

# A Brownian Agent Approach for Modeling and Simulating the Population Dynamics of the Schistosomiasis

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**Abstract** - *Multi-agent simulations have been successfully employed in the studies of population behavior. In this work we present a Brownian agent approach for simulating and modeling the Schistosomiasis infection. Early results suggest that the proposed model describes relevant aspects of the infection conditions.*

**Keywords:** Simulation; Schistosomiasis; Brownian Agents; Population Dynamics

## 1 Introduction

Multi-agent simulations (MABS) have been successfully adopted in the simulation of various problems [1] such as ecological systems modeling, population behavior for predicting crime, biological population dynamics, information spreading, formation of groups, among others [2]. Another important use of Multi-agent based simulations has been made in the context of infection and disease contention such as malaria [3].

In this kind of simulations, it is assumed that individual agents belonging to a major and complex system are endowed with a certain autonomy and intelligence. These agents interact for a purpose, a global behavior, or a specific goal. These interactions between different agents influence the dynamics of the entire system.

Among the various approaches for modeling MABS, a possible one is the Brownian agent. A Brownian agent is characterized by being able to generate a local field of information that can also influence the agent itself or other agents. The advantage of using Brownian agents is given in the context of problems that presents information spreading over time and space, for example, disease spreading [4-5].

In this work we use the Brownian agents to model and simulate the spread of Schistosomiasis disease and also to represent the dynamics of the population involved in the infection.

## 2 Schistosomiasis

The Schistosomiasis is a debilitating disease that can be lethal and it is caused by a worm type parasite of the genus

*Schistosoma* [6]. The disease cycle has two main hosts: the *Biomphalaria* snail which acts as intermediary host, and men as a definitive host. Schistosomiasis occurs in regions where there are streams, ponds and low or nonexistent sanitation. In Brazil, it is still considered a serious public health problem because it affects millions of people each year causing a significant number of serious infection and even death [7].

The disease cycle begins when an infected man releases the worm eggs as excretes in a favorable water region for the parasite development. These eggs hatch in ciliated larvae called miracidium, which penetrate the epidermis and contaminate the *Biomphalaria* snail. After a period of maturation within the snail, these larvae suffer metamorphosis and are released through the skin of the snail, now as tailed larvae, called cercariae, the infective form of the disease. The cercariae seek the definitive host, men, and penetrate their skin. Now without the tail, they are loaded into the bloodstream and when they become adult parasites, they lodge in the veins of the intestine or bladder of the host, thereby causing Schistosomiasis. The adult worms reproduce and generate new eggs that are expelled by men, thus closing the cycle of the disease [6].

The contamination cycle depends on water resources, because the parasites (miracidium and cercariae) survive on this ambient for a short period of time, one or two days long, consuming their internal nutrients reservation. Also the snail usually lives in aquatic habitat.

The measures against the Schistosomiasis disease can be applied by combining two strategies: combating the *Biomphalaria* snail with improvements in sanitation, health care, and application of molluscicide; or applying educational sanitation campaigns for the population. These measures can be taken because the life cycle of the parasite depends on both interactions between larvae and hosts, and on the sanitation conditions for larval development [7].

## 3 Related work

Over the past years there has been an increasing trend in the application of mathematical and simulation models in the studies and control of infectious disease [8]. One of the advantages in using these models is the access of public health professionals and managers, allowing them to analyze and

apply prophylactic measures. Mathematical models have been created to understand the schistosome epidemiology and to the design of control programs.

In this sense, the literature provides a set of works that applies mathematical models for the Schistosomiasis contagion. Complex and detailed models can be used in simulation studies to assist the interpretation of data and to prevent the occurrence of epidemics [9].

Some models of the Schistosomiasis focus on the conditions of the environment and the prophylactic measures, trying to predict the potential efficacy of targeted chemotherapy or focal molluscicide application [10]. A mathematical model for Schistosomiasis transmission must integrate data from diverse sources to aid in designing control strategies, and evaluating surveillance programs [11]. The identified prophylactic measures against Schistosomiasis are: selective mass treatment, targeted mass treatment, mass treatment for animal reservoirs, and health education [12].

