
Mathematical Modeling in the Interface of Ecology, Epidemiology and Environment

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MAHNAZ ALAVINEJAD, York University

Coupled Renewal Equations for Vector-Born Disease Transmission Outbreak Dynamics

We study a class of models, including compartmental models, for vector-transmitted diseases by analyzing the forces of infection formulated as a coupled system of renewal equations. We derive the basic reproduction number and a final size relation for a closed vector and host population. We extend the model to the case where both vector and host populations have demographic dynamics and derive the positive equilibrium and its local stability.

MIROSLAVA CUPERLOVIC-CULF, NRC

Quantification of the metabolic response of wheat to Fusarium Head Blight in changing climate

Diseases of agricultural crops caused by fungi have devastating economic and health effects. Fusarium head blight (FHB) is one of the most damaging diseases of wheat and other small grain cereals. FHB contamination of wheat has been steadily increasing over the last decade leading to an increase in the associated risk of mycotoxin contamination in food and feed. Climate change and associated rise in CO₂ levels are hypothetical causes of this rise but their effects on Fusarium graminearum and the spread of FHB are still unknown. In this study the defense response of wheat plants grown at ambient (400 ppm) and elevated (800 ppm) CO₂ was evaluated and compared. Plant and fungal metabolites play a major role in defense and virulence with significant differences in metabolic response in resistant and susceptible plants. 1D and 2D 1H NMR spectroscopy performed in this work have provided detailed metabolite information leading to possible metabolic markers discriminating metabolic changes in wheat subtypes with different resistance and at changing CO₂ levels. Computational methodology for metabolite quantification from NMR data that automatically aligns spectra of standards and samples prior to quantification utilizing multivariate linear regression optimization of spectra of assigned metabolites to samples' 1D spectra is described and used. Fusarium infection-induced metabolic changes in different conditions will be discussed in the context of metabolic network and resistance.

TROY DAY, Queen's University

The Price Equation and Stochastic Evolutionary Epidemiology

The Price equation has found widespread application in many areas of evolutionary biology, including the evolutionary epidemiology of infectious diseases. I will illustrate the utility of this approach by first deriving a version of Price's equation that can be applied in continuous time and to populations with overlapping generations and then show how it provides a useful perspective on pathogen evolution by considering the epidemiological meaning of each of its terms. Finally, I will extend these results to the case where population size is small and generates demographic stochasticity to show how the particular partitioning of evolutionary change given by Price's equation is also a natural way to partition the evolutionary consequences of such stochasticity. This is joint work with Todd Parsons, Amaury Lambert, and Sylvain Gandon.

CHARMAINE DEAN, University of Waterloo

Spatiotemporal patterns and risk factors of Scarlet fever in Beijing based on a generalized additive modeling framework

Scarlet fever is an acute respiratory infectious disease spread through respiratory droplets or direct contact. In recent years, re-emergence of this disease has been becoming a great threat to global health. However, few studies have investigated its spatial-temporal distribution at the high spatial resolution, the complex interacting effect of environmental factors (temperature, humidity, and PM_{2.5}) as well as the relative importance of risk factors, which are all important for prevention purposes. The surveillance data of Scarlet fever for children aged 1 to 9, in Beijing from 2008 to 2013 from the Beijing Center of Disease Control with detailed and rich geographical information provided us a unique opportunity to explore the spatial-temporal

patterns of Scarlet fever by aggregating the data over a grid of 1041 cells. Generalized additive modeling with a thin plate spline for the spatial coordinates and a tensor product smooth for a three-way interaction of the meteorological variables was used to examine incidence patterns. Due to the differing patterns of incidence over 2008-2010 in comparison with 2011-2013, we analyzed the two time periods separately. Both analyses consistently showed that spatial effects were the greatest significant contributor to the prediction after adjusting for age, gender, month and weather variables. Three-way interaction of meteorological variables revealed a complex interaction with significant effects. Comparatively, demographic variables such as gender and age had a much smaller impact than both the spatial and meteorological interaction effects.

PETER HARRINGTON, University of Alberta
Probabilistic SI Disease Dynamics on a Finite Fixed Network

In this talk a novel probabilistic model is presented for infectious disease transmission on a finite network specified as a fixed weighted digraph. Individuals (network nodes) are classified as either susceptible or infectious, with transmission rates along weighted network arcs. The model is appropriate for diseases with no recovery, or for the initial outbreak of diseases with recovery. Our method to analyze the model yields the exact probability distribution of the time at which a given individual in the network becomes infected. This distribution can be used to compute the probability that any given individual is infected, as well as the expected number of infectious individuals at any time. Nodes can also be identified more generally, such as farms or cities, and the method can be applied to biological networks with estimated transmission rates on the network arcs.

