
Topics in Mathematical Biology: Theory, Applications and Future Perspectives
Thèmes en biologie mathématique : Théorie, applications et perspectives futures
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STEPHANIE ABO, University of Waterloo

Can the clocks tick together despite the noise? Stochastic simulations and analysis

The suprachiasmatic nucleus (SCN), also known as the circadian master clock, consists of a large population of oscillator neurons. Together, these neurons produce a coherent signal that drives the body's circadian rhythms. What properties of the cell-to-cell communication allow the synchronization of these neurons, despite a wide range of environmental challenges such as fluctuations in photoperiods? To answer that question, we present a mean-field description of globally coupled neurons modeled as Goodwin oscillators with standard Gaussian noise. Provided that the initial conditions of all neurons are independent and identically distributed, any finite number of neurons becomes independent and has the same probability distribution in the mean-field limit, a phenomenon called propagation of chaos. This probability distribution is a solution to a Vlasov-Fokker-Planck type equation, which can be obtained from the stochastic particle model. We study, using the macroscopic description, how the interaction between external noise and intercellular coupling affects the dynamics of the collective rhythm, and we provide a numerical description of the bifurcations resulting from the noise-induced transitions. Our numerical simulations show a noise-induced rhythm generation at low noise intensities, while the SCN clock is arrhythmic in the high noise setting. Notably, coupling induces resonance-like behavior at low noise intensities, and varying coupling strength can cause period locking and variance dissipation even in the presence of noise.

JULIEN ARINO, University of Manitoba

Backward bifurcation in an SLIARS model with vaccination

Backward bifurcations are known to occur in a variety of epidemic models when treatment or vaccination are taken into account. In a backward bifurcation situation, there can exist subthreshold endemic equilibria, leading to a bistable situation where the behaviour of the system is initial conditions-dependent. The situation is easy to characterise in a deterministic setting, but more complicated in a stochastic one. To investigate this, we considered an endemic (i.e., including demography) SLIARS model for a disease presenting symptomatic and asymptomatic stages, to which we added vaccination. We showed that the deterministic version of the model can undergo backward bifurcations. We then studied numerically the equivalent (stochastic) continuous-time Markov chain and observed that a backward bifurcation was observable also in this context. Interestingly, a branching process approximation of the stochastic process was unable to pick up the same characteristic. This is joint work with Evan Milliken (U of Louisville).

MARYAM BASIRI, University of Ottawa

Traveling wave solutions for a free boundary problem modeling spread of ecosystem engineers

Ecosystem engineers are species that modify their environment to make it (more) suitable for them. Beavers are a well-known engineering species. We present a novel model for the spread of ecosystem engineers as a free boundary problem: ahead of the front, the habitat is unsuitable for the species, and behind the front, the habitat is suitable. The engineering action of the population moves the boundary ahead. We derive a semilinear parabolic equation from an individual random walk model. The condition for the moving boundary is a biologically derived two-sided condition that models the movement behavior of individuals at the boundary as well as the process by which the population moves the boundary to expand their territory.

We study the model with the Allee growth function and prove the existence of traveling wave solutions of different types. Then we will determine how model parameters affect the ability of an ecosystem engineer species to invade new environments and the speed at which such an invasion occurs.

ELENA BRAVERMAN, University of Calgary

On stability and asymptotics of equations and systems of population dynamics with concentrated and distributed delays

Many differential equations of mathematical biology assume delayed production process and the instantaneous mortality. It is well known that introduction of delay can destroy stability of the unique positive equilibrium and even lead to chaos. However, for some types of equations and systems, lags in the reproduction term do not change stability properties. Consideration of variable, unbounded and distributed delays emphasizes robustness of this 'absolute stability' property.

Some interesting phenomena are observed in equations of population dynamics when the production part includes two different delays. We also consider Hutchinson and Mackey-Glass equations a controlled with a term whose variable coefficient can change its sign.

ROBERT STEPHEN CANTRELL, University of Miami

A two-stage reaction-diffusion system

It is well known that in reaction-diffusion models for a single unstructured population in a bounded, static, heterogeneous environment, slower diffusion is advantageous. That is not necessarily the case for stage structured populations. In earlier work, Cantrell, Cosner and Martinez showed that in a stage structured model introduced by Brown and Lin, there can be situations where faster diffusion is advantageous. In this paper we extend and refine these results on persistence to more general combinations of diffusion rates and to cases where either adults or juveniles do not move. We also obtain results on the asymptotic behavior of solution as diffusion rates go to zero, and on competition between species that differ in their diffusion rates but are otherwise ecologically identical. We find that when the spatial distributions of favorable habitats for adults and juveniles are similar, slow diffusion is still generally advantageous, but if those distributions are different that may no longer be the case. This talk is based on joint work with Chris Cosner and Rachidi Salako.

