Stochastic model of emerging and re-emerging diseases in heterogeneous population

Aadrita Nandi[1] **Linda J. S. Allen**[1]

[1] *Texas Tech University, 2500 Broadway, Lubbock, TX, US, 79409*

aadrita.nandi@ttu.edu
linda.j.allen@ttu.edu

Emerging and re-emerging Infectious diseases are the biggest public health concern globally in the 21st century. Emerging diseases like SARS, MERS, Zika, etc. spillover from animals to humans. Re-emerging diseases like measles, pertussis, etc. had several outbreaks worldwide due to lack of vaccination or waning of vaccination. We have formulated a continuous time Markov chain model to study the probability, duration, and final size of outbreak. For emerging disease model of SARS, we considered that transmission depends on infectivity and divided the population in two groups, depending on their infectivity level. Transmission of measles depends on susceptibility for re-emerging diseases and the population was divided in two groups, depending on their immunity level. When comparing both models, probability of outbreak, duration, and final size shows significant differences. In both models, the probability of outbreak is different depending on which group initiated. Final sizes are also different for both models. Emerging disease model has much higher final size, as opposed to re-emerging disease model.

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