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Agent based modelling of Malaria

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Agent Based Modelling of Malaria

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Dedication

I would like to dedicate this thesis to my children, Trinity and Toby. I hope that it proves to be inspirational to them.

I would also like to dedicate this work to the two mentors of my formative years. Dr. Liz Combes and Dr. Michael Martin. Without you, I would not be the person I am today, nor would I have gained the academic interests and disciplines that brought me to produce this work.

Acknowledgements

Abstract

Malaria is a disease that affects millions of people each year, with 90% of deaths occurring in Africa alone. The subject of this dissertation is the agent based modelling of malaria in populations that are suffering mass migration, living in unsanitary conditions or undergoing other effects of impoverished circumstances. The research is important due to the large numbers of people affected by malaria globally, with about 3.3 billion at risk. A large proportion of those exposed to the risk live in Sub-Saharan African countries.

Agent based modelling is a type of computational modelling which is commonly used for the simulation of interacting, autonomous agents. Using agent based modelling it is possible to assess the effects of interactions between individual agents and populations of agents on the whole system.

There is a limited availability of associated documentation and quantifiable research data in many areas of malaria spread research. To address the problem, three models have been built that investigate different aspects of malaria transmission. The models are developed with flexibility and adaptability as important factors in their use, so that they can provide verifiable results with potentially limited availability of data.

The three models produced are as follows.

- Malaria in Displaced Populations.
- Malaria in Peri-Urban Settlements.
- Malaria and Human Immunodeficiency Virus (HIV) Dual Infection.

The first model simulates malaria spread amongst a migratory population of agents. The second model simulates malaria spread amongst a settled population of agents living in peri-urban conditions with an associated mapping

model used to create custom environments based on real world settlements. The third model visualises the spread of both malaria and HIV through a population of agents that form partnerships to simulate sexual activity. The dual infection of malaria and HIV effects the rate of infection for HIV and the parasite burden of malaria in the hosts.

A further problem to be addressed is that agent based modelling for malaria has lacked a combination of sophistication and flexibility in past work. Modelling that inputs a strictly rigid set of variables, in the case of a complex system like disease spread, does not lend itself well to the simulation of scenarios where some data is unavailable. The models documented here were built with flexibility as an important factor in their design.

The results show that the models produce output that is consistent with real world malaria statistics. They demonstrate both qualitative validation, in the demonstration of realistic trends and also quantitative validation, in output of percentages of infected individuals and other disease related phenomena. There is some evidence of emergence in the Malaria in Displaced Populations model which is of particular interest. The conclusion is that agent based modelling shows promise as a method of evaluating the effects of malaria. The models and the research that accompanies them are important steps toward an understanding of what agent based modelling may contribute to malariology.

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Chapter 1

Introduction

This chapter discusses the motivation for this thesis project. It presents the hypothesis and a set of research questions that form the foundation of the work and the direction it takes. It also summarises the chapters as well as the three models produced.

1.1 Motivation for the research

The unifying theme of the thesis is discovering what can be achieved with agent based modelling techniques, when advancing understanding of a disease transmission subject with a minimal availability of defined variables. Malaria is a vector-borne disease that causes millions of deaths each year. A vector-borne disease is one which is carried via a vector species to another species, with more than one species playing host to the organism. Finding ways of understanding the complex nature of the malaria parasite and its propagation is crucial to its control. Agent based modelling has been closely associated with malaria research in recent years but more effective models are needed.

The work has been undertaken for the purposes of extending available modelling tools for the malaria research academic community. The models are appropriate for use by researchers, academic staff, students or laymen with an interest in discovering how malaria propagates in situations which are not currently well documented scientifically. They have some use in what-if scenarios as predictive models, if accurate data is available to the user.

Where computational models of malaria spread are available, they do not lend themselves well to the modelling of disease spread in scenarios where there is a shortage of

reliable census data or in highly specific but little understood immunological threat. The importance of fulfilling that requirement in modelling is evident in the fact that mass human displacement, widespread habitation in peri-urban townships and multiple disease interactions in human hosts are real and substantial threats to people in regions of high risk of malaria such as sub-saharan African countries. Populations are displaced frequently in these countries, with the resultant change in malaria infection rate from the originating country to the next meaning that the individuals concerned are increasingly susceptible to infection.

The impact of the research is a contribution to the understanding of an internationally recognised ongoing biological threat. Particular focus has been placed on the modelling and understanding of how environmental factors contribute to the threat of malaria in sub-Saharan African countries, where over 90% of malaria infections are recorded. Extending the study further, the impact of another disease transmission issue has been explored and that is the dual infection of HIV with malaria. The dual infection plays a part in increasing the mortality rate of both diseases. Understanding how the disease interaction alters the rate of transmission and the mortality within a population is of great importance. There have, as yet, been only a small number of publications and quantities of research data released on the subject to the general scientific community.

Dividing the problem into three distinct parts, human agents, mosquito agents and environment, each of those parts in themselves constitute problems of disorganised complexity. In order for these three parts to be united in a model with a coherent result, it is necessary to study the characteristics of the whole abstracted system rather than large numbers of individual attributes. The expectation is that if a small number of simplistic features of these problems are brought together, the results will reveal a high fidelity to real world disease spread data that demonstrates the same quality of output as if a greater number of complex features were taken into account. Should it be successful, applying the resultant models to experimental data from less researched disease spread scenarios will reveal a greater understanding of their associated problems.

1.2 Hypothesis

The hypothesis is that with using more advanced agent based modelling techniques, it is possible to contribute to the understanding of malaria transmission where there is limited documentation and quantifiable research data. Flexibility and adaptability are important considerations, so that the models may provide verifiable results with a potentially limited availability of data.

1.3 Specific Research Questions

The following questions were posited to define the direction of the research.

1. What environmental factors can be simulated for a malaria transmission model?

Environmental factors include such things as terrain, temperature, water sources, dwelling places and vegetation.

2. How can human population interactions best be modelled with the minimal of complexity?

Human behaviour and decision making processes are greatly complex problems that are not easily replicated in agent based modelling. This work attempts to produce realistic effects from a combination of the most simplistic of agent behaviours.

3. Using an agent-oriented platform, how much complexity can be achieved whilst maintaining a relatively low computational cost?

It is important to make the models available as teaching and research tools to those working in malariology [38]. In order to make the models useful to researchers, it is necessary to consider that those in the field, working in parts of the world where computer hardware is antiquated or otherwise limited, may not have access to equipment that will support high processing requirements. Likewise, there is not always access to expensive software packages or certain operating systems. For that reason, the models have been developed using an agent based platform that is Open Source, that will work on any Java installation and requires a minimal of processing power.

4. How can multiple disease interactions best be portrayed in an agent based environment?

This final question is addressed in the third model to be produced for the project. It presents issues both programmatically and in terms of creating a suitable visualisation.

The research questions support the hypothesis by defining the practical objectives of the thesis.

1.4 The Agent Based Models

The three models that have been built for the thesis are summarised as follows.

1.4.1 Malaria in Displaced Populations

The Malaria in Displaced Populations model allows the user to simulate real world scenarios relating to malaria transmission amongst Internally Displaced Persons (IDPs). The model offers the ability to upload satellite images of terrain, which may then be enhanced using drawing tools to create extra features for the map. If the user desires it, selecting a button on the interface will trigger the model to automatically identify areas of water present in the map image. The drawn features and any automatically generated water areas, will be recognised by the model and acted upon appropriately by the agents. The human agents are randomly distributed at locations throughout the environment, according to integer values selected from a series that encompasses the number of possible placements on the NetLogo patches. From their point of origin, they will move and act according to which one of the four basic human behaviours the user has selected. Their placement does not exclude terrain which may appear in the selected topography, such as valleys and mountains, but it does exclude areas of water.

The mosquito agents are generated automatically, in quantities selected by the user, on to the water patches. Once generated on water patches, the mosquitoes follow the course of randomised movement throughout the model's environment, interacting with the human agents to transmit malaria. In this model, the malaria transmission occurs

from mosquito to human and from human to mosquito, so that previously uninfected mosquitoes may be infected during the course of the model's run, as well as vice versa.

1.4.2   Malaria in Peri-Urban Settlements

The Malaria in Peri-Urban Settlements model simulates real world scenarios where a human population has settled into a peri-urban housing environment. This model has an associated, secondary model which is used to generate maps for use with the primary model. The associated Map Maker model prompts the user to upload a map image. The image may be a drawing of the user's design or a satellite image taken of the region of interest. Alternatively, the user may draw a map directly into the Map Maker interface. If the user has selected to draw a map over an uploaded image, there are a number of buttons and sliders which, when selected, choose elements that may then be drawn using a computer mouse, onto the view of the interface. Once a map has been successfully created, the Map Maker model allows the user to save it as a image file to any location on their computer.

The Malaria in Peri-Urban Settlements model makes use of the maps generated using the Map Maker model by determining which patch colours are associated with recognised terrain features such as homes, water, vegetation and bare ground. The model may then be set up for an experimental run using sliders, buttons and other input relating to malaria transmission, average family sizes, mosquito numbers, mosquito swarming behaviour specifics and water quality statistics.

1.4.3   Malaria and HIV Dual Infection

The Malaria and HIV dual-infection model simulates a scenario whereby infection with both malaria and HIV is taking place in the same population. Co-infection of malaria with HIV has been found to be responsible for an increase in geographic malaria. This model takes a different approach to the previous two in the fact that there is no simulated environment. This model focuses entirely on the effects of the interacting disease on infection rates in the population.

The transmission of both diseases and the interaction rates of the human agents is user controlled. Other controls include those associated specifically with the spread of

HIV, such as coupling tendency, partnership duration and condom use.

1.5   Summary of Thesis Chapters

Chapter two is a review of relevant background and literature associated with the thesis. It begins by providing the necessary malaria foundation to understand the direction of the work and then details the Susceptible Infected Recovered (SIR) model, which is commonly used as an epidemiology mathematical and system model. The SIR model is used to define state transitions for infection amongst populations. Complex systems and their associated problems are outlined and evaluated in terms of epidemiology. The chapter then goes into the background of agent based modelling and associated techniques that have been applied to disease modelling since the earliest days of the field. The section then moves on to discuss the rationale behind using agent based techniques for the modelling of disease before covering associated and similar work to date, purely in relation to malaria modelling.

Chapter three concerns the Malaria in Displaced Populations model. The chapter begins with a background to the mass migration of human populations that results in a change to the levels of exposure to the malaria parasite. The chapter then goes on to discuss the implementation of the model and the code procedures that make up its functions. The next section describes the interface, the use of its controls and what may be expected from the plots. Agent behaviours are outlined and explained before the chapter moves on to demonstrate how the model may be used with real world data sets. The results from experiments and validation of the output are documented. The chapter concludes with a discussion about the model's use.

Chapter four concerns the Malaria in Peri-Urban Settlements model. The chapter begins with a background to the effects of poor sanitation in peri-urban settlements, that results in an increased proximity of inhabitants to mosquito breeding sites. The chapter then goes on to discuss the implementation of the model and the code procedures that make up its functions. The next section describes the interface and a secondary map making model that has been developed for use with the primary Peri-Urban Settlements model. The results from experiments and validation of the output are documented. The chapter concludes with a discussion about the model's use.

Chapter five concerns the Malaria and HIV Dual Infection model. The chapter begins with a background to the effects of dual infection with malaria and HIV that results in an increased rate of infection from both the virus and the parasite. The chapter then goes on to discuss the implementation of the model and the code procedures that make up its functions. The next section describes the interface and how the visualisation may be interpreted. The results from experiments and validation of the output are documented. The chapter then concludes with a discussion about the model's use.

Chapter six concerns the conclusions drawn from the thesis as a whole and provides an insight into the possibilities of future work. The hypothesis is revisited and then the original research questions are summarised once more, with an evaluation of whether objectives drawn from those questions were met. Limitations of the models that were encountered during the research are discussed. The chapter then outlines potential for future work before concluding by revisiting verification and validation techniques for agent based modelling.

Chapter 2

Literature Review

The purpose of this chapter is to review the literature that is relevant to the thesis. It begins in Section 2.1 by describing the process of Malaria parasite transmission that is required to understand the features of the models and the direction of the research. In Section 2.2 it details the susceptible-infected-recovered model which has been used as the mathematical foundation for producing the disease spread procedures. There follows in Section 2.3, a rationale of agent based modelling as a suitable means for producing the work and a brief section referring to the origins of agent based modelling and its variants in Section 2.4. Section 2.5 discusses the more prominent work in agent based disease modelling, before Section 2.6 specifically details disease modelling in NetLogo [14], the platform used for the modelling produced in this thesis. Section 2.7 concerns geosimulation techniques that are particularly relevant to agent based techniques available to the NetLogo platform. Sections 2.8 and 2.9 are about complex systems and steps that may be taken to deconstruct complexity in a system to be modelled. The alternate approaches to modelling, simple versus descriptive, are the subject of Section 2.10. The agent based platforms discussed in Section 2.11 are reviewed more thoroughly in Section 2.12 and their uses for disease modelling covered in their separate sub-sections. The chapter draws to a close with Section 2.13, a conclusion to the topics covered.

2.1 Malaria Transmission

Malaria is caused by a parasite transferred to the blood via a vector species, namely the sixty types of anopheles mosquito that are able to carry it [62]. The parasite itself is

a genus of protozoa known as Plasmodium. Four species of plasmodia are responsible for causing malaria. These four strains give rise to very different malaria effects in the human host, ranging from the severe and life threatening to the milder, relatively asymptomatic varieties.
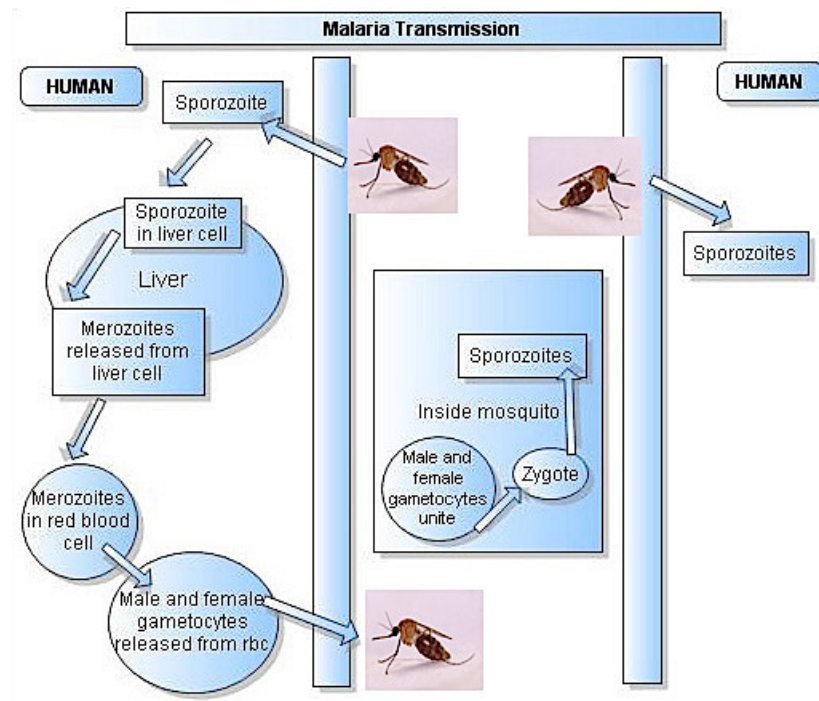
Figure 2.1: Life cycle of the malaria parasite.
Mosquito image courtesy of Muhammad Mahdi Karim, www.micro2macro.net
(accessed 03/02/2014).

Figure 2.1 demonstrates the life cycle of the malaria parasite as it cycles through its journey between human and mosquito hosts. Whilst taking a blood meal from a human host, the infected mosquito injects a form of the parasite known as a sporozoite along with it's saliva. The sporozoites travel in the blood to the host's liver, where they mature and reproduce. Merozoites are formed over the next two to three weeks and these pass back into the blood to transform erythrocytes into self-destructive factories, where they reproduce. Once the erythrocytes disintegrate the merozoites enter other erythrocytes and in the process toxins are released. The cytokines released by the presence of the toxins produce symptoms in the host [62].

The symptoms include fever, sweating, chills and anaemia. An additional effect of the parasite is the damage to fine capillaries (particularly those of the brain) due to disintegrated erythrocytes. Damage to capillaries in the brain results in cerebral malaria, which often leads to death of the host.

When some of the parasites have reached the sexual phase of their life cycle, they are ready to be removed from the human host in a mosquito's next blood meal. Male and female parasites meet in the gut of the mosquito, where they produce offspring. The resultant sporazoites migrate to the salivary gland of the mosquito, where they are ready to begin the cycle again. A great difficulty in combatting the parasite that causes malaria lies in the complexity of it's many stages of life. Each stage requiring a specific immunological response from the host.

2.2   The SIR Model

For the validation of malaria simulation results, the Susceptible Infected Recovered (SIR) model and its variants have been used as a basis for designing the agent interactions. The model is an algorithm that defines three or more states of being, the three basic states are Susceptible to disease, Infected with disease and Recovered from disease [48].

Figure 2.2 shows several state diagrams which explain the Susceptible Infected Recovered model as it was originally conceived, along with some of the many examples of mutations to the original. The topmost digram, Susceptible Infected Recovered, shows a state shift from susceptible to infected to recovered, with no return to a susceptible state from the recovered condition. This use of the model is only accurate in a scenario where recovery from the infection denotes a complete immunity to re-infection. The second state diagram, Susceptible Infected Susceptible, describes a condition whereby none of the infected individuals recover, but may be continuously exposed to the infection, perhaps even gaining an increased burden from the disease as the cycle continues. The Susceptible Infected Susceptible system may relate well to a continued exposure to malaria, since repeated exposure results in increased parasite load in the human host [63].

This second scenario is true for some diseases, including the HIV virus. The third
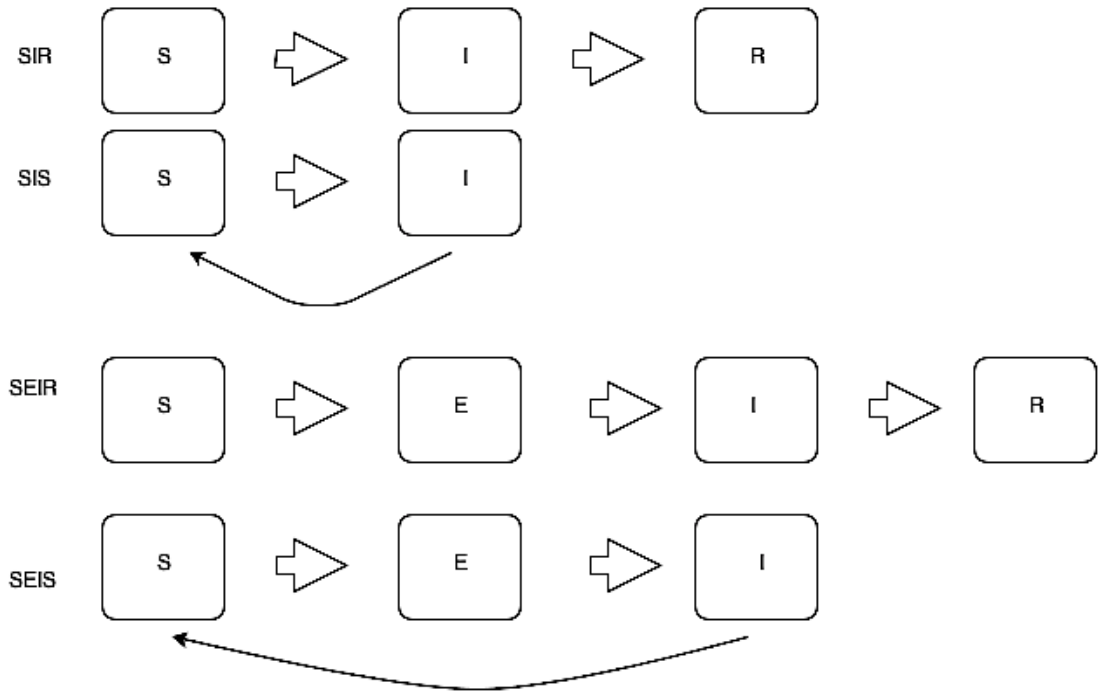
Figure 2.2: Several state diagrams pertaining to SIR model variants.

state diagram is Susceptible Exposed Infected and Recovered, susceptible to disease, exposed to disease, infected by disease and recovered from disease. It is similar to the original SIR version, but with the added state of exposed between the states of susceptible and infected. Adding the exposed state allows for the modelling of a phase of infection whereby the individuals must be exposed to the disease before they become infected. Exposure may come in the form of partaking in some activity for example. In the fourth state diagram, the element of exposure is still in place, but no recovery state exists.

In a similarity to the third state diagram, in the Susceptible Exposed Infected Susceptible variant, the individuals must enter into a situation whereby they are exposed to the infection before becoming infected. The progression goes from susceptible to exposed to infected, before returning in a loop to susceptible. In this final model illustrated, those infected may again become susceptible to being exposed to the infection, but no recovery state is included. This situation is similar to the propagation of the HIV virus, but with greater accuracy to a real world situation, since a given activity is necessary for the individual to enter into the exposed state before becoming infected

[44].

The state diagram shown in Figure 2.3 most accurately visualises the process of transmission of malaria as modelled by the work of this manuscript. The broad, white arrows show the transition from one state to the next and the thin, black arrows show how individuals may also move in to and out of states in additional ways. If a thin, black arrow enter a state from an external location that is not marked by a state, this represents entry to the system due to births or the joining of the population from another population. If a thin, black arrow exits a state, without joining another specified state, this represents deaths of individuals that were previously part of the system. An individual may shift state from susceptible to infected if preventative measures such as anti-malaria drugs or barrier methods like insecticidal spray or bed nets do not offer protection. A person may also shift states from susceptible to immune if a naturally developed immunity is developed or if a course of anti-malarial drugs is taken. An individual may shift states from immune to susceptible if anti-malaria treatment is ceased or if the natural immunity is no longer effective due to a change in malaria exposure from the surrounding environment. An individual may go from a state of infected to immune, if anti-malarial treatment is commenced during infection and is used continuously thereafter.
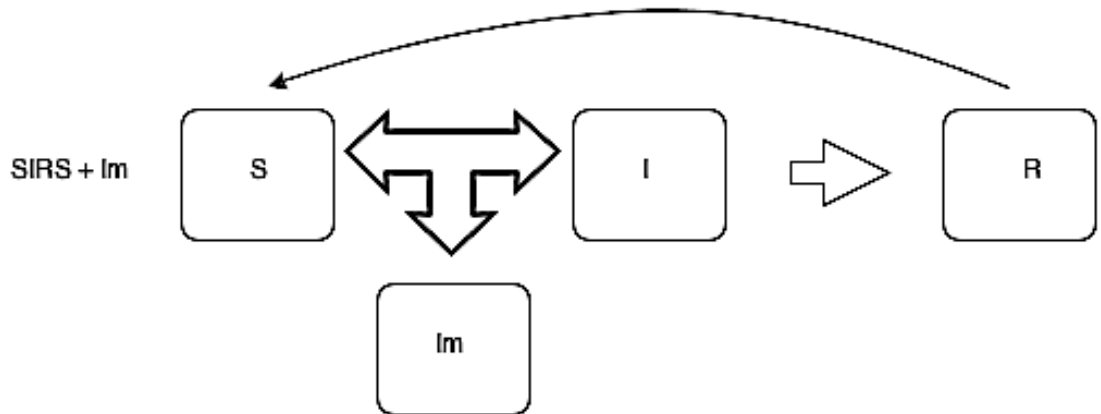
Figure 2.3: A state diagram that describes the parasite transmission of malaria.

The set of differential equations associated with the SIR model would be vital to the production of a mathematical model of disease spread, but due to the fact that the models produced here are agent based, it is only the state transitions that must be

taken into account. The measurement of the numbers of agents existing in each state at any given time may be derived from figures produced as output of the model at any interval. The important numerical data is that found in real world population statistics for rate of malaria transmission in a given region, along with the likelihood of parasite infection after exposure to mosquito bites. Since a vector borne disease like malaria is dependent on the interaction of more than one host species, the shift in states is related to interaction of the first host species with the second host species. In effect it is possible to explore two SIR models shifting in states at the same time, one for each host species, but that is only explored in the first of the three models presented here, the Malaria in Displaced Populations Model.
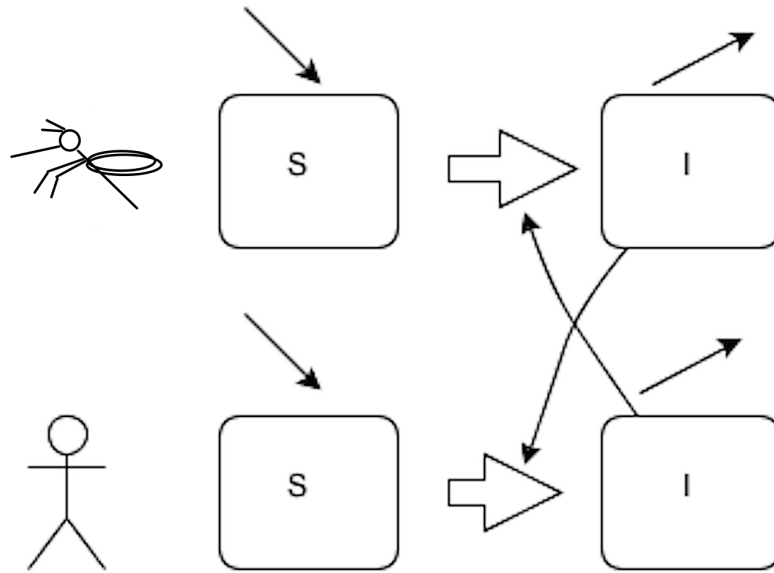
Figure 2.4: A state diagram that describes the inter-related parasite transmission of malaria between human and mosquito hosts.

