AN AGENT BASED MODELING OF MALARIA TRANSMISSION INVESTIGATING THE IMPACT OF BED NET USE AND TEMPERATURE

BY

MUKHTAR GARBA IBRAHIM

SPS/16/MMT/00037

(B.Sc, Mathematics)

(Bayero University, Kano)

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DECLARATION

I hereby declare that this work is the product of my research efforts undertaken under the supervision of Prof. Saminu I. Bala, and has not been presented anywhere for the award of a degree or certificate. All sources have been duly acknowledged.

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MUKHTAR GARBA IBRAHIM

SPS/16/MMT/00037

CERTIFICATION

This is to certify that the research work for this dissertation and the subsequent write-up MUKHTAR GARBA IBRAHIM (SPS/16/MMT/00037) were carried out by under my supervision.

Prof. Saminu I. Bala ———————————-

(Supervisor) Signature

Dr. Abbas Ja‘afar Badakaya ———————————-

(Head of Department) Signature

APPROVAL

This dissertation has been examined and approved for the award of the degree of MASTERS OF SCIENCE IN COMPUTATIONAL MATHEMATICS.

Prof. Ajibade Abiodun Olusegun ———————————-

(External Examiner) Signature/Date

Dr. Isah A. Baba ———————————-

(Internal Examiner) Signature/Date

Prof. Saminu I. Bala ———————————-

(Supervisor) Signature/Date

Dr. Abbas Ja'afar Badakaya ———————————-

(Head of Department) Signature/Date

Prof. S.Y. Mudi ———————————-

(S.P.S Representative) Signature/Date

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DEDICATION

This work is dedicated to my parents, Late Malam Garba Ibrahim and Khadija Abdullahi Yakasai. May Allah (SWA) grant you both highest rank in Jannah, Amin.

Contents

CHAPTER THREE 31

METHODOLOGY 31

List of Tables

List of Figures

ABSTRACT

Malaria is among the most devastating infectious diseases in the world and is caused by plasmodium parasite, which is transmitted through the bites of an infected female Anopheles mosquito. An agent based model (ABM) of malaria is developed using NetLogo software to investigate the impact of Insecticide Treated Net (ITN) on malaria control and temperature under various control strategies. The ABM model incorporate the decrease in ITN effectiveness due to physical and chemical decay, influence of temperature in malaria transmission and mosquito mortality rate. The results of the study show that any intervention which contain ITN as a parameter is effective and temperature has a great influence on malaria transmission dynamics. Furthermore, the results reveal that mosquito mortality rates decreases as ITN effectiveness decreases and vice versa.

Keywords: Agent based model (ABM), NetLogo, Insecticide Treated Net (ITN), and Temperature.

CHAPTER ONE

INTRODUCTION

1.1 Historical Background of Malaria

Malaria has been noted for more than 4,000 years. The term malaria was coined from the two Italian words mal and aria meaning bad and air respectively. Malaria has probably influenced to a great extent human populations and human history. Camillo Golgi, an Italian neurophysiologist, established that there were at least two forms of the disease, one with tertian periodicity (fever every other day) and one with quartan periodicity (fever every third day) [35]. Golgi also observed that the forms produced differing numbers of merozoites (new parasites) upon maturity and that fever coincided with the rupture and release of merozoites into the blood stream. He was awarded a Nobel Prize in Medicine for his discoveries in neurophysiology in 1906. Golgi was the first to describe different species of malarial parasite (based on the frequency of attacks they caused and the number of parasites released once the red blood cells containing them ruptured) [35] . Italian researchers Giovanni Grassi and Raimondo Filetti first put a name to these parasites, classifying P. vivax and P. malariae. Americans William Welch and John

Stephens later contributed the names P. falciparum and P. oval respectively [31]. On August 20th, 1897, Ronald Ross, a British officer in the Indian Medical Service, was the first to demonstrate that malaria parasites could be transmitted from infected patients to mosquitoes. In further work with bird malaria, Ross showed that mosquitoes could transmit malaria parasites from bird to bird. This necessitated a sporogonic cycle (the time interval during which the parasite developed in the mosquito) [33]. Thus, the problem of malaria transmission was solved. For his discovery, Ross was awarded the Nobel Prize in 1902. Discovery of the Transmission of the Human Malaria Parasites Plasmodium (1898 - 1899) led by Giovanni Batista Grassi, a team of Italian investigators, which included Amico Bignami and Giuseppe Bastianelli, collected Anopheles claviger mosquitoes and fed them on malarial patients. The complete sporogonic cycle of Plasmodium falciparum, P. vivax , and P. malariae was demonstrated. In 1899, mosquitoes infected by feeding on a patient in Rome were sent to London where they fed on two volunteers, both of whom developed malaria [31].

