東華大學
DONGHUA UNIVERSITY

University
of Victoria

2022 Donghua - UVic Workshop on Differential Equations and Mathematical Biology

November 12-13, 2022

Donghua University, Shanghai, China

Co-Organizers:

Junling Ma (University of Victoria)

Meili Li (Donghua University)

Program Schedule

Join Zoom Meeting: https://uvic.zoom.us/j/84532631922

Meeting ID: 845 3263 1922

Day 1: Saturday, November 12, 2022 （China Time）

Friday, November 11, 2022 （Victoria Time）

China Time	Victoria Time	Opening Ceremony	
8:20-8:30	16:20-16:30		
Session 1		Chair	Yuan Lou (SJTU)
8:30-9:00	16:30-17:00	Speakers	Mark Lewis (UVIC)
9:00-9:30	17:00-17:30		Yanni Xiao (XJTU)
9:30-9:40	17:30-17:40	**Break**	
Session 2		Chair	Slim Ibrahim (UVIC)
9:40-10:10	17:40-18:10	Speakers	Yuan Lou (SJTU)
10:10-10:40	18:10-18:40		Boualem Khouider (UVIC)
10:40-10:50	18:40-18:50	**Break**	
Session 3		Chair	Junling Ma (UVIC)
10:50-11:20	18:50-19:20	Speakers	Wanbiao Ma (In Chinese) (USTB)
11:20-11:50	19:20-19:50		Yu-Ting Chen (UVIC)
11:50-13:00	19:50-21:00	**Break**	
Session 4		Chair	Zhi Ling (YZU)
13:00-13:30	21:00-21:30	Speakers	Jianshe Yu (GZHU)
13:30-14:00	21:30-22:00		Bo Zheng (GZHU)
14:00-14:10	22:00-22:10	**Break**	
Session 5		Chair	Zhigang Wu (DHU)
14:10-14:40	22:10-22:40	Speakers	Dongbin Zha (DHU)
14:40-15:10	22:40-23:10		Lei Niu (DHU)

Day 2:　Sunday, November 13, 2022　（China Time）

Saturday, November 12, 202　（Victoria Time）

Session 1		Chair	Youshan Tao (SJTU)
9:00-9:30	17:00-17:30	Speaker	Slim Ibrahim (UVIC)
Session 2		Chair	Chunhai Kou (DHU)
9:30-10:00	17:30-18:00	Speakers	Junling Ma (UVIC)
10:00-10:30	18:00-18:30		Guiquan Sun (NUC)

DHU--Donghua University
GZHU--Guangzhou University
NUC—North University of China
SJTU--Shanghai Jiao Tong University
SXU--Shanxi University
USTB--University of Science and Technology Beijing
UVIC--University of Victoria
XJTU--Xi’an Jiaotong University
YZU--Yangzhou University

Host diversification splits epidemic spread into two successive fronts advancing at different speeds

Mark Lewis
Department of Mathematics and Statistics, University of Victoria
Victoria, BC Canada

Abstract Host diversification methods such as within-field mixtures (or field mosaics, depending on the spatial scale considered) are promising methods for agroecological plant disease control. We explore disease spread in host mixtures (or field mosaics) composed of two host genotypes (susceptible and resistant). The pathogen population is composed of two genotypes (wild-type and resistance-breaking). The model is formulated as a system of coupled reaction diffusion equations. We analyse this system from the perspective of spreading speeds. We show that for intermediate fractions of resistant hosts, the spatial spread of the disease may be split into two successive fronts. The first front is led by the wild-type pathogen and the disease spreads faster, but at a lower prevalence, than in a resistant pure stand (or landscape). The second front is led by the resistance-breaking type, which spreads slower than in a pure resistant stand (or landscape). The wild-type and the resistance-breaking genotypes coexist behind the invasion fronts, resulting in the same prevalence as in a resistant pure stand. This study shows that host diversification methods can have a twofold effect on pathogen spread compared to a resistant pure stand (or landscape): on the one hand, they accelerate disease spread, and on the other hand they slow down the spread of the resistance-breaking genotype. This work contributes to a better understanding of the multiple effects underlying the performance of host diversification methods in agroecology.
Joint work with F. M. Hamelin, Y. Mammeri, Y. Aigu, S. E. Strelkov.

