
Mathematical modelling in epidemiology and public health
La modélisation mathématique en épidémiologie et en santé publique
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FRED BRAUER, University of British Columbia

Social distancing in epidemic models

In an epidemic, especially an epidemic of a disease regarded as serious, some individuals change their behaviour in order to try to avoid becoming infected. A fraction of the population reduces the rate of contact with other individuals by a fraction. We examine how this affects the reproduction number of the epidemic. A similar approach may be used to estimate the effect of face mask usage by a fraction of the population.

This work is joint with Fan Bai, Hausdorff Institute for Mathematics, Bonn, Germany.

YUMING CHEN, Wilfrid Laurier University

A new type function for constructing Lyapunov functions

Lyapunov direct method is an effective method to determine the question about stability when it works. However, there exists no general approach for constructing the needed Lyapunov functions. In this talk, we provide a new type function to construct Lyapunov functions. When applied to an SI epidemic model with a nonlinear incidence, the obtained sufficient condition on the global stability of the endemic equilibrium is weaker than the one obtained by using the traditional Volterra-type function.

GERARDO CHOWELL, Georgia State University

Forecasting the COVID-19 pandemic using ensemble modeling approaches

The ongoing COVID-19 pandemic presents with an unprecedented opportunity to evaluate the performance of mathematical modeling frameworks for forecasting the trajectory of the pandemic at different spatial and temporal scales. I will discuss progress on developing new ensemble modeling approaches that can outperform individual models in short-term forecasts without substantially increasing model complexity.

JING LI, California State University Northridge

Modeling the waning and boosting of immunity from infection or vaccination

Immunity following natural infection or immunization may wane, increasing susceptibility to infection with time since infection or vaccination. Symptoms, and concomitantly infectiousness, depend on residual immunity. We quantify these phenomena in a model population composed of individuals whose susceptibility, infectiousness, and symptoms all vary with immune status. We also model age, which affects contact, vaccination, and possibly waning rates. The resurgences of pertussis that have been observed wherever effective vaccination programs have reduced typical disease among young children follow from these processes. As one example, we compare simulations with the experience of Sweden following resumption of pertussis vaccination after the hiatus from 1979 to 1996, reproducing the observations leading health authorities to introduce booster doses among school-aged children and adolescents in 2007 and 2014, respectively. Because pertussis comprises a spectrum of symptoms, only the most severe of which are medically attended, accurate models are needed to design optimal vaccination programs where surveillance is less effective.

MICHAEL LI, University of Alberta

Estimation of the Proportion of Population Infected by COVID-19: Mathematical Models as a Tool for Data Analysis

The COVID-19 has turned into one of the largest pandemics and public health crises in history, with close to 1 million daily cases world-wide by the end of April 2021, and a total death toll of more than 3 million and rising. During the COVID-19

pandemic, mathematical modeling has played a crucial role in informing public health responses and policy. In addition to its well-perceived function of predicting epidemic trends, mathematical models are also being used as an important tool for retrospective data analysis.

In this talk, I present our work using the SIR models to analyze the surveillance data and estimate the proportion of the population in Alberta that have been infected by SARS-CoV-2 during the first wave of the COVID-19. The estimation results have been validated by seroprevalence data. In addition, we are able to estimate the impact of social-distancing measures, the case-infection ratio, and the time dependent infection-fatality rate. A key step of the estimation process is to overcome the nonidentifiability problem in parameter estimation, which is a bottle-neck issue during model calibration from data. This is a collaboration between our research group and Alberta Health.

AARON LIM, University of Bristol

Modelling the impact and costs of hepatitis C virus screening and treatment scale-up to achieve elimination in Pakistan

Background and Aims: Pakistan has the world's second-largest hepatitis C virus (HCV) burden. The World Health Organization (WHO) HCV-elimination strategy advocates for a reduction in HCV incidence by 80% by 2030. We explore how this could be achieved and the costs of doing so in Pakistan.

Methods: A general population HCV transmission, screening, and treatment model was developed and calibrated using available data from Pakistan, incorporating cost data on diagnostics and HCV treatment. We modelled alternative strategies for scaling-up screening and HCV treatment to determine the resulting impact and costs of achieving the WHO HCV incidence target in Pakistan.

Results: One-time screening of 90% of the 2018 population by 2030, with 80% referral to treatment, leads to 14 million individuals being screened and 350,000 treated annually, decreasing incidence by 27% over 2018-2030. Prioritising screening to higher prevalence groups (people who inject drugs (PWID) and adults >30 years) and introducing re-screening (annually for PWID, otherwise 10-yearly) increases the number screened and treated by half and decreases incidence by 51%. Decreasing HCV incidence by 80% requires doubling the primary screening rate, increasing referral to 90%, re-screening the general population every 5-years, and re-engaging those lost-to-follow-up every 5-years. This could cost USD\$8.1 billion, reducing to USD\$3.9 billion with lowest costs for diagnostic tests and drugs, including healthcare savings, and implementing a simplified treatment algorithm. Further including societal benefits of gained productivity suggests that elimination can be cost-saving by 2030.

