A Simulation Model with Community Structure for the Dengue Control

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Abstract

Dengue is an infectious disease with a great impact in tropical and sub-tropical regions, particularly at the Quindío (Colombia). This disease generates a cost overrun in the health care institutions. We propose the implementation of a mathematical tool for the entomological and epidemiological analysis of the Dengue. A simulation model accounting for three random endemic communities has been analyzed. Prophylactic and chemical controls of the mosquito population are used. Finally, it is treated the time evolution of the basic reproduction number using the EpiEstim book of the statistical R software. We have used epidemiological data of Armenia-Quindio from 2012 to 2013.

Keywords: Dengue, Mathematical model, Dynamic systems, Prevention.

1 Introduction

Dengue is a flavivirus that may be transmitted by the vector-mosquito (*Aedes aegypti*) in different tropical and sub-tropical areas. Although some people may be asymptomatic, almost all infected people presents symptoms like: high fever, headache, skin rashes, myalgia, and arthralgia. Each year, approximately 390 millions of persons are infected. Yet, it does not exist a vaccine nor

an efficacious treatment against this disease. That is why, Dengue is considered a public health problem. So then, there exist a massive effort to construct warning systems using statistical techniques and mathematical models. These ones are devoted to understand the disease propagation, incidence, and the infection dynamics in certain entities. Making possible the quickly handling of the disease, avoiding the virus propagation as well as the population mortality [2, 14].

Several mathematical models based in ordinary differential equations, partial differential equations, intregro-differential equations, complex systems, and topological lattices have been reported [7, 16, 11, 8, 13, 9]. Also, mathematical models have been constructed including some climatic factors, as the temperature [15, 1, 6, 12, 4, 5, 10].

2   Model

The mosquito and human populations are involved in the propagation dynamics of the Dengue virus. Geographic expansion in the Quindío generates mobility among several communities, this fact conduces to an influence in the population dynamics due to interactions among communities.

Considering the above statements, we have proposed a mathematical SIR-like model with community structure and without demographic data for the Dengue dynamics in three municipalities of the Quindío, $j = 1, 2, 3$.

The variables and parameters of the model are: x_1^j: average number of susceptible people of the community j, x_2^j: the average number of infected people of the community j, y_1^j: is the average number of non-infected mosquitoes in the community j, y_2^j: average number of virus-carrier mosquitoes in the community j, z^j: average number of immature stages (eggs, larvae, pupa) in the community j, β^j: the probability of virus transmission from mosquitoes to humans in the community j, σ: the preventive measures against the Dengue disease, θ: the infected people recovery rate, α: the infected people mortality rate, η: developing rate of the immature stages to the mature ones, δ^j: probability of virus transmission from humans to mosquitoes in the community j, ϵ: the natural mortality rate of the mature mosquitoes, ω: mortality rate of mosquitoes by chemical control, ϕ: the oviposition rate of the mature stages, K^j: the charge capacity of the mosquito breeding places in the community j, and π: the immature mosquitoes mortality rate.

The non-linear ordinary differential equations that play the dynamics are:

$$\frac{dx_1^j}{dt} = -\frac{y_2^j}{M^j}(1-\sigma)\sum_{i=1}^{3}\beta^j x_1^i \tag{1}$$

$$\frac{dx_2^j}{dt} = \frac{y_2^j}{M^j}(1-\sigma)\sum_{i=1}^{3}\beta^j x_1^i - (\theta+\alpha)x_2^j \tag{2}$$

$$\frac{dy_1^j}{dt} = \eta z^j - \delta^j\frac{x_2^j}{N^j}y_1^j - (\epsilon+\omega)y_1^j \tag{3}$$

$$\frac{dy_2^j}{dt} = \delta^j\frac{x_2^j}{N^j}y_1^j - (\epsilon+\omega)y_2^j \tag{4}$$

$$\frac{dz^j}{dt} = \phi(y_1^j+y_2^j)\left(1-\frac{z^j}{K^j}\right) - (\pi+\eta)z^j \tag{5}$$

with $N^j = x_1^j + x_2^j$ and $M^j = y_1^2 + y_2^j$.

