Assessing the Spatial Impact on an Agent-Based Modeling of Epidemic Control: Case of Schistosomiasis

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Abstract. Given that most mathematical models of schistosomiasis are based on ordinary differential equations (ODE) and therefore do not take into account the spatial dimension of the schistosomiasis spread, we use an agent-based modeling approach to assess environmental impact on the modeling of this phenomenon. We show that taking into account the environment in the modeling process somehow affects the control policies that must be established according to the environmental characteristics of each system that is meant to be studied.

Keywords: Complex systems, mathematical modeling, ODE, Agent-based modeling, Simulation, Schistosomiasis, Epidemic control.

1 Introduction

Epidemiological phenomena often involve a large number of entities - host, vector, pathogen, environment, etc. - that can interact and give rise to complex dynamics ranging over several spatiotemporal scales [9]. These dynamics can have serious health consequences like the spread over large geographical areas and the contamination of a large number of persons. Epidemiological phenomena, because of their evolution that results from the elements interactions, can be described as complex systems. To efficiently study them, it is necessary to go through a process of modeling and simulation [8] in order to produce prediction tools and define prevention and control policies. This is what this paper is meant to, with the specific case of the Schistosomiasis spread.

There are two main approaches to model and simulate epidemiological systems: a mathematical approach based on solving continuous equations and a computational approach resulting on individual-based models. For many infectious diseases including schistosomiasis, mathematical modeling has proved to be a valuable tool for predicting epidemic trends and design control strategies [2]. But, still, they suffer from some conceptual limitations.

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In this paper we thus propose an agent-based model of Bilharzia spread. The approach consists in explicitly representing in the model the individuals, the environment, and their interactions. The methodology adopted is as follows. In a first step, we build a discrete and individual-based model not taking into account the spatial dimension. In that first model, humans, snails and other pathogen agents are randomly distributed and also move in a similar random way. With this model, we run a first simulation to make a sensitivity analysis of some control strategies on the epidemic spread. One can notice that, this proposed model is close to the mathematical description; our simulations indeed produce similar results with respect to a mathematical model of control chosen as reference [1]. In the following step, we extend our model by including the space. The goal is to evaluate and assess the impact of space heterogeneity on the basic individual-based model. Our simulations show that taking into account the spatial dimension influences control strategies. These ones must then be defined according to the study case and the environmental specificities of each system.

After presenting in Section 2 the basic elements and the underlying dynamics of schistosomiasis, we briefly expose in section 3 the mathematical modeling approach, showing how the system could be represented in a continuous way. Section 4 will therefore come back on the way to model with agents a phenomenon that is mathematically described. The so-called agents-based models are then presented in sections 5 and 6 and we terminate the paper in section 7 with the conclusion and some discussions.

2 Schistosomiasis and Its Propagation Dynamics

Schistosomiasis, also known as Bilharzia, is a parasitic disease that is found in tropical and subtropical areas and is caused by a tapeworm called schistosome or bilharzias [1]. Schistosomes are parasites that have two phases of multiplication, one sexual in the definitive host, the human, and the other one asexual in the intermediate host, a freshwater snail (mollusc) [2]. Between the two hosts, the link is freshwater often shallow, quiet and grassy. This water is for snails the main development environment; for parasites the intermediate environment outside the hosts; and for humans a necessary resource. The meeting between these entities is the cause of infections. Indeed, the water is contaminated when it contacts parasite eggs that reside into the urine or feces of an infected human. After coming into contact with water, the eggs hatch and release a ciliated larval form called miracidia. This one whose life is short – only a few hours – swim to meet the snail to penetrate it. Inside the snail, larval development, which lasts about a month, leads to the release of thousands of larvae called cercariae. The liberation of cercariae is largely influenced by the nature of the climate. It is more important when the temperature in water is higher. Cercariae, with a lifetime of 4 to 7 weeks, are repented in water. When a human is in contact with fresh water infested, the cercaria can infect him. It penetrates the skin, releases its tail and becomes schistosomula [16].

Schistosomula spend several days in the skin before settling in the liver where they access through the blood vessels. They remain in the liver until sexual maturity and form pairs. The coupling step happens in the portal system of the liver and leads to lay egg either in the small and large intestines or in the rectal veins according to the different types of schistosomiasis. Much of the eggs are released from the body through the urine or feces and the parasite's life cycle resumes. The other part of the eggs is trapped in the body and makes the person sick [1] [16] [11].

