



Research paper

# Time-spatial model on the dynamics of the proliferation of *Aedes aegypti*



Maury Meirelles Gouvêa Jr.\*

Polytechnic Institute, Department of Electrical Engineering, Pontifical Catholic University of Minas Gerais, Belo Horizonte, Brazil

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## ABSTRACT

Some complex physical systems, such as cellular regulation, ecosystems, and societies, can be represented by local interactions between agents. Then, complex behaviors may emerge. A cellular automaton is a discrete dynamic system with these features. Among the several complex systems, epidemic diseases are given special attention by researchers with respect to their dynamics. Understanding the behavior of an epidemic may well benefit a society. For instance, different proliferation scenarios may be produced and a prevention policy set. This paper presents a new simulation method of the time-spatial spread of the Dengue mosquito with a cellular automaton. Thus, it will be possible to create different dissemination scenarios and preventive policies for these in several regions. Simulations were performed with different initial conditions and parameters as a result of which the behavior of the proposed method was characterized.

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## 1. Introduction

Simulations are studies of real systems using models that can describe and understand the behaviors of real systems and/or to evaluate strategies for their operations [1]. Simulations can be performed in several areas, such as economics, biology, medicine, the social sciences, and computing science. There are several situations in which a simulation may be applied. For instance, when the process does not exist, when it is necessary to understand and analyze a real system, when tests in a real system are not possible, when a real system cannot be disturbed, or for training and education [2]. Using a simulation can offer several advantages, in cost and time, because it can be repeated at lower cost or can represent a long time period in seconds.

Some complex physical systems, ranging from micro systems, such as cellular regulation, to large organisms, such as ecosystems, the economy and societies, can be represented by local interactions between agents. Then, complex behaviors may emerge. A cellular automaton (CA) [3] is a discrete dynamic system with these features. A CA consists of cells that interact with each other, producing a global behavior which can vary from stable to chaotic.

Among the several complex systems, as cited above, epidemic diseases are given special attention by researchers with respect to their dynamics. Understanding the behavior of an epidemic, e.g. by simulation, may well benefit a society. For instance, the speed of proliferation, temporal and spatial, may be estimated. Thus, different proliferation scenarios may be produced and a prevention set, resulting first and foremost in saving lives but also in spending fewer public resources.

\* Corresponding author.

E-mail address: [maury@pucminas.br](mailto:maury@pucminas.br)

Epidemiology provides, by means of observing and analyzing epidemic phenomena, mathematical hypotheses which describe the dynamics of the transmission of infection. Thus, the evolution of epidemics can be studied, and this helps to set prevention and combat strategies [4–8].

In Brazil, some pathologies, such as Dengue, have spread in the form of an epidemic. Dengue is spread by the *Aedes aegypti* mosquito over wide areas. It is infectious and occurs especially in tropical areas [9,10]. Generally, epidemics occur in the summer, during or after rainy periods. Most Dengue infections are mild. However, in about 10% of cases, the disease progresses to dengue hemorrhagic fever, in which leaky blood vessels can, lead to death. Prevention is an important way to combat Dengue, and this is tackled by targeting the focus of stagnant water, where the mosquito breeds, and through setting out public health policies [11].

In general, classical epidemiology theory does not consider the spatial dimension of the transmission of a disease. Thus, this model assumes that infected individuals have the same probability of infecting those susceptible despite the distance between them [12]. Nor does this classical model consider the spatial distribution, which may be important to determine the proximity between individuals in order to start a new infection. Therefore, it is important to consider not only the time variation, but also the distance between individuals.

This paper presents a new simulation method of the time-spatial spread of the Dengue mosquito in a specific region with a cellular automaton. Thus, by using a spatial simulation, it will be possible to create different dissemination scenarios and preventive policies for these in several regions. Simulations were performed with different initial conditions and parameters as a result of which the behavior of the proposed method was characterized.

The rest of this paper is organized as follows. Section 3 introduces the cellular automata theory. Section 3 introduces general concepts of cellular automata. Section 4 the proposed method to simulate the spread of the Dengue mosquito. In Section 5, the results of the experiments which validate the proposed method are presented and discussed. Section 6 concludes the paper and suggests new implementations for future studies.

## 2. Related works

This section presents chronological studies on population model of *A. aegypti*. These studies try to describe the behavior of the population of mosquitoes. Esteva and Vargas [4,13] discussed a model for the transmission of dengue fever in a constant human population. The authors analyzed the results of the theory of competitive systems and stability of periodic orbits in order to establish the global stability of the endemic equilibrium. The control measures of the vector population are discussed in terms of the threshold condition, which governs the existence and stability of the endemic equilibrium. Esteva and Vargas created the human and vector population sizes. In the proposed model, the human population has constant size with birth and death rate constant. The mosquito population has a constant recruitment rate, independent of the actual number of adult mosquitoes. The proposed model is temporal described by the system of differential equations.

Bartley et al. [5] proposed a deterministic ordinary differential equation model of the transmission dynamics of 2 serotypes of dengue virus in the mosquito vector and human host population was developed. The authors analyzed of interactions between dengue serotypes. The model structure is used to explore the seasonal pattern of dengue infection. Empirical data were used to estimate model parameters and these data had been collected in Bangkok.

Otero et al. [6,14] have developed a stochastic model for *A. aegypti* populations based on the life cycle of the mosquito. The authors modeled the evolution of the populations in terms of six different subpopulations and ten random events with transition probabilities prescribed in terms of the biology of *A. aegypti* and the environment. The subpopulations consist of different phases of a mosquito during its growth: eggs, larvae, pupae, female adults not having laid eggs, flyers, and female adults having laid eggs. The evolution of the six subpopulations in each patch is affected by twelve different possible local events: death of eggs, egg hatching, death of larvae, pupation, death of pupae, adult emergence, completion of gonotrophic cycles, death of young adults, oviposition by flyers, death of adults, and death of flyers. Events occur at rates that depend not only on population values but also on temperature, which in turn is a function of time since it changes over the course of the year. The evolution of the populations is modeled by a Poisson process [15,16] where the probability of the state (subpopulations) evolves in time following a Kolmogorov forward equation.

Cruz et al. [8] investigated a natural transovarial infection of *A. aegypti* by a flavivirus, in the Jardim Industriário neighborhood of Cuiabá, Mato Grosso. The eggs were collected with ovitraps during the dry, intermediate, and rainy seasons of 2012. After the eggs hatched and the larvae developed to adulthood, mosquitoes were identified and allocated to pools of 1–10 specimens according to the collection location, sex, and climatic period. After RNA extraction, multiplex semi-nested RT-PCR was performed to detect the four dengue virus (DENV) serotypes, yellow fever virus, West Nile virus and Saint Louis encephalitis virus. The proposed study provides the first evidence of natural transovarial infection by DENV-4 in *A. aegypti*. These results emphasize the need for efficient vector population control measures to prevent arbovirus outbreaks in the state.

## 3. Cellular automata

A cellular automaton is formally defined as a discrete mathematical model, implemented in computers, automated by deterministic rules, and its conduct of an element within a homogeneous set will be based both on the state of its own attributes and those of the neighboring elements [3].

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