The Impact of Demographic Stochasticity on Zika Virus Transmission Dynamics: Disease Extinction Probability, Sensitivity Analysis, and Mean First Passage Time BIOMATH 2024

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Zika virus (ZIKV) is a mosquito-borne virus that has become a worldwide concern, especially among women of childbearing age. We consider an established ZIKV transmission model in this investigation, which includes humanto-human, human-to-mosquito, and mosquito-to-human disease transmission mechanisms. We perform a sensitivity analysis to quantify the dependency of system behavior on the parameters that affect process dynamics. In this work, we use the CTMC process to develop and analyze a stochastic model that captures the random effects that occur during ZIKV transmission. The stochastic model predicts the possibility of disease extinction even though the deterministic model predicts a continuous infection without any prevention, which is the major difference between these two models. We found that the numerically estimated disease extinction probability agrees well with the analytical probability obtained from the Galton-Watson branching process (GWbp). It has been discovered that if the disease arises from infected mosquitoes, it has a higher probability of disease extinction than if it emerges from diseased people. We also looked at how model parameters affect disease extinction probability both locally and globally. In the context of the stochastic model, we derive the implicit equation of the mean first passage time, which computes the average amount of time needed for a system to undergo its first state transition. Finally, a graphic representation illustrates how the parameters affect the mean first passage time.

Keywords: Zika Virus (ZIKV); Basic Reproduction Number; Sensitivity Analysis; Prevalence; Continuous Time Markov Chain (CTMC); Galton-Watson branching process (GWbp); Mean First Passage Time (MFT)

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