Chapter 16
A Framework for Modeling Genetically–Aware Mosquito Vectors for Sterile Insect Technique

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ABSTRACT

Vector-borne diseases account for 16% of the global infectious disease burden (WHO, 2004). Many of these debilitating and sometimes fatal diseases are transmitted between human hosts by mosquitoes. Mosquito-targeted intervention methods have controlled or eliminated mosquito-borne diseases from many regions of the world but regions of constant transmission (holoendemic areas) still exist (Molineaux et al., 1980). To eliminate these illnesses, researchers need to understand how interventions impact a mosquito population so as to identify potential avenues for new intervention techniques. This paper presents a software architecture that allows researchers to simulate transgenic interventions on a mosquito population. The authors present specifications for a model that captures these transgenic aspects and present a software architecture that meets those needs. The authors also provide a proof of concept and some observations about sterile insect technique strategies as simulated by this architecture.

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1. INTRODUCTION

Vector-borne illnesses are transmitted between hosts by an intermediate organism fever, and lymphatic filariasis are mosquitoes. Vector-borne illnesses account for around 16% of the infectious disease burden globally. Malaria is the most serious as it infects 500 million people a year and kills over a million, mostly children under five years of age (WHO, 2004). Malaria occurs throughout the tropics but particularly plagues sub-Saharan Africa, where it is considered a holoendemic disease. Many studies have focused on the mortality of the disease on populations under 5 years of age (Crawley, 2004; Omumbo et al., 2004; Greenwood & Mutabingwa, 2002). In Africa, malaria causes 18% of childhood deaths (Bryce et al., 2005). Eradication of diseases like malaria will save the lives of countless children throughout the world. The United Nations has been successful at local eradication by targeting the mosquito population. Despite these efforts, holoendemic areas of transmission require a different intervention strategies (Gabaldon, 1978). Recently, there has been focus on using multiple, concurrent interventions and research into new intervention avenues. Of these, sterile insect technique (SIT) is arising as a promising method based on its success at controlling other insect populations. In SIT, males are lab-reared to be sterile or carry a dominant lethal gene. Females inseminated by these males pass the lethal gene to her eggs. Those progeny cease development at certain life-stages and die. Modeling and simulation can assist in the effort of looking into new intervention strategies be they combining existing interventions for a complementary effect or looking into avenues of new interventions. Many interventions can be modeled as a behavioral interruption of the insect. For instance, repellent could deflect a mosquito when it seeks a bloodmeal. However, other intervention forms, like SIT, require models to be aware of the populations phenotypes and adjust agent behavior accordingly. Breakthroughs are being made in modeling the transmission of these diseases, their active members and their dynamics (Gu & Novak, 2009; Bomblies et al., 2009), (Craig et al., 1999; Killeen et al., 2003). Among the various modeling techniques available, agent-based methods (Macal & North, 2008) show the most promise. In these models, each member of an interaction or system is treated as an individual with a set of rules dictating their behavior (Macal & North, 2008). By observing the interaction between agents and probing the system at choice times, system-level properties can emerge providing insight into the engine of disease transmission (Bomblies et al., 2008). This approach to modeling is conducive to evaluating the benefit of certain intervention methods and to anticipating possible behavior changes of the mosquitoes.

In this paper, we introduce a software architecture for modeling genetically-aware agents. Though the paper’s scope is the vector for malaria, this architecture can be expanded to other forms of agents by describing their own behavior and attributes. The system is capable of accurately encoding a mosquito’s life cycle and behavior in a structure we call a strategy. The strategy is flexible and can be adapted to accurately characterize a new genus, species or variation within one species. The architecture is designed such that there can be an arbitrary number of nested sub-environments which the agents can interact with when egg-laying and when they are in the aquatic stage of their life cycle. The movement of agents between environments is handled through message passing making this system ideal for parallelization across many cores or many computers with existing tools like OpenMP (Chapman et al., 2007) and MPI (Gabriel et al., 2004). Finally, agents are able to inherit phenotypes from their parents and these attributes can define their behavior.

We discuss the complexity of mosquito vectors first then outline the dynamics needed to capture genetic heredity. Section 4 introduces a software architecture that is capable of simulating genetically-aware agents. Finally, a proof of concept is presented along with a closing discussion.
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