Recent Advance in Disease Dynamics Analysis
Progrès récents en analyse de la dynamique des maladies
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ZHENGUO BAI, Xidian University
A reaction-diffusion malaria model with seasonality and incubation period

In this talk, I will consider a time-periodic reaction-diffusion model which incorporates seasonality, spatial heterogeneity and the extrinsic incubation period (EIP) of the parasite. The basic reproduction number R_0 is derived, and it is shown that the disease-free periodic solution is globally attractive if $R_0 < 1$, while there is an endemic periodic solution and the disease is uniformly persistent if $R_0 > 1$. Numerical simulations indicate that prolonging the EIP and increasing population mobility may be helpful in the disease control, while spatial heterogeneity of the disease transmission coefficient may increase the disease burden. This talk is based on a joint work with Drs. Rui Peng and Xiao-qiang Zhao.

MAX OLIVEIRA DE SOUZA, Universidade Federal Fluminense
On Aedes, Wolbachia and the Control of Urban Arboviruses

Wolbachia is a maternally transmitted bacteria, that has been shown to be capable of blocking the disease transmission of dengue, and recent results suggest that is also able to block chikungunya and zika. We present a model of infection by Wolbachia of an Aedes aegypti population, which take into account both the biology of this infection and athe ecology of the vector. The objective is to use this model for evaluating the sustainable introduction of this bacteria into field population.

We provide a complete mathematical analysis of the model proposed and give the basic reproduction ratio R_0 for Wolbachia. We observe a bistability phenomenon: Two equilibria are asymptotically stable: the mosquito population completely uninfected or completely infected; also a third unstable equilibrium exists. This is a backward bifurcation situation, with the bistability occurring for biological parameter values. This is also an example of an epidemiological model with only vertical transmission.

We use the data of real trial of releases of infected mosquitoes in Cairns (Australia) to calibrate our model. The calibrated model behaves remarkably well vis á vis the observed data. We use it to simulate different scenarios of appearance of dengue. The simulations confirm our findings that a dengue epidemics will not occur if Wolbachia infections is sufficiently prevalent in the Aedes populations. This suggests that the introduction of Wolbachia can become an effective control tool for dengue.

This is joint work with Gauthier Sallet and Abderrahman Iggidr (INRIA), Jair Koiller (INMETRO), Mocayr Silva (FGV) and Claudia Codeço (FIOCRUZ).

KATIA VOGT GEISSE, Universidad Adolfo Ibáñez, Chile
Structured models and their reproduction numbers: Effect of the way of transmission, control measures and social conditions

In this talk we will discuss three deterministic models of coupled differential equations, which are differently structured depending on the way of transmission of the infectious disease that each aims to study. We will pay special attention to the important disease parameter "Reproduction number" for each model, and analyze how it affects its dynamics depending on: specific control measures of the disease studied, intrinsic characteristics of the disease and/or social conditions of the population affected by the pathogen.

HONGBIN GUO, University of Ottawa
Global stability for a class of epidemiological models with multiple age structures

A class of staged-progression models with multiple age of infection structures and/or age of latency structures, are formulated to describe infectious disease progression with long latency and/or infectious period. Global properties of these structured models are studied using the Volterra-type Lyapunov functionals.

This is a joint work with Suxia Zhang from Xi'an University of Technology.

XI HUO, York University
Modelling Antimicrobial De-escalation: Implications for Stewardship Programs

Sequential antimicrobial de-escalation aims to minimize resistance to high-value broad-spectrum empiric antimicrobials by switching to alternative drugs when testing confirms susceptibility. Though widely practiced, the effects de-escalation are not well understood. Definitions of interventions and outcomes differ among studies. We develop a high-dimensional ordinary differential equation system model of the transmission and evolution of Pseudomonas aeruginosa in an intensive care unit to assess the effect of de-escalation on a broad range of outcomes, and clarify expectations. With broad ranges of undetermined parameters and limited hospital data, we statistically analyze the numerical simulation results in order to direct future model simplification and mathematical analysis.

MICHAEL LI, University of Alberta
Nonidentifiability Issues in Fitting Transmission Models with Disease Data

Mathematical models that describe the transmission dynamics of infectious diseases are increasingly applied to analyze public health data. When model parameters are estimated from fitting model outcomes to data, questions such as how many parameters can be fitted or whether the best-fit parameter values are unique often occur. These questions are related to the *nonidentifiability* issue: there are infinitely many best-fit values for certain parameters, which needs to be rigorously resolved for reliable data analysis and model predictions. In this talk, I will show that the nonidentifiability issue is intrinsic to the fitting of transmission models to disease data, and present a new method for detecting nonidentifiability and assessing the degree of nonidentifiability. A case study on parameter estimation of a HIV transmission model from surveillance data is used to demonstrate the concept of nonidentifiability and our method.