With the description of the schistosome dynamics one can see that it is evolving within two hosts: a definitive host, which can be a human or livestock and an intermediate host which is a freshwater snail. It passes from one to the other through the water. This allows dividing the dynamics of the parasite in two parts: an intra-host part and an extra-host part called transmission dynamics, where the parasite interacts with other entities. For this purpose, the modeling of schistosomiasis occurs at two levels [6]:

- Intra-host models: they generally describe the dynamics of the larval stages of the parasite and its interactions with the organs of the body and the immune system [2] [3].
- Transmission dynamics models: they describe the evolution of infection in definitive population hosts [1] [4] [10] [11] [12] [14] [15] [16].

In this paper, we consider transmission dynamics models of the disease.

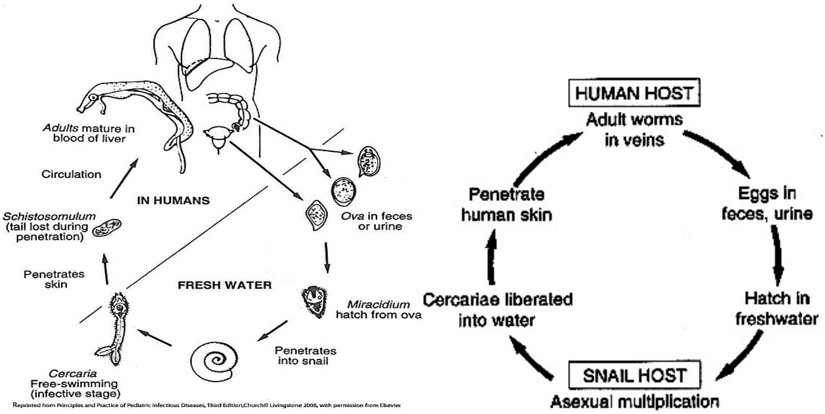

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Fig. 1. Intra- and extra-host dynamics of schistosomiasis parasite

3 The Mathematical Modeling of Schistosomiasis

For many infectious diseases, including schistosomiasis, mathematical modeling has proved to be a suitable tool for the prediction of epidemic trends and the design of strategies [2]. Mathematical models of infectious diseases such as schistosomiasis are composed of two parts: the compartments and rules [10] [11].

Compartments are used to divide the population into subpopulations of homogeneous entities according to the different states of disease or infection, hence the name "compartmental model" used in mathematical modeling of epidemics in general. Considering the human population, for example, it can be partitioned into sub-populations of susceptible (S), infected individuals (I) and recovered individuals (R).

The rules give the proportions of migrant entities from one compartment to another. Example, the rule r($S \rightarrow I$) expresses the proportion of susceptible individuals becoming infected.

Each compartment is represented in the model by an equation and associated rules give the proportions of entities entering and exiting the compartment. Thus, the mathematical model is a set of equations and numerical simulation shows the quantitative evolution of each compartment according to the considered temporal or spatiotemporal scale. Most mathematical models of schistosomiasis are based on ordinary differential equations (ODE) and therefore take into account only the temporal dimension of infections. To illustrate this, we consider the following equation expressing the quantitative evolution of infected individuals over time [1]:

$$\frac{dI}{dt} = \frac{\beta}{1+\alpha P} PS - (\mu + \delta) I \tag{1}$$

The term $\frac{\beta}{1+\alpha P} PS$ involving the susceptible individuals, represented by S, and the cercariae, represented by P, gives the proportion of susceptible individuals becoming infected at a rate $\frac{\beta}{1+\alpha P}$. The term$(\mu + \delta) I$ gives the proportion of infected individuals leaving the compartment I by natural death (at rateμ) or mortality due to disease (at the rateδ).

