

Seasonality effects on Dengue

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Abstract

Dengue is a vector-borne disease transmitted from an infected human to an *Aedes* mosquito, during a blood-meal. A model for dengue disease transmission is presented, composed by human and mosquitoes compartments. The aim of this work is to simulate the effects of seasonality, on the vectorial capacity. Using entomological information about the mosquito behavior under different temperatures, simulations were carried out and the repercussions on the disease transmission were analyzed.

Key words: Dengue; vectorial capacity; seasonality
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1 Introduction

Dengue is a mosquito-borne viral infection that is usually found in tropical and sub-tropical regions around the world. It is a vector-borne disease transmitted by *Aedes aegypti* and *Aedes albopictus*. There are four different serotypes that can cause dengue fever. A human infected by one serotype, when recovered, has total immunity for that one, and only have partial and transient immunity for the other three serotypes.

Unfortunately, there is no specific treatment for dengue. Activities, such as triage and management, are critical in determining the clinical outcome of dengue. Although there

is no effective and safe vaccine for dengue, a number of candidates are undergoing various phases of clinical trials [17].

The life cycle of the mosquito has four distinct stages: egg, larva, pupa and adult. The first three stages take place in water, whilst air is the medium for the adult stage. In urban areas, *Aedes aegypti* breeds on water collections in artificial containers such as cans, plastic cups, used tires, broken bottles and flower pots. With increasing urbanization and crowded cities, environmental conditions foster the spread of the disease that, even in the absence of fatal forms, breed significant economic and social costs (absenteeism, immobilization, debilitation and medication) [2].

Temperature and rainfall are a key environmental determinant in shaping the landscape of dengue. Since temperature influences greatly the vector's survive and transmission capability of dengue virus, it is important to create distinct simulations to predict the effects on the disease transmission [9, 10, 15].

2 The mathematical model

Taking into account the model presented in [3, 4] and the considerations of [12, 13, 14], a mathematical model is here proposed. It includes three epidemiological states for humans:

- $S_h(t)$ — susceptible (individuals who can contract the disease);
- $I_h(t)$ — infected (individuals who can transmit the disease);
- $R_h(t)$ — resistant (individuals who have been infected and have recovered).

These compartments are mutually-exclusive. There are two other state variables, related to the female mosquitoes (male mosquitos are not considered because they do not bite humans and consequently do not influence the dynamics of the disease):

- $S_m(t)$ — susceptible (mosquitoes that can contract the disease);
- $I_m(t)$ — infected (mosquitoes that can transmit the disease).

In order to make a trade-off between simplicity and reality of the epidemiological model, some assumptions are considered:

- there is no vertical transmission, *i.e.*, an infected mosquito cannot transmit the disease to their eggs;
- total human population N_h is constant: $S_h(t) + I_h(t) + R_h(t) = N_h$ at any time t ;
- the mosquito population is also constant, *i.e.*, $S_m(t) + I_m(t) = N_m$;
- the population is homogeneous, which means that every individual of a compartment is homogeneously mixed with the other individuals;

- immigration and emigration are not considered during the period under study;
- homogeneity between host and vector populations, that is, each vector has an equal probability to bite any host;
- humans and mosquitoes are assumed to be born susceptible.

The system of differential equations is composed by

$$\begin{cases} \frac{dS_h(t)}{dt} = \mu_h N_h - \left(B\beta_{mh} \frac{I_m(t)}{N_h} + \mu_h \right) S_h(t) \\ \frac{dI_h(t)}{dt} = B\beta_{mh} \frac{I_m(t)}{N_h} S_h(t) - (\eta_h + \mu_h) I_h(t) \\ \frac{dR_h(t)}{dt} = \eta_h I_h(t) - \mu_h R_h(t) \end{cases} \quad (1)$$

coupled with

$$\begin{cases} \frac{dS_m(t)}{dt} = \mu_m N_m - \left(B\beta_{hm} \frac{I_h(t)}{N_h} + \mu_m \right) S_m(t) \\ \frac{dI_m(t)}{dt} = B\beta_{hm} \frac{I_h(t)}{N_h} S_m(t) - \mu_m I_m(t) \end{cases} \quad (2)$$

and subject to initial conditions

$$\begin{aligned} S_h(0) &= S_{h0}, & I_h(0) &= I_{h0}, & R_h(0) &= R_{h0}, \\ S_m(0) &= S_{m0}, & I_m(0) &= I_{m0}. \end{aligned}$$

The dengue epidemic model makes use of the parameters described in Table 1. In this study three simulations were considered, related to distinct vectorial capacity. Temperature affects the behavior of vector: its population, biting rate, biting capacity, incubation time, daily survival probability or mortality rate, and eggs hatching rate [16]. We only assume differences on transmission capacities and mosquito lifespan. The different values presented for scenarios 1 and 2 are based on [10]. The first one is concerned with a region where the mean temperature is 14°C. The second one is related to a region where the mean temperature is 26°C. The third scenario is created to simulate mild climate. The authors had previously analyzed the outbreak that occurred in Madeira Island, that have a mean temperature between 18°C and 24°C, all over the year. The values used in this last scenario are based on paper [14].