Detailed and complex models focus on realistic features including drug treatment for human hosts, infection age in snail hosts, density-dependent birth rate of snails, distribution of schistosomes within human hosts, and disease-induced mortality in both human and snail hosts [13], representing the biological consequences of applying some control strategies.

In this context, these mathematical models have been applied in stochastic simulations to investigate whether it would be possible to detect patterns predicted by theoretical models [14].

The population dynamics of the Schistosomiasis infection involves human and intermediate snail hosts as well as other possible species competing or serving as intermediary hosts. Some of these models consist in deterministic differential equations for the infected and susceptible subpopulations [15], or the possibility of migration between human habitats [16]. The deterministic system is generalized to a stochastic system of differential equations to account for the random behavior of variables which influences population dynamics [17].

All mathematical models presented in literature represents relevant features of the contagion process [18], like the population dynamics of each species and the environmental, social and economical conditions.

## 4 Brownian agents and the mathematical modeling

The model of this problem can be implemented by the Brownian agents approach. A Brownian agent is characterized by a set of state variables  $u_i^k$  where  $i = 1, \dots, N$  refers to an individual agent  $i$ , and  $k$  indicates their different state variables [4]. In the agents modeling used in the simulation it is adopted two observable variables: space (Eq. 1) and velocity (Eq. 2), presented by all agents as it is assumed that every agent has mobility in space.

There are also two other internal variables: information and energy. The variable internal information (Eq. 3) allows characterizing the nature of the vector agents (men and snails) on the problem of the contagion; it characterizes the state of the agent as infected or healthy. The internal energy of the agent (Eq. 4), allows defining how active an agent will be at a given stage of the simulation. In the case of the proposed problem, this is equivalent to the metabolic reserve of the different parasite population individuals. As pointed out, parasites (Miracidium and Cercariae) survive temporarily consuming their nutrient reserves [19].

$$u_i^1 = \mathbb{P}_i, \quad (1) \quad u_i^2 = d \frac{h_i}{dt} = \mathbb{V}_i, \quad (2)$$

$$u_i^3 = \theta_i, \quad (3) \quad u_i^4 = e_i. \quad (4)$$

The behavior of each agent is modeled by a deterministic and a stochastic component. The deterministic behavior is based on factors that influence the environment where they are inserted. In the case of biological populations, this influence is modeled as constraints associated with the water resources (lakes, rivers and ponds), whereas in the case of human populations, refers to the biological needs of the local population that lead them to an environment of possible contagion. The stochastic component is specified to represent free search along the geographical environment, i.e., each agent may randomly move around a mean position, simulating a wandering in search of resources, such as food. Thus, the dynamics of the variables may be influenced by stochastic and deterministic factors (Eq. 5).

The model of the environment corresponds to a geographical environment, where water resources, essentials for the dynamics of contagion, are modeled as deterministic attractive potentials which affect the three agent populations of miracidium, cercariae and snails. Thus, the water resource can be modeled from a mathematical function that describes an area of influence for the agents mentioned. For characterizing a lake or a pond along the environment, these potentials are represented by circular or elliptical geometry.

According to the discussed models of agent and environment, it is possible to determine the variation of the speed of an individual agent (Eq. 5) and also its energy consumption (Eq. 6).

$$d \frac{u_i^k}{dt} = f_i^k + F_i^{stoch}, \quad (5)$$

$$d \frac{u_i^4}{dt} = -m_i(t), \quad (6)$$

where  $f_i^k$ , represents the deterministic influences (water resources and information fields, described in the following) over the agent,  $F_i^{Stoch}$ , is the stochastic influences and  $m_i$  the parasite metabolic rate.