3   Results and conclusions

We have done all simulations with the ode45 package of the MATLAB code. From this Figure, we can observe that the infected people population tends
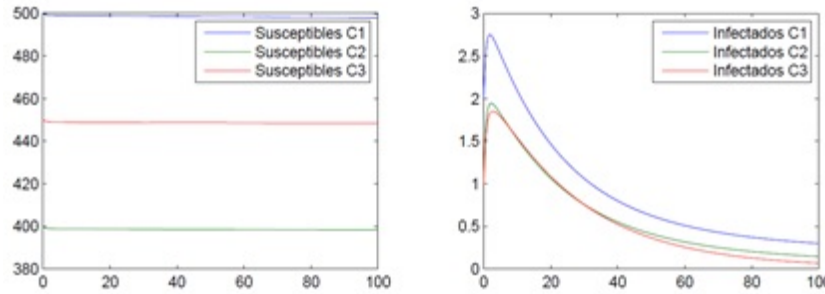

Figure 1: Behavior of the mosquito communities with $\sigma = 0$ and $\omega = 0$.

to achieve fractional values in all communities. This behavior may be understood as a tendency to the extinction of these populations as function of the time. This fact is a direct consequence of the probability of virus transmission from mosquitoes to humans, which is too low (0.02, 0.02, and 0.001 for the first, second, and third community, respectively). The probabilities are not equal to account for different mosquito and human populations. For instance, in a community with more mosquitoes than humans, the probability of virus transmission is higher. Also, we have considered different environmental conditions for each community. In a similar way, it could be understood the carrier mosquito population behavior, where it is evident a trend to small
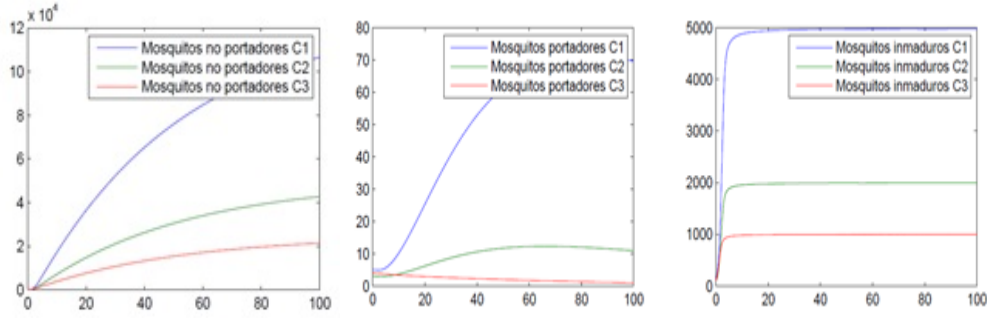
Figure 2: Behavior of the mosquito communities with $\sigma = 0$ and $\omega = 0$.

values of virus-carrier mosquitoes. We also have considered the probability of virus transmission from humans to mosquitoes in all communities.   These
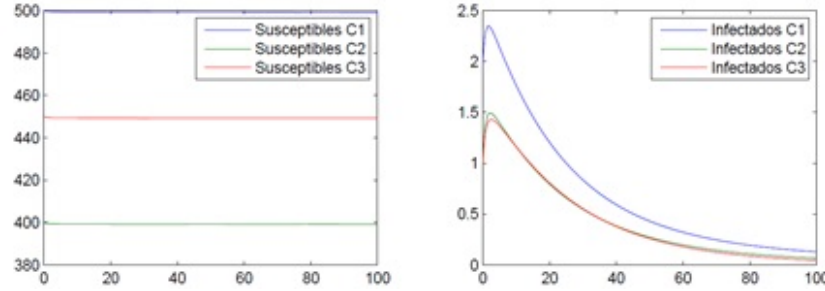