1.2 Malaria Parasite

Malaria is among the most devastating infectious diseases in the world and is caused by plasmodium parasite, which is transmitted through the bites of infected mosquitoes [21]. Malaria parasites are micro-organisms that belong to the genus Plasmodium. Over 100 species of Plasmodium are available in the environment [8]. There are five types of human malaria parasites namely: Plasmodium vivax, P. malarie, P. ovale, P. knowlesi and P. falciparum [52]. P. falciparum and P. vivax are the most common and most deadliest type. P. falciparum is commonly found

in sub-saharan Africa and South East Asia, and is responsible for about 80% of all malaria cases and approximately 90% of deaths [53].

1.3 Life Cycle of Malaria Parasite

As shown in Figure 1.1, the natural life cycle of malaria parasites involves cyclical infection of humans and female anopheles mosquitoes. In humans, the parasites grow and multiply first in the liver cells and then in the red blood cells of the blood. In the blood, successive broods of parasites grow inside the red blood cells and destroy them, releasing daughter parasites (merozoites) that continue the life cycle by invading other red blood cells. The blood stage parasites are those that cause the symptoms of malaria. When certain forms of blood stage parasites (gametocytes, which occur in male and female forms) are ingested during blood feeding by a female anopheles mosquito, they mate in the gut of the mosquito and begin a cycle of growth and multiplication in the mosquito. After 10-18 days, a form of the parasite called sporozoite migrates to the mosquitos salivery glands. When the anopheles mosquito takes a blood meal on another human, anticoagulant saliva is injected together with the sporozoites, which migrate to the liver, thereby beginning a new cycle. Thus the infected mosquito carries the disease from one human to another (acting as a vector), while infected humans transmit the parasites to the mosquito. In contrast to the humans, the mosquito vector does not suffer from the presence of the parasites.

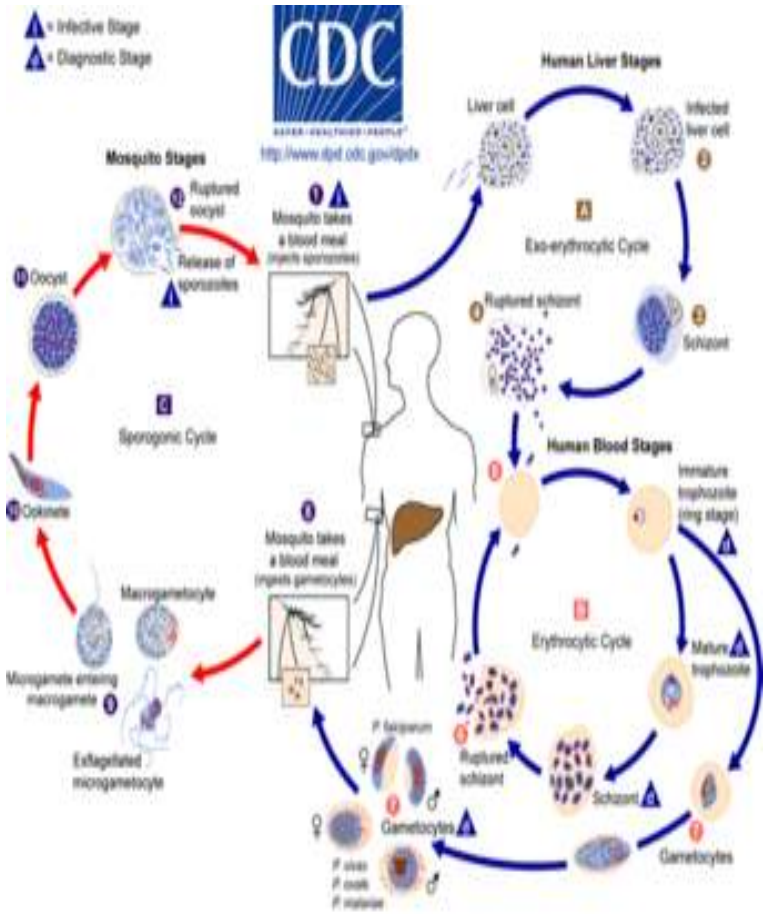

Figure 1.1: Life Cycle of Malaria Parasite [11].

