Mathematical, statistical, and AI modelling of Mpox and related diseases.
Modélisation mathématique, statistique et IA du Mpox et des maladies associées
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JACQUES BÉLAIR, Université de Montréal
Modeling Variable Compliance to Recommended Interventions to Control Outbreaks

Management of the COVID-19 pandemic required, during its early stages, the deployment of non pharmaceutical interventions (NPIs) [social isolation, physical distancing, mask-wearing, hand-washing], and then, as they became available, administration of repeated doses of vaccine. We are interested in the consequences, for the dynamics of the disease, of variable adherence to these measures, and the motivation generating the lack thereof; so we investigate a model for the change in attitude post-infection. A basic SEIRS model is expanded by a. introducing a structure in the infectious class, to reflect the variable severity of symptoms and the presence of asymptomatic cases; and b. considering the population divided into two classes according to their degree of adherence to the NPIs. Analysis of the ensuing model is guided by epidemiological observations in Québec. A recent analysis of a simpler model for compliance pre-infection will be presented.

QING HAN, York University
Adaptive changes in sexual behavior in the high-risk population in response to monkeypox transmission can control the outbreak

Monkeypox, a zoonotic disease, is emerging as a potential sexually transmitted infection/disease, with underlying transmission mechanisms still unclear. We devised a risk structured, compartmental model, incorporating sexual behavior dynamics. We compared different strategies targeting the high risk population: a scenario of control policies geared toward the use of condoms and/or sexual abstinence (robust control strategy) with risk compensation behavior change, and a scenario of control strategies with behavior change in response to the doubling rate (adaptive control strategy). Monkeypox's basic reproduction number is 1.464, 0.0066, and 1.461 in the high risk, low risk, and total populations, respectively, with the high risk group being the major driver of monkeypox spread. Policies imposing condom use or sexual abstinence need to achieve a 35% minimum compliance rate to stop further transmission, while a combination of both can curb the spread with 10% compliance to abstinence and 25% to condom use. With risk compensation, the only option is to impose sexual abstinence by at least 35%. Adaptive control is more effective than robust control where the daily sexual contact number is reduced proportionally and remains constant thereafter, shortening the time to epidemic peak, lowering its size, facilitating disease attenuation, and playing a key role in controlling the current outbreak.

JUDE KONG, York University
An AI-powered, integrated and user-friendly early warning, alert and response platform for disease outbreaks

Disease outbreaks are increasing both in terms of frequency and severity, in part due to accelerating human encroachment into natural landscapes, urbanization, globalization, and climate change. In response to the ever-present threat of disease outbreaks, the need for a comprehensive surveillance and response system has become paramount. In this talk, I will present some of our ongoing work on designing a community-oriented, climate-responsive, integrated, and user-friendly framework called AI-Epidemix for surveilling and managing infectious diseases while democratizing access to data science and machine learning techniques for non-experts. The framework is supported by AI, mathematical models, and a multi-source real-time data collection platform. It utilizes state-of-the-art AI and mathematical models to integrate and model both conventional (historical data, animal data, virus sequencingetc.) and unconventional data (such as Google Trends, Google Trends Rate, social media, satellite data, drug consumption in pharmacies, economic activity data and outdoor containers identified from Google Street View images) to detect possible diseases scenarios and corresponding interventions to suppress disease spread safely with minimal social impact.

IAIN MOYLES, York University

Bifurcations in fear behaviour impact final-size in a disease epidemic

We explore a mathematical model of disease transmission with a fearful compartment. Susceptible individuals become afraid by either interacting with individuals who are already afraid or those who are infected. Individuals who are afraid take protective measures via contact reductions to reduce risk of transmission. Individuals can lose fear naturally over time or because they see people recovering from the disease. We consider two scenarios of the model, one where fear is obtained at a slower rate than disease spread and one where it is comparable. In the former we show that behavioural change cannot impact disease outcome, but in the latter, we observe that sufficient behavioural intervention can reduce disease impact. However, response to recovery can induce a bifurcation where contact reduction cannot mitigate disease spread. We identify this bifurcation and demonstrate its implication on disease dynamics and final size.

