Biomathematics Seminar Series
Department of Mathematics and Statistics

Graduate Student Mini Poster Session
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Aadrita Nandi
The Impact of Population Heterogeneity in Stochastic Models on the Emergence or Re-emergence of Infectious Diseases

Krystin E. Steelman Huff
Modeling the Early Clinical Progression of Hantavirus Pulmonary Syndrome

Md Rafiul Islam
Dynamics of the Emerging Fungal Pathogen *Batrachochytrium salamandrivorans* on the Eastern Newt
**The Impact of Population Heterogeneity in Stochastic Models on the Emergence or Re-emergence of Infectious Diseases**

*Aadrita Nandi*

Recent outbreaks of emerging diseases such as SARS or MERS or of re-emerging diseases such as measles or pertussis are often due to heterogeneity of the population in terms of infectivity potential or susceptibility. In the case of SARS or MERS, superspreaders, highly infectious individuals, were the major contributors to disease spread. However, in vaccine-preventable diseases, such as measles or pertussis, recent outbreaks have occurred in populations with a large proportion of susceptible individuals, where vaccine protection was low. Continuous-time Markov chain epidemic models are formulated that account for these two different types of heterogeneity. Theory from branching processes is used to approximate the probability of an outbreak when one infectious individual from a population subgroup is introduced into the susceptible population. Transmissibility and duration of infection as well as the amount of heterogeneity in the population impact the probability of an outbreak. The models are applied to recent outbreaks of MERS and measles.

**Modeling the Early Clinical Progression of Hantavirus Pulmonary Syndrome**

*Krystin E. Steelman Huff*

Hantavirus pulmonary syndrome (HPS) is a zoonotic infectious disease caused by infection of hantavirus, a virus transmitted by specific rodents. Infection with HPS has a mortality rate as high as 40%. A target-cell limited model describes the dynamics at the cellular level during the early stages of infection. This model is a system of ODEs with healthy cells, infected cells and free virus. When characterizing the clinical stages of HPS, some simplifying assumptions are made in the target-cell limited model. In particular, to compare with clinical data, the free viral level is assumed to be proportional to the number of infected cells. Calculations indicate that the progression of HPS using the simplified model is similar to the actual clinical progression. A sensitivity analysis of the simplified model indicates that the maximum infection level is sensitive to changes in initial infection, rate of infection, and time to immune response. A stochastic differential equation model of clinical HPS, where the infection rate satisfies a mean-reverting process, provides a better understanding of the clinical progression.
Dynamics of the Emerging Fungal Pathogen Batrachochytrium salamandrivorans on the Eastern Newt

Md Rafiul Islam

We developed and analyzed a stage-structured Susceptible-Infection (SI) type disease models for emerging fungal pathogen *Batrachochytrium salamandrivorans* (Bsal). Our models included two routes of pathogen transmission: direct transmission via contact between infected and susceptible individuals and environmental transmission via shed zoospores in the water. Unlike previous models, we categorized individuals into multiple stages of infection (susceptible, latency, and infectious). We found the invasion probability for Bsal (i.e., the basic reproductive number, $R_0$) into a population of the Eastern Newt. We performed numerical simulations and parameter sensitivity analysis using Latin hypercube sampling and partial rank coefficient correlation.