1.4 Mode of Transmission of Malaria

Malaria is transmitted through the bites of female Anopheles mosquitoes that previously had a blood meal from an individual with parasitema [1]. There are over 400 different species of Anopheles mosquito; about 30 are malaria vectors of major importance [54]. All of the important vector species bite between dusk and dawn. Transmission is more intense in places where the mosquito lifespan is longer so that the parasite has time to complete its development inside the mosquito. According to many studies such as ([7],[16], [21] and reference there in) show that temperature plays a vital role in the life span of mosquitoes and the malaria parasite. Temperature affect the number and survival of mosquitoes. In the report of [7], both the mosquito life cycle and plasmodium parasites that cause malaria depend on temperature. In many places, transmission is seasonal, with the peak during and just after the rainy season [54]. The effects of temperature on parasite development and mosquito life history have been acknowledge for many years. Also Clinical immunity is among the factors that favors malaria transmission. Clinical immunity is a situation whereby protection against the clinical symptoms of the disease such as headache, vomiting, diarrhoea, and high fever e.t.c is developed despite the presence of the parasites [30]. An individual who develop clinical immunity serve as a reservoir of malaria disease. In malaria endemic areas, people may develop clinical immunity, allowing asymptomatic infection to occur [24].

1.5 Symptoms of Malaria

In a naive individual, symptoms usually appear 10 to 15 days after the infective mosquito bite [52]. Naive individuals are those who have never been infected with malaria, or who have been infected but do not devlop clinical immunity or those who have lost all immunity ([21],[24],[30]. Malaria symptoms include fever, headache, Vomiting and chills. while in children with severe malaria frequently develop one or more of the following symptoms: severe anaemia, respiratory distress in relation to metabolic acidosis, or cerebral malaria. In adults, multi-organ involvement is also frequent. In malaria endemic areas, people may develop clinical immunity, allowing asymptomatic (no symptoms of malaria) infections to occur [53]. Clinical immunity reduces the probability of clinical disease [51]. Clinical disease is a disease that require treatment.

1.6 Prevention and Control of Malaria

The aim of most current National Malaria Prevention and Control Programs and most malaria activities is to reduce the number of malaria related cases and deaths [11]. That is to reduce malaria transmission to a level where it is no longer a public health problem. According to [11] vector control is the main way to prevent and reduce malaria transmission. If coverage of vector control interventions within a specific area is high enough, then a measure of protection will be conferred across the community. In the report of World Health Organisation (WHO) 2017 [53] recommends protection for all people at risk of malaria with effective malaria vector control. Two forms of vector control, insecticide-treated mosquito

nets and indoor residual spraying are effective in a wide range of circumstances ([53],[11][52]). In the 1960s, dichlorodiphenyltrichloroethane (DDT) was a commonly used insecticide used to control mosquitoes by targeting the mosquitoes that harbor the Plasmodia parasites. Usually insecticides are applied to the walls of homes in areas with a high prevalence of malaria or is used to coat bed nets that also serve to physically keep mosquitoes away. Besides insecticides, mosquito levels can also be regulated by destroying larva before they hatch. A number of strategies have been developed to do this: one is to use biodegradable oils to suffocate developing mosquitoes in their watery habitat [11]. Another is to introduce into environments bacteria or fungi that only infect mosquitoes. Finally, mosquito eating fish have proven effective at reducing the number of larvae in particular large breeding grounds such as lakes [11]. Beyond insecticides, scientists are now developing genetically-modified mosquitoes that can no longer effectively harbor malarial parasites. This is done by introducing foreign genes into the mosquito genome. Two examples of such genes are genes whose protein targets the parasites in the mosquito salivary gland, and genes whose protein prevents the plasmodia from adhering to the wall of the mosquitos digestive system [11]. Furthermore, among the factors that complicates malaria control efforts is clinical immunity. Clinical immunity is 6maintained through repeated infections. A clinically immune individuals harbor parasites and act as a reservoir for malaria transmission.

1.7 Treatment of Malaria

Malaria is curable disease, with good chances of survival, if diagnosed early and given the correct medication [15]. However, according to WHO in [54], malaria can be a severe, potentially fatal disease especially when caused by Plasmodium falciparum and treatment should be initiated as soon as possible. The main objectives of treatment is to ensure complete cure, that is the rapid and full elimination of the plasmodium parasite from the patients blood, in order to prevent progression of uncomplicated malaria to severe disease or death, and to chronic infection that leads to malaria related anaemia [53]. Patients who have severe malaria or who cannot take oral medications should be given the treatment by continuous intravenous infusion. Most drugs used in treatment are active against the parasite forms in the blood. Some of the drugs available today that kill blood borne parasites include: chloroquine, atovaquone-proguanil (Malarone), artemether-lumefantrine (Coartem), mefloquine (Lariam), quinine e.t.c.

1.8 Motivation of the Study

Modeling malaria transmission dynamics is becoming more crucial in handling of such problems, the famous method is equation based modeling. The method make assumptions of homogeneity whereby heterogeneity plays a vital role in malaria transmission. Furthermore, models developed using this method make some simplified assumptions. The model makes assumption of some important factors that influence malaria transmission. In this case we need a method that will overcome or tackle such problem. Some efforts have been proposed to do away with the

shortcomings of equation based model, popularly known as mathematical model. Computer models promise an improvement in representing and understanding the complex social structure as well as the heterogenous patterns in the contact networks of real-word populations determining the transmission dynamics.

