Atlas of Science
another view on science
https://atlasofscience.org

Modeling epidemics and analyzing Ebola incidence data using Numerus Model Builder

Epidemics are quintessentially dynamic with outbreak, peak-incidence, and fadeout phases. The timings of outbreaks are hard to predict, as happened with the 2014 outbreak of Ebola viral disease in West Africa. To evaluate the risks of outbreaks, the presence of the pathogens may be closely monitored. Once an outbreak begins, mathematical and numerical (or computational) models can be used to predict the time of peak-incidence, the size and, perhaps, spatial extent of the epidemic and its duration. These models can also be used to evaluate the impacts of vaccination, prophylactic/educational campaigns, quarantine programs, or assessing the role of early case detection and the efficacy of treatments.

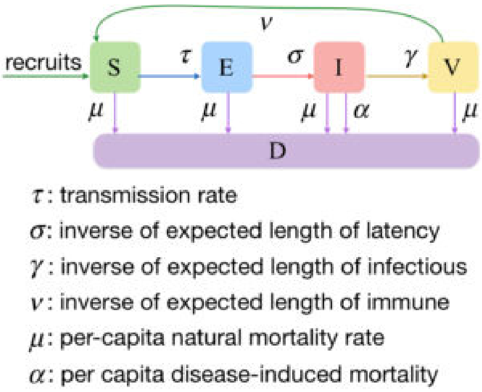

Fig. 1. Compartments S, E, I, V and D respectively represent the number (or density) of susceptible, exposed (infected by not yet infectious), infectious, recovered with immunity, and dead individuals. Individuals start out in state S and move through states E, I, V and back to S at the indicated rates, unless they die (D) due to natural or disease-related causes. New recruits to the susceptible compartment may be newborns in the case of measles, newly sexually active cohorts in the case of sexually transmitted diseases, or migrants in the case of metapopulation settings.

Underpinning all epidemic models is the so-called SEIR (R=V or D) process (Fig. 1). This process can be emulated using: i) numerical methods to solve systems of ordinary differential equations (continuous-time deterministic compartmental formulation); ii) fixed-time-step iterations of a system of difference equations using a competing rates approach; iii) stochastic simulations involving multinomial sampling (Monte Carlo method); iv) stochastic event-driven simulations (Gillespie method); or v). an individual/agent-based fixed-time-step stochastic simulation. With any of these five methods, the most basic approach is to assume the rates of transition, apart from transmission, are constant. Transmission—the transition rate from S to E (i.e., the rate of creating new infection)—is assumed to be either proportional to the density of S and I (mass action assumption) or proportional to S and the fraction of individuals that are infectious (frequency-dependent assumption). Considerations of the impacts of interventions, such as treatment, are included by modifying the various rates in appropriate ways. Thus, for example, one can reduce the transmission rate by isolating infectious individuals or reducing the infectious period by treating individuals.

Numerical simulation of epidemics for any of approaches i)-v) requires the generation of appropriate computer code and a software platform for its implementation. For scientists with limited or no coding experience, Numerus Model Builder (NMB) provides a graphically-driven platform that facilitates rapid, accurate, coding of the model using a hierarchical architecture and codechip design. The NMB platform has two independent components. The first is a set of tools accessed through a graphical user interface that is used to generate a NovaScript (extended JavaScript), which can be run in any suitable runtime environment.

NMB can be used to estimate model parameters; in our case the various rate parameters depicted in Figure 1, by finding the best fitting model to incidence data using least-squares or maximum-likelihood estimation methods. In our paper, we fitted a discrete-time deterministic version of our SEIVD model to the outbreak of Ebola viral disease in Sierra Leone in 2014 (Fig. 2). We found that if we had fitted the model to the first 10 weeks of incidence data, then at that stage of the outbreak, its severity would have been greatly over estimated. Interestingly, repeating this exercise on the first 20 and then 30 weeks of incidence data respectively underestimated and then overestimated the severity of the outbreak. Only when fitting to 40 weeks of incidence data did the model provide a good fit to the remaining period of an outbreak that lasted just over a year.

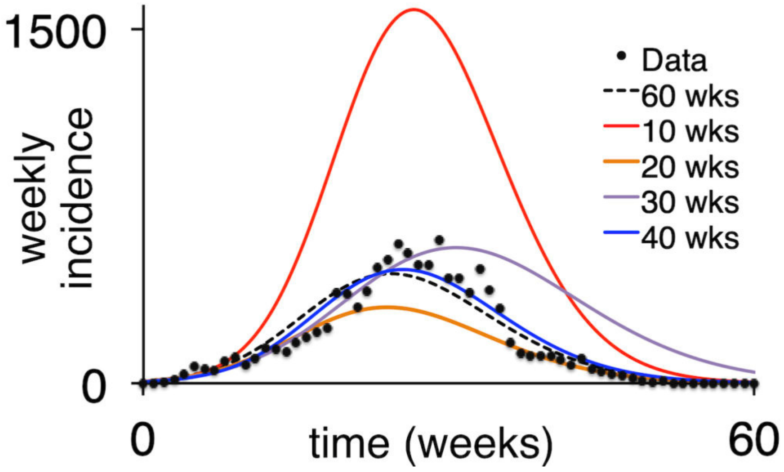

Fig. 2. The black dotted line is a maximum-likelihood (ML) fit to 60 weeks of incidence data from the 2014 outbreak of Ebola viral disease in Sierra Leone. The red, orange, purple and blue plots, simulations were obtained after finding the best ML estimates of model parameters to the first 10, 20, 30 and 40 weeks of weekly incidence respectively. Details of how to build and fit the models to data using NMB are explained in videos that can be accessed through links at the publications supporting website. Also see the NMB website a numerusinc.com for more information.

One conclusion of our study was that SEIVD models remain an important tool for managing epidemics, provided we treat predictions from such models with circumspection. To this end, we demonstrated that NMB provides a tool that allows non-expert coders to explore the behavior and response-to-interventions of SEIVD-elaborated systems in ways previously open only to those trained to code models themselves.

Wayne Marcus Getz
Department of Environmental Science, Policy and Management
University of California at Berkeley, USA

Publication

Modeling epidemics: A primer and Numerus Model Builder implementation.
Getz WM, Salter R, Muellerklein O, Yoon HS, Tallam K
Epidemics. 2018 Dec