Discussion: HCV elimination can bring about substantial societal health and economic benefits for Pakistan.

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.

CONNELL MCCLUSKEY, Wilfrid Laurier University

The effect of heterogeneity in social distancing

A compartmental model for COVID-19 with multiple subgroups that differ only in the level of contacts that members have with others was studied. Numerical simulations were performed for the case of two subgroups: one group that does social distancing and one that doesn't. The number of contacts for the social distancing group was varied, while keeping \mathcal{R}_0 fixed (by changing the relative sizes of the two groups). The peak number of infections changed dramatically, dropping by as much

as 70%, while the initial growth rate and timing of the peak remained constant. This suggests that heterogeneity in social distancing is fundamentally important.

In particular, if \mathcal{R}_0 is determined from a period of exponential growth without accounting for this heterogeneity, then the projections of future cases will be correspondingly affected.

MUHAMMAD ABU SHADEQUE MULLAH AND PING YAN, Public Health Agency of Canada
A Semi-parametric Mixed Model for Short-term Projection of Daily COVID-19 Incidence in Canada

During a pandemic, data are very “noisy” with enormous amounts of local variation in daily counts, compared with any rapid changes in trend. Accurately characterizing the trends and reliable predictions on future trajectories are important for planning and public situation awareness. We describe a semi-parametric statistical model that is used for short-term predictions of daily counts of cases and deaths due to COVID-19 in Canada, which are routinely disseminated to the public by Public Health Agency of Canada. We present the model and the method. Performance indicators are defined and evaluated through extensive sensitivity analyses. We also compare our model with other commonly used models such as generalizations of logistic models (e.g. the Richards model and generalization) for similar purposes, followed by discussions on the limitations.

ZHISHENG SHUAI, University of Central Florida
Impact of Hotspot Arrangements on Disease Invasion

In this talk we consider the spread of an infectious disease in a heterogeneous environment, modeled as a network of patches. We focus on the invasibility of the disease, as quantified by the basic reproduction number R_0 , and investigate how the locations of disease hotspots and the changes in the network structure affect the value of R_0 . These effects can be characterized using new indices for the network average and network heterogeneity, and provide both qualitative and quantitative information for mitigating disease spread among the patches.

STACEY SMITH?, The University of Ottawa
Modelling the daily risk of Ebola in the presence and absence of a potential vaccine

Ebola virus — one of the deadliest viral diseases, with a mortality rate around 90% — damages the immune system and organs, with symptoms including episodic fever, chills, malaise and myalgia. The Recombinant Vesicular Stomatitis Virus-based candidate vaccine (rVSV-ZEBOV) has demonstrated clinical efficacy against Ebola in ring-vaccination clinical trials. In order to evaluate the potential effect of this candidate vaccine, we developed risk equations for the daily risk of Ebola infection both currently and after vaccination. The risk equations account for the basic transmission probability of Ebola and the lowered risk due to various protection protocols: vaccination, hazmat suits, reduced contact with the infected living and dead bodies. Parameter space was sampled using Latin Hypercube Sampling, a statistical method for generating a near-random sample of parameter values. We found that at a high transmission rate of Ebola (i.e., if the transmission rate is greater than 90%), a large fraction of the population must be vaccinated (>80%) to achieve a 50% decrease in the daily risk of infection. If a vaccine is introduced, it must have at least 50% efficacy, and almost everyone in the affected areas must receive it to effectively control outbreaks of Ebola. These results indicate that a low-efficacy Ebola vaccine runs the risk of having vaccinated people be overconfident in a weak vaccine and hence the possibility that the vaccine could make the situation worse, unless the population can be sufficiently educated about the necessity for high vaccine uptake.

QIUYI SU, York University
Impact of variability of reproductive ageing and rate on childhood infectious disease prevention and control

In this study, we propose a stage-structured model of childhood infectious disease transmission dynamics, with the population demographics dynamics governed by a certain family and population planning strategy giving rise to nonlinear feedback delayed effects on the reproduction ageing and rate. We first describe the long-term aging-profile of the population by describing the pattern and stability of equilibrium of the demographic model. Then we investigate the disease transmission dynamics, using

the epidemic model when the population reaches the positive equilibrium (limiting equation). We establish conditions for the existence, uniqueness and global stability of the disease endemic equilibrium. We then prove the global stability of the endemic equilibrium for the original epidemic model with varying population demographics. The global stability of the endemic equilibrium allows us to examine the effects of reproduction ageing and rate, under different family planning strategies, on the childhood infectious disease transmission dynamics. We also examine demographic distribution, diseases reproductive number, infant disease rate and age distribution of disease.