The energy dynamics will be applied only to the parasite population (miracidium and cercariae) because it is assumed that the lifetime of the parasite agent population is much

smaller than the lifetime of the vector population (men and snails). Thus, the number of agents of vector type remains constant during each simulation.

The internal information of the agent is presented only in snails and human agents, and varies according to the conditions for contagion. This variable contributes for building local areas of influence in certain regions of the environment, called information field.

The information field models the interaction between different populations. It is constructed from the individual contribution of each agent according to the value of its current internal information. Thus, the greater the number of agents in a given region of space, the greater is the effect of this field over the other parasite agents that constitute the system. This represents a higher chance for contamination.

Only uncontaminated vectors are assumed to become contaminated and produce regions that have higher chances of contagion for parasite populations. For example, a vector agent already contaminated does not influence the information field accessible to the parasite agents. To simulate the need for searching a host, the parasites agents feel the influence of the field, characterized as a deterministic force that attracts them to the vector agents. Moreover, vectors are generators of the information field contributing to the value of its state at a given point in space.

## 5 Computational model

The simulator development was performed using the oriented-object paradigm. As support technologies, the simulator uses Java based frameworks and Web technologies. Also, it is intended to create a framework as result of this work.

As the initial step, a conceptual model of the agents and the environment was developed and also their relationships. The whole computational model was performed by the MVC design pattern, allowing independence between the interfaces and the business model implemented. It means that it is possible to implement the model presented in this work in any other system architecture.

The simulator modeling process must take into account the elements which compound the problem of the contagion, thus, more attention should be taken in a consistent manner to represent the processes and conditions under which individuals react or modify their behavior during the simulation. For this purpose, the characteristics that distinguish individuals as well as their behavior define the attributes and methods of classes that represent them.

For the specific problem, the classes of the system correspond to the agents of multi-agent simulation, their environment and their interaction. A description of the classes is given in the next sections.

### 5.1 Agents modeling

In the following it is presented a description of the classes that represent the agents of the Multi-agent based simulator (Figure 1):

- Class **BrownianAgent**: This class represents Brownian agents, which have as attributes the set of state variables (internal energy and information) and observable variables (position and velocity), necessary for modeling this problem.

