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**Mathematical modelling in public health**  
**Modélisation mathématique en santé publique**

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**DAIHAI HE**, Hong Kong Polytechnic University

*Resolving the enigma of Iquitos and Manaus: A modelling analysis of multiple COVID-19 epidemic waves in two Amazonian cities*

The nearby cities of Iquitos (Peru) and Manaus (Brazil) experienced the world's highest infection and mortality rates during the first COVID-19 wave in 2020. Key studies suggested that >70% of the city populations were infected in this wave and thus close to herd immunity and protected. It remains an enigma as to why a deadly second wave followed in Manaus worse than the first. To resolve this, we present a data-driven model of epidemic dynamics in Iquitos which we use to help explain and model events in Manaus. The partially observed Markov process model simultaneously fits a flexible "variable  $R_0$ ", estimates long-term immunity waning and impulsive immune evasion, and thus provides a comprehensive framework for characterizing and modeling new variants of concern.

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**XI HUO**, University of Miami

*Vector-borne disease outbreak prevention: linking mosquito trap data to mathematical models*

*Aedes aegypti* is responsible for a few arbovirus transmissions. In this talk, I will present how we connect differential equation parameters with the mosquito trap data collected from 2017 to 2019. The model is then used to compare the *Ae. aegypti* population and evaluate the impact of rainfall intensity in different urban built environments. Our results show that rainfall affects the breeding sites and the abundance of *Ae. aegypti* more significantly in tourist areas than in residential places. In addition, we apply the model to quantitatively assess the effectiveness of vector control strategies in Miami-Dade County in South Florida, USA.

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**MICHAEL LI**, University of Alberta

*An Epidemic Enigma: Challenges in Modeling the Influenza Epidemic in a Boarding School*

I will revisit a classical modeling example of an influenza epidemic in a boarding school in the UK, which was first described in the British Medical Journal (March 4, 1978). The application of an SIR model to describe the epidemic has appeared in well-known textbooks, as well as numerous lecture notes and presentations on the internet. It is shown that the number of infected  $I(t)$  can fit the data very well, allowing estimation of the two model parameters and the basic reproduction number. What the modeling examples failed to check is that the final size, which is the total number or percentage of infected people during the epidemic, predicted by the calibrated models (close to 730 students or 96%) hugely overestimated the final size given in the BMJ paper (512 students or 67%). How to reconcile this huge discrepancy in model predictions and data? I will provide some explanations, outlining several challenges in mathematical modeling of general epidemics. For the influenza epidemic described in the BMJ, there is no known model of any kind in the literature that has correctly described both the time course of the epidemic ( $I(t)$ ) and the final size, and it remains as an epidemic enigma for modellers.

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**MICHAEL WZ LI**, Public Health Agency of Canada

*The Past, Present and the Future of Mathematical Modeling Supporting Public Health*

Mathematical modeling has been critical in supporting public health initiatives, providing valuable insights into disease dynamics, intervention strategies, and resource allocation. This talk explores the past, present, and future of mathematical modeling in supporting public health, highlighting its transformative impact on addressing complex health challenges in different eras.

In the past, mathematical modeling laid the foundations for understanding basic disease transmission dynamics. For example,  $R_0$  provides insights into the potential for disease transmission and helps inform public health interventions; the SIR (Susceptible-Infectious-Recovered) model, allowed researchers to simulate and predict the spread of infectious diseases, aiding in the formulation of effective public health interventions.

In the present era, math modeling has become an indispensable tool in public health research and practice. Advancements in computational power, data availability, and demands for supporting public health policies, practices, and surveillance led to more sophisticated models, incorporating real-world data and parameters. Collaborative efforts with multidisciplinary have opened up many possibilities to advance the state-of-the-art modeling supporting public health.

Looking toward the future, math modeling holds immense promise in transforming public health practices. Advanced modeling techniques provide a more nuanced understanding of disease dynamics, biological mechanisms, and social interactions. Integration of evolving real-time data sources such as genomics, serological, sentinel, and citizen science surveillance enhances modeling. Lastly, to fully leverage the potential of math modeling, interdisciplinary collaborations, and stakeholder engagement are crucial. By involving public health experts, policymakers, scientists, and communities in the modeling process, models can be co-developed to address public health challenges.

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**YIJUN LOU**, The Hong Kong Polytechnic University

*Getting jab or regular test: observations from an impulsive epidemic COVID-19 model*

Several safe and effective vaccines are available to prevent people from getting seriously ill or dying from the coronavirus disease 2019 (COVID-19) and widespread vaccination is believed to be a critical tool to fight the disease. However, individuals with vaccine hesitancy or other medical conditions may choose not to vaccinate, and regular compulsory testing is required in some sectors for such unvaccinated individuals. It is interesting to find that different sectors pose various testing frequencies, for example on a weekly or biweekly basis, and it becomes an important scientific problem to determine the test frequency and identify underlying factors. This talk is going to present a population based model to accommodate different personal decision choices (getting vaccination or regular tests), vaccine efficacies and uncertainties in the epidemic transmission. The model, in the form of impulsive differential equations, uses time instant to represent the reporting date for the test result of an unvaccinated individual. By employing some well-acceptable indices to measure the transmission risk, including the basic reproduction number, the peaking time and the final size, an optimal test frequency is shown to be very sensitive to parameters involved in the transmission process, including vaccine efficacy, disease transmission rate, the test accuracy, and the existing vaccination coverage. The testing frequency should be appropriately designed with the consideration of all these factors, as well as the control objectives measured by epidemiological quantities of great concern.