Figure 3: Behavior of the mosquito communities with $\sigma = 0.5$ and $\omega = 0$.
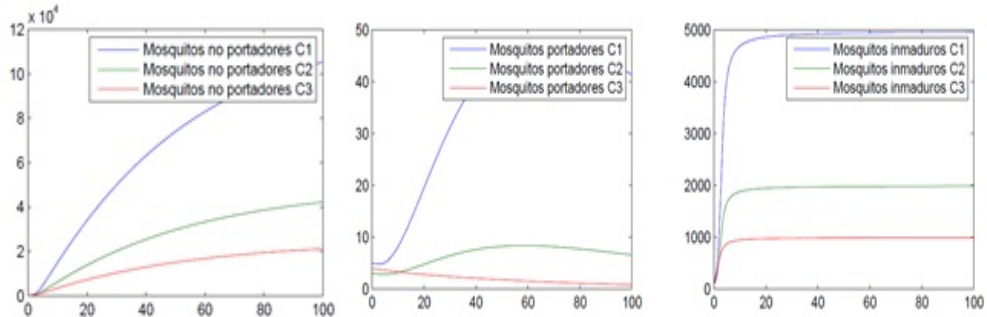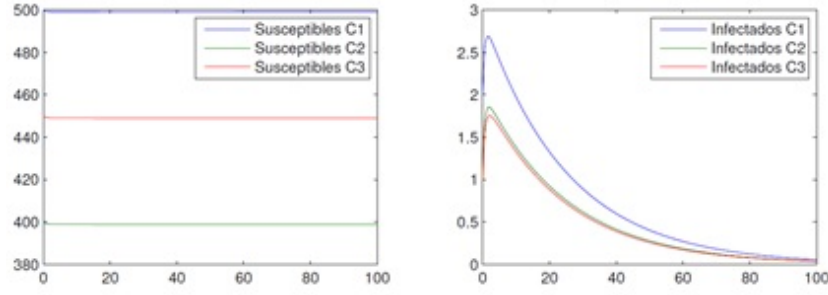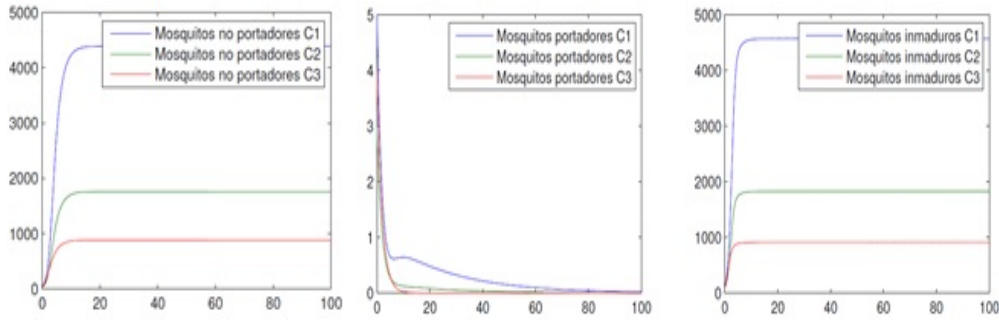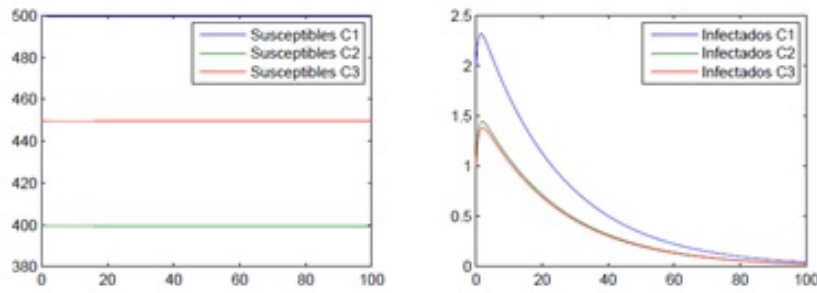

Figure 4: Behavior of mosquito communities with $\sigma = 0.5$ and $\omega = 0$.

simulations show a similar behavior as the one depicted in the previous figure. In this case, it is evident a decrease in the population dynamics of the infected people as consequence of the preventive measures against Dengue ($\sigma = 0.5$). An important decrease of the virus-carrier mosquitoes population is shown in this simulation, with a trend to be extinguished over time because of the chemical control applied to the mature stages.