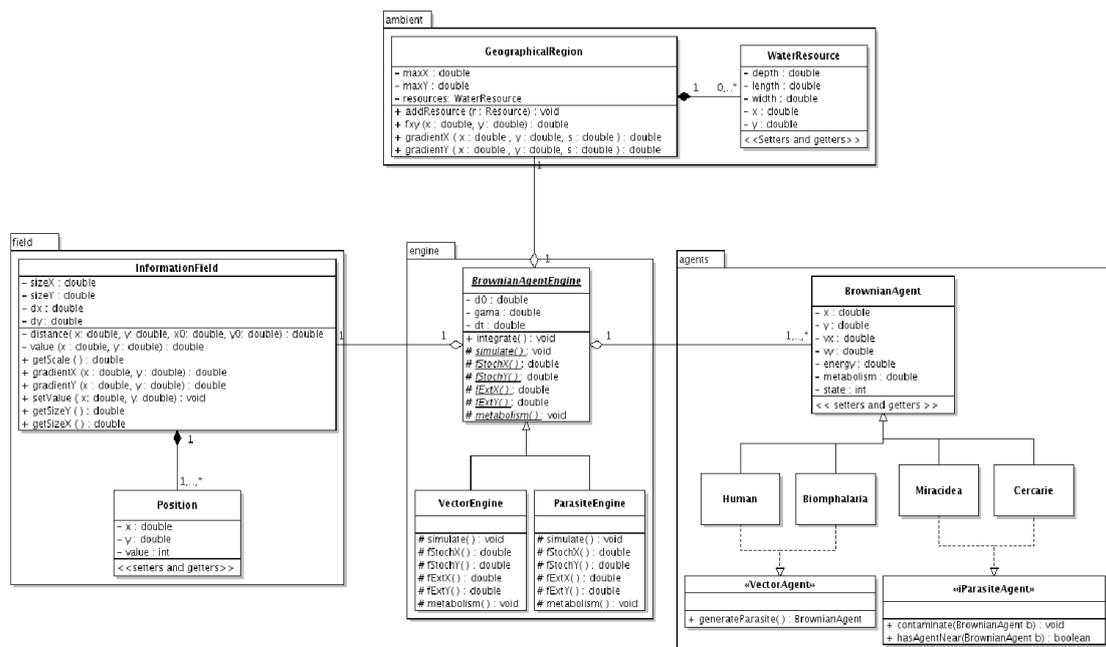


Fig. 1. Class diagram presenting the classes of the model used in the simulator.

- Interface VectorAgent: Presents an abstract method that constructs new Cercariae or Miracidium agents. This method is executed if the Human or *Biomphalaria* agent is infected. It is a method implemented by the classes *Human* and *Biomphalaria* by polymorphism. In particular, according to the life cycle of the *Shistosoma mansoni*, human agents must generate Miracidium agents, in the presence of water resource, and *Biomphalaria* agents must generate Cercariae agents.
- Interface ParasiteAgent: Presents two polymorphic methods to be implemented by classes that represent the parasites (Cercariae and Miracidium). The "hasAgentNear" method is the function that computes in a given simulation step if there is a Vector agent in vicinity. As a polymorphic method, it presents different actions for the different classes. In particular, it is necessary that Miracidium agents only sense the *Biomphalaria* agents and Cercariae agents, only sense the Human agents. The other method called "contaminate" causes a change in the internal information (attribute "state") of the Vector agent previously selected by the "hasAgentNear" method, thus contaminating the vector agent.
- Class Human and Class Biomphalaria: These classes represent the modeling of each vector agent necessary in the life cycle of the *Schistosoma*.
- Class Miracidium and Class Cercariae: Represent a population of parasite agents (Miracidium and Cercariae).

## 5.2 Environment modeling

The environment modeling is carried out by the classes "GeographicalRegion" and "WaterResource". Computer modeling of the environment requires that the species of *Biomphalaria* snails, Cercariae and Miracidium parasites must be found in water resources. Therefore the geographical environment presents a set of water resources.

The environment is modeled as a class called "GeographicalRegion". This class consists of a composition with another class called "WaterResource" which represents the water resources, such as ponds, lakes, standing water, etc. [6-8]. By simplifying assumptions, it is assumed that these resources have circular or elliptical geometry, thus its attributes "length" and "width" represent the semi-axes of an elliptical shape.

In the model, *Biomphalaria*, miracidium and cercariae agents feel the influence of water resource as an attractive deterministic potential, which traps them into the region of the modeled water resource.

The fact described before justifies the method called "fxy" presented in the "GeographicalRegion" class which calculates a component of the deterministic force presented in equation 5

(see section III). This method computes the value of the attractive force felt by the agents, resulting from the sum of all water resources of the geographical area, at a given point with coordinates x, y. The agents which are located near such resource and feel its influence becomes trapped along the elliptical or circular region. It represents the needs of water resources presented by the *Biomphalaria*, cercariae e miracidium population.

In a future model it will also be considered the existence of other resources present in the environment, as well as the motivation for human populations, such as housing, stores, hospitals, schools, etc.

## 5.3 Simulator engine

The simulator engine is composed of some classes which implement the Brownian agents approach and handle the events during the simulated scenarios. The events handled by the engine include computation of all the agents dynamics (Eq. 5 and 6), creation and removal of agents, changes in agents states, creation of the desired environment and creation of the initial population.

The "Simulation" class is the interface between the controller classes and the problem model discussed above (Figure 2). This class presents all the configuration values such as demographic data (number of individuals of all population), the geographical region data and timing sets. Also, it is composed of the "BrownianAgentEngine" class which describes all the computational model of the Schistosomiasis contagion problem.

