Mathematical Biology
Biologie mathématique
(Org: **Abba Gumel** (Manitoba))

AHMED ABDELRAZEC, York University
Spread and control of dengue with limited public health resources

A deterministic model for the transmission dynamics of a dengue disease, with a nonlinear recovery rate reflecting the public health resources, is formulated to study the impact of available resource of the health system on the spread and control of dengue fever. Model results indicate the existence of multiple endemic equilibria; one of them can be driven to change stability, a Hopf bifurcation occurs when parameters vary, in particular the one representing the public health resource. Additionally, our model exhibits the phenomenon of backward bifurcation as a common feature of vector-borne diseases. Our model and results can be helpful for public health plan the resources essential for control of dengue disease.

CAMERON BROWNE, Vanderbilt University
A Nosocomial Epidemic Model with Room Contamination

Nosocomial infections, i.e. hospital-acquired infections, are a major public health concern, especially in light of the spread of antibiotic-resistant bacteria. In this talk, I present a model of epidemic bacterial infections in hospitals which incorporates the infection of patients and contamination of healthcare workers due to environmental causes. The basic reproduction number, $\mathcal{R}_0$, is defined and asymptotic dynamics are analyzed. Under certain conditions, it is proved that the disease-free equilibrium is globally stable when $\mathcal{R}_0 < 1$. However, in general the disease-free equilibrium is only locally stable when $\mathcal{R}_0 < 1$ and there can be multiple positive steady states in this case. Numerical simulations are conducted and the model is interpreted to provide insight for controlling nosocomial epidemics. Furthermore, the problem of antibiotic resistance, along with potential intervention strategies, are discussed.

GERDA DE VRIES, University of Alberta
Formation of Animal Groups: The Importance of Communication

We investigate the formation and movement of self-organizing collectives of individuals in homogeneous environments. We review a hyperbolic system of conservation laws based on the assumption that the interactions governing movement depend not only on distance between individuals, but also on whether neighbours move towards or away from the reference individual. The inclusion of direction-dependent communication mechanisms significantly enriches the model behavior; the model exhibits classical patterns such as stationary pulses and traveling trains, but also novel patterns such as zigzag pulses, breathers, and feathers. The same enrichment of model behavior is observed when we include direction-dependent communication mechanisms in individual-based models.

THOMAS HILLEN, University of Alberta
Mathematical Modelling with Fully Anisotropic Diffusion

Anisotropic diffusion describes random walk with different diffusion rates in different directions. I will present a form of anisotropic diffusion which is called “fully” anisotropic. The fully anisotropic diffusion model does not obey a maximum principle and can even lead to singularity formation in infinite time.

I will derive this model from biological principles, analyse some of its behavior and show how it can be used to model glioma spread and wolf movement.

ALI JAVAME, University of Manitoba
Role of Pap Screening on HPV Transmission Dynamics

Human papillomavirus (HPV), a major sexually-transmitted disease, is known to be the causative agent of cervical cancer (in addition to causing many other cancers in both males and females). Each year, 500,000 women develop cervical cancer (and about 50

JUNLING MA, University of Victoria
Modeling SIS disease dynamics on random contact networks

Contact networks represent persons by nodes and contacts by edges. It is a more realistic model of disease related human contacts than the random mixing model, which assumes that every pair of individuals have identical contact rate. An effective degree SIS epidemic model was developed before, and was shown to have different disease thresholds than an SIR model. This contradicts with the prediction of classic disease models that SIR and SIS models should have the same disease threshold. But this effective degree model is too complex to derive a closed formula for the disease threshold. In this talk, I will introduce a simplified SIS model on random contact networks, which agrees with stochastic simulations and is mathematically tractable. The model yields a disease threshold formula that bears a clear biological meaning: for the disease to spread, the average number of transmissible neighbours times the average number of times a neighbour can be infected must be greater than unity. The threshold converges to that of the SIR model under the homogeneous mixing limit.

DESSALEGN MELESSE, University of Manitoba
Understanding heterogeneity in HIV transmission dynamics among high risk populations: a mathematical modeling approach

Concentrated HIV epidemic is characterized by the transmission of HIV largely in defined vulnerable populations, namely high risk groups: injection drug users (IDUs), sex workers (female, male and transgender), and their sexual partners. As a result, targeted intervention strategies among high risk populations are seen as high public health priorities in many settings. However, heterogeneity in the mixing patterns among these high risk populations has been shown to sustain the epidemic and complicate the delivery of intervention strategies. This talk will focus on understanding heterogeneity in the dynamical interplay between high risk populations using mathematical modeling. This research is in progress.