This research is motivated by the equation based model developed by Gimba and Bala in [21], where malaria transmission dynamics was modeled using systems of ordinary differential equations to investigate the impact of bed net use and treatment on malaria dynamics. Gimba and Bala present a vector-host mathematical model for malaria transmission dynamics of immune and non immune human populations that accounts for the impact of ITN usage and sesonality on the disease. The authors model mosquito biting rate as a function of temperature and ITN usage to mimic seasonality. The study extends the work of [30] by designing a vector-host model for malaria transmission dynamics. The study also extends the work of [3] by modeling the mosquito biting rate as a function of temperature to mimic seasonality.

The work is also motivated by the Agent Based Model developed by Ferreira et al. in [20], where mosquitoes population was considered to be non overlapping generation.

1.9 Statement of the Problem

Many mathematical models were developed to get insight in to malaria transmission dynamics in order to investigate the impact of some control strategies

([21],[30],[41] and reference there in). For simplicity, temperature , bed net efficacy, mosquito mortality rate are considered as parameters independent of time in Gimba and Bala model in [21]. However, in reality the mentioned parameters should be time dependent as they vary with time.

The central idea of this dissertation, is to develop a model that incorporates temperature as a variable, bed net efficacy to decrease with time, and mortality rate of mosquitoes to depend on both temperature and bed net efficacy. A model with aforemention parameters as a variable may result in very complex and non linear models. Agent-based modeling (ABM) is a form of computational modeling whereby a phenomenon is modeled in terms of agents and their interactions [57]. In this work, agents refer to human, mosquitoes and environment. Agent-based modeling (ABM) (ABM, see [57]) approach is chosen to develop a model that investigates the impact of ITN and temperature in malaria transmission dynamics. This is believed to serve as a way hopefully for understanding the dynamics of malaria transmission. ABM can be desgn, develop and formulate using multi agent modeling languages such as StarLogo, StarLogoT and NetLogo.

1.10 Aim and Objectives

Aim

The aim of this research is to develop an agent-based model to simulate the impact of temperature and bed-net use on malaria transmission where the mosquito population is considered to be of overlapping generation.

Objectives

- To assess the effectiveness of insecticide treated bed net usage on malaria transmission.
- To aid in the understanding of transmission dynamics of malaria.
- To assess the impact of temperature in malaria transmission.
- To perform various simulation using the developed ABM model in order to investigate the results of interactions between the human and mosquito agents.

1.11 Scope and Limitation

This research is limited to the effects of temperature and bed-net use on malaria transmission dynamics using ABM approach.

1.12 Methodology

We plan to carry out extensive literature survey to

- to develop an agent-based model using Netlogo software,
- use BehaviorSpace tool for sensitivity analysis, and
- use MATLAB and NetLogo for visualization of the simulation results.

1.13 NetLogo [54]

NetLogo is a programmable modeling environment for simulating natural and social phenomena. It is designed for modeling complex systems. Modelers can give instructions to hundreds or thousands of agents all operating independently. This makes it possible to explore the connection between the micro-level behavior of individuals and the macro-level patterns that emerge from their interaction. It also comes with the Models Library, a large collection of pre-written simulations that can be used and modified. These simulations address content areas in the natural and social sciences including biology and medicine, physics and chemistry, mathematics and computer science, and economics and social psychology. Several model-based inquiry curricula using NetLogo are available and more are under development. NetLogo is the next generation of the series of multiagent modeling languages including StarLogo and StarLogoT. NetLogo runs on the Java virtual machine, so it works on all major platforms (Mac,Windows, Linux, et al). It is run as a desktop application. Command line operation is also supported. NetLogo is a free, open source which can be downloaded from its web site.

1.13.1 Features of NetLogo

Some of the features that can be use in NetLogo programming are:

1. Agents: An agent is a unique and autonomous entities that usually interact with each other and their environment locally. That is, agents usually are different from each other in size, location, history, and do not interact with all other agents but only with their neighbors in geographic space and act

independently of each other to pursue their own objectives. Agents usually also have a graphical component so you can see them on the computer screen. An agent can represent any element of a system. A mosquito agent, for instance, might have properties such as size with value 0.5 units, speed with value 5 meters per second, and heading with a value of the angle it is facing.

2. Environment: Environment is where the agents live and interact, but much more often environment is represented discretely by patches (square cells), usually on a square grid. For example, a landscape can be modeled as a square grid where resource sites (e.g., house holds, breeding sites) are available for the agents.

3. Sliders: Sliders are global variables, which are accessible by all agents. They are used in models as a quick way to change a variable without having to recode the procedure every time. Instead, the user moves the slider to a value and observes what happens in the model.

4. Monitors: Monitors display the value of any reporter. The reporter could be a variable, a complex reporter, or a call to a reporter procedure. Monitors automatically update several times per second.