The equations incorporate coefficients (β, μ, δ, etc.) called model parameters; expressing the rate of infection, incident, transmission, etc. those model parameters play a crucial role in the quality and the efficiency of a model. Their use makes the manipulation of mathematical models flexible. They also allow the development of a better understanding and an effective control of the schistosomiasis infections. Indeed, in the aim of assessing the impact of medical treatment on the dynamics of individual infections, a parameter τ, for example, can be introduced into the equation [1]:

$$\frac{dI}{dt} = \frac{\beta}{1+\alpha P} PS - (\mu + \delta + \tau) I \tag{2}$$

Thus, the proportion of individuals leaving the compartment I become more important. Similarly, the following equation gives the quantitative infected snails I_2 over time [1].

$$\frac{dI_2}{dt} = \frac{\beta_2}{M_0 + \varepsilon M^2} MS_2 - (\mu_2 + \delta_2 + \theta) I_2 \tag{3}$$

The term $\frac{\beta_2}{M_0+\varepsilon M^2} MS_2$ involving the susceptible snails, represented by S_2, and the miracidiums, represented by M, gives the proportion of susceptible snails becoming infected. The term$(\mu_2 + \delta_2 + \theta) I_2$ gives the proportion of infected snails leaving the compartment I_2 by natural death (at rateμ_2) or mortality due to disease (at rateδ_2) or elimination (at rate θ).

Even if this kind of equations is widely used, it still has some conceptual limitations. Indeed, before running the simulation of an equation-based model, one has to give values to the parameters. And yet, for several reasons, these values usually contain a large amount of uncertainty. This can actually affect the accuracy of the simulation [1] [6]. Moreover, since infection depends on the involved species, the climate, the water, sanitation policies, etc. a model that does not take into account the spatial and environmental dimensions is improvable. These remarks, among others, lead us to use computational approaches – for modeling complex systems – to avoid some limits of mathematical models.

Thus, in this paper, we try to assess the spatial impact in the modeling of the transmission dynamics of schistosomiasis. We propose an agent-based model of the phenomenon from a mathematical model of reference established in [1]. The following section then describes the process of deriving the agent-based model from a mathematical model.

4 From the Mathematical Model to an ABM

The mathematical model is based on compartments and does not represent entities individually as perceptible objects. However, in agent-based modeling, it is necessary to explicitly represent the entities considered. Under these conditions, we represent as agent the entities of the same type, even if they are in different compartments in the mathematical model. For example, humans, who are susceptible or infected in the mathematical model, are represented by an agent "*human*". It is the same for snails. Only the status will allow us to distinguish both infected and susceptible human agents and snail agents. It is therefore reasonable to talk about "*human agent*" or "*snail agent*" because, they are reasonably counted. However, considering "*miracidium agent*" or "*cercaria agent*" is not without concerns regarding the uncountable number there may be in the water. Thus, we propose to represent, in the extended model, the water as an agent and link the existence of miracidia and cercariae with the water. We incorporate them in the "*agent water*" as properties and call them the "*content of miracidia in water*" and the "*content of cercariae in water*".

In the mathematical model, the proportion of susceptible humans becoming infected depends on the population of cercaria and the proportion of susceptible snails becoming infected depends on the population of miracidia. In the extended agent-based model, infection of humans will depend on the "*content of cercariae in water*" and infection of snails will depend on the "*content of miracidia in water*". Inversely, the "*content of miracidia in water*" will be determined by infected humans and the "*content of cercariae in water*" by infected snails.

We summarize it below with an UML state diagram of humans and snails, coupled with a class diagram of water, human and snail entities.

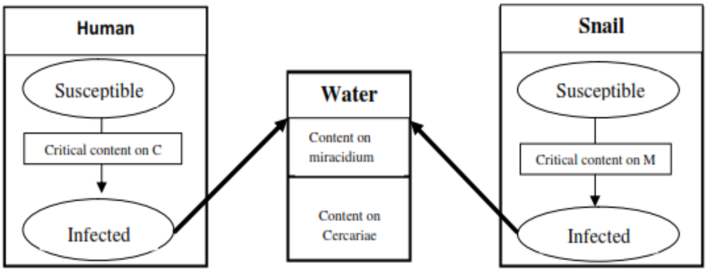

Fig. 2. State diagram of human and snail coupled with a class diagram of water, human and snail

5 A First Agent-Based Model Not Taking into Account the Spatial Dimension

In this model, snail and human agents are randomly distributed on space where they also move randomly. The space is composed of boxes (patches). A box can accommodate a human and / or snail agent and contains a concentration of miracidia and cercariae. A human agent (respectively, a snail agent) present in a box in which the concentration of cercariae (respectively, miracidia) reaches a threshold is contaminated. Similarly, an infected human agent (respectively, an infected snail agent) in a box produces a number of cercariae (respectively, miracidia).

A global agent, commonly called "world agent" in agent-based modeling [7], is created to oversee and synchronize the actions of agents. The interactions between agents are given in the sequence diagram in Figure 3. At each time step, the entire sequence defined in the sequence diagram is executed by the “world agent” using the parameters given in table 1.