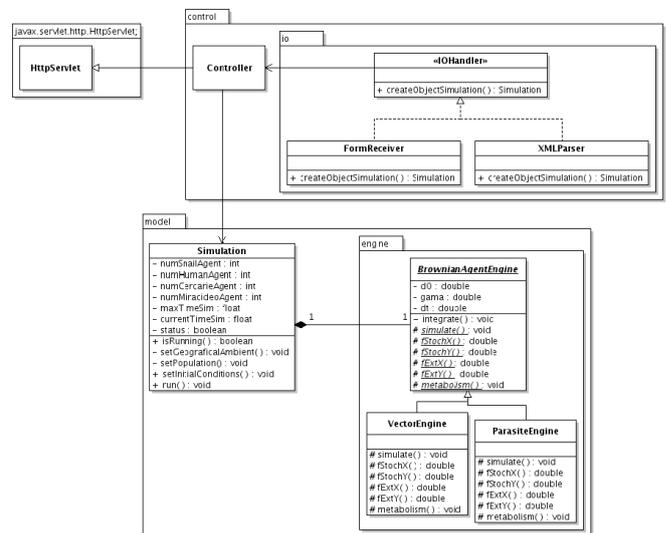


Fig. 2. Class diagram representing the classes that handles the input parameters and the classes responsible for the model simulation.

The "BrownianAgentEngine" class has the task of simulating the dynamics of the populations and handling the events that occur during a scenario simulation. It is an abstract class which presents a set of abstract methods implemented by the classes "VectorEngine" and "ParasiteEngine".

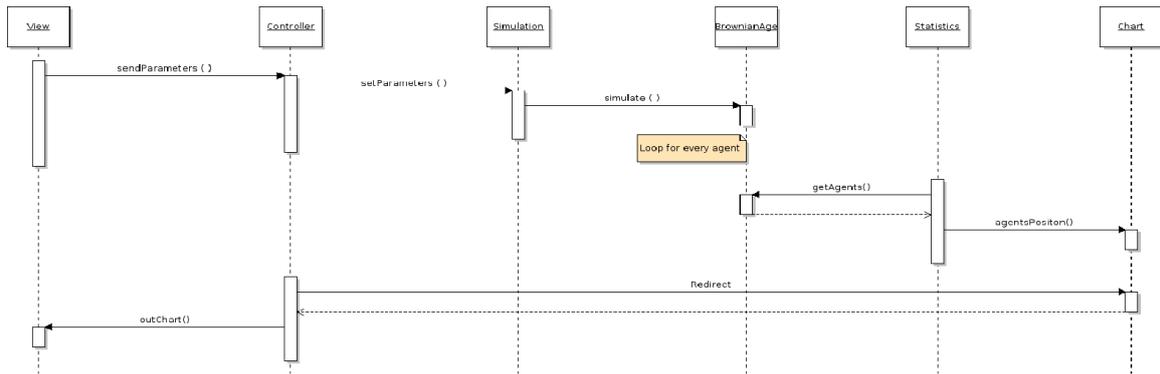


Fig. 3. Sequence Diagram representing the simulation process and all the involved classes.

The “VectorEngine” and “ParasiteEngine” class implements all the abstract methods of the “BrownianAgentEngine” class. As pointed out earlier, the dynamics of each population may be different according to the constraints implied for each population. For example, parasite agents have their energy consumed, simulating the behavior of the real ones. Each of these classes will handle a specified population with their constraints and specific features.

The method “fExtY” and “fExtX” presented in the “BrownianAgentEngine” class computes the sum of all components of the external features which influence the agent, (Eq. 5). When implemented in the “ParasiteEngine” it has also a component related to the water resource and a component related to the information field generated by the Vector agents.

Another method which has great importance in this problem is called “integrate”, which integrates the equation 5 of the model based on the Brownian agent approach. The execution of this method changes the state of the attributes “x” and “y” of all the agents during the simulation, representing its motion along the geographical space.