The multi-scale dynamic models with application to the COVID-19 pandemic

Yanni Xiao
School of Mathematics and Statistics, Xi'an Jiaotong University
Xi'an, Shaanxi China

Abstract Coupling the models in different scales becomes challenging. In this talk I shall briefly give an introduction to modelling approach at both population and individual level. I then present our recent work on COVID-19 infection, including a multi-scale model describing the multiple outbreaks and a stochastic individual based model on complex networks with four layers. We would like to investigate how behavior changes, vaccination, and relaxation of non-NPIs affect the development of COVID-19 infections, and to interpret why children play a different role in the four epidemic waves of COVID-19 pandemic. Finally, I shall give some considerations and thoughts on modelling COVID-19 infections and concluding remarks.

Coexistence of strains in some reaction-diffusion systems

Yuan Lou
School of Mathematical Sciences, Shanghai Jiao Tong University
Shanghai, China

Abstract We study the global dynamics of some reaction-diffusion systems for multiple strains and investigate how the coexistence of strains is impacted by the movement of populations and spatial heterogeneity of the environment. For the case of two strains, general conditions for the existence, uniqueness and stability of coexistence steady states are found. Surprisingly, when there is no coexistence of strains, it is possible for the "weak" strain to be dominant for intermediate diffusion rates, in strong contrast to small and large diffusion cases where the "weak" strain goes extinct. This talk is based on joint work with Rachidi Salako.

Simple models for tropical climate dynamics

Boualem Khouider
Department of Mathematics and Statistics, University of Victoria,
Victoria, BC Canada

Abstract The tropics receive the majority of Earth’s solar energy intake at its surface. To maintain a balanced climate state this energy is transported poleward through various atmospheric and oceanic patterns. The complexity of tropical climate dynamics however, which harbours a wide spectrum of waves and vortices, hinders the clear understanding of the complex interactions between the tropics and extra-tropics and limits weather and climate predictability. In this talk, I will showcase via the use of basic examples how simple mathematical models of reduced dynamics can help shed light on some of such interactions.

Global dynamics of an SI epidemic model with nonlinear incidence rate, feedback controls and time delays

Wanbiao Ma
School of Mathematics and Physics, University of Science and Technology Beijing
Beijing, China

Abstract In this talk, we consider a class of SI epidemic model with nonlinear incidence, feedback controls and four different discrete time delays. By skillfully constructing appropriate Lyapunov functionals, and combining Lyapunov-LaSalle invariance principle, the global dynamics of the model are established.

Stochastic heat equation in two dimensions

Yu-Ting Chen
Department of Mathematics and Statistics, University of Victoria,
Victoria, BC Canada

Abstract The stochastic heat equation arises from interface growth dynamics via the Kardar-Parisi-Zhang equation and from the theory of disordered systems via continuum-directed random polymers. In this talk, I will briefly overview some earlier and recent results for the subject. The emphasis will be on the statistical moments of the stochastic heat equation in two dimensions, with a viewpoint from Schrödinger operators with delta potentials.

Switching ODE models for mosquito population suppression

Jianshe Yu
Guangzhou Center for Applied Mathematics, Guangzhou University
Guangzhou, Guangdong China

Abstract The release of Wolbachia-infected mosquitoes in 2016 and 2017 enabled near-elimination of the sole dengue vector Aedes albopictus on Shazai and Dadaosha islands in Guangzhou. Mathematical analysis may offer guidance in designing effective mass release strategies for the area-wide application of this Wolbachia incompatible and sterile insect technique in the future. The two most crucial questions in designing release strategies are how often and in what amount should Wolbachia-infected mosquitoes be released in order to guarantee the success of population suppression. In this talk, I will introduce our recent works on answering the two questions which have been published in the following three papers.

J. Differ. Equations, 2020, 269(7): 6193-6215.
J. Differ. Equations, 2020, 269(12): 10395-10415.
SIAM J. Appl. Math., 2021, 81(2): 718-740.

By treating the released mosquitoes as a given function, we proposed mosquito suppression models consisting of two sub-equations switching each other. An almost complete characterization of interactive dynamics of wild and released mosquitoes are offered, including the global asymptotic stability of zero solution and the exact number of periodic solutions of these models. It is well known that to obtain existence and also uniqueness conditions for periodic solutions are mathematically challenging for many dynamical systems and there are few such results existed. We hope the methods and techniques used in these three papers can be usefully applied to other model analysis as well.

Switching DDE models for mosquito population suppression

Bo Zheng
Guangzhou Center for Applied Mathematics, Guangzhou University
Guangzhou, Guangdong China

Abstract By including the maturation period τ of wild mosquitoes, we develop a delay differential equation model to study the suppression of wild mosquito population by releasing Wolbachia-infected male mosquitoes with a release period $\tau = mT$ where m is a positive integer. We obtain sufficient conditions for non-existence of periodic solutions and existence of a unique or exactly two periodic solutions by taking the initial function as a solution to the delay-free model. We prove the global asymptotic stability of the unique periodic solution, and that one periodic solution is stable and the other is unstable when there are two periodic solutions.