2.1 Numerical experiments

The software used in the simulations was `Matlab`, with the routine `ode45`. This solver is based on an explicit Runge-Kutta (4,5) formula, the Dormand-Prince pair. That means the numerical solver `ode45` combines fourth and fifth order methods, both of which are similar

Table 1: Parameters in the epidemiological model (1)–(2)

Parameter	Description	Range of values in literature	Value scenario 1	Value scenario 2	Value scenario 3	Source
N_h	total population		112000	112000	112000	[8]
N_m	total mosquito population		$3 \times N_h$	$3 \times N_h$	$3 \times N_h$	[8]
B	average daily biting (per day)		1/3	1/3	1/3	[5]
β_{mh}	transmission probability from I_m (per bite)	[0.1, 1]	0.12	0.99	0.2	[5, 10]
β_{hm}	transmission probability from I_h (per bite)	[0.1, 1]	0.11	0.95	0.2	[5, 10]
$1/\mu_h$	average lifespan of humans (in days)		$\frac{1}{79 \times 365}$	$\frac{1}{79 \times 365}$	$\frac{1}{79 \times 365}$	[8]
$1/\eta_h$	average viremic period (in days)	[1/15, 1/4]	1/7	1/7	1/7	[1]
$1/\mu_m$	average lifespan of adult mosquitoes (in days)	[1/45, 1/8]	0.04	0.03	1/15	[6, 7, 10, 11]

to the classical fourth order Runge-Kutta method. These vary the step size, choosing it at each step an attempt to achieve the desired accuracy.

In this section we examine simulations of system (1)–(2) with the following initial values for differential equations:

$$S_h(0) = 111991, \quad I_h(0) = 9, \quad R_h(0) = 0, \\ S_m(0) = 111900 \times 3, \quad I_m(0) = 1000.$$

Figures 1 to 3 are related to the infected human in the three scenarios, respectively. As expected, Figure 2 presents more infected people. Besides, is also this scenario that reaches the peak of the disease faster, while the third simulation has its higher transmission after 200 days. A situation like this, allows to have time to prepare the fight of the disease, in terms of control measures and medical surveillance.

2.2 Mathematical model with seasonal variation of mosquito

In this subsection, we study the effect of rainfall on the pattern of mosquito reproduction and hence the number of mosquitoes. In this way, we maintain all the assumptions given, except assuming that birth and death rates are equal over time. We incorporate the seasonal effect in the modeling of transmission of the virus, allowing that the total number of mosquitoes varies periodically with time.

Following [9], we include this seasonal pattern in system (1)–(2) by changing the birthrate of mosquitoes to a periodic function

