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Scenarios to Evaluate Techniques for Mollusks Collect in Schistosomiasis Disease Control using Cellular Automata

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Abstract

This article intends to present a proposal to modeling a Cellular Automata to compare two methods of collecting mollusks: one of them using Puçá, and the other one using a Metallic Shell. This modeling had become necessary during the malacological analysis performed on Carne de Vaca beach, north seaboard of Pernambuco/Brazil, between November of 2006 and October of 2007. The main goal is to demonstrate how a Cellular Automata can produce relevant data to prove that Puçá method can be more efficient than the method using the Metallic Shell. In spite of the model proposed in this article had not been tested exhaustively yet, it reproduces, in an accurate way, the patterns of Mollusks movement observed in the nature and illustrates that Puçá method is notably superior when compared with the Metallic Shell.

Keywords: Cellular Automata, Mollusks Collect, Modelling, Python

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1 Introduction

Schistosomiasis (also known as bilharzia) is a parasitic infection caused by Schistosoma flukes, which have complex life cycles involving specific freshwater snail species as intermediate hosts. Infected snails release large numbers of minute, freeswimming larvae (cercariae) that are capable of penetrating the unbroken skin of the human host. Even brief exposure to contaminated freshwater (e.g., during wading, swimming, or bathing) can result in infection. Human schistosomiasis cannot be acquired by contact with salt water (oceans or seas). However, the cercariae of birds and aquatic mammals can penetrate the skin of human beings who enter infested fresh or salt water in many parts of the world, including cool temperate areas. These cercariae die in the skin but may elicit a pruritic rash ("swimmer's itch" or "clam-digger's itch"). Organisms causing hepatic or intestinal schistosomiasis include Schistosoma mansoni, S. mekongi, S. intercalatum, and S. malayanensis. S. haematobium causes urinary schistosomiasis.

This infection occurs widely throughout the tropics and subtropics, affecting some 200 million persons. Schistosomiasis has been considered as a rural endemic disease. In the State of Pernambuco - Brazil - South America, migratory human movements from endemic areas to urban ones with precarious sanitary and environmental conditions, is being pointed out as responsible for expansion and transmission of schistosomiasis. The possibility that schistosomiasis mansoni could reach urban populations of high socio/economic background levels have been neglected. Researchers from CPqAM/FIOCRUZ have been investigated this expansion since 1996.

This work is a part of a larger project from CPqAM/FIOCRUZ (Centro de Pesquisas Aggeu Magalhes/Fundao Oswaldo Cruz) entitled "Eco-epidemiology of Esquistossomose in the Coastline of Pernambuco", which focuses on acute cases of schistosomiasis in coastal areas frequented by tourists and local holiday makers. For example, at the "Praia do Forte" beach on the island of Itamarac, 22 self-reported cases were diagnosed and at the "Praia do Porto" beach in Porto de Galinhas, 600 acute cases were registered, all with accidental exposure (Barbosa et al. 2001). Projects, such as this one, aim to map out and characterise sources and focii of schistosomiasis vectors, and to identify new sites of active transmission, correlating the biological determinants of the illness with the environmental context of their occurrence.

In this context, it becomes relevant to construct models for generating scenarios with a view to assisting the planning and strategic actions of control and prevention of this illness. In addition, this type of instrument not only allows optimised use of public re-sources, but it also provides an important tool for the scientific community studying the epidemiology of health problems.

In this paper, The seat of disease's vector snails and acute cases of schistosomiasis in litoral localities were identified through malacological surveys (collecting mollusks) performed on the coast of Pernambuco between 2006 and 2007 using two kinds of method: Puçá method (Figure 2) and method using the Metallic Shell (Figure 1).

The main goal is to demonstrate how a Cellular Automata can produce relevant



Fig. 1. Collecting Mollusks: method using the Metallic Shell



Fig. 2. Collecting Mollusks: Puçá method.

data to prove that Puçá method can be more efficient than the method using the Metallic Shell.