YUMING CHEN, Wilfrid Laurier University

Threshold dynamics of a viral infection model with defectively infected cells

In this talk, we consider a viral infection model with defectively infected cells. We show that the basic reproduction number serves as a threshold parameter. When the basic reproduction number is less than or equal to unity, the infection-free equilibrium is globally asymptotically stable; when it is larger than unity, the infection equilibrium is globally asymptotically stable. The stability is established by Lyapunov's direct method. Here we provide a procedure to determine whether the derivative of a given type of Lyapunov function candidate is negative (semi-)definite or not.

TIANYU CHENG, University of Western Ontario

A new perspective on infection forces with demonstration by a DDE infectious disease model

In this work, we revisit the notion of infection force from a new angle which can offer a new perspective to motivate and justify some infection force functions. Our approach can not only explain many existing infection force functions in the literature, it can also motivate new forms of infection force functions, particularly infection forces depending on disease surveillance of the past. As a demonstration, we propose a SIRS model with delay. We comprehensively investigate the disease dynamics represented by this model, particularly focusing on the local bifurcation caused by the delay and another parameter that reflects the weight of the past epidemics in the infection force. We confirm Hopf bifurcations both theoretically and numerically. The results show that, depending on how recent the disease surveillance data are, their assigned weight may have a different impact on disease control measures.

MONICA COJOCARU, University of Guelph

Individual risk and discomfort perceptions, NPI policies and the evolution of the pandemic in Ontario 2020

In this work, we provide a granular view of factors affecting COVID-19 disease transmission across Ontario, Canada and the 34 public health units composing it. We estimate the perceived risk of infection and perceived personal discomfort of complying with non-pharmaceutical interventions (NPIs) in each PH region. With the use of dynamic programming and a simple Nash game model, we estimate the expected NPI adoption proportion across Ontario from March to December 2020. Finally, we use an SEIRL compartmental model for Ontario to study the interplay between the estimated NPI adoption from the game and the actual evolution of the infection. Finally, we explore the limitations of our work, discuss the success of our computations and highlight possible avenues of further refinement. This is joint work with: Sarah Smook (U. Guelph), David Lyver (U. Guelph) and Edward W. Thommes (U. Guelph)

TROY DAY, Queen's University

The Epidemiology and Economics of Physical Distancing during Infectious Disease Outbreaks

People's incentives during an infectious disease outbreak influence their behaviour, and this behaviour can impact how the outbreak unfolds. Early on during an outbreak, people are at little personal risk of infection and hence may be unwilling to change their lifestyle to slow the spread of disease. As the number of cases grows people may then voluntarily take extreme measures to limit their exposure. Political leaders also respond to the welfare and changing desires of their constituents. In this talk I will use ideas from the study of differential games to model how individuals' and politicians' incentives change during an outbreak. Motivated by the COVID-19 pandemic, I focus on physical distancing behaviour and the imposition of stay-at-home orders. I show that the dynamic game being played in the population and its consequences are very different depending on the degree of asymptomatic transmission.

This is joint work with David McAdams, Fuqua School of Business and Economics Department, Duke University.

HERMANN EBERL, University of Guelph

Chaos in the Hive and Beyond: A Multiscale Model of Nosemosis in an Apiary

Recent years have seen the emergence of many generic or specific models for the dynamics of honeybee diseases. The vast majority of these studies consider a single hive only. We present and discuss an eco-epidemiological multiscale model of the transmission of Nosemosis in an apiary. For the transmission of the disease on the apiary level, i.e. between hives, we develop a mathematical model of drifting, i.e. "the change of residence of bees from one hive to another" (as Corkins put it in 1932). For the transmission of the disease within a colony, we consider two routes, a direct and an indirect one. This extends our previous work on Nosemosis to the metapopulation setting. It leads to a system of $5N$ nonautonomous ODEs, where N is the number of colonies considered. We explore the model numerically. The main finding is that the apiary level dynamics of the disease can be greatly different (highly irregular chaos vs periodic), depending on which of the two within-hive transmission routes dominates. This is joint work with Nasim Muhammad.

