

An antibody and viral load vector-host dengue fever model

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Dengue fever is a viral infection transmitted from human to human by the *Aedes aegypti* mosquito. It is a significant global public health issue because of its expanding geographical spread and the consequent increase in the disease's incidence. There are different modeling approaches in dengue epidemiological studies in the literature, though we still encounter several challenges in realistic modeling. Some of these challenges include four virus serotypes, complicating the epidemiological dynamics, and the so-called antibody-dependent enhancement (ADE) can occur, in which pre-existing antibodies can enhance the new infection. In this study, we present a preliminary host-vector model, where pathogen transmission occurs through the interaction between vectors and hosts. The model takes into account both microscopic and macroscopic dynamics. The microscopic dynamics consider the viral load and the level of antibodies in the host to define new infections, while the macroscopic dynamics describe the disease transition through population compartments. We present analytical and numerical results for our proposed model with a focus on a single dengue serotype, showing that it represents the expected dynamics of dengue infections.

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