A state diagram that takes in to account the interaction between the human and mosquito hosts has been created and is shown in Figure 2.4. It is based on work produced at the Chalmers University of Technology in Gothenburg [47]. In a simple state diagram, that does not take into account recovery, the above case becomes true. Infection in either host leads to infection in the second, once interaction has taken place. The curving arrows between the infected states of both hosts and the transition point between susceptible to infected, show that connection. Actors are continuously incoming to the susceptible state for both hosts, which would be realistic for a population in

flux due to natural phenomena of births and migration form one population to another. Actors are continuously outgoing from the infected states of both hosts, which would be realistic for a population in flux due to deaths and in the case of the human hosts, being removed from the state diagram by medical interventions or the development of some natural immunity.

The Susceptible Infected Recovered model is dynamic. Although not always the case, it is usual for the numbers in each compartment to fluctuate over time. In cases of a disease with a short infection period, the fluctuation is of particular importance, meaning that the cycles of the outbreaks can be examined. When fully utilising the model for its mathematically deterministic uses, all arrows should be labelled with the transitional rates.

2.3   Rationale of Using Agent Based Modelling

Computational agents are rule-based and dynamically interactive with one another and often also their simulated environments. The modelled systems in which they are utilised are studied for emergent patterns, equilibria or other meaningful output. The ability to generate systems that offer insight into real world phenomena is one of the main contributions of the field to date.

Agent based modelling does not begin with relating equations that work together to create expected or theorised observations. Agent based modelling instead begins with identifying behaviours with which individuals interact and integrate with one another. These individuals have a shared environment. By focussing on defining agents in terms of observables associated with the individual agent and exploring the micro-foundations of global patterns, the modeller moves away from reliance on system-level information. System-level information and observable output does emerge from an agent based model which can be compared to observables that are already known, or in the case of unknown outcomes to complex scenarios, may offer insight into how basic interactions of individuals might lead to global patterns.

It is for these reasons that agent based modelling has been chosen as a method for producing models that allow investigation of the complex scenarios associated with the spread of malaria. With census data and medical records frequently limited or entirely

unavailable, the detailed information required to construct purely mathematically based models may not be accessible. Instead, the information available to researchers in the field of malaria parasitology may come in the form of highly localised statistical datasets, observable human behaviours and knowledge of certain global patterns. Other work using agent based modelling to simulate observed, complex biological trends, in order to provide hints towards working out relevant mechanistic hypotheses, has proven to be successful [30].

2.4 Origins of Agent Based Modelling

Agent based modelling is a computational approach for simulating the actions of agents that interact within an environment. The agents may simulate the interactions of electrical impulses between synapses, the shared chemical stimuli between organs in the human body or travel routes across continents for large population movements. Any study, from the micro to the macro, which can be broken down into two or more separate agents with a definable interaction, is a potential area of research for modellers using agent oriented techniques.

The concept was originally put forward by Stanislaw Ulam and John von Neumann while working at Los Alamos National Laboratory in the 1940s with their cellular automaton. The Von Neumann cellular automata were originally developed to provide an understanding of the logical process for machine self-replication. The first of these cellular automata were produced without the use of a computer [27]. Though far simpler machines have been identified as capable of self-replication, such as crystal growth [53], Von Neumann's automata allow for the study of construction universality and evolution.

The Von Neumann Automata, in its simplest form, is a diamond-shaped neighbourhood that can be used to define a set of cells surrounding another cell. Beginning at the origin of a grid of cells, a two-dimensional cellular automata will radiate out from the origin, in iterations that follow the rule of the Von Neumann Neighbourhood Range. Figure 2.5 is a visualisation of Von Neumann Neighbourhood growth where r is the Manhattan Distance of a set of points from the original cell.

One of the most famous uses of cellular automata is Conway's game of LIfe. Created by the mathematician John Horton Conway in 1970. The Game of LIfe was brought about when Conway drastically simplified Von Neumann's rules of cellular automata.
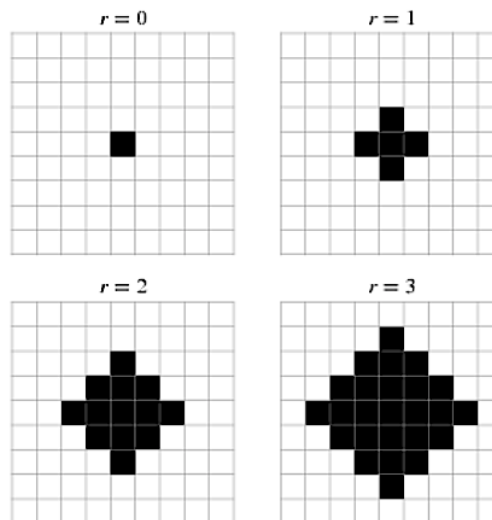
Figure 2.5: Von Neumann Neighbourhood.
Image from Wolfram Mathworld, mathworld.wolfram.com (accessed 03/02/2014).

The universe consists of an infinite two-dimensional grid of square cells, each of which is in two possible states, alive or dead. Each cell interacts with its eight neighbours and in each discrete unit of time, known as a tick, one of four transitions occurs. The first generation is created from each cell adhering to the four rules simultaneously. Conway experimented a great deal before he settled on the rules for the Game of Life. The greatest possible simplicity was the desirable outcome. [10].

The rules were outlined as follows.

- Any live cell with fewer than two live neighbours dies, as if caused by under-population.

- Any live cell with two or three live neighbours lives on to the next generation.

- Any live cell with more than three live neighbours dies, as if by over-crowding.

- Any dead cell with exactly three live neighbours becomes a live cell, as if by reproduction.

The Game of Life produces many different classes of patterns, including still lives, oscillators and spaceships. These patterns grow, in some cases indefinitely, such as

with the Gosper Glider Gun, produced by the Massachussetts Institute of Technology in 1970. Figure 2.6 visualises the Gosper Glider Gun as it produces spaceships. The similarity of the generations to biological processes is notable. The Game has been extensively developed through the years experimentally and discovered to produce some patterns which fire glider shapes that create new objects, including copies of the original shape. A universal constructor can be built, that incorporates Turing's complete computer.
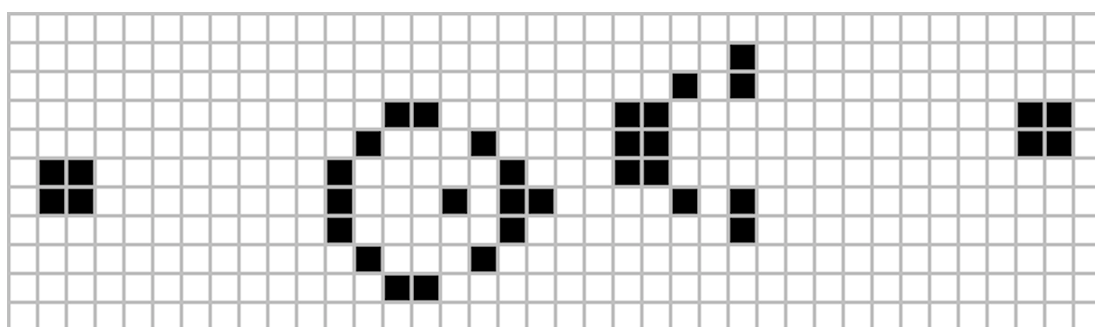
Figure 2.6: Gosper's Glider Gun.
Image Source: Wikipedia Commons.

Turing's complete computer is a hypothetical machine rather than a piece of computing technology. Alan Turing devised the hypothesis in 1936. It has since been used as a means of explaining the functions of a CPU inside a computer and to teach computer scientists the limits of mechanical computation. When a Turing machine is capable of simulating further Turing machines it becomes a Universal Constructor.

These early simulations using rules and behaviours associated with actions on cells over discrete time frames led to the field of Artificial Intelligence known as Artificial Life. Artificial life is a sub-field which includes the study of genetic algorithms. With these first algorithms as a basis, agent based modelling took off as an experimental tool of interest to scientists in all areas of research and also the non-scientific community. Those that wished to study the patterns in traffic flow or the economy for instance. It has never been intrinsically associated with computer science, though it certainly has strong roots in that field and in mathematics.

Cellular automata have since been used to good effect in infectious disease modelling. An strong example of which is the Java based cellular automaton framework

developed by the Institute of Biomedical Engineering in Austria [58]. Using the SIR mathematical model as a basis for mapping transitional states, the framework maps the spacial and temporal aspects of infectious disease spread in large populations. The project simulates the spread of a mock disease similar to the avian flu. As an initial development, the simulation shows promise in the use of cellular automata for the visualisation of disease spread, but it does not demonstrate effects which would be caused by travel or activity along transport routes. Cellular automata have limitations in generating realistic human interactions due to the nature of their rules, which map effects that radiate out from a central point. The neighbouring cells only are affected by the states of the initial cells and so the complex nature of human interaction and travel may be difficult to replicate using a purely cellular automata based framework without some further extension. Figure 2.7 shows a visualisation image produced by the cellular automaton framework from the Institute of Biomedical Engineering in Austria. The warmer colours, ranging from red to orange to yellow, show the highest concentration of infection in those regions of human habitation. The cooler colours, ranging from blue to pale grey, represent the lowest concentration of infections in those areas of habitation.
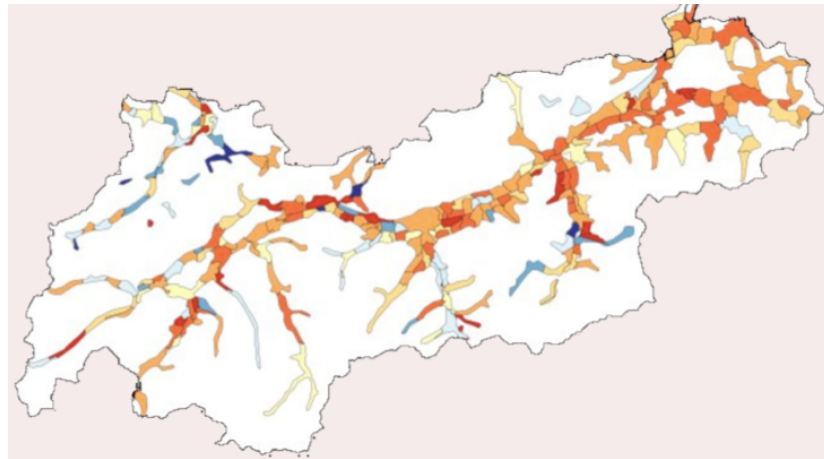
Figure 2.7: A visualisation from the cellular automaton framework produced by the Institute of Biomedical Engineering in Austria.

It is the concept of evolution in a machine process and the resultant emergent properties of a rule set that provided a basis for the foundation of agent based modelling. Due to intensive processing requirements, computational agent based models did not become widespread until the 1990s. The choice to implement a model is usually due to a system being too complex to be analysed purely with mathematical expressions of

other forms of experiment. It may be the case that the experiments are too expensive to otherwise run or are undesirable.

Agents themselves are state-based and contain information based on those states. They may demonstrate reproduction and death. In models of sufficient complexity, the environment in which the agents are situated will have spacial relationships that result in interactions with the agents. Time representation is also an important factor. Time may be represented synchronously as a time-driven model or asynchronously as an event-driven model.

The characteristics of agent based modelling are heterogeneity, agent behaviour specifications, explicit space and complex interactions. A model will usually utilise some randomness in its features and may present emergent behaviour [60]. It is the emergence and evolutionary forms that may arise in agent based models that form the key interest in their development. Emergence is the property of an agent based model that sets it apart from purely mathematically based modelling. Emergent properties of a model system may lead to transparency of understanding of otherwise opaque, disorganised complex systems of vast numbers of attributes that are otherwise not traversable with experiment.

2.5 Agent Based Disease Modelling

It was during the mid-nineties when the computational power available to developers made it possible to create models of the necessary complexity for advances in disease modelling.

One of the most noteworthy and powerful agent based tools developed for epidemic simulation is the EpiSims platform [20]. It has been developed at the same laboratories that Von Neumann worked at during his career in Los Alamos. EpiSims is what is known as a biosurveillance tool, meaning that it it may be utilised for predictive modelling of disease spread scenarios. With output from EpiSims it is possible to analyse an outbreak and determine which control structures might be the most feasible and effective responding to an outbreak in a given region.

The EpiSims environment models the United States. It splits the region into fifteen

sections, each section seeded with around twenty million synthetic individuals. The tool is applied to assess the impact of airborne infectious diseases. Its applications include the following.

- Parameter values for within-host based on demographic or geographic characteristics.

- Targeted mitigation strategies by demographic or geospacial characteristics.

- Impact of disease on workforce absenteeism by more than 1000 industry classification.

- Impact of reactive behavioural modifications such as fear-based home isolation.

Evaluation of the EpiSims model to determine confidence in its results has included comparison of its output statistics with published survey studies [20]. Figure 2.8 is some sample output from the EpiSims model. It shows how a measure of the symptomatic percentage of a population measured against the number of days since epidemic onset is used to determine the predicted length of school closure.

Another large scale disease surveillance system, which is currently under way, is NASA's Malaria Modelling and Surveillance project [51]. The project utilises satellite imagery and other topographical and atmospheric data taken from orbit of the Earth in order to supply an agent based modelling framework with accurate environmental input. It makes use of the Global Situational Awareness Tool (GSAT), which is currently used for risk assessment for U.S. forces. The project is focussed on the study of malaria spread, globally, with a focus on understanding the links between malaria transmission and environmental parameters. In discovering patterns of disease spread through these means, it is hoped that malaria risk will be modelled to a great enough accuracy, that an early warning system may be put into effect in the most highly affected regions. NASA's project does make use of agent based modelling, but the Malaria Modelling and Surveillance project brings together a number of techniques and computational analysis methods of which agent based modelling is one part of a larger system.
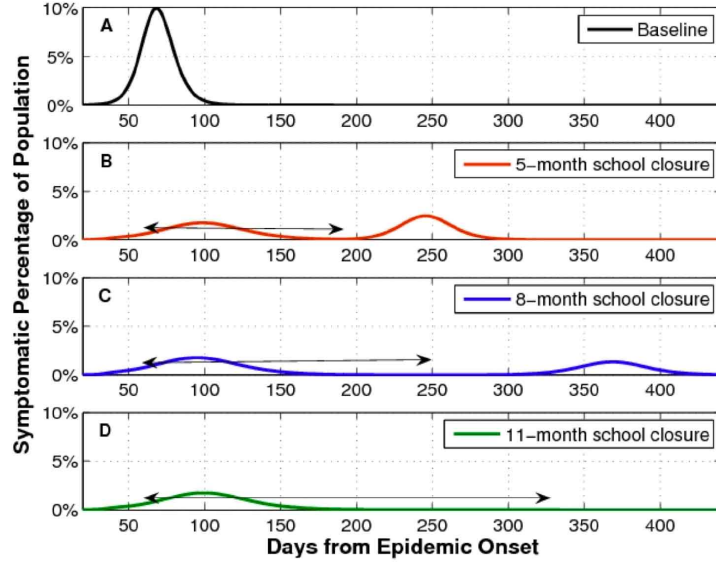
Figure 2.8: EpiSims example output.
Image Source: http://www.lanl.gov/programs/nisac/episims.shtml (accessed 03/02/2014).

2.6 Disease Modelling Using NetLogo

NetLogo is a multi-agent framework used as a modelling environment. Released in 1999 and designed by Uri Wilensky, it was strongly influenced by its predecessors, StarLogo and Logo [13]. NetLogo has several qualities that make it a desirable programming platform for use in creating models that explore the several malaria transmission situations that have been described. Firstly, it is computationally inexpensive to run. In many cases, the researchers that investigate malaria do not have access to computer systems with expensive, efficient hardware or software packages, since they are out in the field in small villages in African countries. Most of rural Africa remains without access to the advancements in computing technologies that are taken for granted in more developed parts of the world. For that reason, the fact that NetLogo models can be run on any computer that supports Java is an important factor in choosing it as a development platform. Secondly, NetLogo is open source. Its accessibility to the NetLogo modelling community via shared online repositories means that it may be tested, distributed and further improved without licensing and copyrighting restrictions. Models produced in NetLogo are contributions to a global network of scientific researchers, with no barrier to entry other than access to a computer system with a Java platform [14].

Prior to the work of this thesis, NetLogo modelling of disease spread has had a low complexity in terms of representing population dynamics and the quantity of disease variables programmed. Table 2.1 documents the NetLogo disease models released to the NetLogo modelling community. The column for transmission contains the form in which the disease is transmitted and the column for diseases represented lists the diseases that the model simulates. Notably, transmission of disease via a vector species only appears as a feature in one previous model, also concentrating on malaria. In terms of interaction between agent population and the modelled environment, NetLogo has much to offer that has yet to be exploited for use in disease modelling. Given how the malaria vector requires particular environmental conditions in order to propagate, the role of the modelled environment is particularly important. NetLogo also provides a solution to maintaining disease statuses associated with spacial characteristics in its use of 'patch' agents, which form the model space and can be programmed with attributes in the same way as the mobile agents, known as turtles. The Netlogo environment acts upon the agents interacting with it so that patches in the environment behave as agents themselves, with attributes and changing states.

Table 2.1: NetLogo disease transmission models

Model Name*	Transmission	Diseases Represented
Disease Solo	Contact	Contact
AIDS	Interaction (contact)	AIDS
Virus	Contact	Contact trans.
Disease in Groups	Contact/airborne	Contact/airborne trans
Disease Doctors	Contact	Contact trans.
Sick Town	Contact/airborne	Contact/airborne trans.
Virus2	Contact	Contact trans.
Bird Flu	Contact/airborne	Bird flu
Disease	Contact	Contact trans.
Malaria Control	Vector	Malaria
Typhoid Fever	Water-borne	Typhoid

* These models are found either in the NetLogo Models Library or the NetLogo User Community Models [14] [15] with the exception of the Bird Flu and Disease models, which are found elsewhere [7].

A review of NetLogo disease modelling approaches has been published in the Triple C open access journal [39]. The review compares three agent based modelling ap-

proaches and evaluates them for the accuracy and clarity of their output. The first is a population based model that represents a host population divided into four infection states. The second is a population based model with the same structure as the first model but with a second population of agents that represent mosquitoes. The third model is an individual based model, operating with the scheme of the second model applied to each individual agent. Its parameters are defined at an individual level rather than a population level as it is in the first two models.

The review concludes that the output of the three models was alike in terms of quantifiable output. The differences between the models were that the individual based model dealt well with details of specific measurements and interventions whereas the population based model performed best with an input of average magnitudes and not particular values. Individual based models are concerned with the output from individual agents in the system, whereas population based models are concerned with the generated output from interactions of the agent population as a whole. The second conclusion was that population based models were easily interpreted numerically in a straightforward quantifiable analysis, but the individual based model required a larger number of simulations in order to read notable outcomes and interesting trends. It was noted in the report that the lack of standardised analytical methods for individual based models continues to be a problem.

2.7 Geosimulation Techniques

Geosimulation is a catch-all phrase that describes a wealth of approaches to modelling that have come to the foreground in recent years. The style offers an alternative to rigid systems that isolate agents and entities in multi-agent models, and particularly those that simulate spacial units and environments. The geosimulation approach seeks to create a flow of data throughout the modelled environment, such that quantifiable attributes are continuously updated throughout the run of agent interactions. In a more traditional approach to multi-agent interactions, the spacial content of the simulated world is separate and isolated from the interaction of the mobile agents [22]

NetLogo, as a platform, is ideally suited to experiment with geosimulation oriented techniques. Its turtle agents that comprise the mobile agents and its patch agents, that comprise its world, all possess the ability to share numeric, boolean and other

data relating to their attributes. The exchange of data is continuous throughout the models' run and therefore may be measured at any given time stamp. It is also possible to simulate real time, by altering the methods by which NetLogo's time units, ticks, are measured and recorded.

Models one and two from this thesis explore the use of mobile agent and environment agent interaction to good effect. In the Malaria in Displaced Populations model, the benefits of agent based modelling over mathematical modelling are made clear with the emergence of an increased infection rate due to the basic obstacle avoidance of areas of water in the world. The interaction of mobile agents with topographical features in the simulated world offers unique insights into potential real world phenomena that would otherwise not arise should the models be purely mathematical in nature.

In model two, Malaria in Peri-Urban Settlements, the separate Map Maker model allows the user to create maps of terrain for use in the model that may closely resemble regions in the real world, if the maps are overlaid onto satellite imagery or some other suitably scaled map image. This second model creates a closer link with the simulated environment and the visualisation of it, through use of maps. The detail in mapping water in particular, lends well to the accuracy of mosquito agent interactions with the water patches.

Due to NetLogo's approach of building a model entirely out of agents, both the environment itself, the stationary artefacts within that environment and the mobile agents, NetLogo is well suited to exploring geosimulation techniques. The NetLogo environment has been created in such a way that flow of information throughout the modelled world can be achieved with ease. All aspects of the world might interact freely and in limitless ways and a simulation of real-time may be achieved with ease. Recording of output using simulated real-time steps is also possible and may be as thorough as the developer or user desires. The following code snippet shows a simple turtle and patch interaction in NetLogo code.

Listing 2.1: NetLogo turtle procedure for detecting water.

```
ask turtles [
     fd 1
   ask patch-here [
```

```
      pcolor blue
]]
```

2.8 Complex Systems Modelling

Epidemiological modelling, and indeed biological modelling as a subject, deals with the analysis of complex systems [25].

Complex systems come in one of three forms or parts. Problems of simplicity, disorganised complexity and organised complexity. An example of disorganised complexity consists of a system of interest that comprises a large number of variables, sometimes in the thousands. In these cases it is necessary to study the characteristics of the whole abstracted system rather than any number of the individual attributes. Creating, in the process, a way of understanding a simple abstraction derived from a complex abstraction. It is only necessary to understand the nature of the input fed into the system and for it to be possible to evaluate the output. Organised complexity presents a different form of structure, such that a medium number (less than those of disorganised complexity), of interrelated attributes produce a whole system. Evaluating systems of organised complexity presents a problem due to the lack of extensive tools available for analysis. The non-linear behaviour present in systems of organised complexity make it difficult to devise useful analytical methods.

In the case of disease modelling we are presented with an example of disorganised complexity. A vast number of variables exist in relation to the spread of disease. Some are clearly identifiable, such as temperature change in the climate, the usual lifecycle of the virus or parasite in question or the rate at which it reproduces. But some are much more difficult to quantify mathematically, such as any natural immunity that the hosts may benefit from over time, or resistance to chemical treatments in the virus or parasite. There are many variables that it may be impossible to adequately account for in a model, such as the complexity of human behaviour in any given situation and the intricacy of creating a natural environment [68].

To account for these issues and still hope to produce a model that offers useful output it is necessary to consider what number of available attributes of the system will likely produce output from the model that are comparable to known real world

data. The most basic attributes to consider are those associated with the propagation of the disease. If the propagation of the disease itself is modelled with enough accuracy to be deemed reliable, all other attributes of the system such as interaction between agents and the layout of the simulated environment, may be as simplified or as elaborate as the developer chooses, for it to be possible to develop models which are valuable as scenario-exploring simulations. To create models that offer a more traditional approach of creating predictive scenarios, it becomes necessary to develop appropriately real-world agent behaviours and environmental features. The work presented in this thesis offers both scenario-exploration and predictive modelling tools.

2.9   Deconstructing Complexity

In order to produce a suite of models that are relevant to current malaria research topics and their associated foundation in real world human populations, it has been necessary to pinpoint certain over-reaching features that the models should possess. These features range from topical environmental features from the sub-Saharan terrain, that is the subject of the models, to certain patterns of human and mosquito behaviour that have been encountered and scientifically documented. To show the selected features as clearly and concisely as possible, each of the three chapters describing the three models has a series of subsections after the Implementation section. The subsections deal with each of the model's basic features and describes both how they are implemented and why they were selected for modelling. There are a number of associated references that corroborate the author's selection of these features, along with the arguments for their validity.

2.10   Simple versus Descriptive Modelling

The KISS principle (Keep It Simple and Short) is widely used in agent based modelling. The approach supports the idea that the whole is greater than its parts, and with that in mind, the simplest possible approach to agent interactions and situation is adopted, with complexity added only if and when it becomes required after a setup of the basics. Another design option has been suggested that is dubbed the KIDS (Keep It Descriptive Stupid) approach [35]. KIDS differs from KISS in that rather than modelling the bare basics of agent variables and attributes, a large range of target phenomena

is considered initially, including widely dispersed evidence that may be anecdotal. A simplification process is then applied, but only if it proves necessary. The argument that the originators of the KIDS principle put forth is that often modellers strive for simplicity even when there is no practicable reason to simplify a construct, such as in the case of clearly defined mathematical equations.