2 Modeling using Cellular Automata

A model can be seen as an approximate representation of some real problem, using a predetermined language (mathematics, logic, geography, physics, etc.) and in accor-dance with one or more theories. Models which use mathematical language are known as mathematical models, and can be represented by a combination of equations and/or expressions. Constructing a model allows the complexity of a real problem to be ana-lysed within a passive logical structure. In this way it is possible to show the results of alternative decisions, the effects previewed, relevant data noted, and various outcomes explored. Computational modelling consists of using abstract computational machines for gene-rating and inferring the rules when the system being modelled does not allow the ma-thematical equations and expressions to described with precision or even estimated. The use of computational modelling is accompanied by mathematical modelling once some of the behaviours of the object being modelled are completely characterised from a be-havioural and descriptive point of view.

Computation theory of Cellular Automata, which represent dynamic systems, where time and space are discrete, came to be used in the literature as computational models for simulation of objects including epidemiological phenomena.

Formally, cellular automata are defined as an evolution of the states of the cells of which they are composed. The state of a cell $\tau_i^t \in \{0, 1\}$ indicates that at a

position i at a time t the cell assumes one of a defined set of states, in this case 0 or 1. Assuming an N-dimensional network of cells, then we have an N-dimensional automaton. The evolution of the state of a cell is given by a function, here a rule of evolution is defined as

$$\tau_i^{t+1} = f(\tau_{i-k}^t, \dots, \tau_i^t, \dots, \tau_{i+k}^t),$$

where k is the index count of iterations. The evolutionary rule is applied simultaneously to all cells. The state of a cell at time t + 1 depends on the state of 2k + 1cells at time t; these other cells are called the cell's neighbours, ilustrated in Fugure 3.

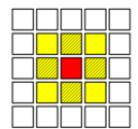


Fig. 3. Cellular automata cell and its neighbourhood

Such systems are able to generate varied solution spaces by setting different configurations of the initial conditions. In this way, it is possible with the assistance of specialists to filter the various scenarios in order to guarantee a degree of confidence in the responses of the model. Equally, when the conjunction of variables is too great, the degree of variation cannot work as a practical application if one wishes to plan strategically according to the response of the models. In addition the computational time required for simulation of such models becomes a restrictive aspect once the models become too complex.

3 The Model

A Cellular Automata has been used to generate the scenarios using the two collecting methods: Puçá method and method using the Metallic Shell. The system is represented by a grid of cells (simulating a hidric collection). The dynamic of the system depends of the interaction between the cells. Each cell represents a mollusk, and depending of its neighbourhood, can move for one if the nine cells (Moores neighbourhood). This model does not consider, dead and born of mollusks. In this case, the population in each simulation is constant. This does not influence the model because we are only interested into compare the two method.

3.1 Defining the variables

Consider:

N1: number of mollusks collected by PuçáN2: number of mollusks collected by Metallic ShellTa: number of neighbors above the MolluskTb: number of neighbors below the Mollusk

T1: number of neighbors at left sideTr: number of neighbors at right sideTn: total number of neighbors a Mollusk has

To represent movements of a Mollusks in a lake and the collect movement from Puçá and the Metallic Shell, it was used the Moore's Neighborhood, illustrated on picture 3; the iteration rules are illustrated on picture 4, where the neighborhood is represented by their coefficients and the Mollusk by a \mathbf{X} .

c _I	c_2	<i>c</i> ₃
<i>c</i> ₄	x	С5
с6	C7	C8

Fig. 4. Schematic representation of Moore's neighborhood, where X represents a cell with a mollusk and C1 to C8, the cells where the mollusk can move to.

The simulation rules are defined below:

1. If Tv=8, the mollusk does not move;

2. If Tv=0, the mollusk will have 50% of probability to move to either c2 or c7. If those cells are already filled in, the mollusk will remain where it is;

3. When Te=1, Td=1, Ta=0 and Tb=0, the mollusk will move to c7. If that cell is already filled in, the mollusk will remain where it is;

4. When Te=0, Td=0, Ta=1 and Tb=1, the mollusk will move to c5. If that cell is already filled in, the next rule will be verified;

5. If both previous rules were not satisfied, the mollusk will have 50probability to move to either c3 or c8;

6. When Te=1, Td=1, Ta=1 and Tb=1, the mollusk will move to c8. If that cell is already filled in, the next rule will be verified;

7. When Tv=4, Te=2, Td=2, Ta=2 and Tb=2, in other words, if there are mollusks in the cells c1, c3, c6 and c8, the mollusk will move to c7;

8. If both previous rules were not satisfied, the mollusk can move for any neighbor cell;

9. When Tv=1 or Tv=3 or Tv=5 or Tv=6 or Tv=7, the mollusk can move for any neighbor cell.

4 Simulations

The simulations were obtained through the combination of all rules previously cited in a scenario with two thousands mollusks randomly distributed following a Normal distribution. The scheme below illustrates the simulation among 4 iterations (Figures 5, 6, 7 and 8). In the pictures, the green square represents the sweep-

ing area of the Puçá, while the red one represents the sweeping area of Metallic Shell.

