Stochastic lattice model describing a vector-borne disease

Tânia Tomé, David R. de Souza, M. J. de Oliveira
Universidade de São Paulo

Suani R. T. Pinho, Florisneide R. Barreto
Universidade Federal da Bahia

We employ the approach of stochastic dynamics to describe the dissemination of vector-borne diseases such as dengue, and we focus our attention on the characterization of the threshold of the epidemic. The coexistence space comprises two representative spatial structures for both human and mosquito populations. The human population has its evolution described by a process that is similar to the Susceptible-Infected-Recovered (SIR) dynamics. The population of mosquitoes follows a dynamic of the type of the Susceptible Infected-Susceptible (SIS) model. The coexistence space is a bipartite lattice constituted by two structures representing the human and mosquito populations. We develop a truncation scheme to solve the evolution equations for the densities and the two-site correlations from which we get the threshold of the disease and the reproductive ratio. We present a precise definition of the reproductive ratio which reveals the importance of the correlations developed in the early stage of the disease. According to our definition, the reproductive rate is directed related to the conditional probability of the occurrence of a susceptible human (mosquito) given the presence in the neighborhood of an infected mosquito (human). The threshold of the epidemic as well as the phase transition between the epidemic and the non-epidemic states are also obtained by performing Monte Carlo simulations.
References: [1] David R. de Souza, Tânia Tomé, , Suani R. T. Pinho, Florisneide R. Barreto and Mário J. de Oliveira, Phys. Rev. E 87, 012709 (2013). [2] D. R. de Souza, T. Tomé and R. M. Ziff, J. Stat. Mech. P03006 (2011).