Malaria spread is a complex systems modelling problem, and therefore, a situation where potentially many thousands of variables may be taken into account. Considered from a KIDS perspective, if anecdotal evidence and empirical data taken into account also, the many associated facts pertaining to the disease and its hosts may well become impossible to account for. For this reason, it has been necessary to approach the model development from the direction of the KISS principle, the more widely accepted approach. This has not been a matter of simplicity for simplicity's sake, but a question of necessity [46].

The models are built from NetLogo procedures that are as simplified as possible in function, with agent behaviours that are basic and associated disease variables that are few. However, from this collection of simplistic programming procedures, it is possible to discover emergent properties that appear pertinent to the behaviour of the agents' real world counterparts. In the case of the Malaria in Displaced Populations model, when negotiating the water present in their environment, in order to traverse the terrain and continue their migration, the agents came into extended contact with the greater part of the mosquito agent population, thus increasing their chances of contracting malaria. In a real world scenario, this behaviour would be unavoidable, when migratory populations come upon large bodies of water, and that is only considering a situation whereby the population is simply moving past the obstacle. If one were to consider that the population may make a camp near to the water for a period of time to make use of it as a resource, then an even greater increase in human-mosquito interaction may take place.

2.11   Biological Modelling with Agent Based Platforms

There are many agent oriented programming platforms that are or have been used for disease modelling specifically or biological modelling generally. These several platforms have varying degrees of portability across operating systems and restrictions of use

due to licensing, processing power and visualisation sophistication. Dependant on use, the restrictions and benefits of each platform become more or less important. For the purposes of the work documented in this paper, NetLogo possesses some of the more favourable qualities as a programming platform.

A benefit of using the interpreted NetLogo environment for the modelling of biological events, is the ability to easily account for time and space dependent events simultaneously [31]. The programming involvement necessary for NetLogo development is considerably less than that required for many other agent-oriented toolkits, either with a proprietary license or available as freeware. NetLogo's visualisation sophistication is relatively high, while it's processing requirement is low enough for use on computer hardware in the low to middle range price bracket.

Table 2.2: Comparison of Agent Based Toolkits Used for Biological Modelling

Platform	Primary Domain	License	OS
NetLogo	General Purpose	Freeware	Java Platform
AnyLogic	General Purpose	Proprietary	Java Platform
Cormas	Natural Resources	Free to modify	L, M, W, U
ECHO	Ecological Models	Open Source	
Framsticks	Evolving Systems	Proprietary	L, M, W
LSD	Social Sciences	GLP	L, M, W
MAML	Social Science	Open Source	L, W
MASON	General Purpose	Free License	Java Platform
MASS	General Purpose	Proprietary	Java Platform
Moduleco	General Purpose	GPL	L, M, W
OBEUS	Urban Sim	Freeware	W, M
Repast	Social Sciences	BSD	Java Platform
SimBioSys	Evolutionary Sim	Artistic	C++ Platforms
Swarm	General Purpose	GPL	L, W, M
VisualBots	Excel Sim	Freeware	W

* Operating System Key: [L] = Linux [M] = Macintosh [W] = Windows [U] = Unix [S] = Solaris

Table 2.2 makes a comparison of agent based toolkits used for biological modelling. There is no framework available specifically for vector-borne disease modelling, despite the relatively high societal impact of this form of disease transmission on a large percentage of the world's population, compared to that of other disease transmission types. The mortality rate of Malaria as an example, already discussed earlier in the thesis, is a

significant problem. A tool of this type would be useful in several capacities, including the planning of medical recovery efforts, prioritisation of relief operations and resource allocation.

2.12 Review of Agent-Based Languages Used for Disease Modelling

Those agent based platforms that are listed in Table 2.2 which have published disease spread models available for review are mentioned in this section.

2.12.1 AnyLogic

The AnyLogic platform allows for the use of three simulation paradigms; discrete event, agent based and system dynamics. It also allows for hybrids of the three. It supports visualisation using a 3D interface, which is greatly customisable. The platform is used to great effect as a dynamic visualisation and simulation tool for presentations. AnyLogic has been utilised as a platform a simple, agent-oriented disease simulation. The epidemic Spread model created by a team from The Institute of Analysis and Scientific Computing at the Vienna University of Technology [37]. The work uses one of the extended SIR models found in epidemiology, the SIRS version mentioned early in this chapter, which allows for recovered individuals to enter back into the cycle of disease, returning to a susceptible status. This model does not extend beyond a basic representation of contact based disease spread.

2.12.2 Cormas

Cormas is a programming environment primarily used for natural resource management. The Cormas framework may be used to develop simulation models which portray coordination modes between individuals and groups that share common resources. A number of tools developed using Cormas are available on the Ecosystem-Based Management Tools Network, an online data base serving the needs of environmental researchers and resource allocation projects [9]. It is of particular interest to those working to improve coastal-marine spacial planning and management decision making. Cormas has been used for epidemiologically related modelling, and an example of this is an event

based model produced by the Australian Bureau of Agricultural and Resource Economics to study the effects of the propagation of a plant disease [36]. Several modules within the model capture characteristics of disease, the farming systems and incursion response and management of an outbreak in a given region.

2.12.3 MAML

The Multi-Agent Modelling Language (MAML), was created by a team of researchers from the Complex Adaptive Systems Laboratory of the Central European University in Budapest, Hungary [42]. The intention was to produce a language that was accessible to modellers without a computer science background. The accessibility of MAML was aimed at reducing the problematic issue of modellers needing to combine a thorough understanding of several aspects of model creation before modelling became accessible to them as a tool. These various aspects being design, parameter space research and result-analysis. Its creators attribute it with a similarity to the Swarm platform, since it adopts the agent-based modelling paradigm within a discrete event simulation framework. A model is made up of a collection of independent agents interacting via messages and events.

MAML may be used with or without a graphic user interface, although responsibility for design of the graphic interface is given to the user, so it has a less immediate visualisation aspect than some similar languages. MAML is mentioned as a tool for potential use in the modelling of disease spread amongst primates in the book Primate Ecology and Conservation [64], but no such model is presented with the text.

2.12.4 MASON

Multi-Agent Simulator of Neighbourhoods (MASON) is a Java based multi-agent simulation library, which is not a stand alone platform. It is intended for use as a foundation for large scale java based simulation. It comes with a suite of visualisation tools for both 2D and 3D development. The MASON libraries have been listed as being used for epidemiological modelling. One instance of disease modelling use with MASON is with a model produced by Liliana Perez and Suzana Dragicevic [57]. The specific focus of that work was to integrate geographic information systems into an agent-based modelling approach with the aim of understanding the spacial diffusion of contagious

disease in an urban environment.

2.12.5 Swarm

Swarm is a suite of modelling tools developed at the Santa Fe Institute [17] by a team of multi-disciplinary researchers led by Christ Langton, the founder of the field of research known as artificial life. The purpose of Swarm was to advance the development of complex adaptive system oriented agent based modelling. Since its inception in 1999, many hundreds of people around the world have contributed to its continued open source development, further extending the applications of the suite of tools. The Swarm development group holds an annual conference known as Swarmfest, typically held at a different research university each year. Contributors, users and researchers gather to present papers and discuss the current state and the future development of Swarm. With a strong following in multi-disciplinary areas, it continues to be a popular modelling platform. It has been used extensively for disease modelling.

2.13 Verification and Validation of Agent Based Models

Currently, epidemiological modelling mainly takes three approaches, those approaches being mathematical, network theory based and agent based. Network theory based models and agent based models often take similar approaches and are complementary to one another. Mathematical approaches to disease modelling, also referred to as Equation Based Models (EBM), are often still verified purely by the SIR model. EBMs that are disease focussed commonly use partial differential equations to evaluate a system.

As with agent based modelling evaluation, partial differential equations allow measurement of events across space and time and attributes specific to representatives of individuals in the system. Equation based modelling expresses connections between observable parts of the system. Agent based modelling begins with an expression of behaviours with which individuals may interact with one another. Those behaviours may be independent of the greater system as a whole, whereas with equation based modelling the system must be considered. [1].

Agent based modelling has been criticised for its lack of reliable validation technique. Many models are validated using informal and qualitative procedures which make it difficult to compare their quality to other models that may be considered similar [23]. Researchers in the field continue to call for the absence of validation structure to be redressed [2].

One important step in the currently accepted process of validation is model alignment, whereby a model is compared to other models of its type that have well validated output. In the case of the models in this thesis, there are no similar models which can be used for the purposes of model alignment. Instead another well recognised method for analysis of an agent based model has been utilised; cross validation. With cross validation, also known as statistical evaluation, a model's output is compared to real world values from appropriate data such as census and other research statistics available.

A system of sensitivity analysis may be used during the process of validation. Sensitivity analysis is a comparison of the input and internal parameters of a model, whereby it is determined how close a relationship those values have to parameters in a real world system [67].

Unlike the classical modelling community, the agent based modelling community has yet to put forward a core set of theoretical models from which to draw comparisons and form a basis for the foundation of successive models. In fact, the very principles involved in agent based modelling promote diversity and innovation. With no core modelling precepts to draw from, comparative evaluation and validation is further hindered [3].

Where similar models do exist, a process of cross validation or cross model validity testing may take place, whereby a new model may be compared in performance to a related one with similar features. It should be understood that no model is strictly correct in producing a correspondence between its own features and that of the real world. With that in mind, cross-validation is considered a flawed technique [66].

The statistical evaluation of the malaria transmission procedures has revealed output data and modelling effects that have a high fidelity to real world malaria statistics. All further modelling procedures were then built upon that foundation of similarity

to real world disease spread. Any hard coded variables that were necessary, and they were very few, since the object of the research was to create flexibility over rigidity, have been taken directly from figures released from census or other available data as referenced in future chapters.

2.14 Conclusion

Agent based modelling of malaria is a subject which has not been widely pursued previously, but is now finding a place in several forms as a means of experimenting with census and statistical data. The two closest competitors to the work of this thesis are the Los Alamos EpiSims project [20] and NASA's Malaria Modelling and Surveillance project [51]. The EpiSims project lacks the flexibility to model multiple regions and differing populations, since its design solely implements a simulation of one, fixed urban area. The models presented in this thesis have the flexibility to model many different terrains and population sizes. NASA's malaria modelling project utilises several computational tools, only one of which is agent based. The modelling presented in this thesis is a unified body of work that purely utilises an agent oriented approach.

An agent based approach is a suitable platform for development of the malaria models of this thesis. It allows the study of observables associated with the individual agents, when using individual based techniques. That means the user may move away from reliance on building and evaluating purely system level data and features. In the case of malaria transmission scenarios that are sparsely documented, building and observing individual based attributes of the model compensates for the absence of complete data sets. The resultant flexibility is desirable.

Cellular automata, as an alternative technique for the modelling of infectious disease spread, lacks the capacity to simulate the complex dynamics of human interaction that agent based modelling provides. By selecting NetLogo as the framework for building models, users of the models benefit from them being open source and cross-platform. The fact that the models will run successfully on any system running a Java platform, even with relatively low processing speeds, meets the objective of creating models that are accessible to researchers working in locations such as small African townships.

The connection between geosimulation techniques and NetLogo's inbuilt methods for integrating its simulated environment with its mobile agents has been discussed

in this chapter. Geosimulation is a strong approach for handling phenomena such as malaria infection, that has many complex interactions between the agents and their environment taking place. The complexity of the subject matter, in terms of the disease itself and the human and mosquito agent behaviours has been discussed. Malaria as a disease represents a disorganised complex system, with many thousand of variables that are difficult if not impossible to fully catalogue and implement programmatically. Approaches for deconstructing that complexity have been put forward in this chapter, such as ensuring that the models are as flexible in what data is required for input as possible.

In the final portion of the chapter, the alternative agent based platforms to NetLogo are evaluated and discussed, along with any notable contributions made to disease modelling that those platforms have been used for. The decision to build the models of this thesis with NetLogo is supported by a table of comparisons with the other platforms.

Chapter 3

Malaria and Population Displacement

This chapter concerns the development and implementation of the Malaria and Population Displacement Model. It begins with a section detailing the subject of human migration and how it effects the transmission of malaria. The chapter then goes on to present the implementation of the model programatically in its various parts. The interface, its development and use, is then described. The next section goes into detail about the model's agent behaviours, which simulate simplistic facets of human behaviours during times of migration and the behaviours of swarms of mosquitoes over land and water. The chapter then reveals how real world data sets were used to run the model and the results that were gained from that analysis. Finally, there is a section that describes how verification of the model's output was obtained and how validation of the model's accuracy was ensured.

3.1   Human Migration

Since many forced population movements occur in areas where malaria constitutes a major health threat, or between areas with differing malaria infection rates, there is room for further scientific investigation into the effects on human mortality and the morbidity of the disease. In recent times, with global initiatives such as Roll Back malaria bringing to light the plight of people involved in complex emergencies and displacement, focus on improving malaria control for these situations has increased [16]. It is unfortunate that due to the high priority of other survival needs by such

displaced populations, malaria control activities have been, retrospectively speaking, given a lower degree of emphasis. Even movement of fairly small numbers of people can change the malaria infection rate in a region. Large irrigation schemes, logging, mining and hunting can bring displaced populations into high malaria risk areas [24].

Table 3.1 shows the large numbers of displaced individuals recorded in recent years. The first column lists the country in which internally displaced individuals are located. The second column provides the number of internally displaced individuals recorded as present and recorded by the listed country. The third column compares the previous figure with the numbers documented by the United Nations in their own surveys. The fourth column provides the date the survey was last carried out.

Table 3.1: Internally Displaced Person Figures for African Countries. *

Country	No. IDPs (rounded)	UN figures	Date of survey
C. African Republic	192,000	192,000	July 2010
DR of the Congo	1.71 million	1.71 million	November 2010
Ethiopia	350,000	300,000	June 2008
Kenya	Undetermined	350,000	June 2008
Nigeria	1,210,000	Not Available	September 2007
Somalia	1.6 million	1,500,000	January 2010
Sudan	4.5-5.2 million	4.1 million	January 2010
Uganda	166,000	166,000	January 2010
Zimbabwe	1,000,000	Not Available	September 2008

* Data provided by the Internal Displacement Monitoring Centre (IDMC), Norwegian Refugee Council, Geneva.

The focus of the media is often concentrated on the political vulnerability of displaced populations, their state of malnourishment and exposure to communicable diseases stemming from close human proximity, such as cholera. The reality of the situation is that frequently the highest death toll stems from entering malarious areas. Lessons learned from malaria control in stable situations are inadequately put into practise in complex emergencies. The reasons for such inadequacy could be attributed to the difficulty in studying the effects of malaria during the period of crisis and within the region of crisis. Often the observations of what may alleviate the effects of malaria can only be made retrospectively. The modelled environment presented in this thesis may be used predictively for estimating the effects of malaria in future population displacement. It forms a foundation for exploring how multi-agent modelling of malaria

spread could be furthered for use in associated research. It should be viewed as an initial step in the process of developing models of increasing complexity and adaptability.

3.2   Design Objectives

The first aim for the design of the Malaria in Displaced Populations model was to model a number of human behaviours that may reasonably be expected in situations of population displacement. Another objective was to design a working system of interaction between mosquito agents and human agents. The third objective was to produce a malaria transmission procedure that realistically simulated transference of the disease between the host and vector species. Another aim for the design of the model was to simulate a realistic transfer of the malaria parasite between the mosquito vector species and the human hosts, with a two way infection procedure. The final objective for the model was to simulate a real world terrain in the model's environment in which water and dry land were differentiated by the agents.

3.3   Implementation

The Malaria in Displaced Human Populations model has been developed using two breeds of agent that are established to interact with the NetLogo patch environment. The NetLogo patches are agents that may take any shape and have variable attributes of their own. They make up the environment in the NetLogo modelling space and may be used to interact with the mobile, turtle agents that move over them. One agent type has mosquito-like attributes and the other has human-like attributes. The movement of both mosquito and human agents is set to be similar to that of the agents' real life counterparts inhabiting sub-Saharan regions, with four simplistic human behaviours available to the user to select and a simple chaotic behaviour associated with the mosquito agents. The possible human behaviours are migration, encampment, chaotic and chaotic around home. Here, in this context, the word chaotic is used to describe movement that has some randomised element of direction change. It is not intended to refer to the modelling of chaos as in a model representing chaos mathematically.

When determining which attributes should be allocated to the modelled environ-

ment and agents, it was necessary to evaluate known factors that influence real world malaria transmission in areas affected by mass human displacement. The following subjects were discovered to be of significance to the work as found in the papers referenced along with them.

3.3.1 Medical assistance

Selecting the most effective treatment and preventative measures for malaria in situations where a population has been displaced from their usual living situation has proven to be a great challenge to aid workers that enter into these often chaotic scenarios [55]. Medical assistance from aid workers is commonly allocated to treating multiple pressing health issues, just as it would be in situations where the patients were not displaced from their homes. However, where the people have been up-rooted form their point of origin and therefore separated from their regular health care regimen and any medical records that may exist, it becomes much more difficult to effectively allocate medicines and care to the individuals concerned. Just as importantly, the pressing health issues that arise from a displaced population, living in often greatly reduced circumstances, are issues that were of lesser concern previous to displacement, such as widespread dysentery and typhoid as well as malaria. Unsanitary conditions, crowded living spaces and limited available shelter are the main causes of these serious health problems [50].

With limited resources and immediate funding available, aid workers must use their judgement to provide assistance to those with the most pressing needs. It is usual to prioritise a health risk such as dysentery, which is seen to have an immediate effect on mortality, over what would appear to be the less pressing issue of malaria, which has a more long term effect on mortality. When the statistics relating to internally displaced people become available after the fact, i.e when monitoring of the population has occurred and records are available for the study of health care provision to these populations, it become clear that malaria is equally, if not more so, a threat to mortality as dysentery or typhoid [24]. Experimenting with the level of health care available to internally displaced people using the Malaria in Displaced Populations model allows the user to determine how much available assistance is necessary to make a difference to malaria infection levels.

3.3.2 Immunity

A varying number of individuals in a given population will have a certain amount of immunity to malaria infection. For instance, nursing infants acquire a limited but significant protection from their mother. Also, those that have been frequently exposed to malaria infection over a sustained period of time may acquire a resistance to the parasite [59].

3.3.3 Water Sources

Areas under the Western Nile region have a lower mosquito spawning intensity than those North of the equator. The mosquitoes are less likely to cluster around vegetation. Giving rise to a greater migratory movement from West to East. When the mosquitoes migrate to their autumnal feeding grounds, they will have less access to the vegetation and hence the nectar that feeds the females in between their gravid stages.
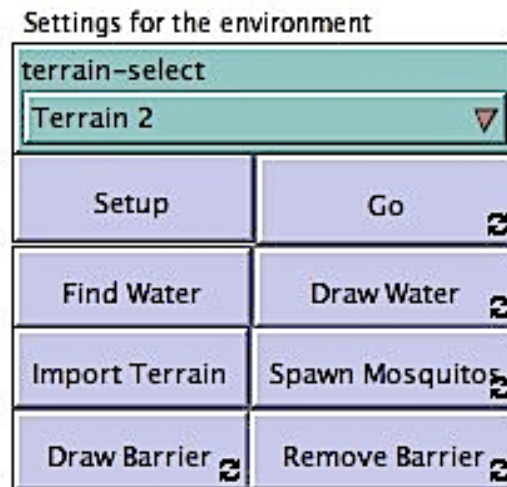
Figure 3.1: The buttons on the model's interface that are used for draw procedures.

Proximity to productive breeding sites for mosquitoes has an impact on malaria infection. Mosquitoes will not oviposit in running water, since it does not provide the necessary environment to promote larval growth, so regarding what is necessary for furnishing the model's environment, only still water need be represented [40]. Water sources may be automatically generated into the environment by using the model's feature of identifying water regions from an uploaded map image. However, if some of

those water sources on the map image are running water, it is recommended that the user draw the still water sources into the model's environment by using the model's Draw Water button and the computer mouse. The model offers the ability to draw several additional features on the model's terrain, that are then interactive with the mobile agents, using the mouse. These features are water patches, insecticidal barriers and encampment areas.

3.3.4   Bed Net Usage

Utilising bed nets during night time hours offers protection against mosquito bites. Provision of bed nets to internally displaced people will only offer beneficial protection from mosquito bites of the individuals have sufficient space and shelter available to properly set up the nets. In many cases these facilities are not available so the user may decide not to set up the model with bed nets available to the human agents. If the model is being used to experiment with modelling conditions where these basic necessities for bed net use are available, there is the option to allocate bed nets to a a percentage of the population. It should also be noted that in the case of setting up the medical assistance feature of the model, the doctor agents, once they have interacted with a regular human agent, will provide that agent with treatment for malaria and a bed net [29].

3.3.5   Insecticidal Spray

Applying insecticidal spray to the perimeter of villages and the perimeter and interior of individual homes offers protection against mosquitoes. The use of insecticidal spray is represented in the model by providing a physical barrier for entry by mosquitoes into the patches surrounded by the insecticidal barrier. Insecticidal barriers may be drawn into the environment by the user with the computer mouse [61].

3.3.6   Human Migration

The displacement of large groups of people from one region to another leaves them vulnerable to malaria infection and propagates the disease into regions where Malaria was previously a lesser known threat [32]. For the purposes of investigating global patterns that arise from simplistic behavioural traits, there are four basic behaviours

programmed into the model for the user to experiment with. The behaviours themselves are described in Section 3.5.

3.3.7 Encampments

Once the migratory period of displacement has passed, it is common for internally displaced people to settle for short or extended periods at encampments provided for them by the host towns and cities, or else by aid workers that have travelled to the region to set up aid camps [24]. The model explores the implications of clustering internally displaced people into encampments. The encampment locations can be drawn by the user by clicking the Draw Encampment button on the interface and using the computer mouse to designate any patches in the environment to be camp facilities that the human agents will seek. It is possible for the user to apply insecticidal spray and nearby still water sources and hence mosquito breeding grounds, to the encampment areas.

The code in Listing 3.1 is taken from the go procedure in the Malaria in Displaced Populations model. The go procedure runs with every tick, initiating the procedures that are listed within it so that they are run continuously unless a stopping point is specified in the code. In the go procedure for this model there is an if statement that ensures the model will cease to run at the user's desired number of ticks. The user specifies the maximum number of ticks via an input parameter on the interface. Two other procedures listed within control the movement of the mosquito agents from their original locations at the model's starting point and also the movement of the human agents, depending on which behaviour has been selected by the user. Finally, the go procedure updates the plots that provide the user with graphs of the model's progress, before moving on to the next tick. The tick is NetLogo's unit of time. The speed at which ticks progress can be coded, so that they correspond to real world units of time.

Listing 3.1: The code of the go procedure in the Malaria in Displaced Populations model.

```
to go
    if ticks > max-days [ stop ]
    spread-mosquitos
    move-humans
```

```
    update-plot
    tick
end
```

3.4 The Interface

The model's interface, seen in F igure 3.1, consists of sliders, buttons and choosers corresponding with malaria transmission and agent and environment related factors which may be altered and adjusted to suit the user's experimental set ups. The central view may also be adjusted so that the world can be seen in 3D, allowing the user to orbit the environment, zoom in and move the viewing angle for closer inspection.
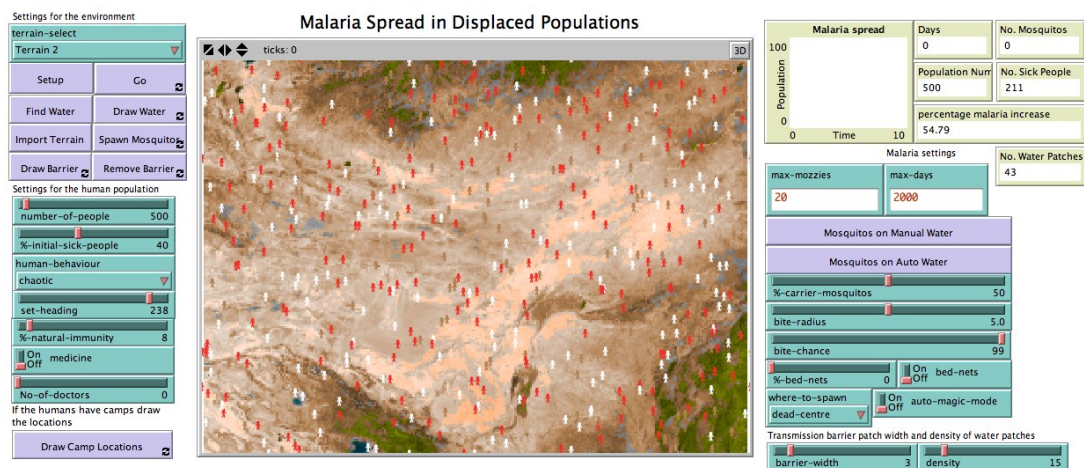
Figure 3.2: A screenshot of the Malaria in Displaced Populations Model Interface.

The patch based environment loads a satellite image which is then converted to colours within the RGB scale recognised by NetLogo. The program checks through the RGB settings of the patches for those that are within the blue scale, then identifying those patches as water. User defined values allow a malaria infection rate to be associated with the environment. The malaria infection rate, adjusted via an interface slider, determines the rate of infection of the disease between the human and mosquito species. Since high to low malaria infection rates provide differing rates of natural immunity in the native populations, an expected percentage of natural immunity can be user defined. By loading a different environment through the terrain selector and

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keeping the population's original natural immunity percentage the same, it is possible to model the effects of greater or lesser mosquito spawning sites on the population once it has been displaced to a new region.