SAMUEL MATTHIAS FISCHER, Osnabrück University & Helmholtz Centre for Environmental Research – UFZ

KDE-likelihood: a tool for fitting stochastic dynamic models to equilibrium data

Stochastic dynamic models are a valuable tool to study the spatial distribution of species and estimate their responses to disturbances and environmental changes. However, fitting such models to observational data can be challenging, because their complexity typically hinders direct application of classical statistical tools such as the likelihood. Hence, modellers often examine the parameter space by applying sampling-based methods (e.g. approximate Bayesian computation, ABC), or they consider aggregated results whose distribution may be approximated via the central limit theorem. However, if the considered species distributions are assumed to be in equilibrium state, reaching these states in simulations requires long runs, making methods such as ABC difficult to apply. At the same time, aggregating results may lead to information loss that could result in identifiability issues corrupting the reliability of the parameter estimates. In this talk, we suggest the kernel-density-estimate-based (KDE-) likelihood as a tool circumventing these issues. The KDE-likelihood allows modellers to exploit the favourable statistical properties of the likelihood function without deriving it in closed form. We showcase the method's advantages in real applications by modelling the distribution of trees in a temperate Chinese forest using the process-based model Formind.

FRÉDÉRIC HAMELIN, Institut Agro

The proportion of resistant hosts in mixtures should be biased towards the resistance with the lowest breaking cost

Current agricultural practices facilitate emergence and spread of plant diseases through the wide use of monocultures. Host mixtures are a promising alternative for sustainable plant disease control. Their effectiveness can be partly explained by priming-induced cross-protection among plants. Priming occurs when plants are challenged with non-infective pathogen genotypes, resulting in increased resistance to subsequent infections by infective pathogen genotypes. We developed an epidemiological model to explore how mixing two distinct resistant varieties can reduce disease prevalence. We considered a pathogen population composed of three genotypes infecting either one or both varieties. We found that host mixtures should not contain an equal proportion of resistant plants, but a biased ratio (80 : 20) to minimize disease prevalence. Counter-intuitively, the optimal ratio of resistant varieties should be biased against the costliest resistance for the pathogen to break. This benefit is amplified by priming. This strategy also prevents the invasion of pathogens breaking all resistances.

This is joint work with Pauline Clin, Frédéric Grogard, Didier Andrivon, and Ludovic Mailleret.

CHRISTOPHER M HEGGERUD, UC Davis

Mathematical comparison and empirical review of the Monod and Droop forms for resource-based population dynamics

Almost all biological models use either the Droop or Monod form to describe the resource-based growth of a living organism. Empirical evidence overwhelmingly suggests the Droop form describes data more accurately than the Monod form, however, the Monod form is more popular due to its simplicity. Focusing on phytoplankton, we illustrate the underlying logics behind these two forms via conceptual comparison, experimental data validation, transient, and asymptotic dynamics. The conceptual illustration provides the primary difference in their mechanisms via a paradox. Data validation is tested via field and laboratory experiments. The Droop and Monod forms have consistent asymptotic dynamics in the closed nutrient case, whereas the transient dynamics are significantly different when the nutrient uptake rate is small.

YU JIN, University of Nebraska-Lincoln

Population dynamics in a habitat with a protection zone

Protecting native species or endangered species has been an important issue in ecology. We derive a reaction-diffusion model for a population in a one-dimensional bounded habitat, where the population is subjected to a strong Allee effect in its natural domain but obeys a logistic growth in a protection zone. We establish threshold conditions for population persistence and extinction via the principal eigenvalue of an associated eigenvalue problem. We then obtain the influences of the protection zone on the long-term population dynamics under different boundary conditions and propose strategies for designing the optimal location of the protection zone in order for the population to persist in the long run.

LAURENCE KETCHEMEN, University of Ottawa

Populations dynamics in fragmented landscapes under monostable and bistable growth dynamics

Many biological populations reside in increasingly fragmented landscapes, where habitat quality may change abruptly in space. A reaction-diffusion model for a single species which grows and disperses in a one-dimensional heterogeneous landscape is presented. The landscape is composed of two homogeneous adjacent patches with different diffusivities and net growth functions (monostable and bistable). An interface condition connects population density and flux between the two patches. We first classify all possible positive steady states using a phase plane approach. We continue by analyzing the stability properties of certain simple possible positive steady states. We end by applying bifurcations theory. Numerical simulations reveal fold bifurcations.