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**BRYCE MORSE**, Florida State University

*The impact of threshold decision mechanisms of collective behaviour on disease spread*

Humans are a hyper social species, which greatly impacts the spread of infectious diseases. How do social dynamics impact epidemiology? How does public health policy best take into account these impacts? Here we develop a model of disease transmission that incorporates human behaviour and social dynamics. We use a "tipping-point" dynamic, previously used in the sociological literature, where individuals adopt a behaviour given a sufficient frequency of the behaviour in the population. The thresholds at which individuals adopt behaviours is modulated by the perceived risks of infection, i.e. the disease prevalence and transmission rate, and the behaviour of others. Social conformity creates a type of "stickiness" whereby individuals are resistant to changing their behaviour due to the population's inertia. In this model, the epidemic attack rate is sensitive to the timing of the behavioural response. Near the optimal response, small errors can result in large increases in the total number infected during the epidemic. And, more surprisingly, we observe a non-monotonicity in the attack rate as a function of various biological and social parameters such as the transmission rate, efficacy of social distancing, the costs to social distancing, the weight of social consequences of shirking the norm, and the degree of heterogeneity in the population.

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**XIAOYING WANG**, Trent University

*Studying the mixed transmission in a community with age heterogeneity: COVID-19 as a case study*

COVID-19 has been prevalent worldwide for about 2 years now and has brought unprecedented challenges to our society. Before vaccines were available, the main disease intervention strategies were non-pharmaceutical. Starting December 2020, in Ontario, Canada, vaccines were approved for administering to vulnerable individuals and gradually expanded to all individuals above the age of 12. As the vaccine coverage reached a satisfactory level among the eligible population, normal social activities resumed and schools reopened starting September 2021. However, when schools reopen for in-person learning, children under the age of 12 are unvaccinated and are at higher risks of contracting the virus. We propose an age-stratified model based on the age and vaccine eligibility of the individuals. We fit our model to the data in Ontario, Canada and obtain a good fitting result. The results show that a relaxed between-group contact rate may trigger future epidemic waves more easily than an increased within-group contact rate. An increasing mixed contact rate of the older group quickly amplifies the daily incidence numbers for both groups whereas an increasing mixed contact rate of the younger group mainly leads to future waves in the younger group alone. The results indicate the importance of accelerating vaccine rollout for younger individuals in mitigating disease spread.

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**YANYU XIAO**, University of Cincinnati

*Investigations the optimal de-escalation strategies during pandemic*

In this work, we examined some optimal paths for contact relaxing strategies during the de-escalation phase of a pandemic.

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**PING YAN**, Public Health Agency of Canada

*A proportional incidence rate model for aggregated data on vaccine effectiveness against COVID-19 hospital/ICU admissions*

We develop a proportional incidence model that estimates vaccine effectiveness (VE) at the population level using conditional likelihood for aggregated data. Our model assumes that the population counts of clinical outcomes for an infectious disease arise from a superposition of Poisson processes with different vaccination statuses. The intensity function in this model is calculated as the product of per capita incidence rate and the at-risk population size, both of which are time-dependent. We then formulate a log-linear regression model with respect to the relative risk, defined as the ratio between the per capita incidence rates of vaccinated and unvaccinated individuals. In the regression analysis, we treat the baseline incidence rate as a nuisance parameter, like the Cox proportional hazard model in survival analysis. We apply the proposed models and methods to age-stratified weekly counts of COVID-19-related hospital and ICU admissions among adults in Ontario, Canada. The data, spanning from 2021 to February 2022, encompass the Omicron era and the rollout of booster vaccine doses. We also discuss the limitations and confounding effects while advocating for the necessity of more comprehensive and timely individual-level data that document the clinical outcomes and measure potential confounders.

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**MINGRAN ZHANG**,

*Modeling the Proliferation and Regulation of CD4+ T Cells During an Immune Response*

Most mathematical models for immune responses incorporating CD4+ T cell dynamics, such as HIV models, overly simplify this proliferation as an exponential growth with a rate less than the death rate of CD4+ T cells. Yet the autocrine reaction of IL-2 and CD4+ T cells suggests a much faster response, and the clearance of activated CD4+ T cells after the infection depends on induced regulatory T cells (Tregs). We prove mathematically that the interaction of IL-2, CD4+ T cells, and Tregs allows two modes of proliferation: the first mode is solely driven by the activation of naive CD4+ T cells, and the second mode is an excitable response in which the Treg population rapidly but briefly increases to a high level. These two modes are characterized by whether the proliferation rate is dominated by the CD4+ T cell death rate. We extend our model to include more realistic regulation terms and fit the models to CD4+ count data. The best-fit model parameters show that the immune system operates in the excitable mode.

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**SICHENG ZHAO**, Queen's University

*A Review of Bond Percolation Methods on Epidemic Network Models*

Bond percolation methods can be used to model disease transmission on complex networks and accommodate social heterogeneity while keeping tractability. Here we review the seminal works on this field by Newman (2002, 2003, 2010), Bansal & Meyers (2012) and Miller, Slim & Volz (2011). We also present a new R package based on these papers that take epidemic and network parameters as input and generates estimates of the epidemic trajectory and final size. This allows us to investigate the interaction between different community structures and disease control strategies, leading to interesting new research directions.