The program allows the user to draw regions of water into the environment manually, for experimentation. Since the mosquito agents are spawned from the water patches to simulate the outward spread of the species from watery regions in the natural environment, adding and subtracting water patches affects the rate of disease transmission. The user may also draw barriers across or around patch areas to model the use of insecticidal spray in those areas, which would protect the human agents from interaction with mosquitos whilst they remain in the region of those patches.

The use of bed nets by the human agents can be added either directly, through a user control, or indirectly, by the addition of access to medicine through doctor agents. The doctor agents cure human agents who enter their vicinity and provide bed nets (in programming terms the agent is provided with long term protection), which allow the cured individuals to avoid reinfection by the malaria parasite. The rate of malaria infection for the set environment can be easily generated and exported for a range of populations, settings and durations. Once output for the initial environment has been recorded, further satellite images may be loaded into the environment and manipulated in the same way, to produce malaria infection rate output for the displaced population in other regions.

3.5   Human and Mosquito Behaviours

Empirical data from historical record of displaced populations supports the understanding that when a large group of people are uprooted from their homes due to conflict or unrest, they flee across often barren and hostile land in order to find a new settlement. These uprooted people will break off into clusters. A cluster of people will journey in a single direction, as a group, until either a humanitarian encampment is reached or else the borders of other villages or cities. Some will remain in the encampments for an extended period of time due to illness or a lack of any guaranteed security elsewhere [12].

An obstacle avoidance crowd behaviour has been programmed for the agents. Crowd behaviour can be influenced by a large number of variables and the complexity with

which crowd behaviour may be modelled is also great. For the purposes of this model, simplistic rules based on Reynolds' boid-like steering behaviours [28] have been used to reproduce similar movement to real world swarming. However, even with the simplest rules, complex emergent properties can become apparent. The NetLogo code that follows shows how the migration behaviour has been implemented. Nested if statements have been used to set the human agents' heading. Checking for the colour of the patch ahead determines whether the patch is land or water. If the patch is water, the agent avoids it as an obstacle and moves around it.

Listing 3.2: Code demonstrating the human agent migration procedure.

```
if (human-behaviour = "migration")
  [
    if (ticks mod time-between-heading-change = 0)
    ; set the agent heading.
      [ set heading set-heading + random 20 - random 20 ]
      ; check the colour of the patch ahead to determine if it is water.
      ; if the patch ahead is water move around it.
    ifelse ([pcolor] of patch-ahead 5 != blue)
    [ fd 1 ]
    [ ifelse (random 2 = 0)
      [ rt 90 ]
      [ lt 90 ]
      ]
```

With just one or two simple behavioural rules put into practise, such as obstacle avoidance followed by a return to original heading and an in-radius searching behaviour, it is possible to observe the emergent result that while traversing the outer edge of water patches for an extended period of time, the agents are exposed to close proximity to mosquito breeding grounds. Should the agents or their real world counterparts possess a behaviour that steered them further from the perimeter of water bodies, close exposure to dense mosquito swarms for an extended period of time would be avoided.

There are four human behaviours that may be selected by the user. They are basic representations of how a human population would be expected to behave en masse in a situation where they have been displaced from their original communities. The migration behaviour sends all human agents toward a set heading in the environment from the point at which the agents are spawned. They will avoid traversing patches

of water, using a boid-like [28] obstacle avoidance behaviour, so that they return to following their set heading as soon as they have moved around the water patches. The migration behaviour is a simulation of real world population displacement shortly after upheaval from the original communities.

The chaotic human behaviour sends the agents wandering from their point of origin to random locations, with the chaotic-close-to-home behaviour beginning in a similar way and then checking the distance the agents have moved from their point of origin. In the second of the chaotic behaviours, the agents will return to their point of origin if they wander a certain distance. In situations of mass population movement, a group of people often move into a temporary location, where individuals remain highly mobile and services are minimal. The model takes this into account, using randomised agent movement within a limited space of the environment. There is no community centre and dwellings are not present.

The encampment behaviour simulates behaviour where a displaced population settles into designated areas in the environment before becoming stationary. The camps are representations of points in real world humanitarian aid facilities where groups of people may gather to take advantage of some provided amenities. One or more camp sites are placed in the environment by the user. The agents, once spawned, will locate the nearest camp site to their location. Upon entering the encampment area, they become inactive for the remainder of the model's run.

The movement of the mosquito agents is accounted for by mosquito habits documented by researchers at the North Dakota State University [41]. Mosquitoes are described as sometimes engaging in long distance flight from their breeding sites but more often only traveling the shortest distance in order to find a blood meal. Due to the variable nature of the expected flight distance of mosquitoes the agents in the model that represent mosquito clusters are programmed to radiate out in a random direction from their breeding site, traveling outwards into the surrounding area. The mosquito cluster agents are then eventually found throughout the environment, beginning in dense numbers near the breeding site and then found in less concentrated quantities throughout the model over time. The dispersal of the agents in this way allows a simulation of both the long and short distance travel expected of mosquitoes. The full code for these behaviours may be found in Appendix 1.

3.6 Application of the model using real world data sets

Figure 3.2 provides a screenshot of the model running after an example setup, viewed with the NetLogo 3D interface option. In the top left hand corner of the image, the blue area indicates a cluster of user-drawn water patches. The mosquito agents, that are visible as the target yellow shapes, have been generated on or near the water patches before they radiated outwards, interacting with the human agents. The black colouration represents a transmission barrier, with a user drawn encampment area at its centre. The human agents outside of the barrier are interacting with the mosquito agents, but those that have moved towards the encampment area and clustered there are no longer in contact with mosquitoes, since mosquitoes are blocked from passing across the barrier.

Figure 3.3: A screenshot of the view corresponding with the Malaria in Displaced Populations model interface during an example run. The agents of brown coloration are uninfected due to immunity. White agents, visible amongst those gathered inside the insecticidal barrier, are uninfected. Those of red coloration have become infected. The yellow, target shapes represent swarms of mosquitoes. The black patches on the terrain represent insecticidal barriers, protecting the agents within from infection. The blue patches on the terrain represent water, where mosquito swarms are spawned.

The mosquito agents have a target shape, to identify them as representing a mobile target area of infection rather than as representations of single mosquitoes. Each single mosquito agent has the effect on a population of human agents of being a cluster of mosquitoes rather than a single mosquito. The reason for this is the relative size of

the mosquito compared to the human. A mosquito agent that represents a cluster of mosquitoes and moves over the patch based environment in the manner of such a cluster, brings a human agent into contact with infection in a manner that is statistically realistic to real world interactions, as demonstrated by the statistical output of the model. For the benefit of the model's users, it also makes the mosquito agents more clearly visible as separate from the environment. If the mosquito agents were individually rendered, to a realistic scale, they would quickly cover the patch environment leaving the other environmental elements such as water, barriers and encampments obscured.

Multiple simulations with a range of different settings can be run automatically using NetLogo's BehaviourSpace tool. The BehaviourSpace tool is NetLogo's associated program for use in controlling and tabulating the results of experiments. However, the user drawn patches of water or encampment areas cause a problem when the model is tested via the BehaviourSpace tool. When experiments are set up through BehaviourSpace, the settings are adjusted with NetLogo commands so user drawn patches cannot be repeatedly selected by the program during the multiple experimental runs. In the case of the user drawn water patches, the model has been adapted to allow the user to enter commands to draw water patches automatically at the setup of multiple experiments rather than manually for each run. The mosquito clusters may also be automatically spawned, to a user defined number, on the automatically generated water patches.

In the case of encampment patches, which are also user drawn, it is not possible to automatically generate them for BehaviourSpace experiments. Due to the complicated arrangement of encampment areas in the environment, an automatic setup would not offer realistic or useful output. In selecting an area on which to place encampment patches, the user takes several things into consideration. Likely proximity to water patches is one such consideration, as is the possible use of insecticidal barriers around one or more encampment area. For these reasons, no automatic drawing feature has been added to this version of the model. Testing involving changes to human agent behaviour have been run through BehaviourSpace for chaotic, migration and chaotic around home behaviours but have been run separately, without BehaviourSpace in the case of the encampment behaviour.

The following shell script must be placed in a file kept in the same location as the

model if the user wishes to utilise the custom headless mode developed for experimental runs.

Listing 3.3: Shell script to run experiments in headless mode

```bash
#!/bin/bash

NETLOGOMODEL=/Location on drive/Folder-name//Malaria-and-Displacement.nlogo
NETLOGOBIN=/Applications/NetLogo\ 4.1.2/NetLogo.jar org.nlogo.headless.Main
EXPERIMENT="exp2"
RESULTS="results-file"

echo "Running Simulation in headless mode"
echo "Model ........ ${NETLOGOMODEL}"
echo "Experiment ... ${EXPERIMENT}"
echo "Results ...... ${RESULTS}"

java    -server -Xmx1024M -cp ${NETLOGOBIN} \
        --model ${NETLOGOMODEL} \
        --experiment ${EXPERIMENT} \
        --spreadsheet ${RESULTS}
```

3.7   Results and Validation

Along with census data relating broadly to sub-Saharan African countries, it is possible to obtain figures and scientific measurements for the malaria situation in many small, localised regions. Both stable and unstable malaria in Africa are highly researched topics in epidemiology. It is therefore possible to program a malaria distribution model with well researched, real world data sets for comparison of cross validated output.

According to data available through UN Data [18], reported cases of malaria in the Central African Republic total forty-five to fifty percent of the population. Using that figure as a guide, the model was run with forty-five percent of the human agent population carrying malaria at the start of the experimental runs.

Bed net coverage needs to be at fifty-sixty percent at the least, in order for a community to reap the maximum benefits. That is due to the fact that bed nets treated

with insecticide provide protection for a given radius, due to the impregnation with chemical agents, rather than acting purely as a physical barrier [24]. As a result of the extended radius of protection offered by impregnated bed nets, he benefit of the nets extends further than just to the individuals using the barrier.

Each mosquito agent represents a cluster of mosquitoes rather than a single mosquito. The model is designed this way to take into account problems of scale and visualisation. Where the human agents are less than the size of a grain of rice the mosquito agents would become invisible to the user. Another difficulty in modelling an accurate ratio of human agents of mosquito agents is that in real world situations where the human population may be subject to a census, the mosquito population vary greatly in numbers across the seasons, with a lifespan of around 3 to 15 days, the fluctuations in mosquito numbers are considerably large. Epidemiological surveys of mosquito numbers involve landing rate counts, mechanical traps and artificial breeding spots called Ovitraps to monitor larval production [21]. None of these methods calculate the true numbers of mosquitoes present in an open area of land effectively.

Each mosquito agent has been used to represent a swarm or localised cluster of mosquito agents so that when a human agent comes into contact with one of the mosquito agents the statistical chance of the human being bitten by a malaria carrying mosquito is calculated by the model and infection occurs as a result. When an increasing number of mosquito agents are placed in the environment an increasing number of malaria infections is expected. In order to correlate the infection rate with known real world infection rates a measure of how many mosquito agents to place in the model must be provided for the user.

Since the environment size is fixed, initially, the model may be set up with ten mosquito agent clusters. These will produce the expected malaria intensity of forty-five to fifty percent malaria infection in the environment, which is an observed figure for several African regions with a high intensity malaria infection rate [18]. Reducing or increasing the number of clusters will decrease or increase the infection rate, respectively. After the initial mosquito agents have been placed in the model, the increase in malaria infection rate in the population is directly proportional to the increase in the number of mosquito agents. The model has been extensively tested to prove that it consistently maintains a disease state in the population within 2 to 4 percent of the expected increase from exposure to greater numbers of mosquito agents.
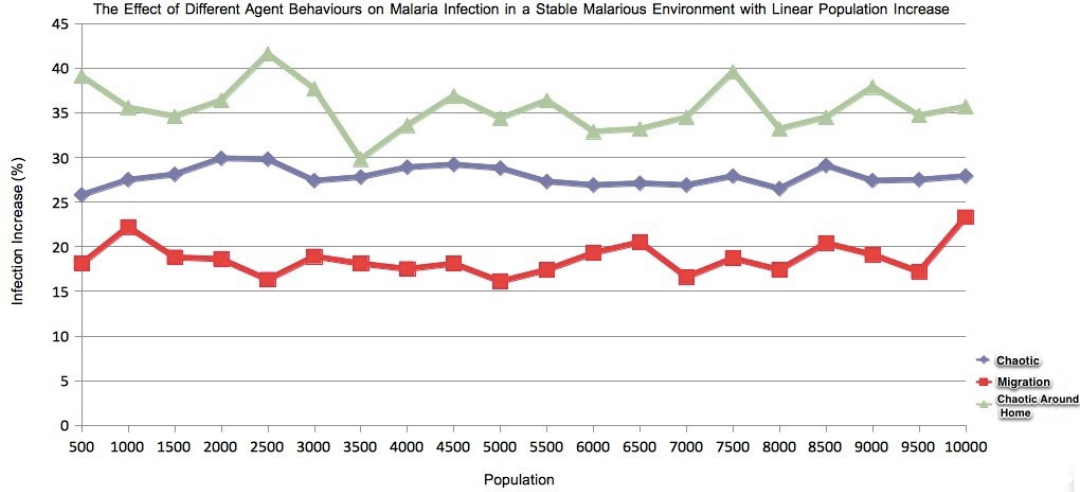
Figure 3.4: The effect of different agent behaviours on malaria infection in a stable malarious environment with a linear population increase.

Each human agent behaviour should have an effect on the rate and level of malaria transmitted between mosquito agents and human agents. It would be expected that a chaotic, randomised human agent movement would increase exposure to mosquito agents and hence increase the transmission rate of malaria between agents. That situation is found to be consistently true with the model. In the case of the Chaotic Around Home behaviour, the decrease in the range of movement of each human agent from its patch of origin means that a proportion of the human agents do not wander into the area where mosquito agents are in their greatest numbers. However, due to their restricted wandering, large numbers of human agents repeatedly traverse patches that are densely covered with mosquito clusters. In that case, the overall effect is a significant increase in the percentage of infected agents in comparison to the migration and chaotic behaviour.

In the case of the migration behaviour, all human agents move in a sweep across the environment, causing a close proximity to areas where mosquito agents are in high numbers at several points throughout the run. In that case, it might be expected that malaria transmission would be increased by the migration behaviour. In the model, the situation is found to be otherwise, with a sweeping across the environment taking the human agents out of the way of areas where mosquito clusters are dense. The same is not found to be true if large areas of water patches are present. In this case, the human agents' avoidance of water by traversing around the edge of the water patches as they

apply their obstacle avoidance behaviour puts them in a more prolonged contact with the malaria carrying mosquito clusters.

In the case of the encampment behaviour, human agents may come into contact with areas highly populated with mosquito agents while they move towards encampments, but the fact that they become stationary once at the encampment and no longer wander into potentially high risk territory should offer the agents greater protection from contracting malaria. As demonstrated by further testing, that is not strictly speaking the case, with only a small beneficial difference for encampment behaviour over chaotic around home behaviour. The reason for this may be that the camps are always situated near to water sources in the model, as they may also be in real world scenarios.

The benefit of the available water sources to individuals at the camps becomes a negative when the water sources are also identified as mosquito breeding grounds. The screenshot provided in Figure 3.4 shows a number of uninfected individuals clustered at the site of an encampment. The encampments placed in the model run shown in the screenshot do not have protective transmission barriers. Due to the camps being distanced from the water patches and areas of greatest mosquito concentration and the fact that human agents become stationary once they have found an encampment, the camps themselves offer some protection from malaria infection.

Adding a transmission barrier to the camps which protects the stationary occupants from mosquito agents, which cannot enter through the barrier, will only offer a marginal improvement in protection from malaria, since the process of traveling to the camps puts many of the individuals into contact with mosquito populations which are heavily located at the nearby water sources. The results offered from testing encampment scenarios with and without barriers and also with and without close proximity to water sources are true to what was expected in these cases. Table 3.2 able summarises those different cases.

The model allows for medical assistance to be offered to the human agent population in the form of doctor agents. If a human agent comes into contact with a doctor agent the human agent's malaria status becomes susceptible rather than infected. By testing the model with increasing numbers of doctor agents over an increasing number of human agents, it was expected that some beneficial trend would emerge and that there would be an optimal number of doctor agents in relation to human agents for

Figure 3.5: A screenshot of the malaria in Displaced Populations model showing the 'encampment' feature. The agents of brown colouration are immune. Agents of red colouration are infected. Agents of white colouration are uninfected. The purple patches in the environment represent encampments, where human agents are attracted. Patches of blue colouration represent water.

Table 3.2: Demonstrating the effect of different encampment scenarios on malaria infection.

Model Setup	Increase in Infection (%)
Camps Near Water	21.75
Camps Distanced from Water	18.2
Camps Near Water with Barriers	19.8
Camps Distanced from Water with Barriers	15.2

medical assistance to have the greatest impact.

No optimal number of doctor agents became apparent before the maximum modelled human population was reached. The reason that no optimal number was identified is possibly due to the fact that the human agents in the model do not have a behaviour that simulates a preference or motivation for seeking out a doctor agent. Coming into contact with a doctor agent is a random occurrence. The real world behaviour of a human population in relation to medical aid provided is not available as qualitative or quantitative data at this time. In terms of developing a more sophisticated interaction

between the doctors and the human agents, a preference and motivation for seeking out a doctor agent is possible for future work.
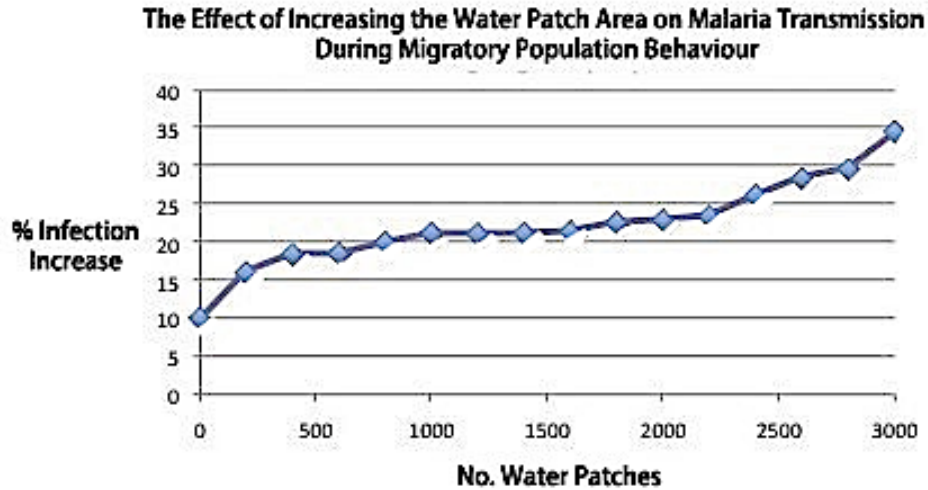
Figure 3.6: The effect on malaria transmission of increasing the water patch area.

Increasing the number of water patches for model setups that use the migratory human agent behaviour results in the agents using obstacle avoidance to move around the water patches and return to their migratory heading. In avoiding the water patches, the agents travel the perimeter of the water and in doing so prolong their contact with areas of high mosquito concentration. As can be seen in Figure 3.5, increasing the area of water patches steadily increases malaria infection in the human agent population.

3.8   Conclusion

The Malaria in Displaced Populations model yields quantifiable output that demonstrates a high fidelity to real world malaria infection statistics. Using the validation methods of sensitivity analysis and statistical verification of results, the model's simulation is well supported.

Some interesting phenomena may be witnessed when experimenting with the model.

One example of such phenomena is the emergent behaviour of the human agents when avoiding patches of water during their migratory behaviour. Following the contours of a large body of water to negotiate it as an obstacle brings the agents into a longer period of exposure to associated mosquito breeding grounds.

The Malaria in Displaced Populations model has a disease interaction between both the human and mosquito agents, whereby the malaria infected mosquito agents may infected human agents and infected human agents may infect uninfected mosquito agents should they interact. The objective of the two way disease interaction was to produce a realistic transfer of the parasite between the two types of agent. In the Malaria in Peri-Urban Settlements model a one way disease transfer from mosquito to human was designed for comparison of the infection rate output for the human agents, which is one of the important subjects of interest. There was no discernible difference between infection rate in humans with the two way disease interaction of the Malaria in Displaced Populations mode and the one way disease interaction of the Peri-Urban model. With no additional benefit to the simulation with the more complex procedures associated with a two way interaction, the simpler one way malaria transference was the preference for design of the other two models.

The two way transference of malaria in the Malaria in Displaced Populations model remains a more accurate modelling of real world phenomena. It may be possible to extend the complexity of the malaria infection procedures in this model so that the two way disease interaction between the different types of agents does become an interesting addition to the simulation. For further extension of the procedure, associated real world quantitative data relating to the rate of transfer of the parasite between human and mosquito would be necessary.

A further example of how the model may be expanded in use and accuracy is in the interaction between the doctor agents and other human agents. Presently, the model situates the doctor agents randomly in the model and interaction with the other agents occurs randomly, should they happen to interact during the course of the several human behaviours that dictate movement. No data was available to support evidence of interaction that may have been suitable for the modelling of a more complex behaviour.

Chapter 4

Malaria in Peri-Urban Settlements

This chapter concerns the development and implementation of the Malaria in Peri-Urban Settlements Model. It begins with a section detailing the subject of poor sanitation in peri-urban settlements, which is a key factor in the propagation of the malaria parasite. It then describes the use of the Map Maker model, which has been created for use as an environment builder for the Malaria in Peri-Urban Settlements model. The implementation section then goes on to explain the various attributes of the main model and how they relate to real world phenomena. The final part of the chapter is comprised of results from testing and the validation of the work.

4.1 The effects of poor sanitation in peri-urban settlements

Peri-urban settlements are found worldwide, throughout developing countries, many of which still have serious issues with untreated malaria. In the Peri-Urban model described in this chapter, it is possible to load maps of any region, not only the previous countries of interest to the thesis in sub-Saharan Africa. Table 4.1 has been taken from the Hogrewe report [45]. It clearly shows the high percentage of urban populations around the world that have no formal sanitation services. These figures were taken in 1987. According to data collected by The World Bank in 2008, 40% of the worlds population live without access to good sanitation.

Parkinson and Taylor [56] state that due to inadequate drainage systems, inhabitants of peri-urban settlements dispose of waste water on to plots that are left vacant. Often the waste water is disposed of in direct proximity to the habitation, for convenience. The water goes stagnant at the sites of disposal, so that it becomes the ideal breeding ground for mosquitoes. Data collected for the report reveals that a centralised waste water management approach is often ineffective due to the large scale of the settlement and the prohibitively costly nature of implementing a centralised drainage system. Decentralised approaches have previously been considered inefficient, but as a cost effective and long term alternative, they are now being considered the better option for peri-urban areas, due to their lesser impact on malarious exposure for inhabitants.

The data provided by the Parkinson and Taylor report is not sufficient to accurately model decentralised waste water systems in a peri-urban environment, but it does offer enough information about the disposal of waste water around habitations that the waste water itself may be modelled realistically. Table 4.1 presents the correlation between the distance of habitation from swamps and streams and the incidence density of malaria in children. The first column lists the geographic variable, either swamp or stream and shows the distance of those features from the homes of the children taking part in the study. The second column indicates the number of children residing in that area. The third column presents the number of recorded malaria infections amongst those children. The fourth column analyses the incidence density. The calculated number of infection incidents per person per year. Since the number of bites is impossible to measure, the parasite load in the hosts's serum is used to gauge the level of exposure.

Table 4.1: The correlation between living distance from swamp land and incidence of malaria infection in children.

Geographic variable	Number of children	Number of infections	Incidence density*
Dist. from swamp >100m	88	32	0.41
Dist. from swamp 1 - 100m	44	39	1.02
Dist. from swamp 0m	173	296	2.22
Dist. from stream $\geq 500m$	72	38	0.16
Dist. from stream <500m	233	329	1.76

Per person, per year

4.2 Design Objectives

One objective was to produce a model that significantly extended the mapping capability of the Malaria in Displaced Populations model. Leading on from the objective to produce a more advanced environment mapping feature, the aim was to enable a greater interaction between the mobile agents and the stationary environment agents. A further objective for producing the Peri-Urban Settlements model was to simulate a population of human agents that were associated with simulated housing. Finally, the aim was to produce a model that had more complex interactions between the mosquito agents and the simulated water sources than the previous model.

4.3 Implementation

The peri-urban model has an associated, secondary model that is used to create custom maps. The use of both models is further detailed in section 4.4

The Malaria in Peri-urban Settlements model has been developed using three types of agent that interact with the NetLogo patch environment. Two of the types represent human agents, both children and adults. The third type of agent represents mosquito agents. The purpose of specifying the difference between adult and child human agents is so that the model may be further developed with a differing malaria infection rate depending on age range. Consistent data sets have not been available for the use of modelling the variance. It is hoped that future work will be dedicated to improving the model by adding a differentiation between adult and child infection rates.

In this model, the human agents are spawned on patches that represent their homes. They have a behaviour which involves a randomised movement within a certain distance from their homes during the daylight hours and a remain-at-home behaviour during the night time hours. The agents move forward, left and right randomly. Once a maximum distance from home, determined by user controls, has been reached, they reset their heading to be towards their home patch. If a human agent is not on their home patch when the night time hours begin, rather than remaining at home they will continue to roam around. The fact that some agents will continue to roam at night adds realism to the set of human behaviours due to the fact that in a real life town or settlement it would be unrealistic to expect all humans to remain stationary and

inactive under a shelter during the night time hours. Having the majority of human agents remain on their home patch to become inactive during the night time hours benefits those agents any benefits that use bed nets or insecticidal spray at their homes offer.

