Mathematical Ecology and Epidemiology
Écologie mathématique et épidémiologie
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FRED BRAUER, Department of Mathematics, University of British Columbia, Vancouver, BC V6T 1Z2
A simple epidemic model with behavioral changes

People change their behavior during an epidemic. Infectious members of a population may reduce the number of contacts they make with other people because of the physical effects of their illness and possibly because of public health announcements asking them to do so in order to decrease the number of new infections, while susceptible members of the population may reduce the number of contacts they make in order to try to avoid becoming infected. We study a simple epidemic model in which these two classes of members reduce contacts by different fractions. This produces a model with heterogeneous mixing, and we analyze the effect of such contact reductions on the size of the epidemic. We assume constant fractional reductions, without attempting to consider the way in which susceptible members might respond to information about the epidemic.

JIGUO CAO, Simon Fraser University, Vancouver, BC
Estimating Differential Equations from Real Data

Differential equations model the rate of change of a dynamic process. They are widely used in medicine, engineering, ecology and a host of other applications. One central and difficult problem is how to estimate DE parameters from noisy data. We have developed the generalized profiling method to solve this problem. DE solutions are approximated by nonparametric functions, which are estimated by penalized smoothing with DE-defined penalty. This method avoids solving DEs numerically and greatly improves the computational efficiency. We can also estimate variances of DE parameters, and provide their confidence intervals. I will demonstrate our method by estimating a predator-prey dynamic model from some real experimental data.

GUIHONG FAN, York University
Oscillations in delay differential equation models for vector-borne diseases

Vector-borne diseases are typical infectious diseases which can cause severe illness in humans or animals. Vectors like mosquitoes or ticks play a critical rule in the transmission and spread of the diseases. To investigate the role of vectors, we formulate a system of delay differential equations to model the transmission dynamics of the diseases between vectors and their hosts. Analytical analyses show that vectors alone can force the system to oscillate. In addition, the interaction between vector and amplification host can also cause oscillations. A case study of WNv will be presented.

This is a joint work with Huaiping Zhu.

MEREDITH L. GREER, Bates College
Can cyanobacterial blooms in nutrient-poor lakes accelerate eutrophication? Perspectives from modeling

Gloeotrichia echinulata is a large nitrogen-fixing cyanobacterium that is causing nuisance blooms in oligotrophic and mesotrophic lakes in northern New England. We hypothesize that *G. echinulata* accelerates eutrophication by alleviating nitrogen (N) and phosphorus (P) limitation. Previous work in eutrophic lakes has established that meroplanktonic *G. echinulata* translocate significant amounts of P from sediments into the water column during recruitment, though the magnitude of N additions has not been previously calculated. Using extrapolations of recruitment data for Lake Sunapee, NH, we suggest that *G. echinulata* may add as much P as a small tributary, and predict that it could become comparable to a major tributary if recruitment continues to increase.

While data collection and analysis have been part of this project for several years, mathematical modeling is a newer component. Initial forays into modeling the interactions between *G. echinulata*, in the different phases of its life cycle, and N and P show that the addition of life-cycle components and the interaction of a second nutrient change the predictions of simple, one-element models. This modeling work is key in predicting the extent to which increases in the duration and extent of *G. echinulata* blooms might impact lake water quality.

ABBA GUMEL, University of Manitoba
Mathematical Analysis of a Model for Quarantine/Isolation

Quarantine (of people feared exposed to a disease) and isolation of those with symptoms constitute one of the oldest infection control methods. The talk will focus on the design and rigorous analysis of a model for the transmission dynamics of a communicable disease subject to the use of quarantine/isolation.

HONGBIN GUO, York University, Toronto
Global dynamics of a stage-structured differential infectivity model for HIV infection

A determistic model with stage-structured differential infectivities for HIV infection is proposed and analyzed. The stage structure allows for HIV patients to move to higher-level subgroups due to education campaign, etc. The global dynamics are completely determined by the basic reproduction number R_0. If $R_0 \leq 1$, then the disease-free equilibrium is globally asymptotically stable and the disease always dies out. If $R_0 > 1$, the disease-free equilibrium is unstable, and a unique endemic equilibrium is globally asymptotically stable, the disease persists at the endemic equilibrium. The global stability of the endemic equilibrium is established using a global Lyapunov function.

This is a joint work with Jianhong Wu and Ping Yan.

