
Infectious Disease Modelling
Modélisation de maladies infectieuses
(Org: **Robert Smith?** (University of Ottawa))

BHAGWAN AGGARWALA, University of Calgary
Mathematical Modeling of HCV

We present a mathematical model which describes the development of HCV, and its resistant variants, in a patient. We assume that, apart from the variants that are already in the patient's blood stream, it requires only one more mutation at a specific nucleotide for an HCV virus to become resistant to the antiviral drug being administered, i.e for $S_{u,0}$ (virus, together with all its variants, present when the treatment starts) to change into $S_{u,1}$, virus which is resistant to the drug (telaprevir). We assume that, in the presence of drug pressure, it is easier for $S_{u,0}$ to change to $S_{u,1}$ than the other way around, so that we assume that the probability of $S_{u,1}$ changing to $S_{u,0}$ is much smaller than the one of $S_{u,0}$ changing to $S_{u,1}$. We also assume that $S_{u,0}$ changes to $S_{u,1}$ after one more mutation at a given nucleotide. The Model will say that there are exactly two outcomes of treatment: either the patient has a REBOUND of virus or SVR, sustained viral recovery. The model will also say a protease inhibitor, like telaprevir, has profound effect on treatment.

STEFANELLA BOATTO, Universidade de Rio de Janeiro
EPIDEMICS DYNAMICS IN A CITY: A NETWORK MODEL AND SEASON VARIATIONS

We are considering a model for dengue epidemics spreading in a densely populated town, where people move daily from one neighborhood to another. For this purpose we consider a network generalization of SIR model with and without birth and death. We are particularly interested in understanding how the geometry of the network, its homogeneity or non-homogeneity, the flux of people and a possible seasonal periodicity of climate have an effect in the occurrence of an epidemics.

[Lucas Stolerma, Stefanella Boatto and Daniel Coombs, "Epidemics Dynamics: the basic Reproduction Number R_0 for the SIR-Network Model" (2013); Lucas Stolerma, Master thesis, Um Modelo em Rede para a dinamica de uma epidemiaem uma cidade' (2012); Bacaer and Gomez, On the final size of epidemics with seasonality', Bulletin of Mathematical Biology, 71 : 1954-1966 (2009); Howard Weiss, A Mathematical Introduction to Population Dynamics', IMPA (2009);]

FRED BRAUER, University of British Columbia
Drug resistance in disease treatment models

We consider a disease treatment model in which treatment may cause the emergence of a drug-resistant strain of the disease. We study the possible equilibria, their stability, and the effects of changing the treatment rate. The possibilities are determined mainly by the reproduction numbers of the two disease strains. This work is joint with Yanyu Xiao and Seyed Moghadas.

NYUK SIAN CHONG, Department of Mathematics and Statistics, University of Ottawa
Filippov Models of Avian Influenza

The growing number of reported avian influenza cases have prompted awareness of the effectiveness of pharmaceutical or/and non-pharmaceutical interventions which aim to suppress the transmission rate. We propose two Filippov models with threshold policy; the avian-only model with culling of infected birds and the SIIR model with quarantine. The dynamical systems of these two models are governed by nonlinear ordinary differential equations with discontinuous right-hand sides. The solutions of these two models will converge to either one of the two endemic equilibria or the sliding equilibrium on the discontinuous surface. Our results provide several useful insights which include the choice that can be made to fix the threshold level. For any desired threshold level that we choose, it can be observed that either the outbreak will be precluded or the infection will be stabilized. A well-defined threshold policy is essential in order for us to efficiently combat the outbreak.

Keywords: Avian influenza; Filippov model; threshold policy; culling of infected birds; quarantine

KEVIN CHURCH, University of Ottawa

A comparison of two malaria vector control strategies with impulsive differential equations

We present a mathematical model of malaria and two vector control strategies: spray insecticide at regular, fixed times and spray at times determined by a function of disease incidence. This model is described by a system of nonlinear impulsive differential equations with different impulse conditions for each strategy. Stability of the disease-free periodic orbit is considered, and the existence of an endemic periodic orbit and its stability is established using techniques from local bifurcation theory. The two vector control strategies are compared with respect to short-term implementation cost (number of spraying events) and disease burden reduction using numerical simulations.

GUIHONG FAN, Columbus State University, Georgia State

A differential delay model for ticks

Abstract: Ticks play a critical role as vectors in the transmission and spread of Lyme disease, an emerging infectious disease which can cause severe illness in humans or animals. To understand the transmission dynamics of Lyme disease, it is therefore necessary to investigate the population dynamics of ticks. Here, we formulate a system of delay differential equations which models the stage structure of the tick population. Temperature can alter the length of time delays in each developmental stages, and so the time delays can vary geographically (and seasonally which we do not consider). We define the basic reproduction number R_0 of stage structured tick populations. The tick population is uniformly persistent if $R_0 > 1$ and dies out if $R_0 < 1$. We present sufficient conditions under which the unique positive equilibrium point is globally asymptotically stable. In general, the positive equilibrium can be unstable and the system show oscillatory behavior. These oscillations are primarily due to negative feedback within the tick system, but can be enhanced by the time delays of the different developmental stages.