Listing 4.1: Human agent movement procedure in the Peri-Urban Settlements model.

```
if not (time-of-day > sunset OR time-of-day < sunrise AND patch-here =
    start-patch)
  [
    set heading random 360
    ifelse ([pcolor] of patch-ahead 5 != 95) ;; human agents should not walk
        on water.
    [ fd 1 ]
    [ ifelse (random 2 = 0)
      [ rt 90 ]
      [ lt 90 ]
    ]
    ; check to see if wandered too far from home
    if ((distancexy original-x-location original-y-location) >
        max-distance-from-home)
      [ ; head back to home
        facexy original-x-location original-y-location ; face your original
            patch.
        fd distancexy original-x-location original-y-location
        ; move forward the distance between the patch you're on and your
            original patch.
      ]
```

In the code section shown, it can be seen that this model utilises some of the code featured in the Malaria in Displaced Populations Model, including the return to home patch code and the obstacle avoidance used to move around water patches rather that across them. The movement of the agents away from their home patches and their subsequent return is dictated by the time of day represented by a modification to how the ticks are measured as time. Unlike in the Malaria in Displaced Populations model, ticks are measured in terms of hours, days and weeks, using some code to calculate how many ticks represent each of those time frames. The sunrise and sunset time, on a 24 hour clock, may be adjusted by the user with an option on the interface.

The human agents possess a chemical, which they drop on the patches as they

move around. The chemical evaporates over time on the patches it is dropped on, but mosquitoes are attracted to it when it is of a high enough concentration. The chemical represents human body odour, which in real life terms is attractive to mosquitoes and can be found in greatest concentrations where humans spend the most time, i.e, during the night at their homes.

The chemical dropping simulates the real world phenomena of mosquitoes being attracted to the chemical secretions of human bodies. In places where the human agents stop for longer periods or pass over the most often, the chemical scent is strongest and will therefore attract more mosquito agent attention.

Listing 4.2: NetLogo procedure for calculating which patches ahead of the mosquito agents that possess the strongest chemical deposit. Mosquito agents move towards the patch with the strongest chemical deposit

```
to look-for-bloodmeal ;; turtle procedure
  ;; go in the direction where the chemical scent is strongest
  if (chemical >= 0.05) and (chemical < 2)
  [ uphill-chemical ]
end
```

The NetLogo procedure seen in the code above shows how the mosquito agents move towards higher concentrations of the chemical once they have located a patch where some amount of chemical is deposited. The uphill-chemical procedure locates a patch direction that has the successive patch marked with a greater concentration of chemical than the previous patch.

The mosquitoes possess two behaviours. One is a swarming that is based on Reynolds' Boid-like behaviours [28], where they will move through the environment as a swarm, not seeking blood meals. The second behaviour is a blood-meal seeking behaviour, which becomes active after a certain number of days in the mosquito life cycle that corresponds with their real world counterparts' reproductive behaviours. If a mosquito has reached a point in it's lifespan that corresponds with a blood meal seeking day, it will actively seek out human prey and bite them, possibly infecting the human with malaria in the process. Unlike in the Malaria in Displaced Populations model, the malaria transmission in this model is strictly from mosquito to human and

does not transfer from mosquito to human.

After a period of time consistent with real world mosquitos' reproductive cycle, a new batch of mosquitoes will be spawned on the original hatching sites of the first generation of mosquitoes. This process will be repeated throughout the model's run, so that as mosquitoes die off from exposure to insecticidal spray or natural causes (each one is programmed with it's own predetermined lifespan), there are further generations of mosquitoes to replace them.

When determining which attributes should be allocated to the modelled environment and agents, it was necessary to evaluate known factors that influence real world malaria transmission in areas where there are peri-urban settlements. The following subjects were discovered to be of significance to the work and well supported by scientific evidence from researchers in the fields of sanitation, environmental sciences and malariology.

4.3.1 Humidity

Humidity, whether from waste water, rainfall or other water sources, may provide viable breeding grounds for mosquitoes [52]. Water quality is a factor that dictates the success of mosquito larval development, so it becomes necessary to program a variable water quality for water patches present in the model dependant on a statistic entered by the user.

4.3.2 House Construction

Selection of building sites for domiciles directly affects the proximity of inhabitants to high concentrations of mosquitoes, dependant on whether these homes are close to standing water sources. Providing either centralised or decentralised wastewater management to homes in a peri-urban environment have their own particular drawbacks in relation to mosquito oviposition [52] [56].

4.3.3 Sanitation and Drainage

Disorganised sanitation practices in peri-urban areas result in an increase in still water close to habitations. Since mosquitoes will lay eggs in wastewater regardless of its chemical composition, even wastewater that is not a viable breeding ground for mosquitoes will still result in large concentrations of adult mosquitoes congregating at the site. In peri-urban environments where there are no formalised sanitation methods, wastewater is spilled over any patch of land between habitations that is not deemed fit for building housing structures [56] [54] [45].

4.3.4 Vegetation

Proximity to dense vegetation increases the exposure of inhabitants of households to adult mosquitoes, due to the fact that adult mosquitoes will congregate in the still air currents above dense vegetation [52]. For the purposes of furthering the Peri-urban Settlements model, vegetation has been added as a patch type, but modelling the hovering mosquito behaviour associated with dense vegetation has not been deemed useful for this version of the model.

4.3.5 Insecticidal Spray

Applying insecticidal spray to the perimeter of villages and the perimeter and interior of individual homes offers protection against mosquitoes. The use of insecticidal spray is represented in the model by providing a physical barrier for entry by mosquitoes into the patches surrounded by the insecticidal barrier. Insecticidal barriers may be added to a percentage of the homes present in the environment by use of a slider on the interface [61]. The protection offered by use of insecticidal spray associated with a home may also be translated as the same benefit that would be offered from all occupants of that household using bed nets.

Listing 4.3: The go procedure from the Peri-Urban Settlements model

```
        repeat 5 [ ask mosquitoes [ fd 0.2 ] display ]
reset-chemical
move-adults
move-children
```

61

```
insecticide-contact
      ask patches [ set chemical chemical * (100 - evaporation-rate) / 100 ]
; slowly evaporate chemical
display
set time-of-day (time-of-day + 1) mod 24
; increment by an hour
      if-else (time-of-day > sunset OR time-of-day < sunrise)
              [ set time "Night" ]
              [ set time "Day" ]
set hours ticks
set number-of-days ticks / 24
set weeks number-of-days / 7
        if (hours mod 24 = 0) and (number-of-days mod 7 = 0)
              [re-spawn-mosquitoes]
        if ticks >= 365
              [set number-of-years ticks / 365]
ask adults [human-age-increment]
ask children [human-age-increment]
ask mosquitoes [age-mosquitoes]
end
```

The go procedure for the Malaria in Peri-Urban Settlements model has a greater complexity than the one for the Malaria in Displaced Populations model. The reason for the greater complexity is that this one deals with several more procedures. In this model human agents have been split into two groups: adults and children. Their actions are handled by separate procedures. In this one there is code to distribute the chemical over the patches. The time of day is altered by an if-else statement. Ticks are calculated to become hours, days and weeks. The correct time for mosquitoes to re-spawn on their home patches, replicating reproduction, is calculated with an if statement. Finally, the two types of human and the mosquito agents have their age incremented. The go procedure is initiated with each tick.

4.4   The Interface

The Malaria in Peri-Urban Settlements model simulates real world scenarios where a human population has settled into a peri-urban housing environment. This model has an associated, secondary model which is used to generate maps for use with the pri-

mary model. The associated Map Maker model prompts the user to upload a map image. The image may be a drawing of the user's design or a satellite image taken of the region of interest. Alternatively, the user may draw a map directly into the Map Maker interface. If the user has selected to draw a map over an uploaded image, there are a number of buttons and sliders which, when selected, choose elements that may then be drawn using a computer mouse, onto the view of the interface. Once a map has been successfully created, the Map Maker model allows the user to save it as a image file to a location on their computer.

Figure 4.1 is an example of a suitable satellite image for use with the Map Maker model. The correct scale is the approximately equivalent of thirty five square meters per home patch when drawing housing from satellite images or maps [11]. The image shown is of a peri-urban settlement on the outskirts of Kananga in the Democratic Republic of the Congo.

Figure 4.1: Satellite image of a peri-urban settlement in the Democratic Republic of the Congo.

Figure 4.2 shows the Map Maker model's interface when it is being used to draw a freehand map. As well as controls that allow the user to draw vegetation, housing and

water patches it is possible to select the percentage of the water patches that will be viable for mosquito reproduction. If that data is available to the user, a greater level of realism can be introduced to the model. If that data is not available, the viable-water slider may simply be set to 100%
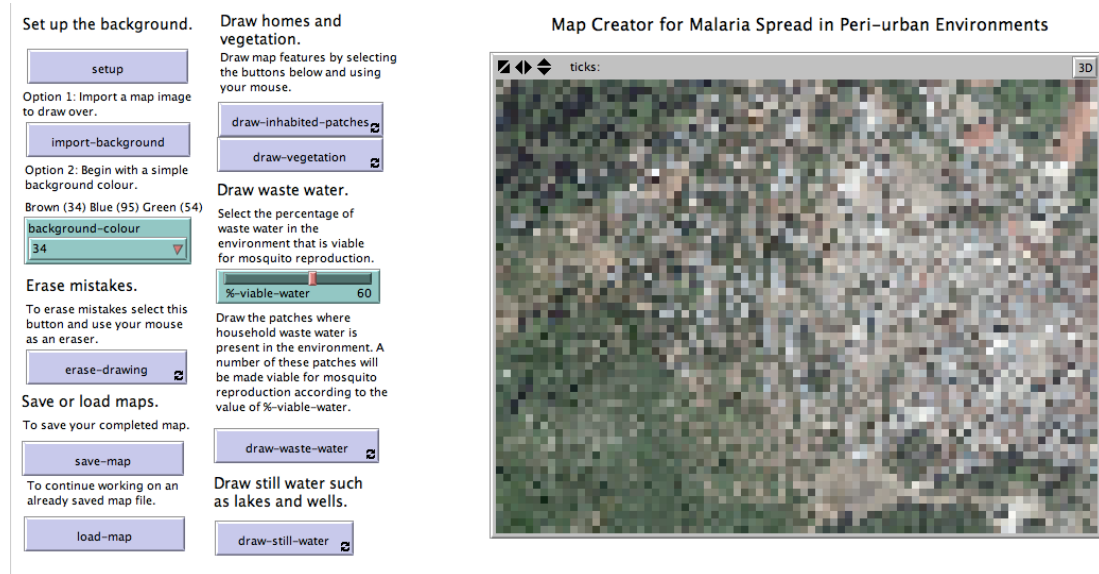
Figure 4.2: A screenshot of the Map Maker model showing how the previous image may be converted into a NetLogo environment using drawing tools.

Figure 4.3 shows the Malaria in Peri-Urban Settlements model with a loaded map environment that has been created from the earlier satellite image from the Democratic Republic of the Congo. Once the environment is loaded, the agent settings may be adjusted and then a set of agents loaded for an experimental run. Since it was not possible to identify water from this particular satellite image, some water patches have been added for the sake of generating some mosquito agents in the simulation.

Figure 4.4 is a screenshot of the Malaria in peri-Urban Settlements model with a loaded map environment and a loaded set of human and mosquito agents. It is possible to reduce the density of human and/or mosquito agents according to the user's requirements by altering the human and mosquito agents controls.

The Malaria in Peri-Urban Settlements model makes use of the maps generated using the Map Maker model by determining which patch colours are associated with
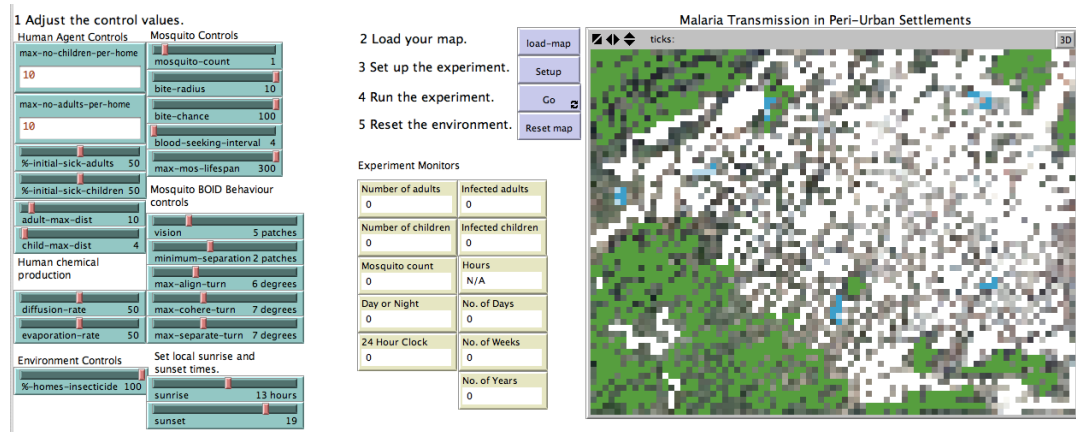
Figure 4.3: A screenshot of the Malaria in Peri-Urban Settlements model with a loaded map environment created with the Map Maker model.
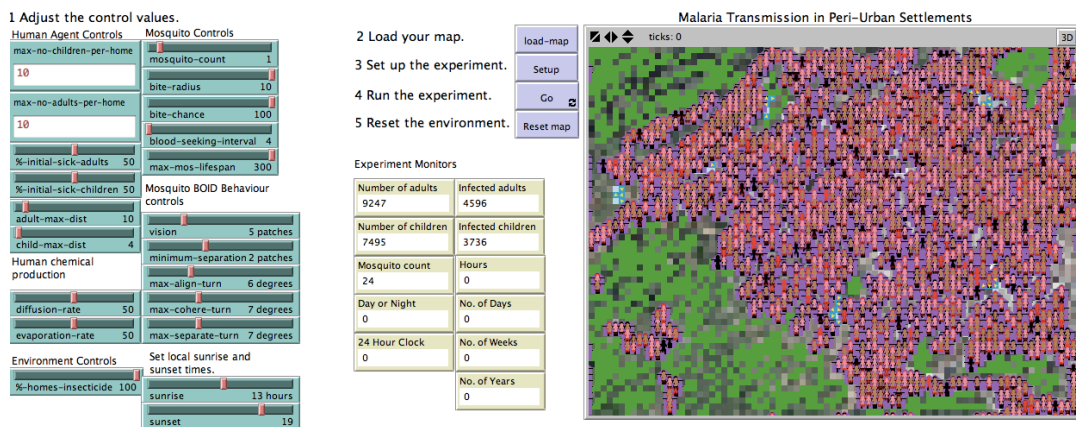
Figure 4.4: A screenshot of the Malaria in Peri-Urban Settlements model with a loaded map environment and a loaded set of human and mosquito agents.

recognised terrain features such as homes, water, vegetation and bare ground. The model may then be set up for an experimental run using sliders, buttons and other input relating to malaria transmission. The interface presents the user with a large number of controls over the model's environment and the agents' behaviours. The controls allow user control over the majority of the model's coded procedures.

Dependent on available data in relation to peri-urban living, there is a great deal of flexibility associated with how the model may be used or become useful. The human agent controls make it possible for the user to create a human-like multi-agent popula-

tion with realistic family sizes, with a set number of individuals that already carry the malaria parasite and also to decide how far the human agents are likely to be travelling from their homes, day to day. The model is also flexible for the user as they can decide how the chemical produced by the human agents works, so that if data is available, a realistic reaction to human odour by mosquitoes is possible. Table 2.4 lists the colour coding of the agents so that the visualisation is clearer.

Table 4.2: Agent Colour Coding

Agent type	Status	Colour
Mosquito	N/A	Yellow
Adult Human	Uninfected	Black
Adult Human	Infected	Red
Child Human	Uninfected	Brown
Child Human	Infected	Pink
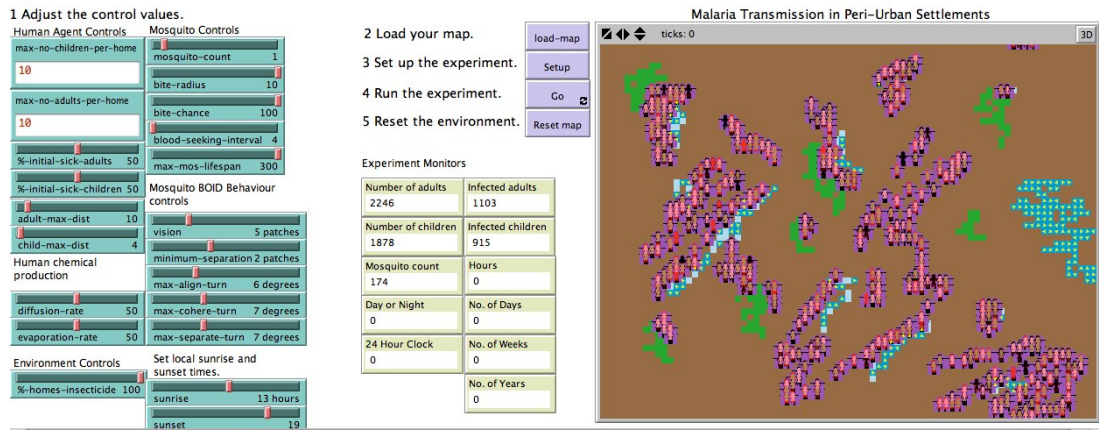
Figure 4.5: A screenshot of the Malaria In Peri-Urban Settlements Model with a free-hand drawn map environment and loaded agents.

The mosquito controls offer flexibility for the user to decide how the mosquitoes will react to their environment and to other agents and to determine the usual lifespan for mosquitoes supplied to the model. The mosquito swarming controls are also available to the user, so that adjustments may be made, allowing for a closer approximation to known mosquito swarming behaviours.

There are controls which allow the user to decide whether or not insecticidal spray

is likely to be used in and around the homes present in the model's environment and to what extent the spray is used, via a slider representing a percentage.

The research of Le Menach and McKenzie *et al* [54] cites that female mosquitoes will gravitate towards suitable places for oviposition with a favourable flight distance to blood hosts. It is irrelevant whether the sites of standing water used for oviposition are of sufficient quality to produce matured mosquito adults from the deposited larva. Therefore, any body of stagnant water can be a source for malaria spread due to the attraction of adult mosquito females to the area, but all bodies of still water may not produce an increase in the localised mosquito population. Figure 4.5 shows a screenshot of the model with a user created map that shows water deposits around areas of housing as it would be found in a peri-urban settlement.

Patches of standing water that are generated amidst the inhabitants of a modelled peri-urban area may or may not be a source for increase in mosquito population size. The percentage of stagnant water sites that are not viable for maturation of mosquito larva are represented by a GUI slider in the interface, to increase the flexibility of the model's environment in accordance with variable data sets.

4.5 Results and Validation

In order to verify the effectiveness of the Peri-Urban model it has been necessary to compare its output to known real world statistics of urban, peri-urban and rural malaria infection. By creating a greater or lesser number of households in the environment, and a greater area of water, it is possible to simulate urban, peri-urban or rural regions, since the physical definition between any of those areas is simply the density of housing and water coverage. To decide on a number of households in the limited modelled environment that constitutes a peri-urban settlement, experimentation was necessary.

As sample data, the work of De Silva and Marshall from the Department of Medicine, Imperial College London has been the comparison [33]. The study by De Silva and Marshall has shown that in Ouagadougou, Burkina Faso, the parasitisation rate is estimated to be 24.1% in the urban centre, 38.6% in its peri-urban surroundings and 68.7% in neighbouring rural areas. With those figures for comparison, the model was setup with various housing densities and water areas. For the purpose of testing only the vector-

borne transmission procedures of the model, the chemical drop sliders were left at 0, no homes were protected by insecticide and the initial sick adults and children left at 0. The agents-per-home figures were kept at 1 for adults and 1 for children, with the coding altered temporarily for the testing, so that it was no longer a maximum number of agents possible per home, but an fixed number. With that set up, there were always twice as many human agents in the model as there are housing patches. The number of mosquitoes to be spawned per water patch was kept at one, so the number of mosquito agents, representing a cluster of mosquitoes, was always equal to the number of water patches. For the other tables of data shown in this chapter and discussed individually, the settings for the experiment may be considered to have been kept within the same parameters, unless specified otherwise, for consistency.

Table 4.3 presents the housing density and water area arrangements for the model that best represent the infection rates expected for rural, peri-urban and urban regions as compared to the estimate for those figures taken from the De Silva and Marshall report. The model settings were fifty homes, meaning that there were one hundred agents in the run each time. Water patches were increased by increments of five patches per experiment. The length of the experiment was capped at 300 ticks. This is purely an arbitrary figure that was found to be enough time elapsed to demonstrate the model phenomena of interest.

Table 4.3: Effects of Varying Water Area

No. Water Patches	Range of Infection* (%)
20	19.3 - 26.2
45	35.0 - 42.7
65	64.9 - 72.5

Figure 4.6 shows the protection levels offered from malarian infection to the human agents with the use of insecticidal spray at their homes. The number of mosquito agents was gradually increased during testing for this experiment to expose the human agents to a much higher infection rate and make it clearer how much protection from exposure to the mosquitoes the insecticidal spraying afforded them. The reason for increasing the mosquito agents was to ensure that an expected increase in malaria infection rate with increased exposure was taking place.

Table 4.5 shows the effect of decreasing the rate of evaporation of the chemical

Reduced use of insecticide, 10 mosquito clusters.

Reduced use of insecticide, 20 mosquito clusters.

Reduced use of insecticide, 30 mosquito clusters

125 145 165 185 205 225 245 265 285 305 325 345 365 385 405 425 445

Infected agents
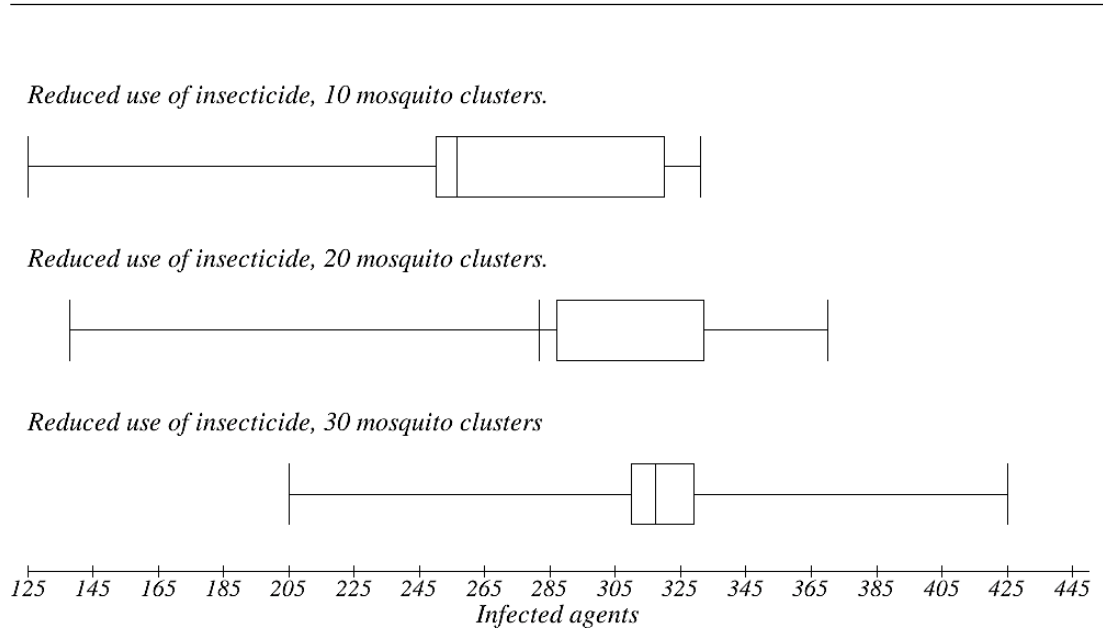
Figure 4.6: Reducing the use of insecticide in domiciles with varying amounts of mosquito agents.

Table 4.4: Effects of decreasing the evaporation rate of the attractive chemical for mosquitoes deposited by human agents.

Evaporation rate % per tick	No. Infected agents after 20 ticks. *
90	20
80	74
70	190
60	232
50	539
40	846

deposited by human agents that represents attractive human chemical emissions for mosquitoes. The chemical is deposited in proximity to the human agent as it moves in the environment. If the human agents' movement is limited to a certain radius of activity in the environment as if is in the Peri-Urban Settlements model, then the chemical remains in proximity to the human agents for an extended period of time, making the area more attractive to mosquitoes. The first column shows the decreasing percentage of evaporation for the simulated chemical in the model while the second column demonstrates the increasing rate of infection for the human agents as the chemical increasingly remains proximate to their location.
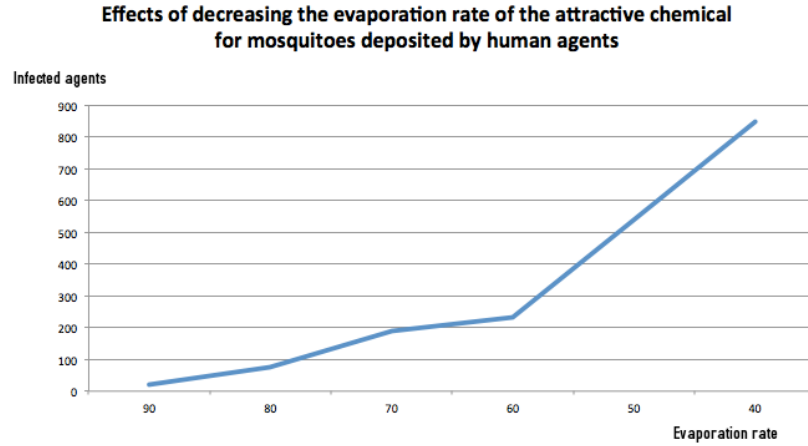
Figure 4.7: The effects of decreasing the evaporation rate.