## 5.4 Population interaction and the information field

The interaction between the agents is essential for the contagion modeling. As discussed earlier, the contagion occurs when different species interact and some specific conditions are satisfied.

In this model it is used the information field as a mechanism for interaction between different population. Recall that the information field is a dynamical field created by the vector agents with individual contributions, what means that the larger the number of vector agents in a given space coordinate the greater will be the chances for vectors to become infected.

This mechanism is created by the following feature: a class named “InformationField” holds the coordinates of all the uncontaminated vectors. A parasite agent in a given coordinate “x” and “y” will sum the contribution of the gradient of the created field along the simulation. This

contribution is given by the methods “gradientX” and “gradientY”.

As an uncontaminated vector agent changes its position coordinate, the value of the field also changes and so the contribution of the gradients calculated by the methods “gradientX” and “gradientY”. Also, if an agent becomes contaminated its contribution to field is zero.

This class takes into account which of the vector agent and parasite agent are involved because the real problem involves the interaction of specific agents in different population. So there must be only one field for the “Human” and “Cercariae” agents and another different for the “Biomphalaria” and “Miracidium” agents.

The mechanism described above is responsible for the disease spreading along the geographical space.

## 6 The simulation process

This section describes the simulation process from the input parameters to the reports generated by the simulator. The sequence diagram in Figure 3 illustrates the process.

The user enters the input data from an XML file to the simulator. These data are sent to a Java class that adjusts the input parameters of the simulation. In general, the parameters are set by the user and grouped into three categories: geographical region, demographics and timing data.

Demographic data is based on population density of the region considered taking into account the population size of humans and snails of the genus *Biomphalaria* inhabiting the region as well as its distribution in geographic space, thus, define a population density space around some points representing, for example, the housing occupation area.

The other group of input parameters is based on the dimensions of the geographical region and the scale used during the simulation. Also, the user sets the parameters associated with water resources, like the size of the resource, the depth and its coordinate location.

Finally, the last set of parameters is associated with the simulation time, for example, duration of the simulation. The

configuration performed by the user, and the initialization of the simulation are given by the sequence diagram shown in the Figure 3.

During the simulation a list of all the agents is kept in memory and must be covered, so all agents who are active in the simulation are modified by the classes "VectorAgentEngine" or "ParasiteAgentEngine".

1. Update the information fields: the list of agents is iterated over for each vector agent (Human or snails) and the associated field is updated, i.e., the value associated with the new positions of the vector agents is changed according to the events that occurred;
2. Proliferation and contamination: contamination occurs as follows: if the agent is the type of Miracidium or Cercariae, and there is a snail or human respectively, in a given radius, these agents are contaminated. A contaminated agent remains in this state, since such agent is not cured. The proliferation occurs as follows: every agent of human type, which is contaminated, generates a new Miracidium agent, which is added to the end of the agents list. The same occurs with the snails that are infected, however the new agent created is a Cercariae agent.
3. Update the positions of agents: position, velocity and energy of all agents in the system are updated. If the energy of a given agent is depleted, its agent is removed from the simulation.

The simulation consists in the implementation of phases 1, 2 and 3, in that order, for a predetermined number of simulation steps.

Initially, it is assumed the existence of at least one human infected by the parasite *Schistosoma* agent that releases its feces or urinates near a water resource. From a computational point of view, when the position of a human agent is domain of the function that describes a water feature, new agents of the class "Parasite" are created.

The Parasite agents alter their dynamics influenced by the information field generated by the population of Vectors agents. This occurs because the information field generates an attractive force that directs the parasites to the vector agents.

If a Parasite agent reaches a Vector agent, the contagion will occur and will trigger the creation of new Parasite agents and will change the attribute "state" of the Vector agent. Vectors agents who are infected will not contribute to the information field. This ensures that Parasite agents will always aim to search for different healthy Vector individuals.