5. Speed slider: Speed slider lets you fast forward your model or see it in slow motion.

6. BehaviorSpace: BehaviorSpace is an open source tool used to collect data from multiple parallel runs of a model.

7. Plots; Plots show data the model is generating.

CHAPTER TWO

LITERATURE REVIEW

2.1 Introduction

In this Chapter we shall discuss some concept of modeling, mathematical modeling, agent-based modeling, malaria models, and some related literature in modeling malaria.

2.2 Modelling [49]

A model is a purposeful representation of some real system. To design models we have to make decisions what to leave out of the model. Real systems often are too complex to be analyzed using experiments. The function of a model is to help us to understand and examine phenomena that exist in the real world in more tractable and efficient ways than by simply observing reality. Mathematicians try to formulate a simplified representation of the system using equations or a computer program that can then manipulate and experiment on.

2.3 Mathematical Modelling [15]

Mathematical modeling is define as the art of using mathematical objects (e.g. differential equations, matrices as well as computer programs) to explain the dynamical or static behaviour of systems/problems we encounter in our day-to-day life. Models describe our beliefs about how the world functions. Mathematical modeling translate those beliefs into the language of mathematics. Mathematical models are used in comparing, planning, implementing, evaluating, and optimizing various detection, prevention, therapy and control programs.

2.4 Computational Modelling

A computational model is a mathematical model in computational science that requires extensive computational resources to study the behavior of a complex system by computer simulation [46]. Computational modeling is the use of computers to simulate and study the behavior of complex systems using mathematics, physics and computer science. A computational model contains numerous variables that characterize the system being studied. A key feature of todays computational models is that they are able to study a biological system at multiple levels [25]. As described in [25] computational model as a model that takes certain input values, manipulates those inputs in an algorithmic way, and generates outputs. Computational modeling and simulation has grown to where it now represents one of the most powerful design tools available in industry, particularly when used to analyze and control dynamic systems. This has been primarily due

to remarkable advances that have taken place in systems theory, computer science, and engineering, as well as other human activities in engineering and science [25].

2.5 Agent-Based Modelling

Agent-based modeling (ABM) is a form of computational modeling whereby a phenomenon is modeled in terms of agents and their interactions [57]. Traditionally, the complexity of scientific models was often limited by mathematical malleability when differential calculus was the only approach scientist had for modeling, they had to keep models simple enough to solve mathematically. With ABM, the limitation of mathematical tractability is removed so we can start addressing problems that require models that are less simplified and include more characteristics of the real systems. ABM is a methodology that can be randomly applied. It can enable us to explore, make sense of, and analyze phenomena and scenarios across a wide variety of contexts and content domains. In the past two decades, scientists have increasingly used agent-based modeling methods to conduct their research. ABM is a transformative representational technology that enables modelers to better understand familiar topics, and make sense of and analyze hitherto unexplored topics, and enable a democratization of access to computational tools for making sense of complexity and change [57].

Components of an ABM

The authors in ([2],[47],[57]) described three major components of an ABM, namely: agent, environment and rules. Rules merge the agents and their environment. These rules can be operated between agent to agent, or agent to environment. For example, agent to agent is the interactions (how one type of agents (e.g., infectious) infect another type (e.g., susceptible)). An agent to environment level rule is the movement which may direct an agent to look around as far as it can, and to look for food, breeding site e.t.c. for instance, a sheep agent might have a rule to eat grass if there is grass available nearby.

In an agent-based model, we imagine a universal clock. When the clock ticks, all agents invoke their rules. If the conditions of the rules are satisfied, (e.g., they are at the edge of a box, or grass is nearby), they enact the behavior (i.e., bounce or eat grass). The goal of agent-based modeling is to create agents and rules that will generate a target behavior. ABM is used to understand a phenomenon through experimentation with rules and properties. The methodology of ABM encodes the behavior of individual agents in simple rules so that we can observe the results of these agents interactions.

2.5.1 Equation based models Vs Agent-based models

Agent-based models, in particular, are distinctive from other modeling approaches in that they were designed in order to understand and explain complex phenomena that otherwise could not be explained through traditional approaches [57]. The

most common form of scientific models is the equation form. In [44], Parunak et al., discussed the differences between ABM and equation-based modeling (EBM)

- Since ABM models individuals, it can model a heterogeneous population, whereas EBM makes assumptions of homogeneity. In many models, heterogeneity plays a key role. Furthermore, when you model individuals, the interactions and results are typically discrete and not continuous. Continuous models do not always map well onto real world situations.