4.6 Conclusion

The malaria transmission procedures from the Peri-Urban Settlements model have been validated using comparison of their output to real world malaria statistics as outlined in the De Silva and Marshall report [33]. It is possible to use the model with the settings outlined earlier in this chapter to produce a realistic simulation of a small section of peri-urban housing. The De Silva and Marshall report placed the infection rate for individuals in a peri-urban settlement at 38.6%. At around 45 patches of water it is possible to model the range of infection between 35.0-42.7%.

Testing of the model revealed that its use in modelling human habitation is not limited to a peri-urban situation. It is possible to match infection rates of urban environments at around 20 water patches, with a modelled range of infection produced between 19.3-26.2%. That output comes close to the findings of the De Silva and Marshall report that place expected figures at 24.1% in urban environments. A rural environment may be modelled at around 65 water patches. Placing the range of infection between 64.9-72.5% in comparison to the 68.7% in the De Silva and Marshall report.

The other aspects of the model, such as the chemical drop procedures and the

mosquito swarming behaviour cannot be well validated due to a lack of availability of relevant data for comparison. However, the controls for these two procedures are well represented by the user interface and might be validated and extended in their use at a future date, should sufficient supporting data and research become available. The testing that has been undertaken for the chemical drop procedure does demonstrate quantitative results that are consistent with expected qualitative phenomena understood in real world scenarios.

Chapter 5

Malaria and HIV Dual Infection

This chapter concerns the development and implementation of the Malaria and HIV Dual Infection model. It begins with a section detailing the subject of increased HIV viral load during dual infection with malaria, which is a factor in the propagation of both the malaria parasite and the HIV virus. The implementation section then goes on to explain the various attributes of the main model and how they relate to real world phenomena. The next section of the chapter is comprised of results from testing and the validation of the work. The concluding part of the chapter is a summary of the model's development and results.

5.1   Increase in HIV viral load during malaria infection

Dual infection with HIV has been responsible for an increase in geographic spread of malaria. The one disease makes the patient more susceptible to the other and in turn sustains a much higher viral and parasitic load of both diseases leading to a proliferation of infected individuals. The number of infected people becomes concentrated in one region and spreads out from that region due to the expected methods of transmission; parasitic transfer between vector species in the case of malaria and the several avenues of serum transfer in the case of HIV. The link between this model and the previous two lies not only in the malaria connection, but in the fact that population mobility has an effect on the spread of HIV just as it does on the spread of malaria. Population mobility has been found to link geographically separate epidemics and intensify transmission by inducing riskier sexual practices [34].

Dual infection with malaria and HIV results in the malaria parasite load promoting

an increase in the cellular propagation of the HIV virus. The implication of the interaction, which is beneficial for the virus and parasite alike, is that both diseases cause a heightened symptomatic state in the individuals concerned. In the case of increasing the viral load of HIV in a subject's serum, transmission of the virus from one individual to the next becomes more likely [19].

5.2 Design Objectives

The Malaria and HIV Dual Infection model was designed with the objective of producing agent based interactions simulating HIV and malaria infection. The aim was to represent the two diseases singularly to achieve model output of realistic infection rates and then combine the two disease to model a third state in the agents that corresponds with known effects of dual infection. A further objective for the design of the model was to explore the complexity of human sexual interaction that is one common method for transmission of the HIV virus.

5.3 Implementation

The basis for the model Malaria and HIV Dual Infection model has been the NetLogo AIDS model produced by Uri Wilensky in 1997 [4]. Only the procedures pertinent to the spread of HIV through a population, such as sexual behaviour, remain from the original model, and those have been made more adaptable to alteration by the user than they originally were. The malaria infection procedures have been added alongside HIV and the increased susceptibility to HIV when infected with malaria has been modelled.

The transmission of both diseases and the interaction rates of the human agents is entirely user controlled, including the infection rates and incidence level of the two diseases in the population. The intention has been to create models with as much user flexibility as possible. The Malaria and HIV Dual Infection model is similar to the two previous models in that it gives the user a choice to alter the values associated with almost all of its procedures.

The model has no complexity to its environment. The agents are not connected to

any homes nor do they interact with the NetLogo patches. The modelling of the dual infection did not require more than a basic patch environment to be implemented. The disease interactions themselves are programmatically complex but without any mobile agent interaction with the environment the visualisation itself and the interface is the simplest of the three models.

The following code is the model's go procedure. As with the go procedures of the previous two models, the code within is executed once every tick. If all turtle agents become infected with HIV the model stops. The infection length, which is the length of time the agent has been infected with HIV is increased by one each time the go procedure executes. If agents are coupled with another agent, the length of time they have been coupled increases by one with every tick. If the agents are not part of a couple, they move position randomly, to potentially come into contact with another uncoupled agent and form a couple. When the uncouple procedure is called in the code, the length of the couples' relationship is determined and if it exceeds their couple length, they uncouple. When the infection procedure is called, the chances of one or both of the coupled agents becoming infected with HIV from their sexual interactions is determined and their infection status updated is appropriate.

Listing 5.1: The go procedure from the Malaria and HIV Dual Infection model.

```
to go
      if all? turtles [HIV-infected?]
              [ stop ]
  check-sliders
       ask turtles
              [ if HIV-infected?
                      [ set HIV-infection-length HIV-infection-length + 1 ]
       if coupled?
              [ set couple-length couple-length + 1 ] ]
      ask turtles
              [ if not coupled?
                      [ move ] ]
;; Person shape 'one' is always the one to initiate mating.This is purely
;; arbitrary choice which makes the coding easier.
      ask turtles
              [ if not coupled? and shape = "person one" and (random-float
                  10.0 < coupling-tendency)
```

```
                  [ couple ] ]
  ask turtles [ uncouple ]
  ask turtles [ infect ]
  ask turtles [ assign-color ]
  tick
end
```

5.3.1   Susceptibility to malaria infection of HIV positive persons

Due to the cellular interactions of HIV within the host, a subject becomes more susceptible to infection by the malaria parasite. The lowered immune response associated with HIV infection then leads on to an inability for the individual to fight the parasitic infection, thus allowing for a swifter and more encompassing parasitic infection to take root. [65]

5.3.2   Duration of heightened viral load during malaria episodes

Viral load in an individual's serum, resulting from HIV infection, is a fluctuating parameter. Viral load is dependant on the success of the virus to propagate in the serum over time, which is in turn dependent on the overall health of the subject and the strength of their immune system. During periods of malaria parasitic infection, there is the added parameter of the destructive cellular effects of the parasite, which result in a more suitable environment for the HIV virus to propagate. The implication is that during malaria and HIV dual infection, the HIV viral load is heightened.

5.3.3   Enhanced HIV mortality in dually infected patients

There is an increased mortality rate associated with the greater HIV viral and parasite load in patients dually infected with malaria.

The following subjects for modelling implementation are quantitative parameters used for a mathematical model created for a journal paper published by Abu-Raddad *et al*., in Science Magazine, 2006 [19]. The core assumptions of the HIV/malaria interaction model produced by Abu-Raddad, *et al*. are reproduced below. Not all modelling parameters from that work have been represented here, only those that relate to the

foundations of this agent-based model.

- The enhanced susceptibility to malaria infection in HIV-infected persons in the chronic stage is 44%.

- The enhanced susceptibility to malaria infection in HIV-infected persons in the chronic stage is 44%, increasing to 103% in the advanced stage. With the 103% representing over a hundred percent increase in parasite load.

- The duration of heightened HIV viral load during malaria episodes is 42 days.

- The fractional reduction in sexual activity during clinical malaria infection is 10%.

- The fractional reduction in sexual activity during nonclinical malaria infection is 3%.

- The fraction of malaria-infected patients developing clinical malaria when HIV negative is 16%.

- The fraction of malaria-infected patients developing clinical malaria when HIV positive is 31%.

- The enhanced HIV mortality in dually infected patients in areas of stable malaria is 0%.

- The enhanced HIV mortality in dually infected patients in areas of unstable malaria is 25%.

5.4   The Interface

The model interface provides the user with a number of sliders that control the population of agents and also the ratio of the population that is infected with either or both of the two modelled disease. The HIV transmission controls allow the user to adjust the behaviour of the agents that brings them into a relationship with another agent, and how long that relationship lasts. While the agents are in a committed relationship, their sexual relations are considered to be monogamous, and therefore, if HIV is not present in one of the paired agents, no infection will occur over that given time period. The condom use of the agents is governed by it's own slider. If at least one partner wishes to use a condom during sexual relations, then the protection that method would

offer the individuals concerned is modelled as a reduced likelihood of HIV infection.

The malaria infection chance is also governed by a slider. The number of individuals already carrying malaria at the start of the model's run is determined by the malaria transmission slider. The effects of dual infection, in terms of increased risk of contracting HIV for those malaria infected agents, is governed by an additional control.
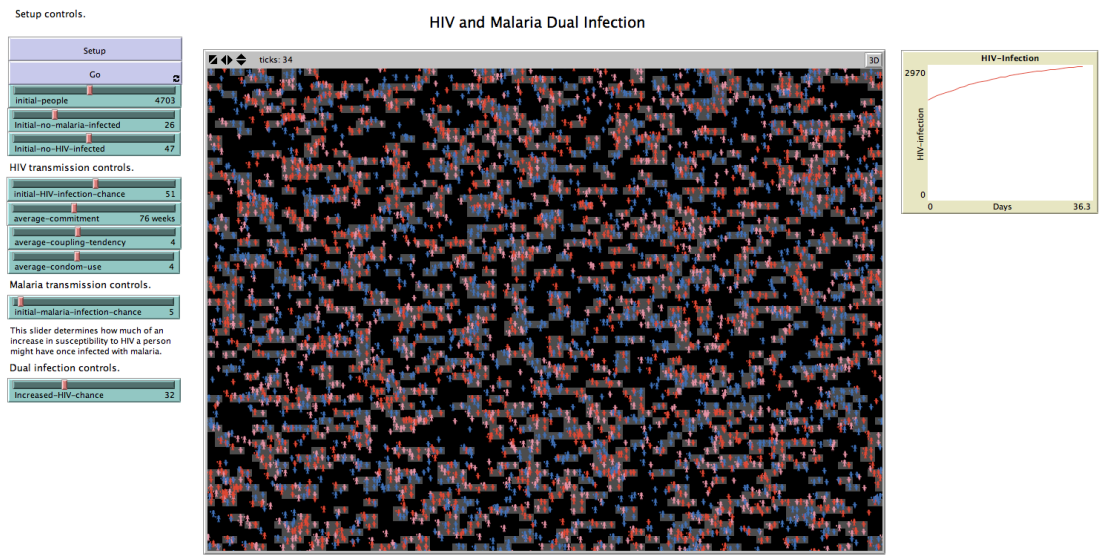
Figure 5.1: A screenshot of the HIV and Malaria Dual Infection model interface.The graph on the right of the interface shows the effect on HIV infection rate over time using the particular settings, also shown. The graph reveals that a total saturation of HIV infection has been achieved in the population after 36 days. That figure results from setting the HIV infection chance unusually high and should not be taken as indicative of the results demonstrated by the use of more realistic settings. This is only an example output from experimentation.

Table 5.1: Agent Colour Coding

Infection Status	Agent Colour
Uninfected	Blue
Dual-Infection	Pink
HIV Only	Red
Malaria Only	Yellow

Table 5.1 lists the agents' colour in relation to their infection state while the model

is running. As with the previous two models, transitions in colour have been used to indicate transitions in infection to the user.

5.5 Agent Behaviour, Infection and Visualisation

All of the agents have a randomised movement and interaction in the environment. They are initially placed in locations determined by a randomly selected integer co-ordinates. The agents then pair with neighbouring agents. Once pairing has ceased, they are relocated to a new set of randomly selected coordinates, where they will seek to pair with neighbouring agents again. It has not been the intention with this model to in simulate real world human behaviour, the purpose of the model is to provide a visualisation of how the dual infection of HIV and malaria propagates through a population. The other purpose of the model, in alignment with the previous work of the thesis, is to further test the boundaries of flexibility in disease modelling, in terms of allowing the greatest amount of user control over the values applied to modelled variables.

Since it is possible to alter the value of the HIV infection chance, the different figures for infection chance due to intercourse of varying types, such as anal and vaginal, may be represented. Limitations in the model mean that the infection chance of only one sort of sexual interaction may be simulated for a single run. According to figures released by the Centers for Disease Control and Prevention [8] some examples of risk of infection from an act of sexual intercourse are 50% for receptive anal intercourse and 10% for receptive vaginal intercourse.

The code below shows how when coupled, HIV infection chance is increased by a percentage input by the user if the agent is already infected with malaria.

Listing 5.2: The infect procedure from the Malaria and HIV Dual Infection code. This procedure determines how malaria and HIV are transmitted to the agents.

```
to infect
; If one of the partners have HIV but neither of the partners has malaria,
; HIV infection is passed on at the normal rate.
if coupled? and HIV-infected?
[if random-float 11 > condom-use or
  random-float 11 > ([condom-use] of partner)
```

```
   [ if random-float 100 < HIV-infection-chance
     [ ask partner [ set HIV-infected? true ] ] ] ]
 ;If one of the partners has malaria, they have an increased risk of
     contracting HIV
  if coupled? and HIV-infected? and Malaria-infected?
 [if random-float 11 > condom-use or
   random-float 11 > ([condom-use] of partner)
   [ if random-float 100 < HIV-infection-chance + increased-HIV-chance
     [ ask partner [ set HIV-infected? true ] ] ] ]
end
```

When a pair of agents become coupled, they become stationary in the model's environment. The couples' cessation of movement is for the purposes of providing a clearer visualisation in the model's view that demonstrates the agents' interactions. There was some concern that by making the coupled agents stationary, there would not be a random interaction achieved once the couples had dissolved into individuals again, since those agents would be positioned close to where they had stopped when part of a couple. The model was run and tested with both the couples moving around together, along with the single agents and with the couples stationary during the time frame of their relationship. It was found that no discernible difference to the flow of infection amongst the agents could be noted either way, and so the model has been returned to its original state of stationary couples to provide the clearer visualisation.

5.6   Implications for malaria intensity in a given region

The connection between the two diseases has a large enough impact on sizeable populations to make a study of it as worthwhile as the study of malaria itself. In a population of 200000, the interaction in the absence of malaria intervention may account for 8500 cases of HIV infection that would otherwise not have come about and 980000 excess malaria episodes since 1980 [19].

In the period between 1990 and 2005 (a period when there was a prevalence of 24% HIV infections in rural Uganda) the fraction of HIV infections attributed to malaria was 4.8% and the malaria promoted by HIV at the time was 9.9%. An HIV prevalence that reached 24% in 1995 would have required two further years to develop to that level without the synergy with malaria.

In areas with malaria status that can support small changes in entomology and transmission parameters the interaction can promote unstable malaria to a status of stable malaria and there lies one of the interesting hypotheses put forward by researchers that has only limited real world evidence and that is the change in malaria status brought about by the disease interaction. It is a good candidate for future work and more complex modelling, since insight may be gained from agent behaviour.

5.7 Results and Validation

For the Malaria and HIV Dual Infection model there is only one output that requires quantifiable validation and that is the increased susceptibility to HIV infection in agents that are infected with malaria. Table 5.2 demonstrates how increasing the number of individuals infected with malaria in a population of five thousand agents (an arbitrary number for the purposes of the experiment), coincides with an increase in HIV infections. The first values entered in the table represent the control values of HIV infection spreading through the population when no malaria is present. The duration of the model runs was limited to 300 hundred ticks throughout testing, for consistency. The number of agents was fixed each run at 5000. Those two figures have been arbitrarily picked for testing, since there is no data to indicate a specific time frame or population size will have differing effects.

The user controls were maintained at fixed values. Initial number of HIV infected agents was 40%. The average condom use was set at 0. The average commitment between couples set at 4 weeks (arbitrary number). The average coupling tendency was set at 10 to have the maximum tendency the model would allow. A figure of 10% was set for the initial HIV infection chance slider. That percentage is the known risk of contracting HIV from receptive vaginal intercourse. The conclusion of this chapter discusses the great limitations in modelling accurate HIV infection rates.

Table 5.2 reveals that 5.5% of agents infected with malaria in a population results in the increase in HIV infection rate expected from the disease interactions of dual infection, as documented from the period of research between 1990 and 2005 in rural Uganda.

Table 5.2: Increased HIV infection rates in agents coinciding with increased numbers of malaria infected agents.

No. agents with malaria	Total infected with HIV	Increased HIV susceptibility %	
0	1270	0*	* Control run.
100	1283	0.26	
200	1451	3.63	
300	1545	5.5	
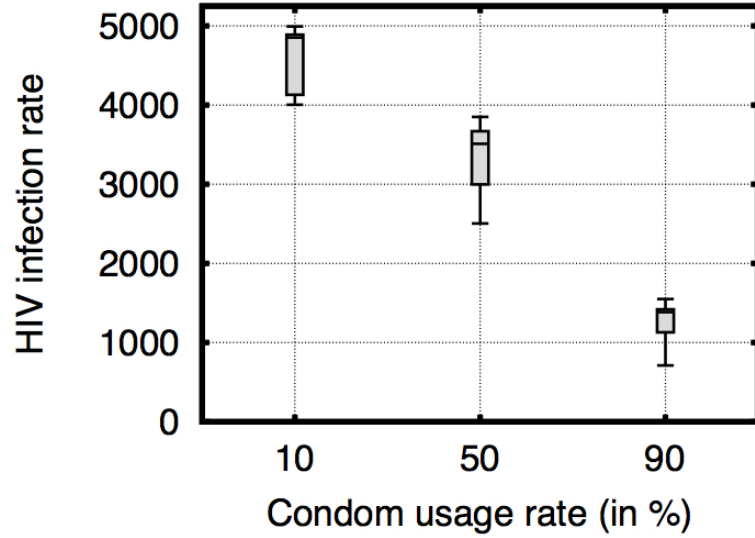
Figure 5.2: HIV infection rate with condom usage.

Figure 5.2 demonstrates the increased rate of HIV infection in human agents that coincides with a decrease in average condom use in the agents when sexual activity takes place. The average condom use is one important factor in limiting the spread of HIV amongst the agents, with the average commitment to monogamous relationships with an agent partner being the other factor that results in an increase or decrease of rate of HIV spread through the agent population. Figure 5.3 shows a correlation between a reduction in the average commitment to a monogamous relationship in agent couples and an increase in the rate of HIV infection.

The output of the model has undergone sensitivity analysis of its malaria and HIV disease transmission procedures. Cross-validation of the model was not possible, since
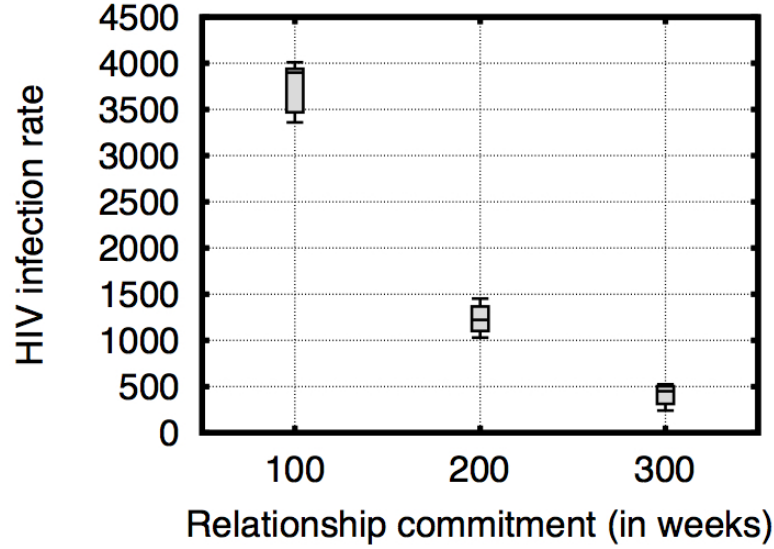
Figure 5.3: HIV infection rate with relationship commitment.

there is no known model of enough similarity to allow that form of testing. The transmittance of malaria and HIV have been individually checked for validity, to determine that they are capable of producing realistic output, such as the 10% infection rate of HIV when considering only receptive vaginal intercourse and the 45% malaria infection rate of a stable malarious region.

5.8 Conclusion

The data available for Malaria and HIV infections separately is extensive, but the study of their interaction is a fairly recent thing. There is however, enough data pertaining to the interaction to allow for model parameters to be set. As with the previous two models, the intention is to allow the user as much freedom with setting the agent attributes and the propagation of the disease as possible.

The Malaria and HIV Dual Infection model lacks the complexity of the previous two models produced for this thesis. The intention was to produce a model with less basis in environmental attributes of malaria than the previous two models, since the environment does not play a well documented part in the choices related to the process of human coupling.

The Malaria and HIV Dual Infection model has significant limitations. In real world scenarios, transmission of HIV is not purely via sexual intercourse. Non-sexual transmission is not taken into account. A further limitation lies in the inability to model multiple types of sexual interaction. For that reason, varying sexual practices between partners and sexual practices between both heterosexual and homosexual partners are not well represented. The nature of sexual relationships presents such a complex problem for modelling that it may not be possible to adequately represent without advancing the model to a level of complexity outside of the work of this thesis.

Chapter 6

Conclusions and Future Work

6.1 Overview

An estimated 219 million cases of malaria were reported in 2010 by the World Health Organisation, and an estimated 660 000 deaths. The importance of dedicating research hours and resources to a resolution of the many associated health risks is undeniable. The question of what agent based modelling can offer to the field has been extensively explored in this thesis. In chapter one, the introduction of the thesis, a unifying theme is outlined as motivation for the research.

"The unifying theme of the thesis is discovering what can be achieved with agent based modelling techniques, when advancing understanding of a disease transmission subject with a minimal availability of defined variables."

The unifying theme of the thesis served to support the hypothesis and the research questions detailed in the same chapter by giving a clear structure to what elements of the research were important in terms of evaluation and discussion throughout. The introduction also outlined in brief the chapters pertaining to the three models themselves.

Chapter two, the literature review, is a study of the relevant publications and any associated models that support the thesis. The sections of the literature review go from the general to the specific. The sections provide a background to malaria as a disease, the SIR model and a rationale of agent based modelling and its origins in cellular automata. The chapter then moves on to outline current research that has similarity to the work of this thesis and notes the limitations and associated problems of using agent

based modelling to simulate real world phenomena.

Chapters three, four and five document the models. The sections of the chapters discuss a background to the subject matter, implementation of the model, the availability of real world data sets for cross validation of the models' output and then a conclusion that draws on the results of testing. The results themselves are validated using a process of sensitivity analysis and statistical evaluation. Their output has been found to have a high fidelity to a number of real world malaria infection rate statistics and related data. The findings of experiments are explicitly stated in the validation sections of the chapters.

6.2 Re-visiting the Hypothesis

The hypothesis presented at the start of this thesis was as follows.

"The hypothesis is that using basic agent based modelling techniques it is possible to contribute considerably to the understanding of malaria transmission in scenarios where there is minimal research data available."

The first model, Malaria in Displaced Populations, went some way towards supporting this hypothesis. Using just a few non-complex reactive agent behaviours and environmental attributes, it was possible to observe some emergent behaviour from the agents. The possibility of discovering emergent properties is one of the principle advantages of using agent based modelling over a purely mathematical approach.

The second model, Malaria in Peri-Urban Settlements, consists of a broader range of agent and environmental attributes. Along with an increase in complexity of the model came a greater obscurity in terms of the ability to discover useful phenomena from its use. It also presented a greater difficulty in thoroughly validating and verifying its procedures.

The third model represents a complex interaction of two diseases, HIV and malaria, using similar agent based procedures as found in the previous two models. Both of the diseases and their propagation through the agents may be viewed as correct in the working of their associated procedures, but the there are significant limitations in

modelling the disease interaction due to the great complexity of human interaction that results in HIV transmission. In order to adequately model the transmission of HIV, a large number of sexual and non-sexual practices would need to be represented in the procedures. The frequency of these practices in a population is not documented in enough detail for that to be possible.

In conclusion, this thesis does support the hypothesis of producing interesting and useful contributions to the understanding of malaria transmission from the creation of very basic agent based models. It provides evidence to support this hypothesis in the results gained from evaluation of the three models.

6.3 Research Questions

This section revisits the research questions and evaluates whether a solution was met that satisfies them.

1) What environmental factors can be simulated for a malaria transmission model?

This question is answered best by the work of the second model, Malaria in peri-Urban Settlements. As the model with the greatest degree of environmental complexity it demonstrates that the majority of topographical features of a terrain and region of human habitation may be represented well by using the patch agents available in the NetLogo platform.

2) How can human population interactions best be modelled with the minimal of complexity?

