Dynamical Systems with Applications to Biology and Ecology
Systèmes dynamiques avec applications en biologie et en écologie
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ISAM AL-DARABSAH, Memorial University of Newfoundland
A Prey-Predator Model with n Patches, Migrations and Delays.

In this talk we investigate the dynamics of a prey-predator model in n patches through the stage structured maturation time delay with migration among patches. We discuss the existence of equilibrium points, the uniform persistence, the local and global stability of boundary equilibrium point with general migration function and the local stability of the positive equilibrium with constant migration rate. Numerical simulations are provided to demonstrate the theoretical results, to illustrate the effect of the maturation time, the migration rate on the dynamical behavior of the system. This is a joint work with Dr. Xianhua Tang and Dr. Yuan Yuan.

ALI GHAROUNI, University of New Brunswick
Recent application of spreading speed theory to the green crab invasion in Atlantic Canada

Spreading speed theory provides a mathematical tool to analyze the demography and dispersal of invasive species. Based on biological records, the secondary spread of the European green crab, *Carcinus maenas*, has maintained a relatively consistent rate of advance for over 120 years covering a wide range of temperate latitudes and local hydrological environments along the Atlantic coast of North America. We analyzed presence/absence data for recently established green crab populations, empirically estimated the crab's spread rate, and employed a discrete-time model to investigate the relationship between the spreading speed and demography and dispersal parameters. The model couples a matrix population model for population growth with integrodifference equations for dispersal. Hydrodynamically-driven dispersal, predominantly larval dispersal, is assumed in our model and estimated by a hydrodynamics model through particle tracking. Our modeling exercise provided insights about the observed pattern of green crab spread, including the possibility of maintaining a consistent spread rate despite stochastic drift which influences larval dispersal. Sensitivity analysis of the model also informed us about possible green crab demographic and dispersal processes that could be targeted by managers.

XIAODI LI, School of Mathematical Sciences, Shandong Normal University
Stability of FDEs with state-dependent delay of unknown bounded

State-dependent delay is a class of special time delays that depends on the state of system and exists in many practical problems. In this talk, he mainly introduce his recent work which is about the stability for functional differential equations (FDEs) with state-dependent delay. Lyapunov method is developed to stability analysis of FDEs and some stability criteria including exponential stability and Lipschitz stability are established, which are easy to check in real problems.

CHUNHUA SHAN, University of Alberta
Turning points and relaxation oscillations in epidemic models of SIR type

We study the effects of disease caused death on the host population via an epidemic model of SIR type. Using the geometric singular perturbation technique and the phenomenon of the delay of stability loss due to turning points, the existence of relaxation oscillations is proved, which contrast sharply to the oscillations via Hopf bifurcation. This work provides a reasonable explanation for large-amplitude oscillations with a long inter-epidemic period observed during the disease transmission.

YUN TIAN, Shanghai Normal University
HIV-1 dynamics of fighting a virus with another virus

In this talk, we propose a mathematical model for HIV-1 infection with intracellular delay. The model examines a viral-therapy for controlling infections through recombining HIV-1 virus with a genetically modified virus. For this model, the basic reproduction number R_0 is identified and its threshold properties are discussed. Some simulations are performed to support the theoretical results. These results show that the delay plays an important role in determining the dynamic behaviour of the system. This is a joint work with Yu Bai and Dr. Pei Yu.

XIAO WANG, National University of Defense Technology
Periodic and almost periodic oscillations in a disease system modeling the transmission of infectious diseases in migrants' home

A delay differential equation model with time dependent coefficients is proposed to study the transmission of infectious diseases in migrants' home residence. It is shown that this model exhibits periodic and almost periodic oscillations. Due to the lack of compactness for the almost periodic function family, it is extremely difficult to establish the existence of almost periodic solutions for delay differential equations via the Schauder's fixed point theorem and the coincidence degree theory. To overcome this difficulty, in this paper, we employ a novel technique to construct a contraction mapping and establish the existence of almost periodic solution by means of the contraction mapping theorem. The coincide degree theory is used to establish the existence of periodic solutions. Global stability results are achieved by the method of Lyapunov functionals.

XIAOYING WANG, western university
Modelling the trait in fear of predators

Recent fields experiments on fear effect of prey due to predators show that anti-predator defence may reduce the reproduction of prey. Based on these observations, a predator-prey model is proposed which incorporates the cost of fear in prey production. Mathematical analysis show that high levels of fear (or equivalently strong anti-predation behaviours) can stabilize the predator-prey system by excluding the existence of periodic solutions. However, relatively low levels of fear can induce multiple limit cycles via subcritical Hopf bifurcations, leading to a bi-stability phenomenon. Compared to classic predator-prey models ignoring the cost of fear where Hopf bifurcations are typically supercritical, Hopf bifurcations in our model can be both supercritical and subcritical by choosing different sets of parameters. Numerical simulations are conducted to explore relationships between fear effect and other biologically related parameters, which further demonstrate the roles that fear play in predator-prey interactions. For example, it is found that under the conditions for existence of a Hopf bifurcation, increase of fear level may alter the direction of Hopf bifurcation from supercritical to subcritical when the birth rate of prey varies accordingly. Simulations also show that the prey is less sensitive in perceiving predation risks with increasing birth rate of prey or increasing death rate of predators, but demonstrates stronger anti-predation defense with larger attacking rate by predators.