MARVIN HOTI, Ryerson University
Local stability analysis on Lotka-Volterra predator-prey models with prey refuge and harvesting

We propose a predator-prey model by incorporating a constant harvesting rate into a Lotka-Volterra predator-prey model with prey refuge. All the positive equilibria and the local stability of the proposed model are studied and analyzed by sorting out the intervals of the parameters involved in the model. These intervals of the parameters exhibit the effects on the dynamical behaviors of prey and predators. The emphasis is put on the ranges of the prey refuge constant and harvesting rate. We show that the model has three type positive boundary equilibria and one positive interior equilibrium. By using the qualitative theory for planar systems, we show that the three type boundary positive equilibria can be saddles, saddle nodes, topological saddles or stable or unstable nodes, and the interior positive equilibrium is locally asymptotically stable. Under suitable restrictions on the parameters, we prove that the positive interior equilibrium is a stable node. It remains open that under what conditions on the parameters is the positive interior equilibrium a focus.

This is joint work with Christopher Chow, Chongming Li and Dr. Kunquan Lan

LIA HUMPHREY, University of Guelph
Optimal shingles vaccine distribution under a multiyear vaccination program

In this work we use a dynamic programming and health economics framework to build an optimal allocation model for preventative shingles treatments among population groups with a single-payer health care provider (such as the Ontario program). We model and analyze whether or not the presence of multiple treatment options on the market may help increase coverage over more age groups under the same budgetary restrictions in a multiyear model. Lastly, we incorporate and discuss two policy options for increasing coverage to age groups currently not in the program's window.

SALAH UDDIN KHAN, University of Guelph

NAZILA AKHAVAN KHARAZIAN, Kings Distributed Systems
Next-generation computing tools to accelerate research, discovery and innovation

Distributed Compute Labs (DCL) is a Canadian educational nonprofit promoting the Distributed Compute Protocol (DCP), a modern, easy-to-use, and powerful computing platform. DCP connects idle computers — e.g. thousands of desktops on a university campus — unlocking latent computing power to support research. DCP enables students, researchers, and industry to process massive mathematical and statistical models with unprecedented ease and speed. In summary, Distributed Compute Labs democratizes access to digital infrastructure, reduces barriers, and unleashes innovation.

MARK LEWIS, University of Alberta

Estimation of spatiotemporal transmission dynamics and analysis of management scenarios for sea lice of farmed and wild salmon

Parasite transmission between farmed and wild salmon affects the sustainability of salmon aquaculture in Pacific Canada. Understanding and managing parasites in aquaculture is challenged by spatial and temporal variation in transmission dynamics. We developed a mechanistic model that connects sea louse (*Lepeoptheirus salmonis*) outbreak and control on farmed salmon (*Salmo salar*) to spatiotemporal dynamics of sea lice on migrating wild juvenile salmon (*Oncorhynchus keta* and *Oncorhynchus gorbuscha*). The model is based on a microparasite infection equations coupled to a partial differential equation describing spatial movement along fjords where the sea louse larvae can spread as the juvenile salmon migrate. We fitted the model to time series of sea lice on farmed salmon and spatial surveys of juvenile wild salmon in the Broughton Archipelago. We used the parameterized model to evaluate alternative management scenarios based on the resulting sea louse infestations and predicted mortality of wild salmon. Early and coordinated management of sea lice on salmon farms was most effective for controlling outbreaks in wild salmon, while uncoordinated treatments led to a resurgence of sea lice on salmon farms during the juvenile salmon migration. This study highlights the importance of incorporating spatiotemporal variability when considering infectious disease dynamics shared by farmed and wild hosts, particularly when migratory wildlife are involved. This is joint work with Stephanie Peacock, Martin Krkošek, and Andrew Bateman.

FELICIA MAGPANTAY, Queen's University

Challenges in modeling the transition period of childhood diseases from the pre-vaccine to vaccine era

Mathematical models of childhood diseases often employ homogeneous time-dependent transmission rates. These models can provide good agreement with data in the absence of significant changes in population demography or levels of transmission, such as in the case of pre-vaccine era measles in industrialized countries. However, accurate modeling and forecasting of transient dynamics after the start of mass vaccination has proved more challenging. This is true even in the case of measles which has a well understood natural history and a very effective vaccine. Here, we demonstrate how the dynamics of homogeneous and age-structured models can be similar in the absence of vaccination, but diverge after vaccine roll-out. We also propose methods to fit such models to long term epidemiological data with imperfect covariate information.

JUNE MURLEY, University of Waterloo

Well-posedness of a coupled PDE model of High Intensity Focussed Ultrasound heating of biological tissue

Over the past decade, High Intensity Focussed Ultrasound (HIFU) has emerged as an important novel therapeutic modality in the treatment of cancers. In this talk, we present a set of equations that model the effects of HIFU on the temperature of biological tissue, where the effects of convection are taken into account. The methods to prove the well-posedness of the model for functions in L^p spaces are outlined. In particular, we describe the use of the Leray-Schauder fixed point theorem to prove existence of solutions to the set of equations and a priori estimates to establish uniqueness.