This question is answered best by the first model, Malaria in Displaced Populations. Using just a few very simplistic agent behaviours that mimicked the movement of human beings in situations of migration and re-settlement, it was possible to visualise and evaluate the effects of those behaviours and interactions in terms of real world data. Revealing a high fidelity to what would be expected from population movement in real world scenarios.

3) Using a agent-oriented platform, how much complexity can be achieved whilst

maintaining a relatively low computational cost?

Netlogo has the capability of running models with agents numbering in the millions. Computational cost increases along with increased numbers of agents but another problem becomes evident also, the problem of producing a readable visualisation. Even with the use of a large screen space to expand the view, a large number of agents that use changing colour or another visual indication of state change such as links formed or an altered patch colour beneath them, become unreadable as a visualisation.

4) How can multiple disease interactions best be portrayed in an agent based environment?

This final question is addressed in the third model to be produced for the project. It presents issues both programmatically and in terms of creating a suitable visualisation. The conclusion presented by this thesis is that the modelling of multiple disease interactions shows promising results but some further work is necessary to ascertain the effectiveness of pursuing that avenue of disease modelling within the bounds of the hypothesis presented here.

The research questions have led to findings that support the hypothesis. In particular, question one has been addressed with the Malaria in Displaced Populations model and the Malaria in Peri-Urban Settlements model. A number of features of the modelled terrain and effects produced by insecticidal spraying have been viable as features for simulation. Question two has led to the discovery that simplistic agent behaviours are sufficient to produce the effect of realistic human behaviours in modelling.

The knowledge gained from fulfilling the remit of the research questions has revealed new possibilities for expanding the field of agent based modelling to benefit the malaria research community. Using agent based techniques to simulate some of the most obscure real world malaria infection scenarios amongst vulnerable populations has yielded interesting results. The results themselves have been validated using sensitivity analysis and have been proven to have a high fidelity to real world quantitative data available. Qualitatively, they have much to offer in terms of interesting phenomena and they may be further developed should their user have access to other pertinent data relating to the subjects of the three models.

6.4 Adaptability and Flexibility

The creation of the first model was an experiment in delivering a working, realistic malaria transmission procedure, and validating that procedure was the priority. In the second and third models, with a well validated, working malaria transmission procedure already in place, the priority became advancing the idea of offering a thorough control of the modelling procedures to the user and testing the limitations of modelling interaction with the agents' environment. As far as possible, all variables belonging to the agents and the environment are adjustable by the user in those later two models. The advantage of this flexibility is that the model is less likely to become redundant in its uses, if the emergence of new, updated research data alters our understanding of how malaria infection takes place.

Due to its open source framework, the NetLogo models may be advanced, altered and updated freely. The code has been supplied along with this thesis, in appendices 1-4.

6.5 Low-cost, Cross-Platform Framework

As a low-cost, cross-platform framework, NetLogo is a lightweight software package that may be run on any machine that supports Java. Although the package itself is low cost in terms of processing power, when run with many thousands of agents, which is the capability of all three models, a degree of processing power will be required. The computers used for testing the models were a MacBook Air, with 1.8Ghz Intel Core i5 processor and 4GB memory and an iMac with 2.9Ghz QC i5 processor and 8GB of memory. The MacBook Air would successfully run up to 5000 agents without slowing the speed of the models and the iMac would successfully run up to 10,000 agents without any reduction in the efficiency of the models. It is possible to run any of the three models with as few agents as the user desires, without effecting the way the models work, should the user have limited access to computer hardware with sufficient processing power.

As described in chapter one, a custom script has been created to enable the running of the malaria in Displaced Populations model in a headless mode, which produces output more efficiently than running NetLogo's own BehaviourSpace testbed application.

6.6 Adaptation to overcome unknown variables

Some variables that would be required to run the models with the best degree of similarity to real world events are not readily available. One example of this is the measure of water quality in waste water deposits in the malaria in Peri-Urban Settlements model. Water quality measurements for a given region may be available to those that are or have been working in the field, but for the purposes of using the model experimentally, any range of values may be supplied. If water quality, and hence the amount of water in the environment that is suitable for mosquito oviposition, is not expected to be a useful feature for the model or its output, that portion of the code may be commented out and the model will run adequately without it.

Modelling of natural and acquired immunity has been handled in the Malaria in Displaced Populations model. Immunity is a difficult measurement to take from a population, but there is data available to support simulation of its effects in some malarious regions. Making the immunity levels of the agent population in that model a user controlled variable allowed for flexibility in experimentation according to data available to the user at the time of use.

6.7 Experiences of Implementation

NetLogo is a useful, flexible platform with which to develop disease related models. It provides an immediate visualisation of programmed procedures, which is as adaptable as the code itself. Troubleshooting of errors is aided considerably by the ability to observe the interactions of agents as soon as they are programmed. With no secondary requirement to learn to use a graphics or other associated package for visualising the model, development takes less time than it may otherwise.

There is some common syntax missing from NetLogo that might be expected by programmers used to other languages such as Java. One unavailable syntax use is the switch statement. With no availability of a switch statement, for shifting between possible outcomes to a code statement, it is necessary to use nested if and if-else. NetLogo has some features that haven't been utilised during the course of producing this thesis,

but may prove of use to advancing disease modelling in the future. One such feature is its capability as a tool for use over a network, with multiple users interacting via a NetLogo model over a network of computers. The usefulness of that type of modelling extension may be of interest to those studying disease spread via transport links and global population movement.

NetLogo has a worldwide community of followers that share their modelling work online, but it does not have a strong base of disease modellers interested in its development at present. In comparison to a platform such as Swarm, which has a worldwide following of immunological modellers, an annual conference and a number of academic collaborations associated with it, NetLogo lacks the support to highlight it as a useful and potentially powerful tool for disease modelling.

The limitations of modelling discovered during the course of this research were not due to deficiencies in the NetLogo platform. These limitations were associated with the Malaria and HIV Dual Infection model, which presented difficulty in adequately modelling HIV as a disease. Its highly complex transmission routes and the extensive detail of their possibilities is not easily simulated.

6.8   Limitations

The modelling of malaria's effects on a population might never be able to take into account enough of the many thousands of inter-related variables associated with the subject. The number of factors, both biological and environmental that effect the transmission of malaria are so great, that it would be impossible to comprehensively cover them within the scope of a single thesis. In fact, due to the constantly evolving nature of both the parasite and its hosts, it is unlikely that any study might be expected to do so. With that limitation considered, there are several factors relating to malaria transmission that have been identified as being of possible interest to future work, building upon this thesis. These areas are noted and explained below.

When a large number of agents are introduced to a mode,l there is a compromise on the quality of the visualisation of agent interactions. For the visualisation itself to be human readable, there must be a visual indication of how the agents are interacting and how their states are being altered by that interaction. When a large number of

agents are introduced to NetLogo's view, which is limited by available screen size, the agents overlap so considerably that their movement cannot be discerned.

The greater the complexity of the modelled environment and behaviours, the greater the difficulty in verifying the output of the model and validating the results produced. With a large number of complex agent interactions taking place, isolating just one feature for validation becomes difficult. One example of difficulty in validating output is evidenced with the Malaria in Peri-Urban Settlements model, where it became necessary to temporarily alter the code in order for the malaria transmission itself to be evaluated on its own.

6.9   Subjects for future work

There are a number of research topics that are related to the content of this thesis and may provide avenues for developments of future models or enhancement of those presented in this thesis.

6.9.1   Drug Resistance

The malaria parasite has developed and continues to develop resistance to many of the anti-malarial drugs that are commonly used. Drug resistant malaria is a well documented and well researched area that is of continued interest to malariology. Drug resistance as a subject would be fitting as the basis for development of a further model but is unlikely to be appropriate for addition to the models of this thesis. [43], [5].

6.9.2   Quality of Housing

The quality of housing available has an effect on the exposure of inhabitants to mosquitoes. Housing that is not structurally sound or well roofed allows entry by mosquitoes and makes those dwelling within susceptible to increased infection risk. There are a number of published works available that document the quality of housing in rural, urban and peri-urban regions globally, but the information is usually purely qualitative. [69].

6.9.3 Rapid Urbanisation

Rapid urbanisation has an impact on the quantity of standing water left near housing. Water is used for mixing building materials and preparing surfaces, so in areas of rapid expansion and settlement there are large amounts of still water available for mosquito oviposition. Rapid urbanisation is a possible avenue for further development of the Malaria in Peri-Urban Settlements model. [49].

6.9.4 Human Behaviours

Human behaviour is a complex subject in itself. When it is attempted in an agent based modelling sense, it is only ever simulated in part, with a small range of attributes, movements and interactions playing a part in creating a basic representation of what it means to be human.

The human behaviours developed for the models presented with this thesis are simplistic. It would be possible to extend those behaviours to add a greater realism to the interactions of the agents. Applying human like behaviours to agent based modelling is an area that continues to have greatly varying approaches. The question of how much detail is necessary in terms of behavioural traits before human behaviours are adequately represented continues to be a subject for debate in agent based modelling literature [26].

One possibility for advancing the human behaviours in the work of this thesis is an increased complexity in the interaction between doctor agents and other human agents in the malaria in Displaced Populations model.

6.9.5 Deficiencies in Verification and Validation

The verification and validation techniques used by agent based modellers do not follow a particular methodology, but rather a number of different techniques with no standardised method. Problems arise in comparing the validity of one model from another, when varying techniques have been used to evaluate the output. With no standardised methodology, it is also true that when models have been validated using the same technique, i.e comparison to real world statistics data and other quantitative sources, due to the data used being of varying quality and correctness, the accuracy of the models

suffers as a result.

The lack of standardised validation techniques in the agent based modelling community gives rise to problems of proving the credibility of models with widely recognised methodologies. It is a difficult issue to address, since in the case of agent based programming, appropriate methods of validation vary considerably depending on the subject of the model itself. It is also important to take into account that some models will require to be validated purely qualitatively rather than quantitatively. Qualitative analysis will always be unique to the subject of the model and therefore not easily standardised [6].

NetLogo Code for the Malaria in Displaced Populations Model

```
; A malaria spread model produced by Jessica S. Rowlands and W. J Teahan
; Bangor University 2011

turtles-own
[ sick?            ;; if true, the turtle is sick
  immune?          ;; if true, the turtle is immune
  community
  nearest-neighbour
]

globals[
  \%immune
  \%humans-infected ;; what \% of the population is infected.
  initial-water ;; how many water patches to begin with
  mos-spawned ;; how many water patches have spawned mosquitos so far
]

breed [mosquitos mosquito]
breed [humans human]
breed [doctors doctor]

humans-own
[
  time-between-heading-change
  original-x-location original-y-location ; used to determine their "home"
       for "chaotic around home" behaviour
  max-distance-from-home
]
```

```
patches-own[
  irrigated? ;; identifies a patch that is part of an irrigation scheme
  water? ;; identifies a patch that is water
  auto-water? ;; identify a patch that is automatically identified as water
  manual-water? ;; identify a patch that is manually identified as water
  camp? ;;identifies a patch that is a human camp centre
  transmissionBarrier? ;;this is used to model a barrier to malaria
      transmission.
  original-patch-color
  camp-x-location camp-y-location ; use to determine the location of camp
      patches
]

to setup
  ;; (for this model to work with NetLogo's new plotting features,
  ;; __clear-all-and-reset-ticks should be replaced with clear-all at
  ;; the beginning of your setup procedure and reset-ticks at the end
  ;; of the procedure.)
  __clear-all-and-reset-ticks
  set-default-shape turtles "square"
  set-default-shape mosquitos "target"
  ask patches with [(random-float 100) < density]
  [ set pcolor brown
    set water? true ]

  set initial-water count patches with [ is-water? pcolor ]
  set mos-spawned 0
  setup-humans
  import-terrain

  if auto-magic-mode [
    ;
    ; **************************************************
    ; * Simulation to run automatically in headless mode
    ; *
    ; * Overview
    ; * --------
    ; *
```

```
; * In order to run multiple simulations without manual intervention, an
;   automatic
; * means of configuring and running the model has been designed. The
;   results can
; * be collected via STDOUT, CSV or XLS format using NetLogo's native
;   headless
; * behaviour space modes.
; *
; * Usage
; * -----
; *
; * In order to take advantage of the additional functionality introduced
;   to the model
; * it's recommended that experiments are spawned from the command line
;   interface, this
; * allows us to utilize Behaviour Space's native ability to collate data
;   from multiple runs
; * of the model, iterating through pre-defined sets of variables and
;   generating vast
; * quantities for analysis by the user.
; *
; * From the command line
; *
; *      NETLOGOMODEL=/Computer-location/file-name/
; *      NETLOGOBIN=/Applications/NetLogo\ 4.1.2/NetLogo.jar
;   org.nlogo.headless.Main
; *      EXPERIMENT="experiment"
; *      RESULTS="results-file"
; *
; *      java -server -Xmx1024M -cp ${NETLOGOBIN} \
; *                          --model ${NETLOGOMODEL} \
; *                          --experiment ${EXPERIMENT} \
; *                          --spreadsheet ${RESULTS}
; *
; * Defining An Experiment Externally
; * ---------------------------------
; *
; * Behaviour space is capable of reading an experiment definition from
;   either a
```

```
; * Netlogo .nlogo file, where the experiment can be configured via the
    GUI or using
; * an external XML definition file.
; *
; * An example experiement definition can be found in 'experiments.xml'
; *
; *
; ******************************************
; set up our mozzies automatically
output-print "we're in auto magic mode!"

output-print "identifying water"
find-water

ifelse where-to-spawn = "auto"
[
  output-print "spawning mozzies on patches automatically identified as
      water"
  auto-gen-mozzies-on-auto-water
] [
ifelse where-to-spawn = "manual"
[
  output-print "spawning mozzies on patches manually identified as water"
  auto-gen-mozzies-on-manual-water
] [
ifelse where-to-spawn = "any"
[
  output-print "spawning mozzies in any port"
  auto-gen-mozzies-on-any-water
] [
ifelse where-to-spawn = "dead-centre"
[
  output-print "looks like we're being run from another program, we'll put
      some water in the centre of the screen and plant some mozzies on it"

  ask patch 0 0 [
    set water? true
    set manual-water? true
  ]
```

```
      output-print "planting some mozzies"

      auto-gen-mozzies-on-manual-water

    ] [
    ;; default case
    ]]]]


  ]
end


;The go procedure intiates the procedures that move the two agent types.
;It also updates the plots and progresses time in the model by adding a tick
    with each iteration.
;The if ticks > max-days [ stop ] code stops the model at the user determined
    time frame.

to go

  if ticks > max-days [ stop ]

  spread-mosquitos
  move-humans
  update-plot
  tick
end


;The setup humans procedure creates human agents.

to setup-humans
  set-default-shape humans "person"
  create-humans number-of-people
  [
    ;Sets the size of the agents and positions them at a random starting
        location.
    ;The original position of each agent is set as a variable so that it may
        be used
    ;later in the model when the agents may be required to return to their
        starting
    ;positions.
```

```
    set size 5.0
    setxy random-xcor random-ycor
    set original-x-location xcor
    set original-y-location ycor

    ;This part of the procedure sets the disease status of the agents

    set sick? false
    set immune? false
    ;If the human behaviour selected by the user is 'migration'
    ;headings are set here and variables time-between-heading-change
    ;and max-distance-from-home are set to be used by behaviours
    ;later on.

    ifelse (human-behaviour = "migration")
    [ set heading 320 + random 10 - random 10 ]
    [ set heading random 360 ]
    set time-between-heading-change 10 + random 40
    set max-distance-from-home random 50

    ;This part of the procedure creates a number of sick agents
    ;determined by the user control \%-initial-sick-people.

    ifelse (random 100 < \%-initial-sick-people)
      [ set color red
        set sick? true ] ; these people start off with malaria
      [ set color white ]
    if (random 100 < \%-initial-sick-people) and (color = white)
    ; if the people use bed nets the people without malaria will be brown and
        can not be bitten by a mosquito
      [ set color brown ]
    if (random 100 < \%-natural-immunity) and (color = white)
      [ set color brown
        set immune? true ] ;;this percentage of the population is calculated
            to possess natural immunity, and will not contract malaria.
]

 set-default-shape doctors "person"
```

```
    ifelse medicine ; if the medicine switch is set to 'on' doctors will be
        placed in the environment
      [create-doctors No-of-doctors ask doctors [(set size 6.0)(set color
          magenta)(set immune? true) (setxy random-xcor random-ycor)]]
      [create-doctors 0]

end

to draw-camps
  ;;draw some water over the imported image
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patches in-cone 3 360
        [ set pcolor 114
          set camp? true
        ]
        die
      ]
      display
    ]
  ]
end

to colour-irrigation
  ;; colour the areas that represent irrigation schemes.
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patches in-cone 3 360
        [ set pcolor 25
          set irrigated? true
        ]
        die
```

```
      ]
      display
    ]
  ]
end

;; MOVE HUMAN AGENT PROCEDURE *********************
;This procedure handles the movement of the agents
;based on the selected behaviour.

to move-humans
  ask humans
  [
    if (human-behaviour = "chaotic") or (human-behaviour = "chaotic around
        home")
    [
      if (ticks mod time-between-heading-change = 0)
        [ set heading random 360]
      ifelse ([pcolor] of patch-ahead 5 != blue)
      [ fd 1 ]
      [ ifelse (random 2 = 0)
        [ rt 90 ]
        [ lt 90 ]
      ]
      if (human-behaviour = "chaotic around home")
        [ ; check to see if wandered too far from home
          if ((distancexy original-x-location original-y-location) >
              max-distance-from-home)
            [ ; head back to home
              facexy original-x-location original-y-location
            ]
        ]
    ]

    if (human-behaviour = "migration")
    [
      if (ticks mod time-between-heading-change = 0)
        [ set heading set-heading + random 20 - random 20 ]
      ifelse ([pcolor] of patch-ahead 5 != blue)
      [ fd 1 ]
```

```
    [ ifelse (random 2 = 0)
      [ rt 90 ]
      [ lt 90 ]
  ]
  ]


  if (human-behaviour = "encampment")
  [
    if ([pcolor] of patch-ahead 5 = 114)
    [Stop]
    if (ticks mod time-between-heading-change = 0)
      [ set heading random 360]
    ifelse ([pcolor] of patch-ahead 5 != blue)
    [ fd 1 ]
    [ ifelse (random 2 = 0)
      [ rt 90 ]
      [ lt 90 ]
    ]
  ]


  ;The following code deals with the chance of infection from mosquito
  ; and human agent interaction as they negotiate their environment.

  let humanColor color
  ask mosquitos in-radius bite-radius
    [
      if (random 100 < bite-chance)
        [
          if (color = green) and (humanColor = red)
            [ set color yellow ]
          if (color = yellow) and (humanColor = white)
            [ ask myself
              [ set color red
                set sick? true ]
            ]
        ]
    ]

    ; If a non-infected mosquito bites an infected person,
    ; the mosquito becomes infected. If an infected mosquito
```

```
; bites a non-infected person, the person becomes infected
; since human agents with the colour brown represent individuals
; with natural immunity the code does not check or alter disease status
    for those agents.
; The chances of contracting the malaria parasite are highest when human
; agents and mosquito agents are interacting near
; the water patches where the mosquitos congregate to breed.

; *******************************************************
; Some risk of contracting malaria exists from interaction with wider
    ranging
; mosquitos in the environment. The following line of code models the
    risk.

; ask humans [if who <= random 10 [set color red]]

; **********************************************

;*******THIS SECTION CREATES DOCTOR AGENTS********
ifelse medicine ;if medicine is available
    [ask doctors in-radius .5 [if any? humans in-radius .5 with [color =
        red]
        [ask humans in-radius .5 with [color = red];doctors will cure
            nearby infectious people

            [ifelse bed-nets
            ;when bed-nets are used, doctors will cure nearby infectious
                people and give them a bed-net
                [ask humans in-radius .5 with [color = red]
                    [set color brown] ]
                    [ask humans in-radius .5 with [color = red]
                    [set color white]] ]]]]

    [ask doctors in-radius .5 [if any? humans in-radius .5 with [color =
        red]
    ;if the switch is off there are no doctors so this will not happen
        [ask humans in-radius .5
            [set color white] ]] ]

] ; Human agent interaction with doctors provides
```

```
        ; them with treatment that prevents malaria.
        ; These individuals then have the same
        ;  status as those with natural immunity.
        tick
end


        ;*********END DOCTOR AGENT SECTION**************



; END MOVE HUMAN AGENT PROCEDURES********************

to-report is-water? [colour]
  ;;reports true if the colour is a shade of blue

  report ((colour > 70) and (colour < 80)) or ((colour > 80) and (colour <
      90))
      or ((colour > 90) and (colour < 100)) or ((colour > 100) and (colour <
          110))

  ;; checks to see if the patches are coloured with one of the colours in
  ;; all ranges of blue recognised by NetLogo
end

;; Create the mosquito turtles
to swarm
  sprout-mosquitos 1
  [ set color green]
  set mos-spawned mos-spawned + 1
end

to spread-mosquitos
  ;spread the mosquito swarm through the surrounding area
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout-mosquitos 1
      [
        set color green
        set mos-spawned mos-spawned + 1
```

```
        ask patches in-cone 2 360
        [ sprout-mosquitos 1
          [
            set color green
            set mos-spawned mos-spawned + 1
          ]
        ]
      ]
      display
    ]
  ]
  ask mosquitos
  [
    rt random 300
    if ([pcolor] of patch-ahead 1 != black)
      [ fd 1 ]
    lt random 300 ;; some randomised movement
    if ([pcolor] of patch-ahead 1 != black)
      [ fd 1 ]
    rt random 300
    if ([pcolor] of patch-ahead -1 != black)
      [ back 1 ]
    lt random 300
    if ([pcolor] of patch-ahead -1 != black)
      [ back 1 ]
  ]
end

to spawn-mosquitos
  ;; spawn mosquitos where the user decides to

  if(mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      if (count mosquitos-here = 0)
      [
        sprout-mosquitos 1
        [
          ifelse (random 100 < \%-carrier-mosquitos)
```

```
                [ set color yellow ]
                [ set color green ]
              set mos-spawned mos-spawned + 1
              ask patches in-radius 1
              [
                if (count mosquitos-here = 0)
                  [
                    sprout-mosquitos 1
                    [
                      set color green
                    ]
                  ]
              ]
            ]
          ]
        display
      ]
    ]
end

to draw-water
  ;;draw some water over the imported image
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patches in-cone 3 360
        [ set pcolor blue
          set water? true
          set manual-water? true
        ]
        die
      ]
      display
    ]
  ]
end
```

```
to import-terrain
  ;; imports terrain from an image
  ask patches
  [ set pcolor white
    set water? false]

  if terrain-select = "Terrain 1"
  [import-pcolors "terrain1.jpg"]
  if terrain-select = "Terrain 2"
  [import-pcolors "terrain2.jpg"]
  if terrain-select = "Terrain 3"
  [import-pcolors "terrain3.jpg"]
  if terrain-select = "Terrain 4"
  [import-pcolors "terrain4.jpg"]
  if terrain-select = "Terrain 5"
  [import-pcolors "terrain5.jpg"]
  if terrain-select = "Irrigation"
  [import-pcolors "terrain6_irrigation.jpg"]


  ask patches with [ is-water? pcolor ]
  [
    set water? true
    set auto-water? true
    ; define the patch as an automatically identified water patch
  ]
  ask patches
  [ set original-patch-color pcolor ]
end

to draw-transmissionBarrier
  ;; draw a transmission barrier
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patches in-cone barrier-width 360
```

```
        [ set pcolor black
          set transmissionBarrier? true
        ]
        die
      ]
      display
    ] ; The transmission barriers model the
      ; use of insecticidal sprays around human settlement.
  ]
end


to remove-transmissionBarrier
  ; removes transmission barriers that have been drawn
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patches in-cone barrier-width 360
        [
          set transmissionBarrier? false
          set pcolor original-patch-color
        ]
        die
      ]
    ]
  ]

end


to find-water
  ; finds patches in the imported image that are coloured in
  ; the blue spectrum recognised by the model.
  ask patches with [water? = true]
  [
    set pcolor blue
  ]
  set mos-spawned 0
end
```

```
to update-plot
  set-current-plot "Malaria spread"
  set-current-plot-pen "sick"
  ;;print count humans with [sick?]
  plot count humans with [sick?]
  set-current-plot-pen "healthy"
  plot count humans with [not sick?]
end

to auto-gen-mozzies-on-manual-water
  ask patches with [manual-water? = true]
  [
    if count(mosquitos) <= max-mozzies [
      sprout-mosquitos 1
      [
        output-print count(mosquitos)
        output-print max-mozzies

        set color green
        set mos-spawned mos-spawned + 1
        ask patches in-cone 2 360
        [ sprout-mosquitos 1
          [
            set color green
            set mos-spawned mos-spawned + 1
          ]
        ]
      ]
      output-print "got here"
      display
    ]
  ]
end

to auto-gen-mozzies-on-auto-water
  ask patches with [auto-water? = true]
  [
    if count(mosquitos) <= max-mozzies [
```

```
      sprout-mosquitos 1
      [
        output-print count(mosquitos)
        output-print max-mozzies

        set color green
        set mos-spawned mos-spawned + 1
        ask patches in-cone 2 360
        [ sprout-mosquitos 1
          [
            set color green
            set mos-spawned mos-spawned + 1
          ]
        ]
      ]
      display
    ]
  ]
end

to auto-gen-mozzies-on-any-water
  ask patches with [water? = true]
  [
    if count(mosquitos) <= max-mozzies [
      sprout-mosquitos 1
      [
        output-print count(mosquitos)
        output-print max-mozzies

        set color green
        set mos-spawned mos-spawned + 1
        ask patches in-cone 2 360
        [ sprout-mosquitos 1
          [
            set color green
            set mos-spawned mos-spawned + 1
          ]
        ]
      ]
      display
```

```
        ]
    ]
end
```