- ABM does not require knowledge of the aggregate phenomena while EBM does. One does not need to know what global pattern results from the individual behavior. When modeling an outcome variable with EBM, you need to have a good understanding of the aggregate behavior and then test out your hypothesis against the aggregate output. For example, in the wolf-sheep (predator-prey) example, to build the EBM, you need to have an understanding of the relationship between (aggregate) wolf populations and sheep populations. To encode this aggregate knowledge, you must have knowledge of differential equations. In contrast, ABM enables you to write simple rules for simple entities, requiring knowledge only of commonsense behaviors of individual wolves and sheep and yet still observe the aggregate result by running the model. Thus, even if you have no hypothesis as to how the aggregate variables will interact, you can still build a model and generate results.

- Since agent-based models describe individuals, not aggregates, the relationship between agent-based modeling and the real world is more closely

matched. It is therefore much easier to explain what a model is doing to someone who does not have training in the particular modeling paradigm. This is beneficial because it means that no special training is required to understand an agent-based model. It can be understood by all of the stakeholders in a modeling process. Moreover, with some ABM languages like NetLogo, the syntax is so readable that stakeholders without knowledge of how to build a model can often read the model code and understand what is going on. This helps improve the verifiability of the model. This approach to modeling enables all interested parties to talk about the model all the way down to its most basic components.

- Also the results generated by ABMs are more detailed than those generated by EBMs. ABMs can provide both individual and aggregate level detail at the same time. Since ABMs operate by modeling each individual and their decisions, it is possible to examine the history and life of any one individual in the model, or aggregate individuals and observe the overall results. This bottom-up approach of ABMs is often in contrast with the top-down approach of many EBMs, which tell you only how the aggregate system is behaving and do not tell you anything about individuals. Many EBMs assume that one aspect of the model directly influences, or causes, another aspect of the model, while ABMs allow indirect causation via emergence to have a larger effect on the model outcomes.

  Among the features of agent-based modeling, is that it is easy to incorporate randomness into your models. Many equation based models and other

modeling forms require that each decision in the model be made deterministically. In agent-based models this is not the case; instead, the decisions can be made based on a probability.

- There are often times when we simply do not know enough about how a complex system works in order to build a completely deterministic model. In many of these cases the only type of model that we can build is a model with some random elements. Agent based modeling and other modeling forms that allow you to incorporate random features are essential to studying these kinds of systems.

The comparison between EBMs and ABMs is summarised in Table 2.1.

Table 2.1: **Comparison Between EBMs and ABMs**

Criteria	EBM	ABM
Theoretical basis	Aggregation	Segregate
Compute requirements	Minimal	Intensive
Assumption about individuals	Homogenous	Heterogeneous
Assumption about interactions	Implicit	Explicit
Time, Events and Dynamics	Continuous	Discrete
Level of granularity in implementation	Low	High
Complexity of model	Low	High
Practical use	Evaluation of what if scenarios	Observing patterns of emerging behavior
Decision support in	Operations	Planning

2.5.2 Advantages of ABM

ABM has some advantages over equation-based-model (EBM). Some of the advantages are:

- Agent-based models enable us to easily examine different mechanisms and attributes of a system and see what effect those modifications have on the overall behavior of the system. By varying these different attributes or parameters and observing their effect on the behavior of the system.

- Agent-based models can be used as a vehicle for communication and education. An agent-based model allows us to expand beyond static knowledge, enabling learners to conduct experiments much as scientists do. If someone has a hypothesis as to how a particular mechanism works, they can implement that mechanism and see whether it can account for observed behavior.

- Agent-based models provides us with an unambiguous representation of the problem that we are examining, and thus is useful not only within the scientific community but also in other realms such as policy analysis.

2.5.3 Disadvantages of ABM

Almost, all methods or tools have some disadvantages. Agent-based models also have some drawbacks, some of which are mentioned below:

- ABM can be computationally intensive: Simulating thousands or millions of individuals can require great computing power [57].

- Speed: ABMs run slowly than the other modeling techniques [2]. A lot of agent based toolkits include performance limitations, with a large number

of agents, execution speed drops considerably. Usually these tools are not designed for extensive simulations.

- Cost: Relatively high costs (in both time and effort) are involved compared to the equation-based models because of the finer granularity of information [42].

- Result Analysis: For the consequence of the finer granularity and massive data requirement, it is often hard to detect whether the results generated by an ABM are the cause of a programming error or a groundbreaking insight [24].

- Verification and Validation: Verification and Validation activities sometimes demand more resources [42].

- Programming Language Requirement: Development of an ABM requires knowledge of programming languages. Also, once developed, it may still be diffcult to comprehend by many people [2].

- Sensitivity to initial conditions: Agent-based models are very sensitive to the initial conditions and to small variations in interaction rules [19].

- Multiple run requirements: To get robust result, agent-based computation requires multiple runs by systematically varying initial conditions or parameters [2].

Despite all these disadvantages we want to adopt this method because of the complex structure of our model.