$$\mu_m \left(1 + \alpha \cos \left(\frac{2\pi t}{365} \right) \right) \tag{3}$$

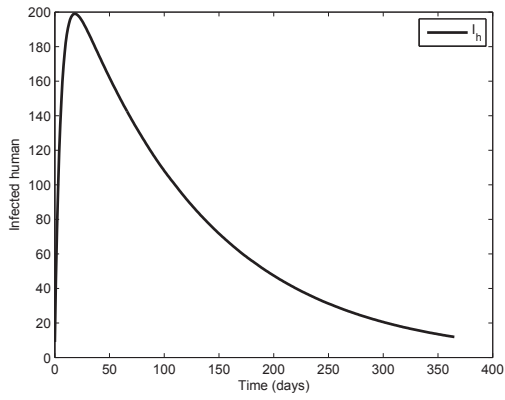


Figure 1: Infected human in scenario 1

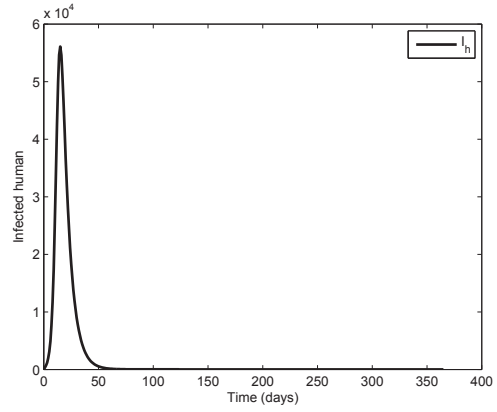


Figure 2: Infected human in scenario 2

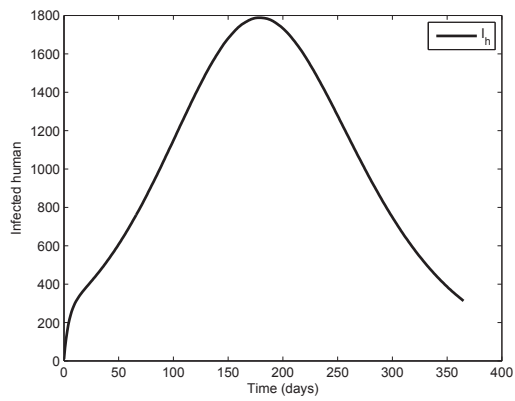


Figure 3: Infected human in scenario 3

where μ_m is the per capita death rate of mosquitoes and α is the amplitude of the seasonal variation, with $0 < \alpha < 1$. So, the differential equation (2) related to the susceptible mosquitos is transformed into

$$\frac{dS_m(t)}{dt} = \mu_m \left(1 + \alpha \cos \left(\frac{2\pi t}{365} \right) \right) - \left(B\beta_{hm} \frac{I_h(t)}{N_h} + \mu_m \right) S_m(t). \tag{4}$$

For numerical experiments, we considered $\alpha = 0.3$. In this way, the mosquito reproduction is lowest around 190 days after the beginning of the year.

Figures 4 to 6 present these simulations: with solid line is showed the situation described in subsection 2.1 with all the parameters fixed; in dashed line is represented the simulation with the periodic function. In all situations, the simulations with the seasonal pattern have conducted to more infected people. In scenario 1, the peak of the disease with the periodic function reached after the fixed one, while in scenario 3 the situation is reversed.

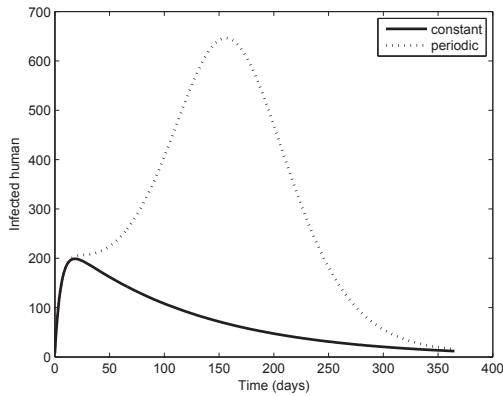


Figure 4: Infected human in scenario 1

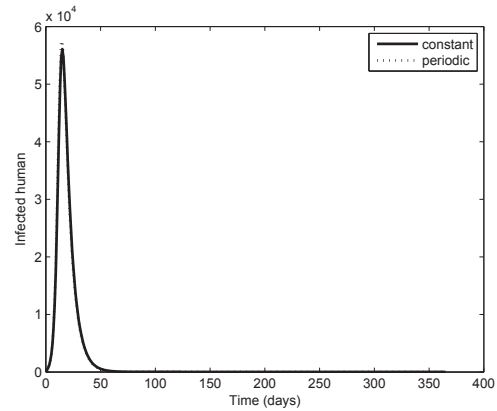


Figure 5: Infected human in scenario 2

3 Conclusion

Temperature and rainfall can be either an effective barrier or a facilitator of vector borne diseases. As climate changes over the last few decades, the ambient temperature increase has possibly contributed to the drastic increase of the dengue cases. In this paper we showed that small changes in the parameters of the model, related to vectorial competence, can provoke great changes in the study of dengue disease. In most regions where the disease is present, there is at least two seasons, with distinct temperature and humidity. In this way, a periodic function that allows to fit the mosquito population along the year, can be an interesting tool to the design of mathematical models.

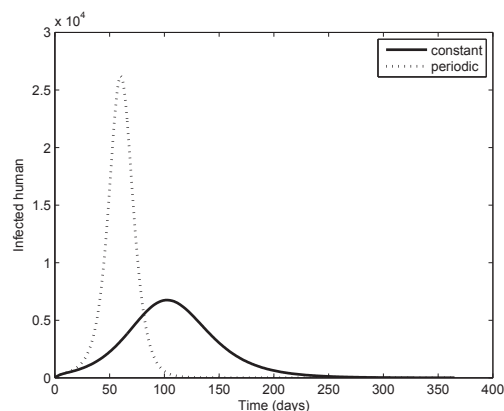


Figure 6: Infected human in scenario 3

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