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.

Keywords: Biological modelling, Malaria, Amazon, SIR, SEI

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].

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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:

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

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

$$\frac{dR_H}{dt} = \gamma I_H$$

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

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

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

The parameters are given in Table 1, while the variables are given in Table 2.

Table 1: List of model parameters.

Symbol	Description	Formulation
$b(R,T)$	Mosquito birth rate (day^{-1})	$\dfrac{B_E p_E(R) p_L(R,T) p_P(R)}{(\tau_E + \tau_L(T) + \tau_P)}$
$a(T)$	Biting rate (day^{-1})	$\dfrac{(T - T_1)}{D_1}$
$\mu(T)$	Mosquito mortality rate per capita (day^{-1})	$-\log(p(T))$
$\tau_M(T)$	Duration of sporozoite cycle (days)	$\dfrac{DD}{(T - T_{min})}$
$\tau_L(T)$	Duration of larval development phase (days)	$\dfrac{1}{c_1 T + c_2}$
$p(T)$	Daily mosquito survival rate	$e^{(-1/(AT^2 + BT + C))}$
$p_L(R)$	Probability of larval survival dependent on rainfall	$(\dfrac{4 p_{ML}}{R_L^2}) R(R_L - R)$
$p_L(T)$	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 (day^{-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	$S_H(t) + I_H(t) + R_H(t)$

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