DAIHAI HE, McMaster University
Plug-and-play inference for disease dynamics: measles in large and small populations as a case study

Statistical inference for mechanistic models of partially observed dynamic systems is an active area of research. Most existing inference methods place substantial restrictions upon the form of models that can be fitted and hence upon the nature of the scientific hypotheses that can be entertained and the data that can be used to evaluate them. In contrast, the so-called plug-and-play methods require only simulations from a model and are thus free of such restrictions. We show the utility of the plug-and-play approach in the context of an investigation of measles transmission dynamics. Our novel methodology enables us to ask and answer questions that previous analyses have been unable to address. Specifically, we demonstrate that plug-and-play methods permit the development of a modelling and inference framework applicable to data from both large and small populations. We thereby obtain novel insights into the nature of heterogeneity in mixing and comment on the importance of including extra-demographic stochasticity as a means of dealing with environmental stochasticity and model misspecification. Our approach is readily applicable to many other epidemiological and ecological systems.

Joint work with Edward L. Ionides and Aaron A. King.

JANE HEFFMAN, York University, Toronto, Ontario
The influence of a backward bifurcation in a model describing HBV or HCV infection in-host

Failure of liver transplantation to cure chronically infected hepatitis B or hepatitis C patients suggests that a second compartment of infection may exist for both of these diseases, namely the blood. We have developed a mathematical model describing hepatitis B virus (HBV) or hepatitis C virus (HCV) and immune system dynamics in-host that incorporates two compartments of infection: the liver and the blood. Analysis of the model shows the existence of a backward bifurcation, which depends on the production term of new virus particles and the death rate of infected cells in both compartments. Extending the model to include drug therapy, we find that, if drug therapy is highly effective in one compartment of infection, but not very effective in

the other, the backward bifurcation exists and virus clearance is difficult to achieve. This result has important implications for the development of new drug therapies against HBV and HCV for chronically infected and liver transplant patients.

DAVID IRON, Dalhousie
A threshold area of organic to conventional agriculture ratio causes recurrent pathogen outbreak

We consider the effect of increasing the area of agricultural land under organic practises. We assumed that organic agriculture does not have effective means of pathogen control. We model pathogen dispersal with a diffusive logistic equation in which the growth/death rate is spatially heterogeneous. We find that if the ratio of the organic plots to conventional plots is below a certain threshold, the pest population is kept small. Above this threshold, the pest population in the organic plot grows rapidly. In this case, the organic plot will act as a source of pest to the surrounding regions, and will always infect organic plots as they become more closely spaced.

MAJID JABERI-DOURAKI, University of New Brunswick
Dynamics of a honeybee model on regulation of work distribution

In this talk, we study age-related activities of honeybees (Apis mellifera L.) first by illustrating the life cycle of honeybee which exhibits a combination of individual traits and social cooperation, and then by constructing an age structured model given by a system of difference equations as follows

$$\mathcal{H}_{n+1} = \mathcal{F}(\mathcal{H}_n) = \big(\mathcal{A}(\mathcal{H}_n) - \mathcal{D}\big)\mathcal{H}_n + \mathcal{B} \quad n \geq 1$$

where the initial conditions $\mathcal{H}_1$ is positive, $\mathcal{B}$ represents the broods, $\mathcal{H}_n$ denotes the population of bees divided into $(k+1)$ classes with respect to their ages, and $\mathcal{A}(\mathcal{H}_n)$ is a lower triangular matrix representing progression or maturation to the next stage of their life involving hive bees and foraging bees, $\mathcal{D}$ indicates the matrix of death rate with subdiagonal entries μ_i and others zero. In fact the distribution of most activities and behavioural/physiological maturation are regulated through primer and releaser pheromones from the queen, worker bees, and brood; we include such dynamical organization, as important characteristics for the honey bee, by introducing numerous parameters in the model. Using extensive numerical simulations, we conjecture that this system has a unique positive steady state which is globally asymptotically stable. We are able to prove analytically the global stability (basin of attraction) of feasible solution of such dynamical system with biological relevant special cases.

YU JIN, University of Alberta, Department of Mathematical and Statistical Sciences
Seasonal Influences on Spatial Population Dynamics

Dynamics of many populations is greatly influenced by time-varying environments (e.g., due to seasonal variation). We describe this seasonal influence as time-periodic functions and investigate a nonlocal periodic reaction-diffusion population model with stage structure. In the case of an unbounded spatial domain, we establish the existence of the asymptotic speed of spread and show that it coincides with the minimal wave speed for monotone periodic traveling waves. In the case of a bounded spatial domain, we obtain a threshold result on the global attractivity of either zero or a positive periodic solution.

