

Agent-Based Models in Human Infectious Disease Epidemiology

Brian Fernando Morales Arredondo
Alejandra Ossa Yepes
Andrés Felipe Tamayo Arango

Junio de 2019

Abstract

In the present article we give an approach to the agent-based modelling and simulation for infectious disease epidemiology based on Kermack-McKendrick model. For all the modelling and simulation process we work on NetLogo platform.

Keywords– Agent based simulation, epidemiological model, SIR model, disease, population, transmission, Kermack-McKendrick.

1 Introduction

One of the best advantages of agent-based modelling in epidemiology is that we can assume that the population is not homogeneous. In fact, this is a big restriction of the equation based models, because requires a large number of complex equations and each population in the model need different set of parameters. In this regard, agent-based simulation models are a great alternative to equation based models while they provide a large number of scenarios and possibilities. It is well known that ABMs allows agents to interact with other agents and the environment on a set of rules [Railsback and Grimm, 2010], and for this ABMs is ideal for an epidemiological study when it is not feasible to run an experiment. When we are creating an agent-based model for infectious disease epidemiology there are four main components that we have to consider: disease, society, transportation and environment. In this regard, when modelling disease one must determines how the infectious disease is transmitted between agents and how the disease progresses in an infected agent. Modelling the society implies modelling the population whereas the disease is being transmitted through the agents in contrast with modelling the transportation determines how the agents will move through the environment. In the other hand, the environment is modelling like the space in which the agents will interact.[Elizabeth Hunter, 2017]

2 Overview

2.1 Purpose

In the present article, our aim is to give an approach to the ABMs on epidemiology and infectious disease based on the Kermack-McKendrick model. Following the taxonomy for an agent-base model in human infectious disease epidemiology, we want to see if our model accomplish this taxonomy.

2.2 Entities, state variables and scales

2.2.1 Entities

- Susceptible individuals
- Infected individuals
- Removed individuals

2.2.2 State variables

If we consider that an agent's state is defined by its properties, we can say that the state variables are: Time infection, Recovered time, ability to reproduce, ability to die.

2.2.3 Scale

Hours 1/hour by step

2.3 Process

Susceptible individuals: They can walk around the world and get a disease and to reproduce
Infected individuals: They can give a disease, walk, reproduce and die
Recovered individuals: They can walk and to reproduce

3 Design concepts

3.1 Basic principles

3.1.1 General concepts

Kermack-McKendrick model is used to predict the number and distribution of an infectious disease through a population over time. It was constructed in principle by A.G. McKendrick and W.O. Kermack in 1927. In this first paper, the start with the assumption that all members of the community are tart with the assumption that all members of the community are initially equally susceptible to the disease, and that a complete immunity is conferred after the infection. In this regard, the population is divided in susceptible, infected and removed individuals. This kind of models are known as SIR models or general epidemic process. So SIR is a dynamical system that models epidemics over time. The basic SIR model can be represented by a nonlinear dynamical system of three differential equations [Russell Connell and Skvortsov*, 2009].

$$\frac{dS_t}{dt} = -\alpha \cdot S_t \cdot I_t \quad (1)$$

$$\frac{dI_t}{dt} = \alpha \cdot S_t \cdot I_t - \beta \cdot I_t \quad (2)$$

$$\frac{dR_t}{dt} = \beta \cdot I_t \quad (3)$$

Where

- S_t is the number of susceptible individuals
- I_t is the number of infected individuals

- R_t is the number of recovered individuals
- $\alpha = \alpha_1 \cdot \alpha_2$ considering that α_1 is the rate per unit time that an individual comes into contact with any other individual and α_2 is the probability of that an individuals of I_t infecting an individuals of S_t when they meet.
- β is the probability an infected person will recover per unit time.

The initial conditions to this model are $I_0 > 0$, $S_0 > 0$ and $R_0 = 0$

3.1.2 Modeling approaches

3.2 Emergence

The model's important outputs are the recovered population, infected population and susceptible population

3.3 Adaptation

The adaptive behaviors that the agents have are:

- If the susceptible individuals get an infection, they start to moving slowly
- If the incubation period is advanced, they go to the quarantine zone.
- If an individual is sick for more than the 75 percentage of the time, and it is no in quarantine zone, they died
- If an infected individual is in the quarantine zone, gets heal

3.4 Interaction

The model's agent interact by random movements, and if an individual is infected, he goes through the quarantine zone.