RONGSONG LIU, University of Wyoming

An Age-structured Model of Bird Migration

An approach to modelling bird migration is proposed, in which there is a region where birds do not move but spend time breeding. Birds leave this breeding region and enter a migration flyway which is effectively a one-way corridor starting and ending at the breeding location. Mathematically, the flyway is a curve parametrised by arc-length. Flight speed depends on position along the flyway, to take account of factors such as wind and the pausing of birds at various locations for wintering or stopovers. Per-capita mortality along the flyway is both position and age-dependent, allowing for increased risks at stopover locations due to predation, and increased risks to immature birds. A reaction-advection age-structured equation models population dynamics along the flyway and, using a Laplace transform technique, the model is reduced to a scalar delay differential equation for the number of adult birds at the breeding location. Extinction and persistence criteria are obtained for the bird population and the results of computer simulations are presented.

XINZHI LIU, University of Waterloo

Multi-group flocking control of multi-agent systems

As a fascinating collective behavior, flocking is observed in a variety of biological species such as beasts, birds, fish, bees, and ants. In such situations, each individual acts as an autonomous agent and interacts only with its nearby neighbors, while the entire group displays coordinated behavior and can accomplish very complex tasks. Inspired by such collective intelligence of animal groups in nature, there has been an increased research interest in flocking control of multi-agent systems around the world in recent years. This talk discusses the flocking control problem of multi-agent systems with multi-group tracking various virtual leaders. Hybrid protocols are proposed to take into consideration of continuous communications among agents and intermittent information exchanges at a sequence of discrete times. It is shown, by employing results from graph theory and dynamical systems, that agents may be divided into multiple subgroups to follow different leaders while maintaining desired sub-formation configurations as well as collision-free motions.

CHUNHUA OU, Memorial University of Newfoundland

Dynamics of Diffusive Lotka-Volterra competition systems in a shifting environment

We studied the existence, uniqueness and stability of forced traveling waves for the Lotka-Volterra competition system in a shifting habitat. Based on the asymptotic behaviors of the wave profiles and by means of upper-lower solution method coupled with sliding technique, we showed that the forced wave for the system exists and is unique, when the forced speed lies in a specific interval. Explicit expressions of the two end points of this interval were derived and our finding indicated that they are related to the Fisher-KPP-type invasion speed. Furthermore, we established a squeezing theorem to show the local stability of the forced waves. With the aid of comparison principle and Xinfu Chen's idea (1997), we established the global stability of the forced waves when the initial data were properly assigned. Finally, a gap formation between two species were studied when forced traveling wave doesn't exist.

WEIWEI QI, University of Alberta

Noise-induced transient dynamics

Many complex processes exhibit transient dynamics - intriguing or important dynamical behaviors over a relatively long but finite time period. A fundamental issue is to understand transient dynamics of different mechanisms. In this talk, we focus on a class of randomly perturbed processes arising in population dynamics where species only persist over finite time periods and go to extinction in the long run. To capture such transient persistent dynamics, we use quasi-stationary distributions (QSDs) and study their noise-vanishing asymptotic. Special attention will be paid to essential differences between models with and without environmental noises. The talk ends up with some discussions.

SHIGUI RUAN, University of Miami

Imperfect and Bogdanov-Takens Bifurcations in Biological Models: From Harvesting of Species to Removal of Infectives

The bifurcation induced by small perturbations of a system (on already existed bifurcations) that leads to more complex bifurcations simplifying into separate saddle and node equilibrium points is called an imperfect (perturbed) bifurcation. In

this paper, we examine two types of biological models that Fred Brauer made pioneer contributions: predator-prey models with stocking/harvesting and epidemic models with immigration/isolation. First we consider a predator-prey model with Holling type II functional response whose dynamics and bifurcation are well-understood. We will show that that introducing constant stocking/harvesting of predators induces imperfect bifurcation: For the case with stocking, the model has one positive equilibrium and one negative equilibrium when stocking constant increases from zero. For the case of harvesting, the model has none, one, or two positive equilibria when harvesting constant varies; then we explain that the unique positive equilibrium is a cusp of codimension 2 and the model undergoes Bogdanov-Takens bifurcation. We also consider an epidemic model with constant importation/isolation of infective individuals and observe similar imperfect and Bogdanov-Takens bifurcations when the constant perturbation rate varies. (Based on a joint work with Dongmei Xiao).