JAMES WATMOUGH, University of New Brunswick
Ecological models with multiple stable states

Many important questions in ecology and immunology involve dynamical systems with multiple stable states. We present a simple example of intra-guild predation which exhibits a variety of bi- and tri-stabilities. Intra-guild systems can be viewed as a coupling of two predator-prey systems by allowing one predator to additionally prey on the other. The two predators and the resource can coexist in equilibrium, in periodic solutions, and in chaotic solutions. One basic model of intra-guild predation is the system

$$
\begin{aligned}
R'(t) &= rR(t)\left(1 - \frac{R(t)}{K}\right) - c_1 R(t)N(t) - c_2 R(t)P(t), \\
N'(t) &= e_1 c_1 R(t-\tau)N(t-\tau) - c_3 N(t)P(t) - m_1 N(t), \\
P'(t) &= e_2 c_2 R(t)P(t) + \epsilon_3 c_3 N(t)P(t) - m_2 P(t).
\end{aligned}
$$

Here R is a prey species, N and P are predator species, and P additionally preys on N. In contrast with the simple predator-prey model, where delay tends to destabilize the dynamics, we show that the delay in this intra-guild predation model can have both stabilizing and destabilizing effects. In addition we study the appearance and dissapearance of an invariant torus in a related model without delay, but with saturating functional and numerical responses:

$$
\begin{aligned}
R'(t) &= rR(t)\left(1-\frac{R(t)}{K}\right) - c_1R(t)N(t) - c_2R(t)P(t),\\
N'(t) &= e_1c_1R(t)N(t) - \frac{c_3N(t)P(t)}{1+b_3N(t)} - m_1N(t),\\
P'(t) &= \frac{e_2c_2R(t)P(t)}{1+b_2R(t)} + \frac{e_3c_3N(t)P(t)}{1+b_3N(t)} - m_2P(t).
\end{aligned}
$$

Both models illustrate the wide variety of alternate steady-states that are possible in even simple ecological models.

GAIL WOLKOWICZ, McMaster University
Sensitivity of the Rosenzweig–MacArthur model to the form of the functional response: a bifurcation theory approach

The equations in the Rosenzweig–MacArthur predator-prey model have been shown to be sensitive to the mathematical form used to model the predator response function even if the forms used have the same basic shape: zero at zero, monotone increasing, concave down, and saturating. Here, we revisit this model to help explain this sensitivity in the case of Holling type II, Ivlev, and Trigonometric response functions. We consider both the local and global dynamics and determine the possible bifurcations with respect to variation of the carrying capacity of the prey, a measure of the enrichment of the environment. We give an analytic expression that determines the criticality of the Andronov-Hopf bifurcation, and prove that although all three forms can give rise to supercritical Andronov-Hopf bifurcations, only the Trigonometric form can also give rise to a subcritical Andronov-Hopf bifurcation and has a saddle node bifurcation of periodic orbits giving rise to two coexisting limit cycles, providing a counterexample to a conjecture of Kooij and Zegeling. We also revisit the ranking of the functional responses, according to their potential to destabilize the dynamics of the model and show that given data, not only the choice of the functional form, but the choice of the number or position of the data points can influence the dynamics predicted.

This is joint work with Gunog Seo, Colgate University.

YANYU XIAO, University of Alberta
Impact of viral drift on vaccination dynamics and patterns of seasonal influenza

Much research has been devoted to the determination of optimal vaccination strategies for seasonal influenza epidemics. However, less attention has been paid to whether this optimization can be achieved within the context of viral drift. The purpose of this work is to investigate the effect of viral drift on optimal vaccination for minimizing the total number of infections. We developed a mathematical model that links different intra-seasonal dynamics of vaccination and infection. Given the uncertainty in the timing and nature of antigenically drifted variants, our findings highlight the difficulty in determining optimal vaccination dynamics for seasonal epidemics. Our study suggests that the short- and long-term impacts of vaccination on seasonal epidemics should be evaluated within the context of population-pathogen landscape for influenza evolution. This is a joint work with S. Moghadas.

WENJING ZHANG, York University
Recurrent viral infection may need no exogenous trigger

Recurrent infection is characterized by short episodes of high viral reproduction, separated by long periods of relative quiescence. This recurrent pattern is observed in many persistent infection, including the “viral blips” observed during chronic infection with the human immunodeficiency virus (HIV). Previous models of the dynamics of these viral blips used either stochastic components or forcing terms as the triggers to simulate the phenomenon. We present an established 4-dimensional HIV antioxidant-therapy model which exhibits viral blips, take advantage of dynamical systems theory and bifurcation theory to reinvestigate the 4-dimensional model, and show that an increasing, saturating infectivity function contributes to the recurrent behavior. The four conditions for the existence of viral blips in a deterministic in-host infection model is proposed, and employed to derive the simplest (2- and 3-dimensional) infection model which produces viral blips. The complete parameter range is identified for the 3-dimensional model in which blips are possible. Further, we find that a 5-dimensional immunological model satisfies the conditions and exhibits recurrent infection even with constant infectivity. Thus, the increasing, saturating infectivity is not necessary if the model is sufficiently complex. This is a joint work with Dr. Lindi Wahl and Dr. Pei Yu.

HUAIPING ZHU, York University

A temperature driven difference equation model with stage-structured for the abundance of culex mosquitoes

The culex mosquitoes are the vector for West Nile virus. The development and distribution of such mosquitoes are closely related to weather, in particularly the daily temperature and precipitation. In this talk, I will introduce a temperature driven difference equation model with stage-structure to describe the development and the abundance of culex mosquitoes. I will introduce some basic dynamical properties of the model. In the end, I will present the application of the model in Peel region Ontario which shows a reasonable match with the surveillance data from the region. This is a joint work with Lie Wang.