YIJUN LOU, Hong Kong Polytechnic University
Modelling Lyme Disease Transmission

Lyme disease imposes increasing global public health challenges and is acknowledged as a common infectious disease for the most of the world, especially in Europe and North America. This talk is devoted to modeling efforts on understanding the ecological cycle of Lyme disease transmission.

CHUNHUA SHAN, The University of Toledo
Oscillations and complex dynamics in mosquito-borne diseases

In this talk I will introduce a deterministic model to study the impact of limited health resources on transmission dynamics of mosquito-borne diseases by incorporating a nonlinear recovery rate. The model exhibits multi-steady states, and the phenomenon of backward bifurcation as a common feature of vector-borne diseases. Oscillations are discovered and studied in this model, which may help to reveal the recurrence mechanism of mosquito-borne diseases in undeveloped countries.

ZHISHENG SHUAI, University of Central Florida
Coupled Infectious Disease Models via Asymmetric Movements

Many recent outbreaks and spatial spread of infectious diseases have been influenced by human movement over air, sea and land transport networks, and/or anthropogenic-induced pathogen/vector movement. These spatial movements in heterogeneous environments and networks are often asymmetric (biased). The effects of asymmetric movement versus symmetric movement will be investigated using several epidemiological models from the literature. These investigations provide a better understanding of disease transmission and control in the real life application.

BRENDA TAPIA-SANTOS, Universidad Veracruzana
A model for the dynamics of nonsterilizing HIV vaccines

We present a model that considers a vaccination policy represented by the vaccine application rate, waning and an index of reduction of viral load. The model also incorporates the possibility of escape mutants that avoid vaccine action. The main result is that we can show the existence of an endemic equilibrium point when R0 is less than one. The reason behind it is the existence of escape mutants that promote an increased rate of infection large enough to trigger an increase in the density of infected people even in the subthreshold case.

JIANHONG WU, York University
Epidemic models with multiple delays: impact of diapause

We consider the dynamic vector-host-pathogen interaction motivated by such tick borne diseases as tick-borne encephalitis and Lyme disease. We stratify the vector population in terms of the stage before and after the contact with the host when co-feeding transmission may take place, and we consider the case where vector development may involve two time lags due to diapause. We derive and calculate the critical rate for the model to exhibit nonlinear oscillations. Our objective here is to use our simple mechanistic dynamic model to show that this structured epidemic model involving diapause and motivated by co-feeding transmission may generate periodic and irregular oscillations even when seasonal variations of the environmental conditions are ignored. This oscillation is not necessarily in synchrony with the seasonality of vector development and hence one should expect complicated oscillatory patterns of vector-borne disease dynamics in the filed observation and surveillance. This is based on a joint work with X. Wu and X. Zhang.

XIAOTIAN WU, Shanghai Maritime University;Université de Montréal
Model-based and data-driven pharmacokinetic parameter estimation

Steady-state volume of distribution (Vdss) is a key pharmacokinetic parameter. Its estimation generally refers to data-driven non-compartmental analysis (NCA), historically based on the available plasma concentration date of linear pharmacokinetic models with central elimination. However, many drug compounds, such as granulocyte colony-stimulating factor (G-CSF), erythropoietin (EPO) and thrombopoietin (TPO) which are widely used during chemotherapy, often exhibit complex nonlinear mechanism, and their Vdss estimation has not been addressed to date. In this talk, two-compartmental pharmacokinetic models with simultaneous first-order and Michaelis-Menten elimination are studied, the corresponding model-based expressions of Vdss and their relationships to data-driven NCA estimation are derived. The impact of non-linearity and peripheral elimination is explicitly delineated in these formulas. Being concerned with the issues of model identifiability and indistinguishability, an interval estimate of Vdss is suggested. This is a joint work with Prof. Fahima Nekka and Jun Li at Universite de Montreal.

YANYU XIAO, University of Cincinnati
Seasonal impact on vector-borne disease dynamics

We will explore the seasonal impact on the transmission and dispersal of some vector-borne diseases in this work.