Table 1. Values of parameters

Parameter	Value	Reference
Human’s birth rate	8 daily	Estimated
Snail’s birth rate	200 daily	1
Miracidia’s Production rate	0.696 daily per infected person	1
Cercariae’s Production rate	2.6 daily per infected snail	1
Miracidia’s natural mortality rate	0.9 daily	1
Cercariae’s natural mortality rate	0.004 daily	1
Infection rate of Human	$(\beta_1 * C * S_1) / (1 + \alpha * S_1)$	1
Infection rate of snail	$(\beta_2 * M * S_2) / (M_0 + \varepsilon * S_2^2)$	1
Human’s natural mortality rate	0.0000384 daily	1
Snail’s natural mortality rate	0.000569 daily	1
Human’s mortality rate due to infection	0.0039 daily	1
Snail’s mortality rate due to infection	0.0004012 daily	1
Snail’s elimination rate for control	0.1 daily after 15 simulation days	1
Cercaria’s elimination rate for control	0.05 daily after 15 simulation days	1
Human’s treatment rate for control	0.03 daily after 15 simulation days	1
β_1	0.0000000306	Estimated
β_2	0.615	1
S_1: Susceptible humans visiting rivers	Calculated	
S_2: Susceptible snails	Calculated	
C: *content of cercariae in water*	Calculated	
M: *content of miracidia in water*	Calculated	
M_0: initial *content of miracidia in water*	10000	Estimated
ε	0.3	1

We have to recall that in this model, our goal is to show that we can, with agent-based modeling, reproduce similar results to those of the mathematical model with particularly the application of the same control policies used: controls consisting firstly to eliminate cercariaes, secondly to eliminate snails, thirdly to treat infected humans and fourth to combine the three control policies. Our simulation results are given in Figures 4, 5, 6, 7 and 8.

This first model does not take into account the spatial dimension of the phenomenon of the spread of schistosomiasis. Simulations of this model have produced results, especially in Figure 4 (left), which represent the temporal evolution of infections people. This figure shows that there is nearly 100% of infection after 100-days of simulations without any control policies. Our goal now is to show the

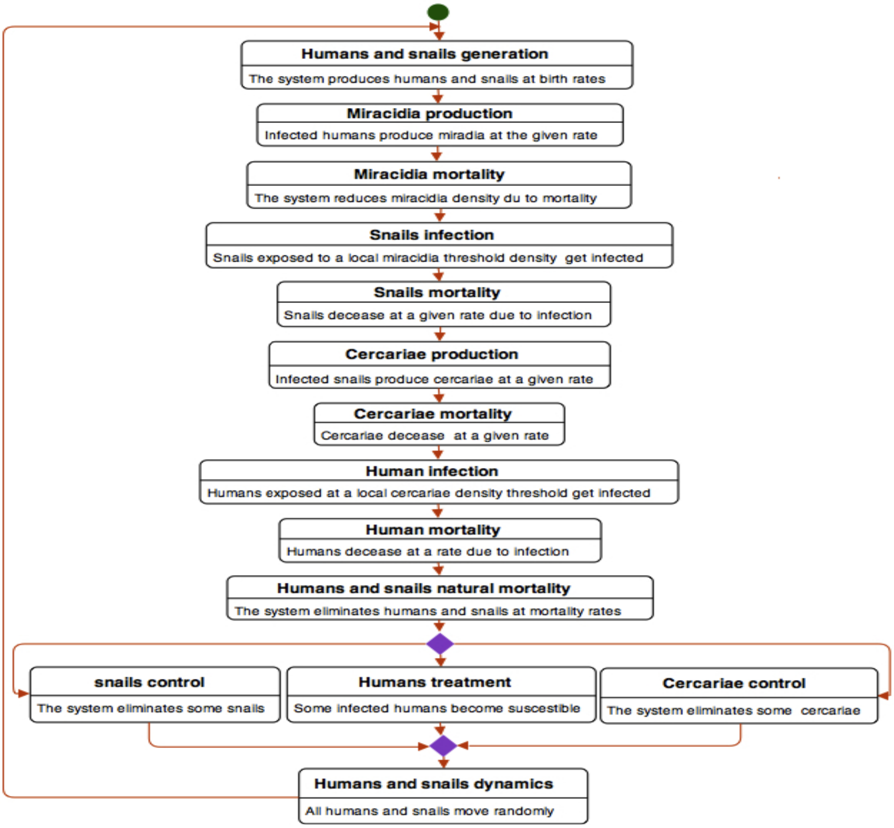

Fig. 3. Transition diagram in the model not taking into account spatial dimension