JING LI, The University of Ottawa, 585 King Edward Avenue, Ottawa, ON K1N 6N5
Can we spend our way out of the AIDS epidemic? A world halting AIDS model

There has been a sudden increase in the amount of money donors are willing to spend on the worldwide HIV/AIDS epidemic. Present plans are to hold most of the money in reserve and spend it slowly. However, rapid spending may be the best strategy for halting this disease. We develop a mathematical model that predicts eradication or persistence of HIV/AIDS on a world scale. Dividing the world into regions (continents, countries, etc.), we develop a linear differential equation model of infectives which has the same eradication properties as more complex models. We show that, even if HIV/AIDS can be eradicated in each region independently, travel/immigration of susceptibles could still sustain the epidemic. We use a continent-level example

to demonstrate that eradication is possible if preventive intervention methods (such as condoms or education) reduced the infection rate to two fifths of what it is currently. We show that, for HIV/AIDS to be eradicated within five years, the total cost would be $\approx$ \$63 billion, which is within the existing \$60 billion (plus interest) amount raised by the donor community. However, if this action is spread over a twenty year period, as currently planned, then eradication is no longer possible, due to population growth, and the costs would exceed \$90 billion. Eradication of AIDS is feasible, using the tools that we have currently to hand, but action needs to occur immediately. If not, then HIV/AIDS will race beyond our ability to afford it.

MICHAEL LI, University of Alberta
Co-existence of Multiple Stable Periodic Solutions in in-host Viral Models with Delayed Immune Response

Stable periodic oscillations have been shown to exist in mathematical models for the CTL response to HTLV-I infection *in vivo*. These periodic oscillations can be the result of mitosis of infected target $CD4^+$ cells, of a general form of response function, or of time delays in the CTL response. In this study, we show that time delays in the CTL response process to HTLV-I infection can lead to the coexistence of multiple stable periodic solutions, which differ in amplitude and period, with their own basins of attraction. Our results imply that the dynamic interactions between the CTL immune response and HTLV-I infection are very complex. Different routes or initial dosages of the viral infection may lead to quantitatively and qualitatively different outcomes.

This is joint work with Hongying Shu of Harbin Institute of Technology.

YIJUN LOU, Memorial University of Newfoundland, St. John's, Newfoundland
A reaction-diffusion malaria model with incubation period in the vector population

Malaria is one of the most important parasitic infections in humans and more than two billion people are at risk every year. To understand how spatial heterogeneity and extrinsic incubation period (EIP) of the parasite within the mosquito affect the dynamics of malaria epidemiology, we propose a nonlocal and time-delayed reaction-diffusion model. We then define the basic reproduction ratio and show that it serves as a threshold parameter that predicts whether malaria will spread. Furthermore, a sufficient condition is obtained to guarantee that the disease will stabilize at a positive steady state eventually in the case where all the parameters are spatially independent. Numerically, we show that the use of the spatially averaged system may highly underestimate the malaria risk. The spatially heterogeneous framework in this work can be used to design the spatial allocation of control resources.

This talk is based on a joint work with Dr. Xiaoqiang Zhao.

JUSTINE GUNOG SEO, University of Ottawa, Department of Mathematics and Statistics, 585 King Edward Ave, Ottawa, ON K1N 6N5
The effect of temporal variability on persistence conditions in rivers

There has been great interest in the invasion and persistence of algal and insect populations in rivers. Recent modeling approaches assume that the flow speed of the river is constant. In reality, however, flow speeds in rivers change significantly on various temporal scales due to seasonality, weather conditions, or many human activities such as hydroelectric dams. In this talk, I study persistence conditions by looking at the upstream invasion speed in simple reaction-advection-diffusion equations with coefficients chosen to be periodic step functions. The key methodological idea to determine the spreading speed is to use the exponential transform in order to obtain a moment generating function. In a temporally periodic environment, the averages of each coefficient function determine the minimal upstream and downstream propagation speeds for a single-compartment model. For a two-compartment model, the temporal variation can enhance population persistence.

Joint work with Frithjof Lutscher, U. Ottawa.

ROBERT SMITH?, The University of Western Ontario
When zombies attack! Mathematical modelling of an outbreak of zombie infection

An outbreak of zombification wreaked havoc recently in Canada and the rest of the world. Mathematical models were created to establish the speed of zombie infection and evaluate potential scenarios for intervention, mainly because mathematicians don't have anything better to do with their time. Anecdotal evidence suggests that zombies can be defeated by guns, the army, eventual starvation or Dire Straits records. Should we be unable to contain the outbreak, we face the extreme possibility of a world whose population is made up entirely of mathematicians and zombies. One of these groups spends all its time lurking in the darkness, with wild eyes, hair askew and brains that don't work like those of normal humans. And the other group is the zombies.

SHAUN STROHM, University of British Columbia–Okanagan, 3333 University Way, Kelowna, BC V1V 1V7
Dispersal of Mountain Pine Beetle and Impacts of Management

Efforts to control the Mountain Pine Beetle infestation in British Columbia and Alberta include large-scale landscape manipulations such as clearcutting, and cost-intensive techniques such as green attack tree removal. Unfortunately, it is unclear just how effective these techniques are in practice. In order to determine and predict the effectiveness of various management strategies, we need to understand how MPB disperse through heterogeneous habitat, where heterogeneity is measured in terms of species composition and tree density on the landscape. In this talk I will present a spatially-explicit hybrid model for the Mountain Pine Beetle (MPB) dispersal and reproduction. The model is composed of reaction-diffusion-chemotaxis PDEs for the beetle flight period and discrete equations for the overwintering stage. Forest management activities are also included in the model. I will discuss the formation of beetle attack patterns in the PDE model.