CHUNHUA SHAN, The University of Toledo

Transmission dynamics and periodic phenomena in a model of West Nile virus with maturation time

West Nile virus is a typical vector-borne disease transmitted to humans and animals by *Culex* mosquitoes, where avian birds serve as amplification hosts for the virus. To investigate the role of mosquitoes in the transmission dynamics of West Nile virus, we formulate a system of delay differential equations with a standard incidence rate to model the interaction between mosquitoes and birds. We show that the maturation time of mosquitoes affects disease transmission in sophisticated ways. It turns out that a large maturation delay will lead to the extinction of mosquitoes and the disease, a small maturation delay will stabilize the epidemic level of the disease, and an intermediate maturation delay will cause sustainable oscillations of mosquito population, recurrence of diseases, and even mixed-mode oscillation with an alternation between oscillations of large and small amplitudes.

ZHONGWEI SHEN, University of Alberta

Coexistence in random environments

We study the evolution of a community modelled by systems of stochastic differential equations with demographic noises, which exhibit coexistence dynamics only over finite periods. To capture such coexistence dynamics, we study the solution process before one species goes extinct and use quasi-stationary distributions (QSDs) to capture dynamical states governing the coexistence. In this talk, I will report some ideas and recent progress about dynamical properties of QSDs.

JUNPING SHI, College of William & Mary

Turing type bifurcation in reaction-diffusion models with nonlocal dispersal

In reaction-diffusion models describing biological and chemical interactions, some dispersal and interaction can be of nonlocal nature. We show that when a nonlocal dispersal occurs instead of classical diffusion, how the mechanism of Turing diffusion-induced instability and pattern formation changes. It is shown that Turing type instability and associated spatial patterns can be induced by fast nonlocal inhibitor dispersal and slow activator diffusion, and slow nonlocal activator dispersal also causes instability but may not produce stable spatial patterns. The existence of nonconstant positive steady states is shown through bifurcation theory. This suggests a new mechanism for spatial pattern formation, which has a different instability parameter regime compared to the Turing mechanism. This talk is based on joint work with Shanshan Chen, Xiaoli Wang and Guohong Zhang.

SABRINA H. STREIPERT, University of Pittsburgh

Introduction and Application of the Augmented Phase Portrait

We introduce the next-iterate operators and corresponding next-iterate root-sets and root-curves associated with the nullclines of discrete planar systems. The signs of these next-iterate operators are used to augment the standard phase portrait that includes the direction field and the nullclines, to determine whether a point is mapped above or below the corresponding nullcline. This method identifies positively invariant regions and regions that can give rise to periodic solutions. The construction of the

augmented phase portrait is demonstrated using an example of a rational planar map that arises in population modeling. We show that the augmented phase portrait can provide an elementary, alternative approach for determining the global dynamics of this model. The potential and limitations of the augmented phase portrait are explored using several examples that have applications in population dynamics, epidemiology, and delay difference equations.

HAO WANG, University of Alberta
Cognitive Animal Movement Modelling

Based on our recent efforts in spatial memory modelling and analysis for cognitive animal movement, I will briefly review this topic and mention challenges in modelling and rigorous analysis. Some showcases will be given as idea illustrations.

XIAOQIANG ZHAO, Memorial University of Newfoundland
Spatial Dynamics of Species with Annually Synchronized Emergence of Adults

In this talk, I will report our recent research on the spatial dynamics of species growth with annually synchronous emergence of adults by formulating an impulsive reaction-diffusion model. With the aid of the discrete-time semiflow generated by the one-year solution map, we establish the existence of the spreading speed and traveling waves for the model on an unbounded spatial domain. It turns out that the spreading speed coincides with the minimal speed of traveling waves, regardless of the monotonicity of the birth rate function. We also investigate the model on a bounded domain with a lethal exterior to determine the critical domain size to reserve species persistence. Numerical simulations are illustrated to confirm the analytical results and to explore the effects of the emergence maturation delay on the spatial dynamics of the population distribution. In particular, the relationship between the spreading speed and the emergence maturation delay is found to be counterintuitively variable.

HUAIPING ZHU, York University