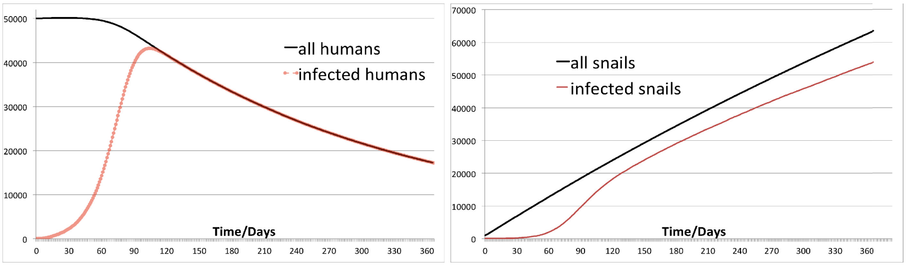

Fig. 4. Results of simulations without any control policies. (Left): The evolution of the human infection. (Right): The evolution of the snail infection.

impact of taking into account the spatial dimension in the spread of the disease. To do so, let us find out the time required to approach 100% infection, in a model taking into account spatial dimension, in order to compare the results with the first model.

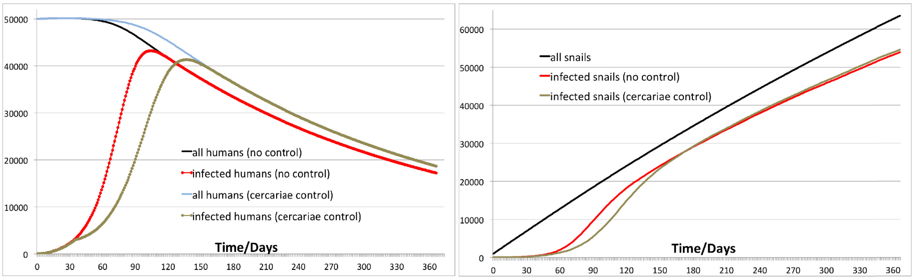

Fig. 5. Results of simulations with a cercariae control policy three time stronger than in table 1. (Left): The evolution of the human infection. (Right): The evolution of the snail infection.

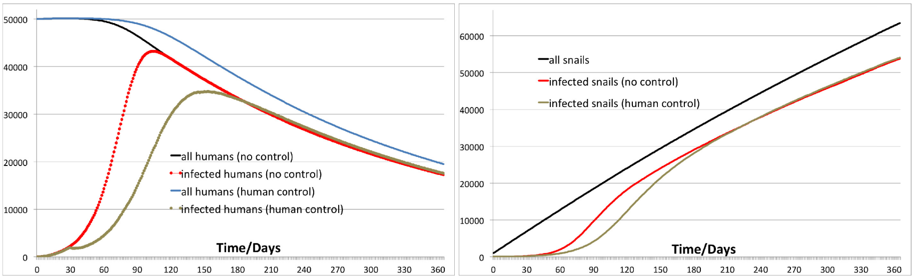

Fig. 6. Results of simulations with a human control policy three time stronger than in table 1. (Left) The evolution of the human infection. (Right) The evolution of the snail infection.

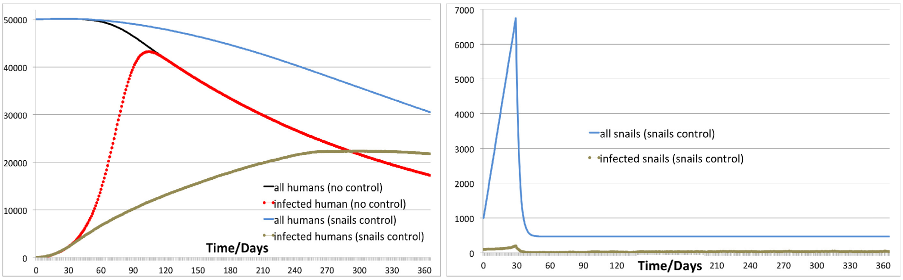

Fig. 7. Results of simulation with a snail control policy three time stronger than in table 1. (Left) The evolution of the human infection. (Right) The evolution of the snail infection.