FERESHTEH NAZARI, Manitoba

ZHIPENG QIU, Nanjing University of Scinece and Technology/York Yniversity
Complex dynamics of a nutrient-plankton system with nonlinear phytoplankton morality and allelopathy

Understanding the plankton dynamics can potentially help us take effective measures to settle the critical issue on how to keep plankton ecosystem balance. In this paper, a nutrient-phytoplankton-zooplankton (NPZ) model is formulated to get insight into understanding the mechanism of plankton dynamics. To account for the harmful effect of the phytoplankton allelopathy, a prototype for a non-monotone response function is used to model zooplankton grazing, and nonlinear phytoplankton mortality is also included in the NPZ model. The main purpose of the paper is to analyze the complex dynamics of the NPZ model, particularly focus on understanding how the phytoplankton allelopathy and nonlinear phytoplankton mortality affect the plankton population dynamics. We first examine the existence of multiple equilibria and provide a detailed classification for the equilibria of the NPZ system, then stability and local bifurcation are also studied. Sufficient conditions for Hopf bifurcation, Bogdanov-Takens bifurcation and zero-Hopf bifurcation are given respectively. Numerical simulations are finally conducted to confirm and extend the analytic results. The theoretical and numerical findings imply that the phytoplankton allelopathy and nonlinear phytoplankton mortality may lead to a rich variety of complex dynamics of the nutrient-plankton system. The results of this study suggest that the effects of the phytoplankton allelopathy and nonlinear phytoplankton mortality should be received additional consideration in understanding the mechanism of plankton dynamics.

MICHAEL YODZIS, University of Guelph
Dynamics of Pollution-induced Illnesses in Fishing Communities, with Social Feedbacks

Pollution-induced illnesses are caused by toxicants that result from human activity and should be entirely preventable. However, social pressures and misperceptions can undermine the efforts to limit pollution, and vulnerable populations can remain exposed for decades. This talk presents a human-environmental system model for the effects of water pollution on the health and livelihood of a fishing community in the developing world. It incorporates dynamic social feedbacks that determine how effectively the population recognizes the injured, and acts to reduce the pollution exposure. The model, which is motivated by an incident from 1949-1968 in Minamata, Japan (where methylmercury effluent from a local factory poisoned fish populations and humans who ate them), will be rigorously analysed to gain insight into its dynamical features. In particular, conditions that allow for the outbreak of a pollution-induced epidemic will be derived. This research is joint work with Dr. Chris Bauch.

SANLING YUAN, University of Shanghai for Science and Technologgy; University of Victoria
Dynamics of a stochastic model for algal bloom with and without distributed delay

In this talk, two stochastic models for algal bloom with and without distributed delay are investigated. We introduce white noise into the equation of algae population to describe the effects of environmental random fluctuations, and a delay into the nutrient equation to account for the time needed for the conversion of detritus into nutrient. The existence and uniqueness of the global positive solutions for both models are proved. By constructing Lyapunov function(al)s, sufficient conditions for the stochastic stability of the washout equilibrium are obtained for both models. Furthermore, for the model without delay, we give an estimate of the deviation of the solutions to the stochastic model from the positive equilibrium of its corresponding determinate model; for the delayed model, our theoretical results show that it has the same long term behavior as the one without delay, which means that the delay does not affect the long term behavior of the system, though the numerical simulations reveal that it may reduce the level of algae population initially.

HUAIPING ZHU, York
Modeling and forecasting of West Nile virus

West Nile virus is a mosquito-borne flavivirus typically transmitted between birds and mosquitoes, and can infect humans and other domestic mammals. It has become a threat for public health since 1999 in North America. Like other mosquito-borne or vector-borne diseases, the transmission and dynamics of the West Nile virus can be very complicated due to climate and environmental impact on vector mosquitoes density, seasonal impact on amplification host birds and biting incidences of the vectors. In this talk, I will talk about the modeling and dynamics of the virus, including bifurcation analysis of some compartmental models. I will briefly introduce our effort on using surveillance data, weather and landscape data to model and weekly real-time forecast of culex mosquito abundance, minimum infection rate (MIR) for risk assessment and human infection of West Nile virus in Ontario, an effort towards toolkit development for public health, and the establishment of Early Warning and Response System (EWARS) for vector-borne diseases in Ontario, Canada.