BOUCHRA NASRI, Université de Montréal

Mathematical modeling of mpox: a scoping review

Mpox, a disease that was formerly found in Africa, saw its global epidemic in 2022 and has since spread to several other parts of the world, posing a threat to global public health. The application of appropriate mathematical modelling techniques is required for well-informed policies intended to manage and control the spread of this disease. To identify the model classes that are most frequently used, their underlying assumptions, and the modelling shortcomings that need to be addressed in light of the epidemiological features of the current mpox outbreak, we will discuss mathematical models that have been used to study mpox transmission in the literature in this talk. This is a joint work with Jeta Molla, Idriss Sekkak, Ariel Mundo Ortiz, Iain Moyles.

JHOANA P. ROMERO-LEITON, University of Manitoba

Mathematical modelling of the first HIV/ZIKV co-infection cases in Colombia and Brazil

In this work, we present a mathematical model to investigate co-infection with HIV/AIDS and zika virus (ZIKV) in Colombia and Brazil, where the first cases were reported in 2015-2016. The model considers the sexual transmission dynamics of both viruses and vector-host interactions. We begin by exploring the qualitative behaviour of each model separately. Then, we analyze the dynamics of the co-infection model using the thresholds and results defined separately for each model. The model also considers the impact of intervention strategies, such as, personal protection, antiretroviral therapy (ART), and sexual protection. Using available parameter values for Colombia and Brazil, the model is calibrated to predict the potential effect of the intervention strategies on the co-infection spread. According to these findings, transmission through sexual contact is a determining factor in the long-term behaviour of these two diseases. Furthermore, it is noted that co-infection with HIV and ZIKV may result in higher rates of HIV transmission and an increased risk of severe congenital disabilities linked to ZIKV infection. As a result, control measures have been implemented to limit the number of infected individuals and mosquitoes, with the aim of halting disease transmission. This study provides novel insights into the dynamics of HIV/ZIKV co-infection and highlights the importance of integrated intervention strategies in controlling the spread of these viruses, which may impact public health.

Keywords: Stability, Equilibrium points, Optimal control, Personal protection, Sexual protection, Antiretroviral therapy.

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IDRISS SEKKAK, École de santé publique de l'Université de Montréal

An analysis of a Multigroup mpox epidemic model incorporating public health measures

Epidemiological models help researchers and public health officials understand the dynamics of infectious diseases, predict their spread, and plan effective intervention strategies. For this matter, an analysis of a mpox epidemic model with heterogeneous mixing is conducted by incorporating several functions and parameters that model public health measures. Our analysis focuses on investigating how various public health measures, such as vaccination campaigns, and quarantine protocols, influence the spread of mpox within and between these population groups. Consequently, we investigate the proposed dynamical systems through both analytical and numerical methods in order to shed light on the effectiveness of these measures in mitigating the mpox epidemic across diverse demographic segments.

WOLDEGEBRIEL ASSEFA WOLDEGERIMA, York University

Quantifying the Basic Reproduction Number and the Underestimated Fraction of Mpox Cases: Mathematical Modelling and ML Study

The current global outbreak of mpox, which started in April 2022 has different epidemiological and clinical features compared to previous mpox outbreaks. Sexual contact has been hypothesized as the major transmission route for the disease in this outbreak, with the community of men having sex with men (MSM) disproportionately and dramatically affected. To better understand the transmission dynamics of the disease, it is essential to understand its dynamics during the early stages of the outbreak. In this article, we estimate the basic reproduction number and the ascertainment fraction of the reported cases of mpox around the world. We divide the population of each country into two groups (high-risk and low-risk groups) and consider two routes of transmission: sexual and non-sexual. Our estimate of the basic reproduction number of mpox in the considered countries ranges between 1.37 (Canada) and 3.68 (Germany). Furthermore, our estimates of the ascertainment fraction for the reported cases of mpox show a large variation in the under-reporting of cases in the high-risk population around the world with ascertainment fractions between 0.25 and 0.93, and a more consistent ascertainment fraction for the low-risk population, which ranges from 0.65 to 0.85. Our estimates can help public health decision- and policymakers better understand the mpox outbreak, in terms of how many underestimated cases can occur in several countries, and how the epidemic can spread differently.