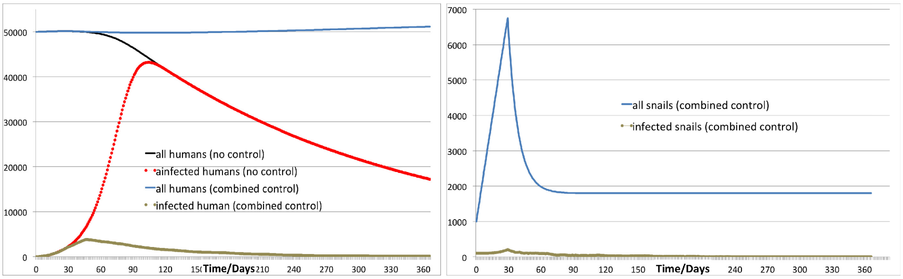

Fig. 8. Results of the simulation with a combined control policy, same values in table 1. (Left) The evolution of the human infection. (Right) The evolution of the snail infection.

6 Agent-Based Model Taking into Account the Spatial Dimension

We propose in this section a model integrating a space located household environment and an actual river (or rivers). The basic behavior of the system described by fig.3 is maintained, only the dynamics of agents will change. Indeed they will no more randomly move, but will adapt their motion on their need to access the water.

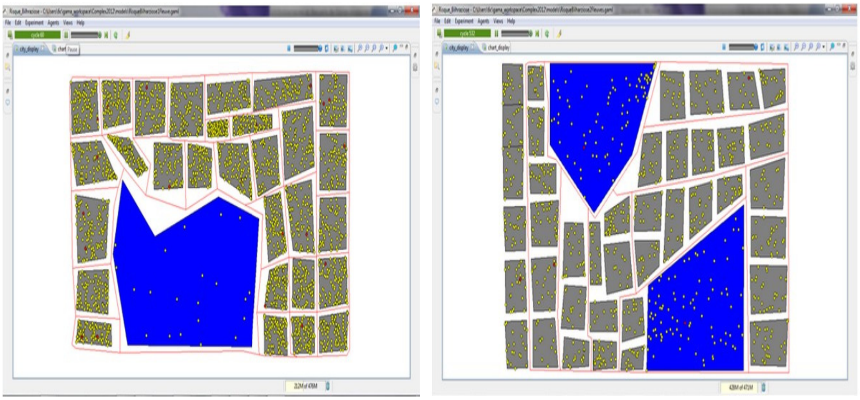

Fig. 9. Simulation environments: (Left): with single river. (Right): with 2 rivers.

Basically, a human agent has a habitat where he leaves to go to the river and where he should return after. Under these conditions the only place where agents can be infected is the river. So a human is exposed to risk when he goes to the river. This was not the case in the first model where the water is not located somewhere on space. That means in this extended model, everyone has not the same risk of exposure. This is the case in reality. We thus divide the population of human agents into three groups. One group, composed of 10% of the population, which has a regular attendance to the river (5 to 7 times per week), a second group, composed of 40% of the population, with an attendance to the river about 1 to 3 times a week and a third group, the rest of the population which has a rare attendance river (about 1 to 3 times every 15 days). To formalize this, each human agent, at the first beginning, has an attribute representing its attendance rate of the river. Those of the first group are more likely higher than those in the second group, also more likely higher than those in the third group. Each human agent also has a “decision mechanism” that assesses, according to the group membership of the agent, the conditions necessary for him to go to the river during the day (the time step).

The river and houses are here modeled as agents as well as human and snail agents. The river agent has attributes *miracidiums_content* and *cercaires_content* that allow infecting snails and humans visiting it.

6.1 Model with a Single River

To infect a person (respectively a snail), we use the same parameters (given in Table 1) of the mathematical model. In this case we can have the same inputs for both the models and be able to compare outputs. The only thing that we modified and adapted from the mathematical inputs is the rate of infection of individuals. Indeed, this rate is applied, at each time step, to all the susceptible persons in the mathematical model; this is not the case here. We apply it only to persons who may have visited the river. The simulation outputs are given in Figure 10 (left).