Figure 5: Behavior of the mosquito communities with $\sigma = 0$ and $\omega = 0.5$.

Figure 6: Behavior of the mosquito communities with $\sigma = 0$ and $\omega = 0.5$.

Application of preventive measures and chemical control to the mature stages generates a decrease in the infected people population as well as in the virus-carrier mosquitoes population. We can observe that even after application

Figure 7: Behavior of the mosquito communities with $\sigma = 0.5$ and $\omega = 0.5$.

of these controls, the susceptible people population remains unaffected (as expected). However, such measures generate changes in other populations as following:

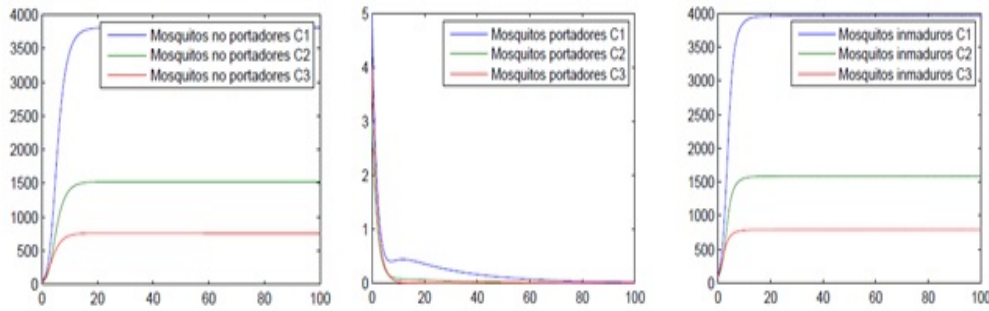- The size of the infected people population in all communities decreases

Figure 8: Behavior of mosquito communities with $\sigma = 0.5$ and $\omega = 0.5$.

after application of preventive measures against Dengue.

- The dynamics of different mosquito populations presents a decrease in all communities when chemical control to the mature stages is applied. Principally, in the virus-carrier mosquitoes population, where the population size decreases drastically.
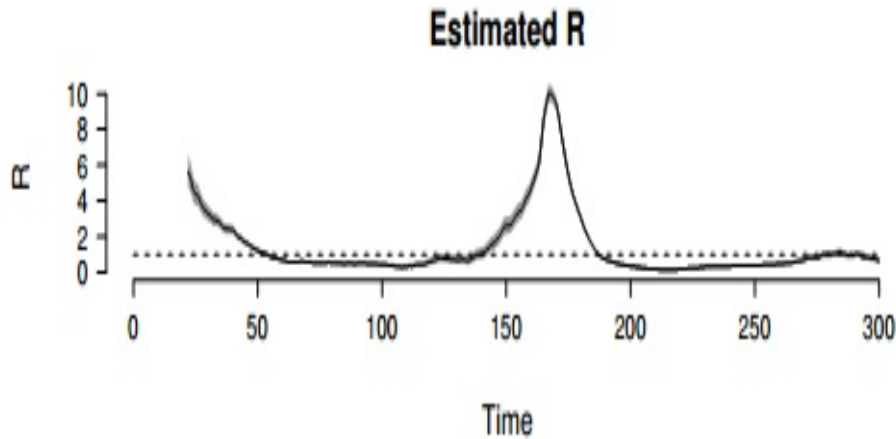

Figure 9: Time-dependent evolution of R_0.

We also can note that the size of all populations in the community 1 are above the size of populations in the community 2, at the same time, this one is above the size of community 3. This fact may emerge since in the simulations are considered different population sizes. Moreover, we expected different sizes in the mosquito population for all communities.

We have estimated the basic reproduction number using the R software by means of the EstimateR function of the EpiEstim book, with emphasis in the

NonParametricSi methods [15].

From the previous figure we observe that R_0 is always higher than 1, indicating a constant presence of Dengue, without possibility to be extinguished over time. Furthermore, there exists an outbreak between the 150 and 180 week, being this time where the virus presents a highest degree of infection in the population. Finally, it is very important to encourage the intervention of the health care institutions to control the virus propagation in the population.

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