Towards the Creation of an Agent-Based Model to Simulate Dengue Dynamics in Human Populations

Héctor Sánchez and Edgar Vallejo

Instituto Tecnológico y de Estudios Superiores de Monterrey
Carretera al Lago de Guadalupe km 3.5, Atizapán de Zaragoza,
Estado de México, México
{a00466118,vallejo}@itesm.mx
http://www.itesm.edu/

Abstract. Dengue is a vector-borne viral disease that is spread throughout the tropical regions of the world. In the latest years the spread and cases of the disease have increased rapidly which has raised some alert in health organisations. The disease's dynamics involve a phase in a mosquito host which complicates the creation of models that are flexible enough to allow the thorough study of the interactions in the population. ABM's can provide flexible environments to test the biological system under different circumstances and configurations to analyse the different ecological variations that occur in these scenarios [1].

1 Motivation and Research Objectives

On 2012 up to 2.5 billion persons lived in risk of contracting the disease with 50 million infections and 22000 deaths (mainly in children) [2]. The virus is mainly transmitted by females of the *Aedes Aegypti* mosquito that need to feed on human blood for reproductive purposes. This is why the main control measures that have appeared in an effort to stop the spreading of the disease involve attacking the vector itself (two of the latest ways to do this are: biological *Wolbachia* control [3] and male sterilisation [4]).

Agent-Based Ecology is a discipline that is focused on the creation of models in which the biological entities are simulated with computational agents. The main advantage of using ABE's as an alternative to mathematical modelling is that it provides a more natural mapping of the model and gives us the ability to make predictions on ecological outcomes of changes in individuals' behaviours, heterogeneity between them, adaptations to environment, migration, etcetera; by making slight modifications to our model without the need of a new one [1].

This project is aimed at the creation of a flexible small-scale ABM that is able to simulate the main human-mosquito dynamics so that the data of the simulation can be used in a larger model to generate a larger population simulation with some control measures analysis. Other secondary objectives involve the exploration of hypothetical scenarios (such as a vaccine finding), social network analysis, combination of control measures, predation, fitness reduction and

other scenarios in which it is difficult to apply traditional population dynamics methodologies [1].

2   Previous Work

Modelling of vector-borne diseases has been generally not as popular as modelling of human contact transmitted diseases [5]. This in part due to the complex non-linear dynamics that come into play when several stages of diseases exist. Still some efforts and successes have taken place in this field such as the simulation conducted by Focks and his colleagues which focused on biological variables of the mosquitoes to analyse the spread of the disease taking into account population and weather conditions [6]. Other teams have focused on the creation of frameworks and large-scale concurrent mosquitos simulations [7–9] but there are still gaps to fill in the application of these models so that they are more than mere simulations and become something more useful to control the vector and ultimately the disease.

3   Methodology

This research will be divided in three phases that will use their own methods and techniques:

 – ABM: Probably the most crucial phase of the research as it is in it that the relevant biological variables and behaviours are defined and implemented. Great care in doing this has to take place so that the model is complex enough to be useful but not more, so that parametrization is a problem [1]. This stage will rely on thorough research on biological literature as well as statistical and optimization methods to calibrate parameters of the system.
 – Medium-Scale Model: Using the ABM in a large scale is currently infeasible due to the limited computational resources and scope of the project. In an effort to extract the behavioural relationships of the model we are proposing an intermediate step that would act as a bridge between the small-scale ABM and the large scale simulation. In this step the use of feed-forward neural networks and their ability to infer non-linear relationships could prove to be useful.
 – Large-Scale Simulation: Once the medium-scale model a large scale simulation can be created. One of the approaches we would like to explore is the use of cellular automata due to the fact that spacial relationships can be easily mapped to these models.

4   Research Progress

This work is still in an exploratory stage. Some tests and preliminary experiments have taken place in ABM phase in order to properly define the behaviours and limitations that are relevant to be able to characterize the variables to take into account when the system is further improved.

5 Preliminary Results

Early-stages experiments have been performed on a "sandbox" model of 200 mosquitos with basic biological behaviours. These experiments are aimed at exploring the capabilities and limitations of our system and although they are still in no shape to be extrapolated to the real world, we are exploring some ideas we expect to verify in the future. Some of these ideas and results are:

- optimization methods tests show that it is possible to use real-world data to calibrate some variables of the model.
- It seems to be possible to eradicate an isolated population of mosquitos by introducing sterile males.
- If female mosquitoes are allowed to mate more than once in their life cycle *Wolbachia* pathogen fixates in the population with the introduction of less infected individuals (figure 1). This could be an indicator that if the pathogen has some severe life-shortening consequences it could be difficult to achieve fixation.
- A baseline simulation with 5 humans moving randomly in the environment yields the expected result of a uniform Markovian distribution of probabilities and no small-world structures. Would the simulation a realistic scenario (with social groups) create cliques and small-world structures? [10] Early experiments show that this could be possible in a scenario where individuals alternated going to and back from work or that have a certain social behaviour during their day to day activities (figure 2).
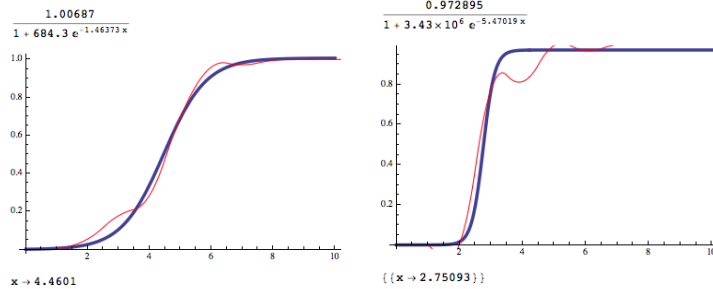
(a) Single Mating   (b) Multiple Mating

Fig. 1: Initial ratio of mosquitos introduced with Wolbachia (multiplied by a factor of 10) against the final ratio of mosquitos infected with Wolbachia after one month. The logistic function fit is shown on the superior part of the figure with the inflection point highlighted in the bottom. The graph on the left shows a scenario in which the female mosquitos were allowed to mate only once while the one in the right shows the same scenario but with the mosquitos being allowed to mate on multiple occasions.

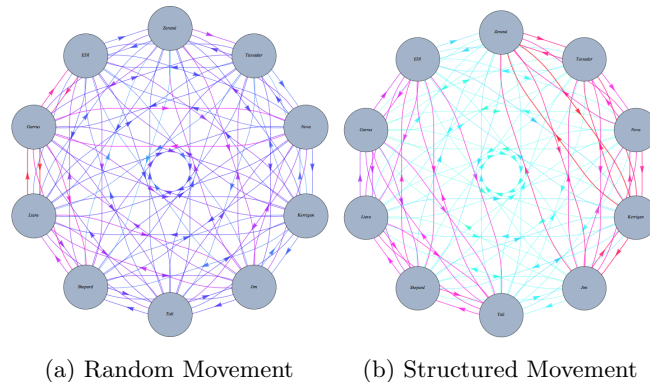(a) Random Movement   (b) Structured Movement

Fig. 2: Markov graphs of initial social experiments. The color and width of the line represent the probability of a mosquito biting a person at one point and then biting the connected individual on a following occasion (being light blue and thin lines the least probable and red and thick the most probable connections). Individuals were set to walk in a random pattern (graph on the left) and in a structured way (graph on the right) for each one of the experiments. It can be observed that the difference in behaviour impacts greatly the probability of contagion of the vector-borne disease.

References

1. Volker Grimm and Steven F. Railsback. *Individual-based Modeling and Ecology: (Princeton Series in Theoretical and Computational Biology)*. Princeton University Press, 2005.
2. WHO: Global Alert and Response. Impact of Dengue, 2012.
3. A A Hoffmann and B L Montgomery. Successful establishment of Wolbachia in Aedes populations to suppress dengue transmission. *Nature*, 476(7361):454–7, August 2011.
4. Renaud Lacroix and Andrew R McKemey. Open field release of genetically engineered sterile male Aedes aegypti in Malaysia. *PloS one*, 7(8):e42771, January 2012.
5. James O Lloyd-Smith and George. Epidemic dynamics at the human-animal interface. *Science (New York, N.Y.)*, 326(5958):1362–7, December 2009.
6. DA Focks and E Daniels. A simulation model of the epidemiology of urban dengue fever: literature analysis, model development, preliminary validation, and samples of simulation results. *American Journal of . . .*, 53(5):489–506, November 1995.
7. Carlos Isidoro, Nuno Fachada, F Barata, and Agostinho Rosa. Agent-based model of Dengue Disease Transmission by Aedes aegypti Populations. *Advances in Artificial Life*, 2011.
8. Chengbin Deng, Haiyan Tao, and Zhiwei Ye. Agent-Based modelling to simulate dengue spread. volume 7143, pages 71431O–71431O–10, October 2008.
9. James E Gentile and Gregory J Davis. A Framework for Modeling Mosquito Vectors. *Proceedings of the 2010 Summer Computer Simulation Conference*.
10. Rada Mihalcea. *Graph-based Natural Language Processing and Information Retrieval*. Cambridge, 2011.