4 Details

4.1 Input data

The input data in the model is:

- Initial population
- Recover probability
- Infected probability
- Average recovery time
- Birth rate.

5 Background

- Kasereka, S., Kasoro, N., Chokki, A. P. (2015). *A hybrid model for modeling the spread of epidemics: Theory and simulation*. IEEE Xplore, 133. [Chokki, 2014]
- López, E. D. (2016). *Analysis of mathematical models of prediction of the behavior of epidemics in social groups through simulation based on agents*. SABER,CIENCIA, 110. [Efraín De La Hoz Granadillo, 2017]

These two articles make a great contribution to the understanding of the aborted agreements in our article, besides mentioning antecedents of this topic as it is the analysis of the interactions of the agents in an environment that was studied by Quezada and Cannesa (2010), who expressed that the SBA is a tool that responds to problems characterized by a "Bottom Up" type behavior, that is, systems that observe emerging behaviors based on the individual behavior of the social actors, in which the behavior of each subject exerts a disturbance mutual with the rest of the population [Efraín De La Hoz Granadillo, 2017].

6 Implementation on simulation platform

.pdf .pdf .png .png .jpg .jpg .mps .mps .jpeg .jpeg .jbig2 .jbig2 .jb2 .jb2 .PDF .PDF .PNG .PNG .JPG .JPG .JPEG .JPEG .JB

Figure 1: Simulation of epidemiological model in the simulation platform Netlogo

7 Verification and validation

The data used for the validation is on the table 1 [Johnson, 2009]

<i>Variables</i>	<i>Rank</i>	<i>Value</i>
Initial-people	50-400	100
Infection-chance	10-100	85
Recovery-chance	10-100	95
Average-recovery-time	0-300	120
Birth-rate		0.64

For the verification and validation process we are going to made a comparison with the results of our model and the results obtained from the article "*Mathematical Modeling of Diseases: Susceptible-Infected-Recovered (SIR) Model*"[Johnson, 2009]. In this regard, we analyse the principals output, this is, the effect of the infectious rate on the susceptible, infected and recovered population. We are going to use an infectious rate of the 85 percent.

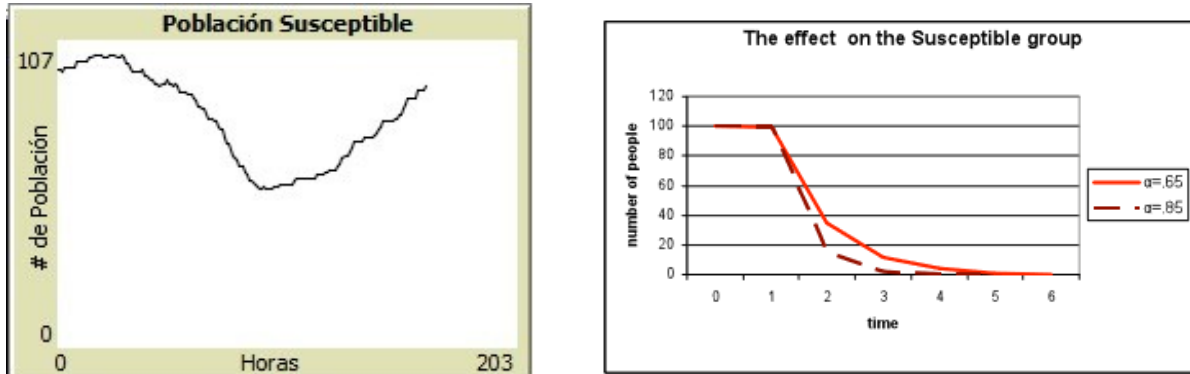


Figure 2: Comparison of the output

The figure 1 is the graphic that represents the susceptible population who has been infected around the time. In the right side we can see how is the susceptible population infected, it is simple to see that it stabilize. In the other hand, the susceptible population does not reach stabilization because of the factor of the birth rate that we add to our model; the individuals who born have the same probability of infection than the susceptible individuals. By this reason, the population after of come down, go up again.

