

Utilization of environmental and epidemiological indicators in the study of malaria dynamics

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ABSTRACT

This paper aims to analyze the behavior of malaria transmission in the Amazon region based on climatic and environmental changes, such as temperature, precipitation and deforestation, through proposed modifications to the SIR and SEI models, in order to contribute to the study of applications of external effects on the evolution of the disease. The Trajetórias Project, developed by the Synthesis Center on Biodiversity and Ecosystem Services (SinBiose/CNPq) was used as an initial reference for the study. This work employs a modified SIR/SEI methodology, based on work from Parham and Michael (2010) which takes into account rainfall and temperature, with further modifications to avoid delay equations. Primary results show that the model is too sensible on some parameters, and using values indicated by other papers did not give the same results, opening up future work to compare the modified model equations with the originals. With the obtained results, it was possible to verify a strong effect caused by increased contact of host and vectors on the transmission of the disease.

1. Introduction

The Amazon is one of the largest and most biodiverse tropical forests in the world, harboring numerous species of plants, animals, and microorganisms, including vectors and pathogens responsible for the transmission of various diseases. Among them, one of the most common is malaria, caused by protozoa of the genus *Plasmodium*, transmitted by the bite of the infected female mosquito of the genus *Anopheles*. It is present in 22 American countries, but the areas with the highest risk of infection are located in the Amazon region, encompassing nine countries, which accounted for 68% of infection cases in 2011 [1]. Although malaria is prevalent in the Americas, it is not limited to this continent and is found in countries in Africa and Asia, resulting in more than two million cases of infection and 445,000 deaths worldwide in 2016 [2].

Notably, vector-borne disease transmission is closely related to environmental changes that interfere with the ecosystem of both transmitting organisms and affected organisms. In the case of the Amazon, agricultural and livestock settlements are among the factors that most favor disease transmission, both due to the deforestation they cause for establishment and the clustering of people in environments close to the vector's habitat [3], especially by clustering non-immune migrants near these natural and artificial breeding sites [4].

Additionally, other factors such as rainfall, wildfires, and mining also significantly influence disease transmission in the region. These events result in habitat loss, ecosystem fragmentation, and climate changes, affecting the distribution and abundance of vectors and hosts, as well as their interaction with pathogens. Furthermore, population growth

and urbanization also play a crucial role in disease spread, increasing human exposure to vectors and infection risks.

In this context, this work aims to investigate vector-borne disease transmission in the Amazon and analyze how environmental impacts influence the dynamics of malaria transmission, the ecological and socioeconomic factors affecting this spread, and possible prevention and control strategies. The main reference for this research is the Trajetórias Project, developed by the Center for Biodiversity and Ecosystem Services (SinBiose/CNPq), which is a dataset including environmental, epidemiological, economic, and socioeconomic indicators for all municipalities in the Legal Amazon, analyzing the spatial and temporal relationship between economic trajectories linked to the dynamics of agrarian systems, whether they are family-based rural or large-scale agricultural and livestock production, the availability of natural resources, and the risk of diseases [5].

2. Model formulation


Based on previous work developed to model the transmission of malaria based on precipitation and temperature dynamics [6], we focus on two different sets of compartments: susceptible hosts (S_H), infected hosts (I_H), recovered hosts (R_H), susceptible vectors (S_M), exposed vectors (E_M) and infected vectors (I_M). The equations that describe the transmission are given as:

$$\frac{dS_H}{dt} = -ab_2 \left(\frac{I_M}{N} \right) S_H \quad (1)$$

$$\frac{dI_H}{dt} = ab_2 \left(\frac{I_M}{N} \right) S_H - \gamma I_H \quad (2)$$

$$\frac{dR_H}{dt} = \gamma I_H \quad (3)$$

$$\frac{dS_M}{dt} = b - ab_1 \left(\frac{I_H}{N} \right) S_M - \mu S_M \quad (4)$$

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$$\frac{dE_M}{dt} = ab_1 \left(\frac{I_H}{N} \right) S_M - \mu E_M - ab_1 \left(\frac{I_H}{N} \right) S_M l(\tau_M) \quad (5)$$

$$\frac{dI_M}{dt} = ab_1 \left(\frac{I_H}{N} \right) S_M l(\tau_M) - \mu I_M \quad (6)$$

