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## A reaction-diffusion model to investigate the spread of Aedes

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In this work, we developed a reaction-diffusion mathematical model to describe the spread of dengue infection in a two-dimensional domain. In our mathematical model, we took into account the interaction between the populations of dengue mosquitoes and humans. In the case of humans, the population was divided into susceptible  $(H_S)$ , infected  $(H_I)$  and recovered  $(H_R)$ , according to the epidemiology of the disease. Winged mosquitoes can be infected  $(M_I)$  or uninfected (susceptible)  $(M_S)$ , considering that the life of the vectors is not long enough to the recovery of an infection. Moreover, a compartment for the aquatic phase of mosquitoes was considered. We assumed that there was no ongoing immigration of infected humans and the circulation of a single serotype of dengue.

The local characteristics are expressed in the model by parameters of the transmission of disease and by the invasion of *Aedes aegypti*, as described in [4]. The temperature can affect transmission dynamics, influencing rates of development and mortality of immature mosquitoes, as well as the number of eggs deposited, conform [9, 10]. The dependence of the ovipositional rate on the temperature can be modeled considering the values of ovipositions published in [11], making it possible to define scenarios for the disease considering different temperatures. In addition, environmental carrying capacity and mosquito mortality rates may vary, depending on the local rainfall and the temperature, as described in [2].

Access accepting eggs are extremely resistant to the dry season. In cases where there are favorable conditions to their development, the eradication may be considered impossible [8]. Therefore, efficient mechanisms need to be found to control the disease, reducing the transmitting mosquito population [7]. In this context, we studied an optimal mechanical control over a large geographic region regarding only the education and sanitation campaigns in the mosquito compartment [1,3,6], in order to analyze the dynamics of both mosquito and human populations.

We aimed to understand how the disease spreads from a specific location to another, considering the diffusion coefficients of both infected populations, mosquitoes and humans. Our contribution provides an in-depth analysis of the optimal control problem and it outlines a more explicit modeling framework based on real spatial-temporal data, available at [5]. We compared the focus of the control between the whole vector population and aquatic phase to draw conclusions on the investment effect in each case.

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