2.6 Literature Review of Malaria Models

Among the first to introduce the first deterministic model of malaria is Sir Ronald Ross in the early 1900 [48]. Ross model the relationship between the number of mosquitoes and incidence of malaria in humans. Ross model showed that reduction of mosquito numbers below a certain figure (Transmission threshold) was sufficient to counter malaria. Later in the 1950s, George Macdonald [38] modified Ross model by adding exposed class in mosquitoes due to malaria parasite development. This provided for a massive World Health Organization (WHO) campaign, which concentrated on using the insecticide dichlorodiphenyltrichloroethane (DDT) that killed mosquitoes. In 1991, Anderson and May [4] introduced Latency of infection in humans in Ross-Macdonalds model making the additional Exposed class in humans.

In 2005, Chitnis [15] model malaria transmission using ordinary differential equations in order to compare intervention strategies for malaria control for two areas of high and low transmission. Based on his findings, use of insecticide-treated bed nets, diagnosis and treatment of infected individuals are the most effective methods for malaria control.

In 2013, Agusto et al [3] formulated a mathematical model that considers the transmission dynamics of malaria infection in human and mosquito population and investigated the impact of bed-net use on malaria prevalence. They model the mosquito biting rate by a linearly decreasing function of treated bed-net usage, b

$$\beta(b) = \beta_{max} - b(\beta_{max} - \beta_{min}), \quad 0 \leq b \leq 1, \tag{2.6.1}$$

Where the parameters βmax, βmin are the maximum and minimum biting rates respectively, and b is the proportion of bed-net usage. The study showed that if 75% of the population were to use ITN, malaria could be eliminated.

In 2013, Cristiana J. Silva and Delfim F. M. Torres [50] consider a mathematical model presented in [31] for the impact of ITN on the transmission of malaria infection. They introduce a time-dependent supervision control in the model in order to minimize the number of infectious humans while keeping the cost low. They found that information, education, communication (IEC) campaigns and post-distribution hang-up campaigns are strongly recommended for the optimal control of malaria transmission.

In 2014, Ngonghala et al.,[40] study the impact of decrease in ITN effectiveness in Malaria transmission dynamics. They authors model mortality rate of mosquitoes as

$$\mu_v\left(b_{\mu_v}(t)\right) = \mu_{v0} + \mu_{v1} b_{\mu_v}(t), \tag{2.6.2}$$

where

$$b_{\mu_v}(t) = \frac{2^n+1}{2^n}\left(\frac{-1}{2^n+1} + \frac{1}{1+\left(\frac{t mod T}{T/2}\right)^n}\right) b_0. \tag{2.6.3}$$

μ_v is natural mortality, μ_{v1} is a positive constant and b_{μ_v} measures the efficacy of ITNs in killing mosquitoes that land on them. The authors discovered that ITN replacement and coverage in malaria control depend on the level of contact rate. In low mosquito contact rate, regular replacement and about 50% coverage will eliminate malaria, while in high mosquito contact rate, regular replacement and about approximately 90% coverage will be needed to bring malaria under control.

In 2016, Ngonghala et al.,[41] explore the effect of natural decay in ITN-efficacy overtime in malaria transmission dynamics. The authors consider two situations in malaria models one with constant ITN efficacy and the other with the decline in ITN efficacy over time. The authors consider mosquito mortality rate defined in Ngonghala et al.[40]. The studies show that a model with constant ITN efficacy underestimate disease prevalence.

In 2013, Lunde et al [34] study how malaria models relate temperature to malaria transmission. The authors compared six temperature dependent mortality models for the malaria parasites. Among the models compared by Lunde et al. are

- Martins Scheme 1 shows the relationship between daily survival probability (P) and temperature (T).

$$P(T) = -0.0016.T^2 + 0.054T + 0.45. \tag{2.6.4}$$

- Martin 2 model a temperature dependent function of daily survival probability of mosquitoes as

$$P(t) = e^{-\frac{1}{-4.4+1.3t-0.03t^2}} \tag{2.6.5}$$

- Bayoh-parham included the effects of relative humidity and parameterized survival probability as

$$P(T,RH) = \exp^{-(T^2\beta_2+T\beta_1+\beta_0)^{-1}}. \tag{2.6.6}$$

Where β_0, β_1, and β_2 are constants related to Relative Humidity (RH).

which increases the daily survival probability of mosquitoes at higher temperatures. They found that different mortality calculations can influence Malaria transmission dynamics.

In 2013, B. Johnson et al., [7] study the effect of temperature in the survival rates of both the Anopheles mosquitoes and the Plasmodium parasites that cause malaria. They formulated temperature-dependent, stage-structured delayed differential equation model. They also include the full mosquito life cycle in the model. The report shows that the Mosquito population abundance is more sensitive to temperature because it is influenced by the dynamics of the juvenile mosquito stages whose vital rates are temperature dependent.