KYEONGAH NAH, York University

Dynamical modeling of tick-borne encephalitis transmission with climate projection

We introduce a mathematical model for retroactive analysis of weather fluctuation on tick-borne encephalitis (TBE) prevalence in Hungary. The model couples a TBE virus transmission dynamics among ticks with multiple development stages, animal

hosts and humans, with the stochastic observation process of human TBE reporting given infection. By fitting human incidence data in Hungary to the model, we estimate key parameters relevant to the tick-host interaction and tick-human transmission. Then we compute the basic reproduction number which determines the long-term behaviors of the periodic system of integro-differential equations - the TBE transmission dynamics. We then show that the developed model provides an effective tool for projecting TBE virus transmission risk in the enzootic cycle by integrating climate projection with emerging knowledge about the region-specific tick ecological and pathogen epidemiological processes.

POURIA RAMAZI, Univesrity of Alberta
Predicting Infestations Using Machine Learning

Predicting future infestations is crucial to forest management. The many successes of machine learning across a variety of tasks, have motivated us to explore this approach for this important task. There are, however, many subtle challenges here: how to identify the best learning models, the best subset of the available covariates, and importantly, how to properly evaluate the models to avoid misleading performance measures (which are unfortunately common). We explore these ideas in the context of predicting the chance of a mountain pine beetle outbreak in the Cypress Hills area, over the years of 2006–2018, seeking the learned models with the best performance at predicting 1 year (resp., 3, 5, 7 years) infestation. We have found a generalized boosted regression tree (GBM) predicting the future 1 and 3-year infestations with 97% and 89% AUC, a neural network (NN) with one hidden layer predicting future 5-year infestations with 88% AUC, and a novel mixed model predicting future 7-year infestations with 80% AUC. We also show how incorrect model evaluations can lead to wrong performance measures: If the train and test datasets are obtained from a random split of the original dataset (rather than the appropriate year-based split), a generalized linear model, for example, would score 77% instead of the more accurate 62%. We then investigate how the prediction accuracy varies with respect to the provided history length of the covariates, and find that GVM, NN, and naive Bayes predict more accurately as the history length increases.

QIUYI SU, York University
A stage-structured model to investigate persistence of pertussis

In this study, we construct a multi-stage age-stratified demographic model and the corresponding epidemiological model of pertussis transmission dynamics. We calculate the positive equilibrium of the demographic model. Under the assumption that the population distribution has reached this positive equilibrium, we analyze the asymptotic behavior of the disease incidence of different age groups and conclude that the disease will die out if the basic reproduction number is smaller than the unity and the infectious population distribution will converge to a unique positive equilibrium when the basic reproduction number is larger than the unity. For a specific birth function, we investigate the impact of changes of the threshold productive age and birth rate parameters on the demographic distribution and infant disease incidence rate.

MARCO TOSATO, York University
A Simple Spatial Model for Tick Dynamics Involving Diapause

Ticks are the second most effective means for vector-borne diseases worldwide. There has been a northward spread of ticks across Canada due to various factors including climate change.

In this talk, we consider tick dynamics with a special focus on diapause. Here we analyze how several ecological factors and environment variations affect this phenomenon. Then, we present one of our recent ongoing research projects which incorporates Delay Differential Equations (DDE) to model tick growth and diapause in a two-patch environment. We examine the existence and stability of equilibria and the occurrence of Hopf bifurcations. This is based on a joint work with Xue Zhang and Jianhong Wu.

VITALI VOUGALTER, University of Toronto
Solvability of some integro-differential equations with anomalous diffusion in higher dimensions

The work deals with the studies of the existence of solutions of an integro-differential equation in the case of the anomalous diffusion with the negative Laplace operator in a fractional power in R^d , $d = 4, 5$. The proof of the existence of solutions relies on a fixed point technique. Solvability conditions for non Fredholm elliptic operators in unbounded domains are used.

RAPHAEL XIMENES, University Health Network / THETA

Development and calibration of a dynamic microsimulation of a disease history model for Zika virus (ZIKV) infection

Purpose: While generally causing self-limited and mild illness, Zika virus (ZIKV) infection can cause significant morbidity including congenital Zika syndrome, newborn Zika syndrome, and Guillain-Barré syndrome (GBS). However, our understanding of the population-level impact of the disease on longer-term health outcomes is limited. This presentation describes the development and calibration of a ZIKV disease history model and quantifies the population-level burden of disease of ZIKV for Colombia.

Method: We developed a ZIKV disease history model using a stochastic, individual-level microsimulation approach. We simulate a dynamic cohort of uninfected individuals over one year using data from the published literature and local census data to parameterize the model and surveillance data from Colombia to calibrate the model. We calibrated five parameters: infection risk, and probabilities of: pregnancy, neurological complication, GBS, and CZS using the Nelder-Mead method and evaluated goodness of fit using the sum of squared differences between simulated proportions and desired proportions.

Result: For the best-fitting parameters the goodness of fit obtained was $6.79 \cdot 10^{-10}$, the incidence of ZIKV infection was 220 per 100,000 people (222 observed), CZS was 4 cases per 1,000 ZIKV infected people (6 observed), neurologic syndrome was 9 cases per 1,000 ZIKV infections (6 observed) and GBS was 9 per 1,000 ZIKV infections (4 expected).

Conclusion: Our model is well calibrated to predict the incidence of ZIKV infection, which will be helpful in understanding the long-term disease burden and cost-effectiveness of ZIKV interventions.