NetLogo Code for the Malaria in Peri-Urban Settlements Model

```
; Malaria in peri-urban settlements model by Jessica S. Rowlands 2012

globals [time hours time-of-day number-of-days weeks number-of-years
    mosquito-lifespan]
patches-own [start-patch chemical vegetation standingWater]

breed [houses house]
breed [adults adult]
breed [children child]
breed [mosquitoes mosquito]

houses-own [site mosquitoBarrier]
adults-own [human-age adult-infected adult-susceptible adult-recovered
    original-x-location original-y-location max-distance-from-home
    dist-home-from-water]
children-own [human-age child-infected child-susceptible child-recovered
    original-x-location original-y-location max-distance-from-home
    dist-home-from-water]
mosquitoes-own [mosquito-age swarm-mates nearest-neighbour
    original-x-location original-y-location]

to setup
  reset-ticks
  create-patches
  set time-of-day 0 ;; In order that the distinction can be made between
      night time and day time.
end
```

```
to reset
  ask turtles[
    die
  ]
end
; The go procedure controls the movement of the human and mosquito agents.
; It also controls the chemical diffusion in the environment and iterates the
; time in the model. Time is measured in ticks but the handling of those ticks
; is dealt with to work more like hours, days and weeks in the model for a
    more
; natural real-time measurement.
; The age of the humans and the mosquitoes is incremented, but currently only
; the aging of the mosquitoes has an effect on their lifespan.
; No procedure exists to limit the lifespan of the human agents.
; Should the user require the age to the human agents to be
; incremented and their lifespans limited, it would be possible to add
; a further procedure to utlilize the attributes already coded.

to go
  tick
  ask mosquitoes [swarm]
  repeat 5 [ ask mosquitoes [ fd 0.2 ] display ]
  reset-chemical
  move-adults
  move-children
  insecticide-contact
  ask patches [ set chemical chemical * (100 - evaporation-rate) / 100 ]
  ; slowly evaporate chemical
  display
  set time-of-day (time-of-day + 1) mod 24
  ; increment by an hour
  if-else (time-of-day > sunset OR time-of-day < sunrise)
    [ set time "Night" ]
    [ set time "Day" ]
  set hours ticks
  set number-of-days ticks / 24
  set weeks number-of-days / 7
   if (hours mod 24 = 0) and (number-of-days mod 7 = 0)
     [re-spawn-mosquitoes]
  if ticks >= 365
```

```
  [set number-of-years ticks / 365]
  ask adults [human-age-increment]
  ask children [human-age-increment]
  ask mosquitoes [age-mosquitoes]
end

to create-patches
  ask patches
  [
    if pcolor = 9.9 ;; HOMES
    ; This colour represents patches that have homes on them.
    [
    sprout-houses 1 [set shape "house" set size 3

              ifelse (random 100 < \%-homes-insecticide)
                  [ set color 115
                  ask patch-here [set pcolor 115]
                  ; colour the patch beneath the house turtle the same colour
                      as the house.
                   ;; homes protected by insecticidal spray
                    set mosquitoBarrier true ]
                  [ set color brown ]
                  ;; unprotected homes are brown in colour.

      ]

    sprout-adults random max-no-adults-per-home + 1
    ; Sprout adult human agents on patches that have homes associated with
        them.
            [set shape "person"
            set size 2
            set human-age random 64 + 16
            set original-x-location xcor
            set original-y-location ycor
            set start-patch patch-here
            ; Associate agents with their original home patches.
             set max-distance-from-home random adult-max-dist
              ; Set a maximum distance from home patches that the agents will
                  travel.
```

```
                    ifelse (random 100 < \%-initial-sick-adults)
                    ; The number of agents that are initially sick is
                       dependent on
                     ; the value provided with the \%-initial-sick-adults
                        slider.
                     [ set color red
                       set adult-infected true ] ; these adults start off
                          with malaria
                        [ set color black
                          set adult-susceptible true] ; these adults are
                             susceptible to contracting malaria

                    ]

   sprout-children random max-no-children-per-home
   ;Sprout child human agents on patches that have homes associated with
       them.
        [set shape "person"
        set size 1.5
        set human-age random 16 + 1
        set original-x-location xcor
         set original-y-location ycor
         set start-patch patch-here
         ; Associate agents with their original home patches.
        set max-distance-from-home random child-max-dist
         ; Set a maximum distance from home patches that the agents will
             travel.

                ifelse (random 100 < \%-initial-sick-children)
                       [ set color pink
                        set child-infected true ] ; these children start off
                           with malaria
                       [ set color brown
                        set child-susceptible true] ; these children are
                           susceptible to contracting malaria.
                   ]

   display
]
    if pcolor = 95 ;; WATER
```

```
    ; If a patch is coloured bright blue (pcolor 95) is is viable
    ; for mosquito breeding and mosquito agents are sprouted on it.
    [
    sprout-mosquitoes mosquito-count
    ;; sprout a number of mosquito swarms up to the maximum user value for
        mosquito-count.
            [set size 1
            set color yellow
            set mosquito-age 0
            set mosquito-lifespan random 100
            ; set a random lifespan for the mosquito agents up to a
            ;  maximum that corresponds with real world mosquitoes.
             set original-x-location xcor
             set original-y-location ycor
             set start-patch patch-here]

    display
    ]

    if pcolor = 54 ;; VEGETATION
    [
      set vegetation true
      ; For future work and development, vegetation is associated with it's
          own attribute.
    ]


  ]
end


to human-age-increment ;; increment the age of the human agents
set human-age human-age + number-of-years
end


to move-adults
  ; Adult agents have a movement that takes them forward in a
  ; random direction away from their home patches.
  ; If they reach a distance that is heir maximum distance from
  ; home they return towards their home patches.
  ask adults
  [
```

```
    if not (time-of-day > sunset OR time-of-day < sunrise AND patch-here =
        start-patch)
    [
      set heading random 360
      ifelse ([pcolor] of patch-ahead 5 != 95) ;; human agents should not walk
          on water.
      [ fd 1 ]
      [ ifelse (random 2 = 0)
        [ rt 90 ]
        [ lt 90 ]
      ]


      ; check to see if wandered too far from home
      if ((distancexy original-x-location original-y-location) >
          max-distance-from-home)
        [ ; head back to home
          facexy original-x-location original-y-location ; face your original
              patch.
          fd distancexy original-x-location original-y-location
          ; move forward the distance between the patch you're on and your
              original patch.
        ]
    ]
;******HANDLING THE TRANSFER OF MALARIA BETWEEN MOSQUITOES AND HUMANS*****

    ; If a mosquito is in a close enough proximity to bite (according to
        bite-radius)
    ; Check disease status of the agent. If the status is 'succeptible' it is
        changed to 'infected'
    Let adultColour color
    ask mosquitoes in-radius bite-radius
    [
      if (random 100 < bite-chance)
      [
        if (adultColour = black)
        [ask myself [ set color red set adult-infected true]
        ]
      ]
    ]
```

```
;******END MALARIA HANDLING********************
     ]
  stop
end

to move-children
  ; Child agents have a movement that takes them
  ; forward in a random direction away from their home patches.
  ; If they reach a distance that is heir maximum distance
  ; from home they return towards their home patches.
  ask children
  [
      if not (time-of-day > sunset OR time-of-day < sunrise AND patch-here =
          start-patch)
      [
      set heading random 360
      ifelse ([pcolor] of patch-ahead 5 != 95)
      ; human agents should not walk on water.
      [ fd 1 ]
      [ ifelse (random 2 = 0)
        [ rt 90]
        [ lt 90 ]
      ]
    ; check to see if wandered too far from home
          if ((distancexy original-x-location original-y-location) >
              max-distance-from-home)
            [ ; head back to home
              facexy original-x-location original-y-location
              fd max-distance-from-home
            ]
          Let childColour color

;******HANDLING THE TRANSFER OF MALARIA BETWEEN MOSQUITOES AND HUMANS******

          ask mosquitoes in-radius bite-radius
          [
            if (random 100 < bite-chance)
            [
              if (childColour = brown)
              [ask myself [ set color pink set child-infected true]
```

```
                    ]
                  ]
                ]
;******END MALARIA HANDLING*************
          ]
  ]
    stop
end


;;;;;;;;;;;;;;;;;;BOID-LIKE SWARMING BEHAVIOUR FOR MOSQUITO
    AGENTS;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;

to swarm
  ifelse (mosquito-age = blood-seeking-interval) and (hours mod 24 = 0) and
      (number-of-days mod blood-seeking-interval = 0)
  ; if the mosquito is at the age to find a blood meal to
  ; reproduce, trigger this behaviour or otherwise swarm.
  [look-for-bloodmeal]
  [
  find-swarm-mates
  if any? swarm-mates
    [ find-nearest-neighbor
      ifelse distance nearest-neighbour < minimum-separation
        [ separate ]
        [ align
          cohere ] ]
  ]
end

to find-swarm-mates ;; turtle procedure
  set swarm-mates other mosquitoes in-radius vision
end

to find-nearest-neighbor ;; turtle procedure
  set nearest-neighbour min-one-of swarm-mates [distance myself]
end

;***SEPARATE

to separate ;; turtle procedure
```

```
    turn-away ([heading] of nearest-neighbour) max-separate-turn
end

;***ALIGN

to align ;; turtle procedure
  turn-towards average-swarm-mate-heading max-align-turn
end

to-report average-swarm-mate-heading ;; turtle procedure
  ;; We can't just average the heading variables here.
  ;; For example, the average of 1 and 359 should be 0,
  ;; not 180. So we have to use trigonometry.
  let x-component sum [dx] of swarm-mates
  let y-component sum [dy] of swarm-mates
  ifelse x-component = 0 and y-component = 0
    [ report heading ]
    [ report atan x-component y-component ]
end

;***COHERE

to cohere ;; turtle procedure
  turn-towards average-heading-towards-swarm-mates max-cohere-turn
end

to-report average-heading-towards-swarm-mates ;; turtle procedure
  ;; "towards myself" gives us the heading from the other turtle
  ;; to me, but we want the heading from me to the other turtle,
  ;; so we add 180
  let x-component mean [sin (towards myself + 180)] of swarm-mates
  let y-component mean [cos (towards myself + 180)] of swarm-mates
  ifelse x-component = 0 and y-component = 0
    [ report heading ]
    [ report atan x-component y-component ]
end

;;; HELPER PROCEDURES

to turn-towards [new-heading max-turn] ;; turtle procedure
```

```
    turn-at-most (subtract-headings new-heading heading) max-turn
end

to turn-away [new-heading max-turn] ;; turtle procedure
  turn-at-most (subtract-headings heading new-heading) max-turn
end

;; turn right by "turn" degrees (or left if "turn" is negative),
;; but never turn more than "max-turn" degrees
to turn-at-most [turn max-turn] ;; turtle procedure
  ifelse abs turn > max-turn
    [ ifelse turn > 0
        [ rt max-turn ]
        [ lt max-turn ] ]
    [ rt turn ]
end




;******END OF MOSQUITO SWARMING BEHAVIOUR SECTION******

to insecticide-contact
  ; this procedure acts on mosquitoes that come into proximity to
      insecticidal spray
  ask mosquitoes[
  if (count patches in-radius 2 with [pcolor = 115] > 0)
  [die
   print "Died due to insecticide"
    ]
  ]
end

to age-mosquitoes
  ; age mosquitoes and give them a realistic lifespan.
  ask mosquitoes[
    set mosquito-age number-of-days

    print (word "Aging: " mosquito-age " " mosquito-lifespan)
    if mosquito-age >= mosquito-lifespan
    [die
```

```
      print (word "Died due to aging: " mosquito-age " " mosquito-lifespan)
        ]
    ]
end


to re-spawn-mosquitoes
  ;if number-of-days = 7
  ;[ ;; this should be every seven days.
  ask patches with [pcolor = 95] ;; WATER
    ; If a patch is coloured bright blue (pcolor 95)
    ; is is viable for mosquito breeding and mosquito agents are sprouted on
        it.
    [
    sprout-mosquitoes mosquito-count
    ;; sprout a number of mosquito swarms up to the maximum user value for
        mosquito-count.
            [set size 1
            set color yellow
            set mosquito-age ticks / 24
            set original-x-location xcor
            set original-y-location ycor
            set start-patch patch-here]

    display
    ]
  ;]
end


;****BEGIN HUMAN chemical PRODUCTION AND MOSQUITO BLOOD MEAL SEEKING
    PROCEDURES****


; If the time of day is the evening hours then the
; humans produce an amount of mosquito attracting chemical.
; The chemical then evaporates over the daylight hours
; according to the user selected evaporation rate.
to reset-chemical
  ;; spread a chemical scent over the whole world -- stronger near the human
      agents
  if time-of-day >= 19
```

```
  [
    ask adults [set chemical 200 - distancexy 0 0]
    ask children [set chemical 200 - distancexy 0 0]
  ]

end

to look-for-bloodmeal ;; turtle procedure
  ;; go in the direction where the chemical scent is strongest
  if (chemical >= 0.05) and (chemical < 2)
  [ uphill-chemical ]
end

;; sniff left and right, and go where the strongest smell is
to uphill-chemical ;; turtle procedure
  let scent-ahead chemical-scent-at-angle 0
  let scent-right chemical-scent-at-angle 45
  let scent-left chemical-scent-at-angle -45
  if (scent-right > scent-ahead) or (scent-left > scent-ahead)
  [ ifelse scent-right > scent-left
    [ rt 45 ]
    [ lt 45 ] ]
end

to-report chemical-scent-at-angle [angle]
  let p patch-right-and-ahead angle 1
  if p = nobody [ report 0 ]
  report [chemical] of p
end

;***END chemical AND BLOOD MEAL SEEKING PRCEDURES****

; To save patches to file.
to save-patches
  file-open user-new-file
  ask patches
  [
    file-write (word "[" pxcor " " pycor " " pcolor "]")
  ]
  file-close
```

```
  [
    ask adults [set chemical 200 - distancexy 0 0]
    ask children [set chemical 200 - distancexy 0 0]
  ]

end

to look-for-bloodmeal ;; turtle procedure
  ;; go in the direction where the chemical scent is strongest
  if (chemical >= 0.05) and (chemical < 2)
  [ uphill-chemical ]
end

;; sniff left and right, and go where the strongest smell is
to uphill-chemical ;; turtle procedure
  let scent-ahead chemical-scent-at-angle 0
  let scent-right chemical-scent-at-angle 45
  let scent-left chemical-scent-at-angle -45
  if (scent-right > scent-ahead) or (scent-left > scent-ahead)
  [ ifelse scent-right > scent-left
    [ rt 45 ]
    [ lt 45 ] ]
end

to-report chemical-scent-at-angle [angle]
  let p patch-right-and-ahead angle 1
  if p = nobody [ report 0 ]
  report [chemical] of p
end

;***END chemical AND BLOOD MEAL SEEKING PRCEDURES****

; To save patches to file.
to save-patches
  file-open user-new-file
  ask patches
  [
    file-write (word "[" pxcor " " pycor " " pcolor "]")
  ]
  file-close
```

```
end

; To load patches from saved map files.
to load-map
  clear-all
  let input []
  let input-string ""
  let px 0
  let py 0

  ask patches
  [ set pcolor white ]
  file-open user-file
  while [not file-at-end?]
  [
    set input-string file-read
    set input read-from-string input-string

    set px (item 0 input)
    set py (item 1 input)
    ask patch px py
    [
      set pcolor (item 2 input)
    ]
  ]
  file-close
end

to report-distance-to-water

  let nearest nobody
  let dist 0

  ask adults
  [
    set nearest min-one-of patches with [pcolor = 95] [distance myself]
    set dist-home-from-water distance nearest
  ]

  ask children
```

```
  [
    set nearest min-one-of patches with [pcolor = 95] [distance myself]
    set dist-home-from-water distance nearest
  ]

  report dist-home-from-water
end
```

NetLogo Code for Map-Maker Model

```
; Allows you to draw a map specifically for use by the Malaria Spread in
    Peri-Urban Environments model
; Created by Jessica S. Rowlands 2012

patches-own [original-patch-color]

; The setup procedure clears the view and
; sets the background patches to the colour
; selected by the user with the background-colour selector.

to setup
  clear-all
  ask patches [set pcolor background-colour] ;; set background colour
end

; The import-background procedure imports the rgb
; colours of the user's selected file into the
; NetLogo's environment patches.

to import-background
  import-pcolors-rgb user-file
end

; The draw-inhabited-patches procedure
; colours the patches the user selects with a mouse click

to draw-inhabited-patches
```

```
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patch-here
        [ set pcolor 9.9
        ]
        die
      ]
      display
    ]
  ]
end


; The draw-waste-water procedure colours
; the patches the user selects with a mouse click.

to draw-waste-water
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patch-here
        [
        ifelse (random-float 100) < %-viable-water
        [ set pcolor 95]
        [set pcolor 98]
        ]
        die
      ]
      display
    ]
]
end
```

```
; The draw-still-water procedure colours the patches
; the user selects with a mouse click.

to draw-still-water

  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patch-here
        [ set pcolor 95
        ]
        die
      ]
      display
    ]
  ]
end


; The draw-wasteland procedure colours the patches the
; user selects with a mouse click.

to draw-wasteland
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patch-here
        [ set pcolor 6
        ]
        die
      ]
      display
    ]
  ]
end
```

```
; The draw- vegetation procedure colours the patches
; the user selects with a mouse click.

to draw-vegetation
  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patch-here
        [ set pcolor 54
        ]
        die
      ]
      display
    ]
  ]
end

; The erase drawing procedure will remove previously drawn
; pacth colours when the user mouse clicks on the patches.

to erase-drawing

  if (mouse-down?)
  [
    ask patch mouse-xcor mouse-ycor
    [
      sprout 1
      [
        ask patch-here
        [
          set pcolor background-colour
        ]
        die
      ]
    ]
  ]
```

```
end

; The save-map procedure saves the patch environment
; to a file that will then be saved on the user's computer.

to save-map
  file-open user-new-file
  ask patches
  [
    file-write (word "[" pxcor " " pycor " " pcolor "]")
  ]
  file-close
end

; The load-map procedure loads a previously saved map.

to load-map
  let input []
  let input-string ""
  let px 0
  let py 0

  ask patches
  [ set pcolor white ]
  file-open user-file
  while [not file-at-end?]
  [
    set input-string file-read
    set input read-from-string input-string

    set px (item 0 input)
    set py (item 1 input)
    ask patch px py
    [
      set pcolor (item 2 input)
    ]
  ]
  file-close
end
```

NetLogo Code for HIV and Malaria Dual Infection Model

```
; Malaria and HIV Dual Infection Model Created by Jessica S. Rowlands 2013

globals [
HIV-infection-chance
Malaria-infection-chance

slider-check-1
slider-check-2
slider-check-3
]

; The turtles-own procedure sets the attributes the turtles
; possess that may then be manipulated elsewhere in the code.

turtles-own [
HIV-infected?
Malaria-infected?

HIV-infection-length
Malaria-infection-length

coupled?
couple-length
coupling-tendency
condom-use
partner
commitment
```

]

; The setup procedure clears the view, then sets up the globals
; detailed in the setup-globals procedure. Ticks are reset.

```
to setup
clear-all
setup-globals
setup-people
reset-ticks
end

to setup-globals
set HIV-infection-chance initial-HIV-infection-chance
set Malaria-infection-chance initial-Malaria-infection-chance
set slider-check-1 average-commitment
set slider-check-2 average-coupling-tendency
set slider-check-3 average-condom-use
end
```

; The setup-people procedure places the agents at random coordinates
; in the NetLogo environment. Initially all the agents are set as uncoupled
; and without partners. Half of the agents are set as one human shape and the
   other
; half set as a second human shape. If this model is being re-created using
; the code provided here, the shapes used for the two human types may be set
   as
; any preferred or convenient shape from the NetLogo turtles editor.

```
to setup-people
crt initial-people
[ setxy random-xcor random-ycor
set coupled? false
set partner nobody
ifelse random 2 = 0
[set shape "person one"]
[set shape "person two"]
```

; This part of the procedure sets a number of the agents as infected with
; malaria and HIV. It assigns their commitment, coupling tendency and

```
; condom use according to the values selected by the user with the
; interface controls.

set Malaria-infected? (who < initial-people / 100 *
    Initial-no-malaria-infected)
set HIV-infected?    (who < initial-people / 100 * Initial-no-HIV-infected)
assign-commitment
assign-coupling-tendency
assign-condom-use
assign-color ]
end

; The assign-colour procedure assigns colour to the agents according to what
    diseases
; they are infected with. It is intended to provide a visualisation that may
    be
; understood by the user. To reference the colours associated with each
    disease
; there is a table provided in the associated chapter of the thesis.

to assign-color

if-else not malaria-infected? and not HIV-infected? [ set color blue ] [
if-else HIV-infected? and malaria-infected?    [ set color pink] [
if-else HIV-infected? and not malaria-infected? [ set color red ] [
                                                  set color yellow
]]]
end

to assign-commitment ;; turtle procedure
  set commitment random-near average-commitment
end

to assign-coupling-tendency ;; turtle procedure
  set coupling-tendency random-near average-coupling-tendency
end

to assign-condom-use ;; turtle procedure
  set condom-use random-near average-condom-use
end
```

```
to-report random-near [center] ;; turtle procedure
  let result 0
  repeat 40
    [ set result (result + random-float center) ]
  report result / 20
end


;***GO PROCEDURES

to go
  if all? turtles [HIV-infected?]
    [ stop ]
  check-sliders
  ask turtles
    [ if HIV-infected?
        [ set HIV-infection-length HIV-infection-length + 1 ]
      if coupled?
        [ set couple-length couple-length + 1 ] ]
  ask turtles
    [ if not coupled?
        [ move ] ]
  ;; Person shape 'one' is always the one to initiate mating.This is purely
  ;; arbitrary choice which makes the coding easier.
  ask turtles
    [ if not coupled? and shape = "person one" and (random-float 10.0 <
        coupling-tendency)
        [ couple ] ]
  ask turtles [ uncouple ]
  ask turtles [ infect ]
  ask turtles [ assign-color ]
  tick
end


to check-sliders
  if (slider-check-1 != average-commitment)
    [ ask turtles [ assign-commitment ]
      set slider-check-1 average-commitment ]
  if (slider-check-2 != average-coupling-tendency)
    [ ask turtles [ assign-coupling-tendency ]
```

```
      set slider-check-2 average-coupling-tendency ]
  if (slider-check-3 != average-condom-use)
    [ ask turtles [ assign-condom-use ]
      set slider-check-3 average-condom-use ]

end

;; update all the sliders.

to move ;; turtle procedure
  rt random-float 360
  fd 1
end

;; People have a chance to couple depending on their tendency to have sex and
;; if they meet. To better show that coupling has occurred, the patches below
;; the couple turn gray.

to couple ;; turtle procedure -- person shape one only.
  let potential-partner one-of (turtles-at -1 0)
                         with [not coupled? and shape = "person two"]
  if potential-partner != nobody
    [ if random-float 10.0 < [coupling-tendency] of potential-partner
      [ set partner potential-partner
        set coupled? true
        ask partner [ set coupled? true ]
        ask partner [ set partner myself ]
        move-to patch-here ;; move to center of patch
        move-to patch-here ;; partner moves to center of patch
        set pcolor gray - 3
        ask (patch-at -1 0) [ set pcolor gray - 3 ] ] ]
end

;; If two peoples are together for longer than either person's commitment
   variable
;; allows, the couple breaks up.

to uncouple ;; turtle procedure
  if coupled? and (shape = "person one")
  ;; Person one has been picked arbitrarily to initiate coupling.
```

```
      [ if (couple-length > commitment) or
          ([couple-length] of partner) > ([commitment] of partner)
        [ set coupled? false
          set couple-length 0
          ask partner [ set couple-length 0 ]
          set pcolor black
          ask (patch-at -1 0) [ set pcolor black ]
          ask partner [ set partner nobody ]
          ask partner [ set coupled? false ]
          set partner nobody ] ] ;; uncouple.
end

to infect
  ; If one of the partners have HIV but neitehr of the partners has malaria,
  ; HIV infection is passed on at the normal rate.
  if coupled? and HIV-infected?
  [if random-float 11 > condom-use or
    random-float 11 > ([condom-use] of partner)
    [ if random-float 100 < HIV-infection-chance
      [ ask partner [ set HIV-infected? true ] ] ] ]

  ;If one of the partners has malaria, they have an increased risk of
      contracting HIV
   if coupled? and HIV-infected? and Malaria-infected?
  [if random-float 11 > condom-use or
    random-float 11 > ([condom-use] of partner)
    [ if random-float 100 < HIV-infection-chance + increased-HIV-chance
      [ ask partner [ set HIV-infected? true ] ] ] ]
end

to-report HIV-infection
  ifelse any? turtles
    [ report (count turtles with [HIV-infected?] / count turtles) * 100 ]
    [ report 0 ]
end
```

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