

MSIS-Robertson: A stochastic multi-host model for West Nile virus

Suzanne Robertson^{1*}, Emily B. Horton¹

¹*Department of Mathematics and Applied Mathematics, Virginia Commonwealth University, Richmond, VA 23184*
srobertson7@vcu.edu

West Nile virus (WNV) is a vector-borne disease spread primarily between birds and mosquitoes that exhibits high spatial and temporal variability. The species of hosts and vectors present in a location are known to have a large influence on disease dynamics. For deterministic ordinary differential equation models of WNV transmission, an outbreak occurs when the disease is introduced into a susceptible population if the basic reproduction number R_0 is greater than one. For a stochastic model, however, disease extinction events can occur even when R_0 is greater than one and outbreaks are not guaranteed. For diseases such as WNV with multiple types of infected individuals, the probability extinction occurs depends on how the disease enters the population. Here we present a Continuous-Time Markov Chain (CTMC) model for enzootic WNV transmission between two species of avian hosts and a single mosquito vector, derived from a corresponding deterministic model. We use multi-type branching process theory to compute the probability of disease extinction based upon the type of individual initially introducing the disease into the population (an exposed vector, infected vector, or infected host of either species). We explore how the probability of disease extinction varies with the competence of each host species, the vector biting rates on each host species, and the relative abundance of the host species, as well as the overall vector abundance. Theoretical predictions for the probability of disease extinction are compared to the outcome of stochastic simulations. We find that the community composition of hosts and vectors, along with the means of disease introduction, can greatly affect the probability of disease extinction.