After running the simulation, the data from each step of the simulation are sent to the framework JFreeChart for subsequent data rendering.

## 6.1 Results

A series of simulations were performed aiming the investigation of the population dynamics of the Schistosomiasis contagion. To do this, we analyze the influence of the locations, water resources and population humans and snails. As we have already discussed, the cycle of transmission of the disease is complex and involves the interaction of different populations. Thus, an initial set of simulations were executed.

All simulations were performed in a maximum of 500 steps. The speed of spread of infection was calculated at the end of each simulation. For each scenario tested, 30 simulations were performed. The simulations are initiated with the diverse populations of agents arranged along the geographic space. The human agents will be arranged randomly, simulating a disordered occupation usually common in regions with low sanitation. The other populations that depend on water resources are allocated along the dimensions of these resources.

The factors mentioned before (size and distribution of the water resources and population density) directly influence the spread of information over time and space. In Figure 4, it is shown that the size of vector populations influences the propagation speed of the contagion. The distribution and size of water resources, influences directly the snails distribution. This means that a greater number of humans living around these resources become susceptible to the infection.

A high occupancy of humans allows rapid snails infection (Figure 5). The same behavior is observed with the number of snails. In both cases it appears that the significant increase of the population of individuals of parasites increases the possibility of infection from the individual vectors. These factors also increase the spread of the disease over the geographical space. This happens because the infected vectors create new parasites, closing the cycle of disease. This behavior was expected according to the characteristics of the disease cycle as previously discussed.

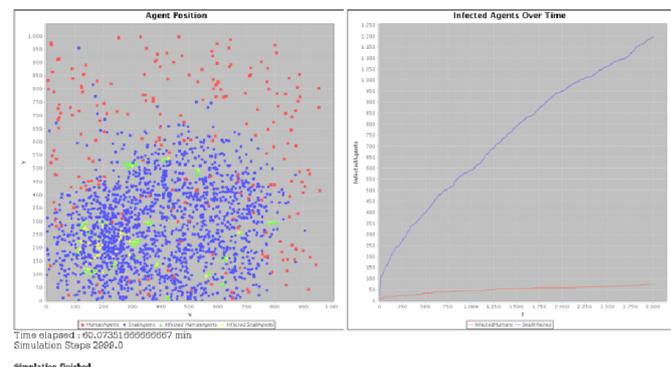


Fig. 4. The simulator interface presenting the calculated data. In red, it is shown the healthy human population, in green contaminated human population, in blue healthy snail population, and in yellow the contaminated snail population.

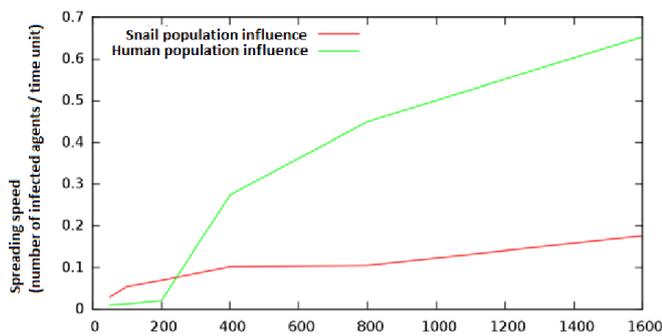


Fig. 5. Influence of the human and snail populations on the contagion spread rate.

## 7 Conclusions

A multi-agent approach based on the Brownian agent model has been used for modeling and simulating the population dynamics in the Schistosomiasis contagion. In general, the results obtained from the simulation showed that the location is a determining factor for infection, and this factor is influenced by the population density of vectors found along the geographic space. The simulator has undergone a series of tests checking various parameters, and in general, it represented relevant aspects to demonstrate the dynamics of populations in the Schistosomiasis contagion.

Model validation with real data will be performed in future work. Due to the complexity of real-world scenarios, the simulation will require the connection with models of real spatial data, and due to the high number of agents a version of the simulator that uses parallel processing will also be needed.

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