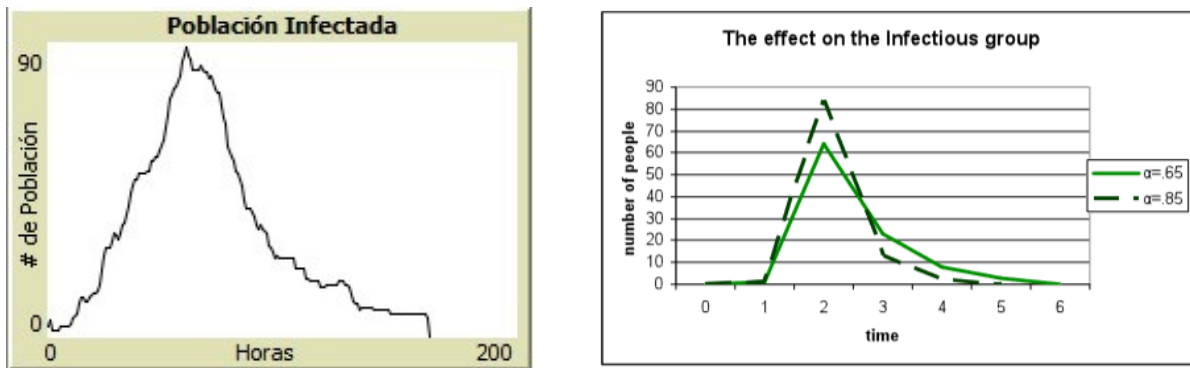


Figure 3: Comparison of the output 2

The figure 2 represents the infected population through the time. We can see that both graphics have some level of similarity. The higher pick can be interpreted as the higher percentage of infectious disease. After this, the individuals get heal.

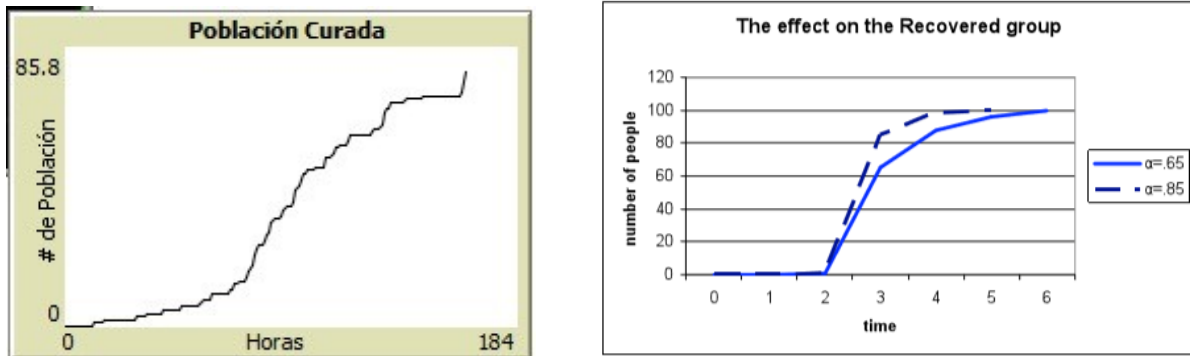


Figure 4: Comparison of the output

The figure 3, make evident the high recovering rate of the infected people because of the conditions of the model and the quarantine zone.

8 Experimentation

We first see the simulation of the probability of infection at 10 percent and the probability of recovering at 10 percent for the behavior of the infected population and of the recovered population is almost equal.

