Project 2: Environmental Heterogeneity in Zoonotic Infectious Diseases

Zoonotic infectious diseases are spread from animals to humans. It is estimated that over 60% of human infectious diseases are zoonotic and 75% of them are emerging zoonoses. The majority of emerging zoonotic infectious diseases are caused by viruses including avian influenza virus, Ebola virus, rabies virus, severe acute respiratory syndrome coronavirus-1 (SARS-CoV-1), SARS-CoV-2, Middle East respiratory syndrome coronavirus (MERS-CoV), West Nile virus, Nipah virus, Hendra virus and hantaviruses. A zoonotic spillover occurs when the pathogen from an infected animal host enters a human host, either directly from a natural reservoir, an intermediate animal host or indirectly from virus in the environment. Avian influenza often spills over to humans from an intermediate host (domestic poultry) rather than from the natural reservoir (waterfowl including ducks and geese). For hantaviruses, spillover into humans generally occurs through contact with infected excreta from the natural reservoir, such as rats, mice or voles. Animal reservoirs vary considerably, but bats and rodents are the majority of natural reservoirs for viral zoonoses originating in the wild. The natural reservoirs for rabies virus, coronaviruses, Ebola virus, Nipah virus and Hendra virus are bats.

Environmental factors, such as seasonal variations in temperature, humidity or rainfall impact the contact rate, individual behavior and the spread of zoonotic infectious diseases. Susceptible-infectious-recovered (SIR) epidemic models for animals and humans are a simple framework for development of stochastic models with environmental heterogeneity. In Figure 1, the subscripts a and h denote animals and humans, respectively. A stochastic model formulation accounts for both demographic and environmental variability. In a continuous-time Markov chain (CTMC), the random variables are discrete-valued, $S_a, I_a, R_a \in \{0, 1, \ldots, N_a\}$ and $S_h, I_h \in \{0, 1, \ldots, N_h\}$, and the events of transmission or recovery occur with a given probability that depends on the number of susceptible and/or infectious individuals.

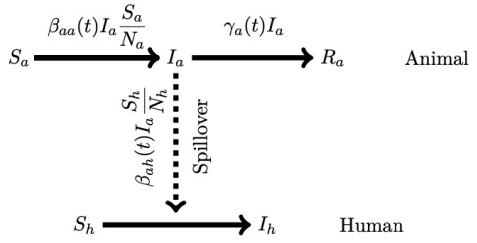

Figure 1: Compartmental diagram of the SIR spillover from an animals to humans.

CTMC models and methods from branching processes will be used to approximate the probability of spillover of infection from animals to humans and to estimate the probability of a disease outbreak in a population. From Figure 1, a spillover from animals to humans during a small interval of time Δt occurs with approximate probability

$$\mathbb{P}\{(\Delta S_a, \Delta I_a, \Delta S_h, \Delta I_h) = (0, 0, -1, 1) | (S_a, I_a, S_h, I_h)\} = \beta_{ah}(t) I_a S_h \Delta t / N_h.$$

For the disease to continue spreading within the human population and resulting in an outbreak depends on human-to-human transmission. Estimates for probability of human spillover and the probability of a disease outbreak can help identify times of greatest risk for human infection. Some references: [1, 2, 3, 4, 5].

Timeline: Week 1: Background information on zoonotic diseases, mathematical and computational methods with problem solving, computer training in Maple/MatLab and discussions. Weeks 2-3: Search for appropriate data and biological information on zoonotic diseases from the literature to formulate a stochastic model for a specific zoonotic infectious disease. Also, identify relevant questions to address with the model and data. Weeks 4-6: Mathematical analyses, development of computer codes and simulation of new stochastic zoonotic infectious disease models. Weeks 7-8: Verify analytical and numerical results, summarize findings, interpret results and write a paper.

References

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