Infectious Disease Modeling and Dynamics
Dynamique et modélisation des maladies infectieuses
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SAFIA ATHAR, York University
Decision making and dynamics changes during Influenza epidemic under Media effects

Media plays a vital role in controlling the decision making of the population in an epidemic. Influenza, a disease that affects every age group and causes mortality in many cases, is always a concern for public health, and a vast number of mathematical models have been used to study it. The role of mass-media reports on Influenza is reviewed in " The effects of media reports on disease spread and essential public health measurements." by Jane H. et.al. In the mentioned paper, the authors employed a stochastic agent-based model to provide a quantification of mass media reports on the variability in crucial public health measurements. We adapted the model presented by Jane H. et al. and added sub-compartments to susceptible and vaccinated populations. The purpose of the research is to study the movement of the population in the sub-compartments during an epidemic. Also, we want to explore the role of mass media, and how decisions of the population change under the influence of media. Furthermore, how the media's role contributes to the control or spread of the influenza epidemic. For this purpose, we use an evolutionary game theory approach to quantify the decision making of the population under the effect of disease and mass media reports.

DAVID DICK, Western University
Modeling the evolution of HIV-1 across the within- and between-host scales

HIV-1 is a rapidly replicating retrovirus with dramatically different numbers of replications between scales: within host there are an estimated 4 million cells newly infected each hour whereas between hosts, in the majority of cases, new infections are started by a single virus strain. The rate of evolution of the virus between these fitness landscapes differs, with a greater rate within than between hosts.

We simulate the within-host evolution using a compartmental model with a latent reservoir and stochastically simulate the transmission bottleneck. As the virus evolves within-host, this increased evolution is coupled to between-host fitness by allowing transmission fitness to drift. i.e. there is greater variance of transmission fitness when the virus is a member of a more evolved within-host compartment.

Linking the within- and between-host scales through a stochastic, competitive transmission bottleneck, our results suggest that both the HIV latent reservoir and bottleneck effects contribute to the observed rate of between-host evolution, over the epidemic.

GUIHONG FAN, Columbus State University
Global stability and Hopf bifurcation in a tick population model with delays

Abstract: Transmitted by ticks, Lyme disease is an emerging infectious disease that can cause severe problems for human health. The reproduction and development of ticks are closely related to the environmental factors, in particular, the daily temperature. We study a three-stage population model for ticks with three delays to reflect the impact of average daily temperature on the developmental stages. We define the basic reproduction number R^* of the tick population. The tick population is uniformly persistent if $\mathcal{R}^* > 1$. Besides if $1 < \mathcal{R}^* < e^2$, then the unique positive equilibrium point (L^*, N^*, A^*) is globally asymptotically stable. If $\mathcal{R}^* > e^2$, the positive equilibrium could lose stability through the occurrence of a Hopf bifurcation and the system shows oscillatory behaviors. Recently, we established the existence of global Hopf bifurcation using delays as bifurcation parameters. To illustrate our theoretical results, we present some global Hopf bifurcation diagrams as delays vary and some numerical solutions of the model. This is joint work with Prof. Zhu (York University) and Prof. Thieme (Arizona State University)

MEGAN GREISCHAR, University of Toronto
The elusive when & why of synchrony in malaria infections

Malaria parasites can proliferate in periodic, synchronized bursts within the host, dynamics underlying the regular fevers associated with the disease. Whether proliferation is synchronized or not has the potential to influence parasite transmission and the efficacy of antimalarial drug treatment. Yet the causes of synchrony remain elusive, including to what extent hosts versus parasites influence the timing of infection dynamics. Disentangling the drivers requires robust statistical methods for quantifying the degree of synchrony within an infection, a considerable challenge. I use a heuristic model (a Leslie matrix) to show that existing methods to quantify synchrony are inadequate. To develop improved methods, I simulate time series from experimental rodent malaria infections, using a system of delayed differential equations to specify different levels of synchrony. I incorporate realistic sampling error to mimic infections from replicate 'mice' and use these simulated data to validate a new method to quantify synchrony. This new approach could identify diversity in the timing of parasite life cycles within the host, a necessary step towards understanding how that timing alters disease spread and host health.