LIN WANG, University of New Brunswick
Impact of travel between patches on disease spread

In this talk, I will present some results addressing the impacts of travel between patches on disease spread. We show that the impacts of travel are very complex and vary on model assumptions. This talk is based on several joint papers with my collaborators.

XIAOYING WANG, Trent University
Studying social awareness of physical distancing in mitigating COVID-19 transmission

Since the initial identification of a COVID-19 case in Wuhan, China, the novel disease quickly becomes a global pandemic emergency. In this paper, we propose a dynamic model that incorporates individuals' behavior change in social interactions at different stages of the epidemics. We fit our model to the data in Ontario, Canada and calculate the effective reproduction number \mathcal{R}_t within each stage. Results show that $\mathcal{R}_t > 1$ if the public's awareness to practice physical distancing is relatively low and $\mathcal{R}_t < 1$ otherwise. Simulations show that a reduced contact rate between the susceptible and asymptomatic/unreported symptomatic individuals is effective in mitigating the disease spread. Moreover, sensitivity analysis indicates that an increasing contact rate may lead to a second wave of disease outbreak. We also investigate the effectiveness of disease intervention strategies. Simulations demonstrate that enlarging the testing capacity and motivating infected individuals to test for an early diagnosis may facilitate mitigating the disease spread in a relatively short time. Results also indicate a significantly faster decline of confirmed positive cases if individuals practice strict physical distancing even if restricted measures are lifted.

JAMES WATMOUTH, University of New Brunswick
Case importation and community spread: controlling disease-spread in low density populations.

For most of the pandemic, Canada has kept case numbers relatively low through a combination of community quarantine and travel restrictions. In theory, this has implications for how to approach and manage the new normal of endemic SARS-CoV-2. I will focus on what this might mean for Atlantic Canada, using simple SIR-type compartmental models with importation and waning immunity.

GAIL WOLKOWICZ, McMaster University
A Delay Model for Persistent Viral Infections in Replicating Cells

Persistently infecting viruses remain within infected cells for a prolonged period of time without killing the cells and can reproduce via budding virus particles or passing on to daughter cells after division. The ability for populations of infected cells to be long-lived and replicate viral progeny through cell division may be critical for virus survival in examples such as HIV latent reservoirs, tumor oncolytic virotherapy, and non-virulent phages in microbial hosts. We consider a model for persistent viral infection within a replicating cell population with time delay in the eclipse stage prior to infected cell replicative form. We obtain reproduction numbers that provide criteria for the existence and stability of the equilibria of the system and provide bifurcation diagrams illustrating transcritical (backward and forward), saddle-node, and Hopf bifurcations, and provide evidence of homoclinic bifurcations and a Bogdanov-Takens bifurcation. We investigate the possibility of long-term survival of the infection (represented by chronically infected cells and free virus) in the cell population by using the mathematical concept of robust uniform persistence. Using numerical continuation software with parameter values estimated from phage-microbe

systems, we obtain two-parameter bifurcation diagrams that divide parameter space into regions with different dynamical outcomes. We thus investigate how varying different parameters, including how the time spent in the eclipse phase, can influence whether or not the virus survives.

This is joint work with Hayriye Gulbudak and Paul Salceanu of the University of Louisiana, Lafayette

JIANHONG WU, York University

A renewal equation model for disease transmission dynamics with contact tracing

Contact tracing is one of the most cost-effective and widely adopted non-pharmaceutical interventions to counteract the spread of infectious diseases in the absence of effective treatments and vaccines. We have developed a deterministic model for disease transmission dynamics, structured by time since infection, that includes diagnosis of symptomatic individuals and contact tracing. A mechanistic formulation of the processes at the individual level leads to an integral equation (delayed in calendar time and advanced in time since infection) for the probability that an infected individual is detected and isolated at any point in time. This is then coupled with a renewal equation for the total incidence to form a closed system describing the transmission dynamics involving contact tracing. When applied to the case of SARS-CoV-2, our results show that only combinations of diagnosis of symptomatic infections and contact tracing that are almost perfect in terms of speed or coverage can attain control, unless additional strong measures to reduce overall community transmission are in place. Under constraints on the testing or tracing capacity, the interruption of contact tracing may be irreversible and, depending on the overall growth rate and prevalence of the disease, may lead to outbreaks even in cases when the epidemic was initially under control. This is based on joint work with Francesca Scarabel and Lorenzo Pellis (University of Manchester, UK) and Nicholas H Ogden (PHAC, Public Health Agency of Canada).