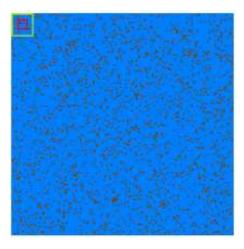


Fig. 5. First Iteration: N1=19 and N2=3.

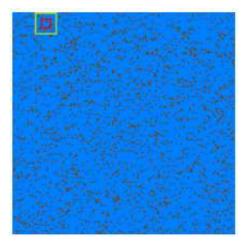


Fig. 6. Second Iteration: N1=17 and N2=3.

The total amount of mollusks collected by Metallic Shell was 23, while the amount of mollusks gather by Puçá was 156 during ten iterations. The graph in Figure 9 illustrates the amount of mollusks collected by each method among the iterations.

5 Final considerations

One of the main goals of the Mathematical Epidemiology is to gather information on how the disease propagates itself in a population aiming to determinate actions to prevent e/or combat such propagation.

Despite of the simplicity of the mollusks collect using Puçá, the Metallic Shell is still widely used to collect the mollusk transmitter of schistosomiasis.

Looking through the simulations it is possible to see that, for any map disposition (as demonstrated in the Figures 5, 6, 7 and 8), Puçá method proved to be more

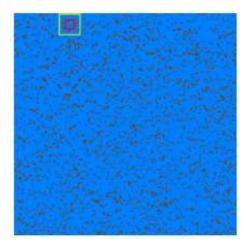


Fig. 7. Third Iteration: N1=15 and N2=2.

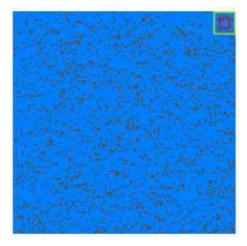


Fig. 8. Tenth Iteration: N1=18 and N2=1.

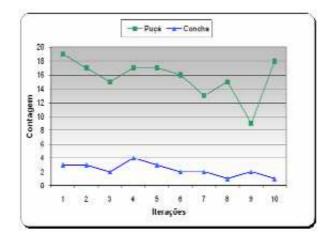


Fig. 9. Comparative analysis of the number of mollusks collected by Puçá and Metallic Shell among ten iterations.

efficient than Metallic Shell.

The graph displayed in the picture 9 illustrates the performance difference of both methodologies among the iterations of this simulation, even considering unrealistic

parameters. For those assumptions, the data was underestimate intentionally to not benefit the Puçá.

To completely eliminate the hypothesis that the data used in this simulation are tendentious, a new simulation is being conducted on real scenarios, on the water resources of Carne de Vaca Pernambuco Brazil.

The Figures 10 and 11 show the tool Cellular Automata Simulator Expansion of Snails, developed in Python. This tool can be downloaded through xiscanoe website: www.xiscanoe.org.

Welcome to Cellular Automata Simulator - Expansio	in of Snails!
To start to use our simulator, please insert the number of its the images that will be used to simulate the snalls. After th	
Number iterations: 50	
Select the image to be used as background of iterations:	
C /Breno/siscance/v4.0/input/input.bmp	Browse
Select the edited image containing the areas where the snals will be distributed	
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Fig. 10. Comparative analysis of the number of mollusks collected by Puçá and Metallic Shell among ten iterations.

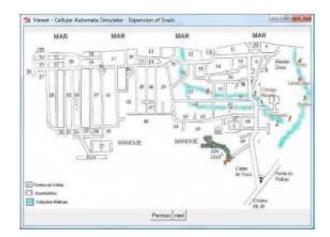


Fig. 11. Simulation on the water resources of Carne de Vaca Pernambuco Brazil.

Looking through the results obtained with the model proposed in this article it is possible to conclude that modeling based on Cellular Automata is able to validate and improve other techniques used in Epidemiology. Beyond the endemic models, this work intends to gather relevant information that might support the study of epidemic models and accelerate the analysis process e comprehension of the epidemics in general.

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