JUN LI, Xidian University
Complex dynamics and bifurcations of a synthetic drug model with psychosocial and environmental influence

Synthetic drug addiction is a growing global problem. In this talk, we establish a synthetic drug model with psychosocial and environmental influence. Meanwhile, our model also incorporates relapse and drug supply chain functions. From the dynamic analysis of this model, we find the system may have many rich dynamical phenomena including saddle-node bifurcation, Hopf bifurcation, and elliptic type nilpotent singularity bifurcation of codimension 3. We also present the bifurcation diagram, corresponding phase diagrams and give some epidemiological explanations for these complex dynamics phenomena. This is joint work with Prof. Huaiping Zhu.

JUNLING MA, University of Victoria
The disease threshold condition for SIS dynamics on a random contact network

It is know that, on a random network, the basic reproduction number of an SIS model is larger than that of an SIR model. It has also been shown that, there is no disease threshold on a scale free network with finite second moment of the degree distribution. These results contrast the prediction of the classical heterogeneous mixing models. We should that, for any positive transmission rate, as long as the network contains nodes with large enough degree, the disease persists on the network, independently to the degree distribution of the network.

CHUNHUA SHAN, The University of Toledo
Periodic phenomena and driven mechanisms in transmission of West Nile virus with maturation time

In this talk we will formulate a compartmental model with bird demographics and maturation time of mosquitoes during metamorphosis to study the impact of ambient temperature on the transmission and recurrence of the disease. We show that avian birds serve as a reservoir of viruses, whilst maturation time affects disease transmission in sophisticated ways. It turns out that large maturation delay will lead to the extinction of mosquitoes and the disease; small maturation delay will stabilize the epidemic level of the disease; and intermediate maturation delay will cause sustainable oscillations of mosquito population, recurrence of diseases, and even mixed-mode oscillation of diseases with an alternation between oscillations of distinct large and small amplitudes. With bifurcation theory, we prove that temperature can drive the oscillation of mosquito population, which leads to recurrence of WNv through the incidence interaction between mosquitoes and hosts, while the biting and transmission process itself will not generate sustained oscillations. Our results provide a sound explanation for understanding interactions between vectors and hosts and driven mechanisms of periodic phenomena in the transmission of WNv and other mosquito-borne diseases.

ASHLEIGH TUITE, BlueDot
Using transmission models to understand the epidemiology of sexually transmitted infections in the United States

The overall burden of sexually transmitted infections (STI) in the United States is large and increasing, and there are marked disparities by race/ethnicity and sexual orientation. In the case of gonorrhea, increasing antibiotic resistance limits treatment options. We have developed a suite of compartmental transmission models with the aims of understanding current epidemiologic trends in syphilis and gonorrhea and evaluating the impact of screening on disease burden. We have also developed a model to investigate the potential utility of a point-of-care test for gonorrhea that reports antibiotic susceptibilities. These novel transmission models provide a platform for evaluating the impact of interventions in a way that captures important population characteristics and disease dynamics. We find that taking into account changing epidemic context is important for controlling STI and ensuring that screening is reaching the appropriate populations at the right time. We also show that although rapid diagnostics have the potential to extend the lifetime of existing antibiotics for the treatment of gonorrhea, ongoing surveillance of resistance patterns will be critical.

PEI YUAN, York University
Dynamics complexity of generalist predatory mite and the pest leafhopper in tea plantation

The tea green leafhopper *Empoasca onukii* Matsuda (Hemiptera: Cicadellidae) is one of the most important insect pests threatening the tea production in China, Vietnam, Japan, Indonesia and other countries in Asia. Both nymph and adult of *E.onukii* suck the tea buds, leaves, and shoots and make wounds in tea plants which finally leads to the symptom from blade curling, bronzing, shriveling, necrosis to stand loss, even severe hopperbum, affecting the quality and yield of the tea. The pesticides were the commonly applied which caused the pest resistance, pest resurgence and the undesirable pesticide residues on brewed tea. Therefore, the biological control methods have received widespread attention in recent years. A potential biological control agent, the mite *Anystis baccarum*(L.) is an important predator of the leafhopper in various agricultural systems. A good understanding of generalist predatory mite and the pest leafhopper population dynamics is crucial for tea pest suppression. We propose a predator prey model with generalist predator and aim to understand the dynamics of leafhopper pest *E. onukii* and predatory mite *A. baccarum*, and to make some endeavor to present a plausible control mechanism. The dynamics of the model are very complicated, with saddle-node bifurcation, Hopf bifurcation, Bogdanov-Takens bifurcation and nilpotent singularities of codimension 3, even nilpotent singularities of codimension 4. We also present the bifurcation diagram near the nilpotent singularities of codimension 3.