The parameters are given in Table A1, while the variables are given in Table A2, which can be found in the Appendix. The selected human population was from the rural area of Manaus, between the years of 2004 to 2008, as this locality had the highest incidence of malaria caused by *P. vivax* in the Amazon region [5]. This species of *Plasmodium* was chosen as it is responsible for the highest number of malaria cases in Brazil [8, 9]. With the incidence function [5] we have that

$$\text{Inc} = \frac{\text{Cases}(d, m, z, t_1, t_2)}{\text{Pop}(m, z, (t_1 + t_2)/2) \times 5 \text{ years}} \times 10^5, \quad (7)$$

where $\text{Cases}(d, m, z, t_1, t_2)$ is the number of cases of disease d in zone z of municipality m , and t_1 and t_2 are the initial and final years of the interval, while $\text{Pop}(m, z, (t_1 + t_2)/2) \times 5 \text{ years}$ is the population in zone z of municipality m in the middle of the period multiplied by the total number of observation years. In this case, we could indicate as:

$$\text{Inc}(\text{Vivax}, \text{Manaus}, \text{Rural}, 2004, 2008) = \quad (8)$$

$$= \frac{\text{Cases}(\text{Vivax}, \text{Manaus}, \text{Rural}, 2004, 2008)}{\text{Pop}(\text{Manaus}, \text{Rural}, 2006) \times 5 \text{ years}} \times 10^5 \Rightarrow \quad (9)$$

$$\Rightarrow 184030.8 = \frac{78745}{5\text{Pop}} \times 10^5 \Rightarrow \text{Pop} \approx 8558 \quad (10)$$

Using data on the total population of Manaus in this period, with an incidence of 3106.429047 and a number of cases of 262264, the total population of the municipality was estimated to be 1688524 inhabitants, which corresponds to the value found in the official census [10]. Thus, the rural population could be considered as approximately 0.5% of the municipality's population.

Having estimated the percentage size of the rural population in the city, it was possible to calculate this population for each of the years of the analysis through linear interpolation using historical series data from IBGE [11]:

Table 1
Manaus' rural population from 2004 to 2009.

Year	Estimated rural population
2004	7717
2005	7889
2006	8061
2007	8233
2008	8492
2009	8751

Given there was only population data for the years of 2000, 2007, and 2010, interpolations were performed with

different initial and final points, using data from 2000 to 2007 for 2004-2007 and from 2007 to 2010 for 2008-2009, ensuring the correct use of the 2007 population.

As for the theory behind environmental factors, according to [12], the removal of tree canopies allowed the resurgence of malaria in South America. In deforested areas, without tree canopies covering the ground, water puddles under sunlight attract mosquitoes of the species *Anopheles darlingi*, the main vector related to human malaria in the Amazon [13]. They are usually less commonly found in still intact forests. This is because light and heat favor the development of larvae and pupae, in addition to a greater availability of algae for larval feeding [14]. The increase in ambient temperature also favors the vectorial capacity of mosquitoes.

Deforestation also attracts and brings humans closer to take part in logging, agriculture, and road construction activities, bringing individuals infected with *Plasmodium* to an area where both the vector and the environment have already been modified to favor transmission. Furthermore, agriculture also promotes river sedimentation, providing suitable environments for breeding sites. Therefore, it can be considered a relevant change for the model to take into account deforestation, the increase in survival probabilities of eggs, larvae, and pupae, as well as increasing the proportion of bites that lead to infection, due to the increased human population density in areas near mosquito breeding sites.

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A. Appendix

Table A.1

List of model parameters.

Parameter	Definition	Formulation
$b(R, T)$	Mosquito birth rate (days^{-1})	$B_E p_E(R) p_L(R, T) p_P(R) / (\tau_E + \tau_L(T) + \tau_P)$
$a(T)$	Biting rate (days^{-1})	$(T - T_1) / D_1$
$\mu(T)$	Mosquito mortality rate per capita (days^{-1})	$-\log(p(T))$
$\tau_M(T)$	Duration of sporozoite cycle (days)	$DD / (T - T_{min})$
$\tau_L(T)$	Duration of larval development phase (days)	$1 / c_1 T + c_2$
$p(T)$	Daily mosquito survival rate	$e^{(-1 / (AT^2 + BT + C))}$
$p_L(R)$	Probability of larval survival dependent on rainfall	$(4p_{ML} / R_L^2) R(R_L - R)$
$p_L(T)$	Probability of larval survival dependent on temperature	$e^{-(c_1 T + c_2)}$
$p_L(R, T)$	Probability of larval survival	$p_L(R) p_L(T)$
$l(\tau_M)(T)$	Probability of mosquito survival during sporozoite cycle (days^{-1})	$p(T)^{\tau_M(T)}$
$M(t)$	Total population of mosquitos	$S_M(t) + E_M(t) + I_M(t)$
$N(t)$	Total population of humans	$S_H(t) + I_H(t) + R_H(t)$