CHENGJUN SUN, University of Manitoba, Winnipeg, Manitoba
The effect of extra infection during travel on disease transmission

In this paper, we revisit an SIS patch model with infection during transport. By studying and comparing the dynamics of models with and without infection during transport, we find that infection during transport can cause a larger magnitude of infection and makes the disease less controllable.

HUI WAN, York University
The backward bifurcation in compartmental models for West Nile virus

There have been several compartmental models for the transmission of the West Nile virus in the mosquito-bird cycle, usually the basic reproduction number serves as a crucial control threshold for the eradication of the virus. In this talk, we first review and give a comparison of the four compartmental models for the virus, and focus on one model proposed by Gustavo et al. to explore the backward bifurcation in the model. Our study suggests that backward bifurcation can be a common property of all the available compartmental models for West Nile virus with host birds satisfying a logistic or linear growth. Whether the virus can become endemic depends also on the initial state.

LIN WANG, University of New Brunswick, Fredericton
Threshold Dynamics in Disease Models with Latency and Relapse

In this talk, I will present a general mathematical model for a disease with an exposed (latent) period and relapse. Such a model is appropriate for tuberculosis, including bovine tuberculosis in cattle and wildlife, and for herpes. For this model with a general probability of remaining in the exposed class, the basic reproduction number is identified and its threshold property is discussed. Two special cases, which result in an ODE system and a DDE system, respectively, are discussed in details.

JAMES WATMOUGH, University of New Brunswick
A model for the regulation of foraging in honey bee colonies

Honey bees show a remarkable ability to coordinate activities in a colony. It is thought that this coordination is accomplished through the production and response to pheromones produced by the queen, brood and workers. This talk presents a model

for the regulation of the onset of foraging based on the hypothesis that foragers and brood produce a pheromone that represses worker development.

BRAD WILLMS, Bishop's University, 2600 College Ave., Sherbrooke, QC J1M 1Z7
Doomsday, Friday November 13, 2026; Is it Really Coming?

In 1960, Dr. Heinz von Foerster et al. published a surprisingly accurate model for human population history. Using twenty-four estimates of world population gathered from the literature, and ranging temporally from 0 to 1958 A.D., von Forester best-fit them to a simple, two-parameter model of depensatory growth, $\frac{dN}{dt} = a_o N^{1+k}$. The best-fit value for k is approximately 1, and so the model predicts blow-up in finite time, resulting in what is now known as von Foerster's "doomsday equation", complete with a predicted doomsday: Friday, November 13, 2026 (*Science* **132**, Nov. 4, 1960). At half-way to "doomsday" (1994), human population was actually ahead of schedule. In 2010, as humanity enters the final quartile until "doomsday", it is fitting to revisit von Foerster's celebrated equation and the premise on which it is posited. Appending data from 1960 to the present, we first update the prediction, demonstrating (thankfully) that the data no longer supports the model. We then propose alternatives: the power law logistic and (a special case of) the hyperlogistic equation, whose solutions possess five free parameters. While no general closed form solution of the power law logistic is available, restriction of the free powers to the rationals allows a closed form solution suitable for curve-fitting. Adding a little help from Maple we are thus able to predict a carrying-capacity for the planet, thereby canceling our date with von Foerster's doomsday.

GAIL WOLKOWICZ, McMaster University
Affect of Delay on the Dynamics of the Classical versus the Chemostat Predator-Prey Model

We address the question: "Does refining predator-prey models to include delay to model the time that it takes for the predator to process the prey, affect the possible dynamics of the model?" In particular, we restrict our attention to predator-prey models that have a globally asymptotically stable equilibrium when delay is ignored and investigate whether delay can destabilize this equilibrium resulting in sustained oscillatory behaviour. We compare the affect of including delay on the dynamics of both the classical predator-prey model and the predator-prey model based in the chemostat.

JIANHONG WU, York University, Toronto, Ontario, Canada
Impact of Environmental Changes on Migration Strategies and its Consequence for Spatial Dynamics of Northern Pintails

The North American population of northern pintails (Anas acuta) has suffered a huge decline since 1970s, reflecting long-term reductions in recruitment and alteration of migration routes in response to habitat conditions in migration stopovers. To understand the impact of environmental changes on the population using different migration strategies, we derive and analyze a spatially stratified time-delay differential equations model of seasonal migration for Northern Pintails along the Pacific Flyway.

This talk is based on joint work with Lydia Bourouiba, Yiming Du, Stephen Gourley and Rongsong Liu.