Joint work with Horst Thieme (Arizona State University) & Huaiping Zhu (York University)

ABBA GUMEL, University of Manitoba

Mathematics of HPV Vaccines

Human papilloma virus (HPV) is a major sexually-transmitted disease that inflicts significant public health burden globally. HPV causes various anogenital cancers and warts in females and males. The talk is based on the use of mathematical modeling and analysis to gain insight into the population-level impact of the two currently-available anti-HPV vaccines. This is a joint work with Aliya Alsaleh.

JOHANNA HANSEN, Queen's University

Coinfection and the Evolution of Resistance

Recent experimental work in the rodent malaria model has shown that when two or more strains share a host, there is competitive release of drug resistant strains upon treatment. This within-host effect is predicted to have an important impact on the evolution and growth of resistant strains. However, how this effect translates to epidemiological parameters at the between-host level, the level at which disease and resistance spreads, is yet to be determined. Here we present a general between-host epidemiological model that explicitly takes into account the effect of coinfection and competitive release. Although our model does show that when there is coinfection competitive release may contribute to the emergence of resistance, it also highlights an additional between-host effect that determines the overall effect of coinfection. It is the combination of these two effects, the between-host effect and the within-host effect, that contribute to the overall outcome of coinfection on the emergence of resistance. Therefore even when competitive release of drug resistant strains occurs it is not necessarily true that coinfection will result in the increased emergence of resistance. These results have important implications for the control of the emergence and spread of drug resistance.

ROBERT SMITH?, The University of Ottawa

Predicting the HIV/AIDS epidemic and measuring the effect of mobility in mainland China

HIV has spread widely in mainland China, but there is significant geographic variation in the severity of the epidemic. We aimed to assess the HIV/AIDS epidemic in mainland China accurately, and address the effect of population mobility on it. Markov-Chain Monte-Carlo simulations and Latin Hypercube Sampling were used to estimate the basic reproductive ratio and its sensitivity to parameter variations. We estimated a mean reproduction number of 1.708 (95% CI 1.440–1.977). Our analysis using national surveillance data indicates that HIV-positive individuals most likely move from economically developed regions to regions with more numerous HIV cases, while mobility of AIDS patients likely flows in the opposite direction, due to the current policy that AIDS patients must return to their registered residence to receive free antiretroviral therapy. Our results based on a spatially stratified population dynamical model show increasing mobility rates of HIV/AIDS cases can have a significant effect on the number of HIV/AIDS cases per province and has the potential to decrease the overall number of HIV/AIDS cases in the country. We recommend that the community-based HIV/AIDS support and care program should be implemented by some local governments (especially in epidemically severe areas) to mitigate HIV infections in China.

STEVE TULLY, University of Guelph

Exploring the relationship between HIV awareness and personal preference towards sexual actions.

Risk perception shapes individual behaviour, and is in turn shaped by the consequences of that behaviour. Here we explore this dynamic in the context of human immunodeficiency virus (HIV) spread. We construct a simplified agent-based model based on a partner selection game, where individuals are paired with others in the population, and through a decision tree, agree on unprotected sex, protected sex, or no sex. An individual's choice is conditioned on their HIV status, their perceived population-level HIV prevalence, and the preferences expressed by the individual with whom they are paired. HIV is transmitted during unprotected sex with a certain probability. As expected, in model simulations, the perceived population-level HIV prevalence climbs along with actual HIV prevalence. During this time, HIV- negative individuals increasingly switch from unprotected sex to protected sex, HIV+ individuals continue practicing unprotected sex whenever possible, and unprotected sex between HIV+ and HIV- individuals eventually becomes rare. We also find that the perceived population-level HIV prevalence diverges according to HIV status: HIV- individuals develop a higher perceived HIV prevalence than HIV+ individuals, although this result is sensitive to how much information is derived from global versus local sources. This research illustrates a potential mechanism by which distinct groups, as defined by their sexual behaviour, HIV status, and risk perceptions, can emerge through coevolution of HIV transmission and risk perception dynamics. Recent medical advances will also be discussed as well as their potential impact on the HIV epidemic.

JAMES WATMOUGH, University of New Brunswick

A simple in-host treatment model exhibiting sustained immunity

In many epidemiological models, treatment works by lowering the reproduction number of the pathogen below a threshold. However, in these models, the pathogen reestablishes itself if the treatment is stopped. We present a simple example of a model where treatment can be stopped without reemergence of the pathogen. A situation referred to as sustained-immunity. This is possible because a stable infection-equilibrium coexists with a stable infection-free or low-infection state. Treatment, if applied for a sufficient time, can move the system into the basin of attraction for the infection-free equilibrium, and immunity is sustained after treatment is stopped. This is joint work with Norah Alshobrami and Lin Wang.

HUAIPING ZHU, York

Modeling the transmission of West Nile virus with weather conditions

Weather (temperature and precipitation) can affect the abundance and the behavior of vector mosquitoes for West Nile virus. In this study, we incorporate the daily weather conditions to model the transmission of West Nile virus in birds and mosquitoes. Using the mosquito abundance from a statistical model, surveillance data and daily weather from the Peel Region, Ontario,

we explore how the weather conditions effect the mosquito behaviors through the biting rate and death rate. Some simulation results under different weather patterns will be presented to illustrate the complex dynamics of the transmission.