Bulletin of Mathematical Biology (2019) 81:4311–4312
https://doi.org/10.1007/s11538-019-00672-3

EDITORIAL

Current Trends in Mathematical Epidemiology

Julien Arino[1] **· James Watmough**[2]

Published online: 14 November 2019

The study of epidemiology using mathematical approaches has had a long history, starting from classic work by Ross on malaria and Kermack and McKendrick on the SIR (Susceptible–Infected–Removed) model roughly a century ago. This work has been characterized by both elegant mathematics and real impact on understanding the dynamics of diseases in humans and animals and consequently contributing to the management of diseases. Yet, there are many important and interesting biological aspects that will potentially change our understanding of disease dynamics. The papers in this special issue illustrate how mathematics has continued to provide insights. We expect that the work presented here will contribute to a better understanding of disease dynamics and spur future work. An overview of the specific contributions to this issue illustrates both current and potential future directions.

While there has been great success using the classic SIR model in explaining the basic features of both the epidemic and endemic forms of disease transmission in a population, it omits many factors thought to be important, leaving many features of epidemics unexplained. These details are of great interest both theoretically and to efforts to predict and control the spread of an infectious disease. Milwid, Frascoli, Steben and Heffernan (1) illustrate the complexity possible in the simple SIR framework in their comparison of several screening, treatment, and vaccination strategies for the control of Human papilloma virus transmission. Smirnova, deCamp and Chowell-Puente (2) present a novel approach to nonparametric modelling and forecasting of epidemics from early case-incidence data.

Despite their apparent complexity, many models feature globally stable endemic and disease-free equilibria and a simple threshold, the Basic Reproduction Number, $\mathcal{R}_0$, separating the two dynamics. Many researchers, both in mathematical and applied epidemiology, are interested in understanding the limits of the Basic Reproduction

Both the authors are associated with Centre for Disease Modelling/Centre pour la modélisation des maladies (http://www.cdm-cmm.org/).

✉ James Watmough
watmough@unb.ca

1 Department of Mathematics & Data Science Nexus, University of Manitoba, Winnipeg, Manitoba, Canada

2 Department of Mathematics and Statistics, University of New Brunswick, Fredericton, NB, Canada

Number and similar simple thresholds in predicting global dynamics of epidemics. Kamgang, Harism and Yakubu (3) examine the global dynamics of a model for malaria transmission and extend our understanding of the conditions under which $\mathcal{R}_0$ is a threshold for transition from globally stable disease-free dynamics to globally stable endemic equilibrium dynamics. Yakubu and van den Driessche (4) extend our understanding of stability and persistence of the solutions of discrete-time SEIR models.

At the other extreme, we are gaining an understanding in many ecological, epidemiological and immunological systems of the role of delays in destabilizing the endemic equilibrium. Cao explores the transitions between stable and periodic endemicity under delays in an age-structured model.

The dynamics of vector-borne infections are complicated by host and vector behaviour. Several aspects of this lend themselves to options for control. Rivera and Barradas (5) develop a model based on the hypothesis that host feeding preference evolves as a protective mechanism in both the host and vector to reduce infection. Malagn and Bernal (6) examine the role of host diversity on transmission dynamics. Mata, Greenwood (7) and Tyson present an analysis of the role of environmental transmission routes. Another important aspect is the movement of hosts, who can spread infection to heretofore uninfected areas. To investigate such problems, Harvim, Zhang, Georgescu (8) and Zhang consider a model for Zika Virus, with both vector-host and between-host sexual transmission, set in a metapopulation framework.

The study of epidemics should not be separated from the study of within-host dynamics. Theoretically, the dynamics share similar structures and the mathematical tools developed give insight to both scales. Assefa, Teboh-Ewungkem and Ngwa (9) extend a model for in-host malaria parasite dynamics to include late state gametocytes and increase our understanding of asymptomatic infections and how they are sustained by repeated exposure.