Some results on one-dimension systems of quasilinear wave equations

Dongbin Zha
College of Science, Donghua University
Shanghai, China

Abstract In this talk, for one-dimension systems of quasilinear wave equations with null conditions, we will introduce the following results:

1. Global existence of classical solutions for the Cauchy problem in the small data setting.
2. Global stability of large solutions, including traveling wave solutions and general large solutions with suitable decay property.
3. Global existence of classical solutions for the initial-boundary value problem in the small data setting.

Some related unsolved problems will be also discussed.

Dynamics of three-dimensional Lotka-Volterra competition model with seasonal succession

Lei Niu
College of Science, Donghua University
Shanghai, China

Abstract In this work, we will discuss the dynamics of the discrete-time dynamical system induced by the Poincaré map of the three-dimensional Lotka-Volterra competition model with seasonal succession. We provide a classification via the equivalence relation relative to local dynamics of boundary fixed points. We show that there are a total of 33 stable equivalence classes which are described in terms of inequalities on parameters. Classes 1-18 admit no positive fixed point and every

trajectory tends to some fixed point on the boundary. Class 27 has a heteroclinic cycle. Classes 19-33 have at least one positive fixed points, and moreover, every trajectory tends to a fixed point in classes 19-25 and 33 when they have a unique positive fixed point. We prove that classes 26 and 27 can have multiple positive fixed points and may admit attracting invariant closed curves. In particular, when the intrinsic growth rates are the same, we give the sufficient and necessary conditions guaranteeing the uniqueness and non-uniqueness of the positive fixed point. Moreover, we prove that there are a total of 37 dynamical scenarios. In 34 cases, every trajectory converges to a fixed point, while in the remaining three cases, one has a heteroclinic cycle attracting all positive points except a positive fixed point, one has a family of invariant closed curves, and one has an asymptotically stable fixed point, a family of invariant closed curves, and a heteroclinic cycle coexisting.
Joint work with Yi Wang (University of Science and Technology of China, Heifei, China), Xizhuang Xie (Huaqiao University, Quanzhou, China).

Disease threshold of the generating function effective degree SIR model

Slim Ibrahim
Department of Mathematics and Statistics, University of Victoria
Victoria, BC Canada

Abstract The effective degree SIR model is a (large) ODE system that gives precise model for the SIR disease dynamics on a homogeneous network with finite degree distributions. Using new generating function approach, we can rewrite the system as a PDE that allows infinite degree distributions. In this talk, I'll give a brief derivation of the PDE effective degree model, analyze the nonlinear stability threshold of the disease-free steady state solution, and show that the threshold is still determined by the basic reproduction number. Our method has the potential to provide a new tool to study the effective degree SIS model, which basic reproduction number has been elusive so far.
Joint work with M. Kurtis, M. Li, and J. Ma.

A contact tracing SIR model for randomly mixed populations

Junling Ma
Department of Mathematics and Statistics, University of Victoria
Victoria, BC Canada

Abstract Contact tracing is an important intervention measure to control infectious diseases. We present a new approach that borrows the edge dynamics idea from network models to track contacts included in a compartmental SIR model for an epidemic spreading in a randomly mixed population. Unlike network models, our approach does not require statistical information of the contact network, data that are usually not readily available. The model resulting from this new approach allows us to study the effect of contact tracing and isolation of diagnosed patients on the control reproduction number and the number of infected individuals. We also estimate the effects of tracing coverage and capacity on the effectiveness of contact tracing.

On the dynamics of a diffusive foot-and-mouse disease model with nonlocal infections

Guiquan Sun
School of Mathematics, North University of China
Taiyuan, Shanxi China

Abstract Foot-and-mouth disease (FMD) is an acute and highly contagious infectious disease of cloven-hoofed animals. In order to reveal the transmission dynamics and explore effective control measures of FMD, we formulate a diffusive FMD model with a fixed latent period and nonlocal infections. The threshold dynamics of the FMD model are determined by using the basic reproduction number R_0. Further, we obtain the effect of diffusion on the time from initial values to steady state when $R_0 > 1$. Moreover, we carry out some sensitivity analysis of R_0 (> 1) and the equilibrium value of the infectious individuals I^* in terms of direct contact infection rate β_1 and indirect contact infection rate β_2. The above results indicate that stamping out the infected individuals and blocking the epidemic spots and areas are effective in preventing and controlling the spread of FMD.