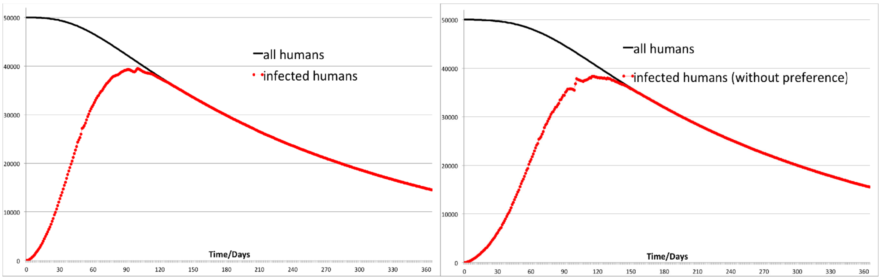

Fig. 10. (Left): Results of the simulation with a single river. (Right): Results of simulation with 2 rivers without specific properties.

6.2 Model with Two Rivers

We consider three scenarios:

Scenario 1: In this scenario, the two rivers do not have distinctive special properties. Our simulation outputs are shown in figure 8 (right). In this case, the disease spread is almost the same in the two environments; the first one with only one river and the second one with two rivers.

Scenario 2: Here, the two rivers are endowed with special properties making them attract a particular group of people. One river has properties attracting more humans with rare frequentation of rivers and the other attracts more the other groups. Under these conditions, a human agent, in its “decision mechanism”, will choice before going into a river. In such a scenario, a river is frequented by almost the same people. Simulation results are given in Figure 11 (left).

Scenario 3: Compared to scenario 2, we add in this scenario control policy of eliminating snails. According to [1], this is the best control policy. Simulation results are given in Figure 11 (right).

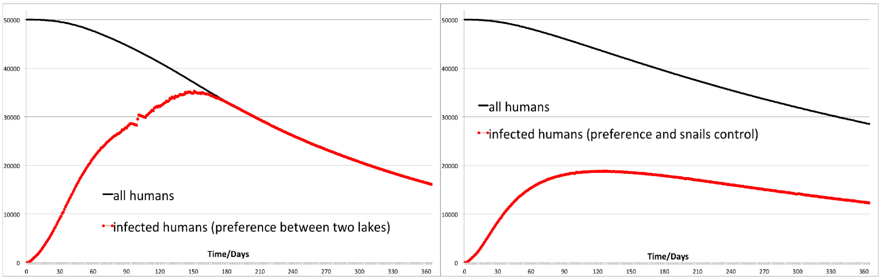

Fig. 11. (Left): Results of the simulation with 2 rivers where each river attract a specific group of persons. (Right): Applying the three control policies.

7 Discussion

In this paper, we assessed the environmental impact on the process of modeling the spread of schistosomiasis. The main objective was to show the influence of taking into account the environment on control policies of schistosomiasis.

In Section 5, we have established a first model that does not take into account the spatial dimension. Simulations of this model show that:

- Without the application of a control policy, one tends towards 100% of infection after 100 days: Figure 4 (left).

- With the application of the control policy consisting to eliminate snails, the disease tends to disappear after 300 days: Figure 7 (left).

In section 6, we have extended the previous model by incorporating the environment into the modeling process. We considered four scenarios.

In the first scenario, we have an environment with a single river. Here, our simulations produce approximately the same outputs as the model that does not take into account the spatial dimension: Figure 10 (left).

In the second scenario, we consider an environment with two rivers. Compared to the previous, our simulations show that without control, one tends towards 100% of infection after 120 days: Figure 10 (right).

In the third scenario, we still have an environment with two rivers. But this time, rivers have properties allowing them to attract a particular group of people. Our simulations show that without control, one approaches 100% of infection after 145 days: Figure 11 (left).

In the fourth scenario, we apply the control policy consisting to eliminate snails on the model of scenario 3. Compared to output in Figure 7 (left), simulations show here that the disease tends to disappear after 120 days: Figure 11 (right).

We can conclude from the simple implemented scenarios that taking into account the environment have a significant impact on the quality of the models of schistosomiasis spread. The “space-less” model and even the one with the only river give approximately the same result that equations-based model could give, especially on control policies. It is a good way to proceed. Nevertheless, when making some kind of realistic scenarios like river preference the outputs change a lot and so should the control policies. We can therefore state that control policies must be defined according to the environmental characteristics of each system that need to be modeled and the approach that we followed can help doing so. Agent-based modeling thus allows having general results and also going into details on some eventual cases study. Indeed, in our work, we use GAMA platform [13] which is an agent-oriented platform allowing GIS data loading to provide a graphical simulation environment faithfully representing the selected system (see figure 9).

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