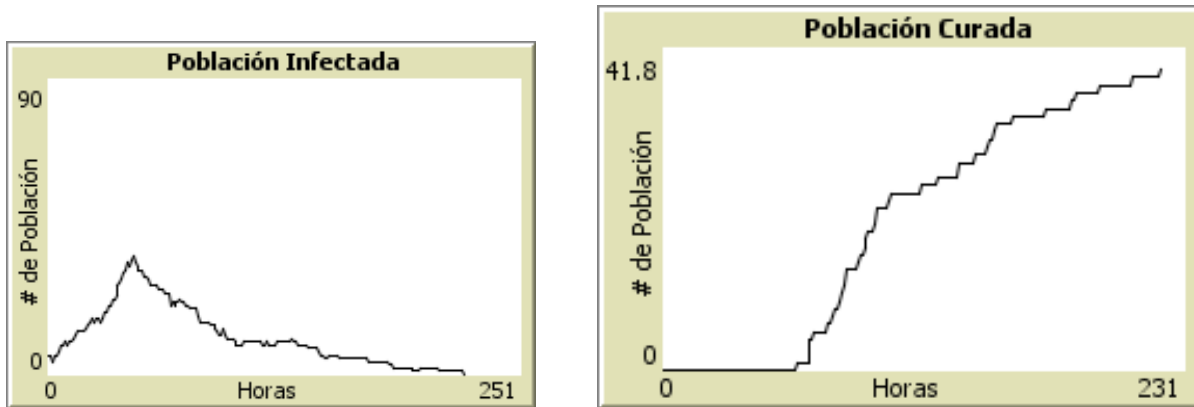


Figure 5: First experimentation

In the other hand, the behavior of the susceptible population grows up

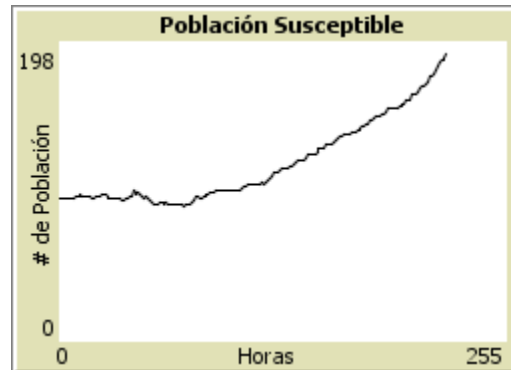


Figure 6: Second experimentation

Now, increasing the probability without going to the quarantine zone, the deaths of the population grows of a considerable way:

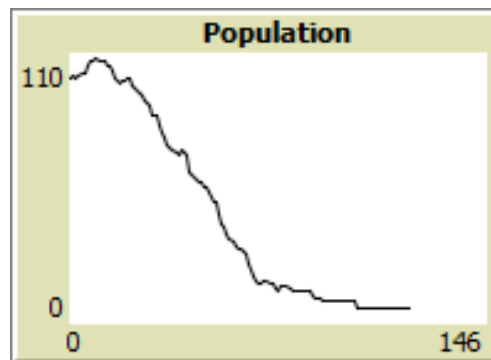


Figure 7: Third experimentation

In contrast with the initial scenario in which the population grows:

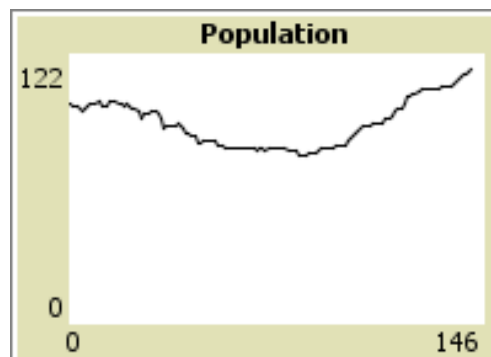


Figure 8: Fourth experimentation

9 Conclusions

- Agent-based models are an important tool in studying the mathematical modelling of infectious disease.
- In the introduction we provide the taxonomy of an ABMS for infectious disease epidemiology, i.e. all of this kinds of models should model the disease, society, transportation and environment. In this regard, our model achieve all this components. Disease is transmitted between the agents with some probability, the society is all the population in the model, transmission is given by the random movements of the agents and the environment is basic.
- SIR models, even being basic epidemiological models, are good approximations to diseases like the varicella or malaria.

References

- [Chokki, 2014] Chokki, S. K. . N. K. . A. P. (2014). A hybrid model for modeling the spread of epidemics: Theory and simulation. Recovered the day 3/06/2019 de <https://ieeexplore.ieee.org/abstract/document/7033457>.
- [Efraín De La Hoz Granadillo, 2017] Efraín De La Hoz Granadillo, L. L. P. (2017). Analysis of mathematical models of prediction of the behavior of epidemics in social groups through simulation based on agents. Recovered the day 3/06/2019 de <https://repository.unilibre.edu.co/handle/10901/13347>.
- [Elizabeth Hunter, 2017] Elizabeth Hunter, Brian Mac Namee, J. K. (2017). A taxonomy for agent-based models in human infectious disease epidemiology. Recovered the day 3/06/2019 de <http://jasss.soc.surrey.ac.uk/20/3/2.html>.
- [Johnson, 2009] Johnson, T. (2009). Mathematical modeling of diseases: Susceptible-infected-recovered (sir) model. Recovered the day 3/06/2019 de <http://op12no2.me/stuff/tjsir.pdf>.
- [Railsback and Grimm, 2010] Railsback, S. F. and Grimm, V. (2010). *Agent-Based and Individual-Based Modeling*. 1er edition.
- [Russell Connell and Skvortsov*, 2009] Russell Connell, P. D. and Skvortsov*, A. (2009). Comparison of an agent-based model of disease propagation with the generalised sir epidemic model. Recovered the day 3/06/2019 de <https://pdfs.semanticscholar.org/f8eb/8d2c494541a4301c9997961f79da02f47071.pdf>.