In 2015, Ciota et al., [16] investigate the effect of temperature on life history traits of some selected mosquitoes species. They measured temperature dependent variation in development time, immature survival, adult survival, mosquito size, blood-feeding, and fecundity both among species and between colonized and field-derived populations. The report demonstrate that temperature affects all of these traits significantly. The report shows that temperature affects all of these traits significantly.

In 2008, Aguas et al., [24] collected clinical data from eight endemic regions in sub-Saharan Africa and formulated a mathematical model to address prospects for malaria eradication from the regions. The study divide human population into four compartment of susceptible naive individuals, infected naive individuals refer as those with clinical malaria, recovered clinically immune individuals and infected clinically immune individuals as those with asymptomatic malaria. The report found that acquisition of clinical immunity alter the duration of infections,

which in turn is responsible for the identification of a regime of bistability. Bistability is the existence of two stable equilibria for the same parameter values which occurs when recovery from a clinical infection is faster than from asymptomatic infections. This provides an identification of regimes where malaria control is sustainable which has important implication for public health. The report show that recovery time for clinically immune individuals is about six times higher than those with clinical malaria. The work suggested that interventions that reduce transmission should be combined with effective management of clinical cases to prevent any undesired increase in disease burden.

In 2013, Keegan and Dushoof [30] formulate a dynamical model of malaria transmission to investigate the possibility of clinically immune causing bistability. The authors use the idea of compartmental modeling and divide the population in to susceptible naive, infected naive, susceptible clinically immune, and infected clinically immune and simulate the model under low and high level of infectiousness of clinically immune. The authors found that relative transmission effectiveness of clinically immune individuals and the time scale at which clinical immunity is wane are the key parameters determining the occurrence of bistability.

In 2017, Gimba and Bala [21] formulated an equation based model to study the impact of temperature on bed-net use and treatment on malaria transmission dynamics. The authors divided the human population into four compartment of susceptible naive, infected naive, susceptible clinically immune, and infected clinically immune individuals. Gimba and Bala modified mosquito biting rate define in [3] as

$$a = \beta_{max} - \beta(\beta_{max} - \beta_{min}), where \beta = \exp^{-h(T/T-T_0)^2}. \tag{2.6.7}$$

β represents the proportion of ITN usage and the parameters T_0 and h are location and scale parameters measured in ^oC respectively. The study shows that temperature has effect on Malaria transmission dynamics and any control strategy which combine treatment and usage of ITN is effective for malaria control. They further suggest that Provision of relatively colder environment will also help in malaria control.

Apart from equation-based models some agent-based models (ABMs) also have been developed to model Malaria transmission dynamics.

In 1968, Macdonald et al., were the first to consider the idea of stochasticity in a model to assist the design of control programmes [39]. They modeled malaria transmission through simulations based on four key epidemiologic parameters: the mosquito biting rate, the mosquito mortality rate, the human recovery rate, and the reproduction number. The model simulations incorporated seasonal changes but no incubation period of the infection. According to MacDonald et al. [39], computational approaches are better for malaria modeling, if the model contains detailed study of various preventive measures and the process of eradication, which cannot be handled by a deterministic approach that deals only in numbers, which never reach very low finite levels.

In 2009, Gu and Novak [22] developed an agent-Based model to trace the status and movement of the mosquitoes. They used two stage processes for mosquito blood searching in the model namely the random flight and the directional flight. A random flight is when the mosquito does not detect the target source, while directional flight is when the mosquito detect the target source. The two types of mosquito foraging had been analyzed to show how the target source reduction can be effective to reduce malaria incidences. The authors also extended

the agent-based model by incorporating intricate intervention between mosquitoes and treated bed nets to investigate the dynamics of the local vector species. The study had shown that reduction of malaria transmission depended on the high killing effects of treated bed-nets (ITNs).

In 2012, Briet et al.,[8] used a stochastic simulation-based tool to evaluate, among other LLIN-effectiveness factors, the impact of physical and chemical decay and discovered that the decay rate of insecticides and the attrition rate of ITN play big roles in assessing malaria transmission.

In 2014, Yokley et al., [59] developed a simple agent-based model of malaria transmission investigating intervention methods and acquired immunity. The authors divided the human population into two compartments of susceptible and infectious individuals as in the Ross-Macdonal model. Similarly, mosquitoes population was also subdivided into two compartments of susceptible mosquitoes and infectious mosquitoes. They considered both the population of mosquitoes and the population of humans to be constant. Seasonality was not included in the model. Furthermore, mosquito mortality rate, ITN efficacy, recovery rate of infected individuals and all other model parameters were assumed to be constant despite the fact that it is not a deterministic model. The authors compared their model to Ross-Macdonal model in order to ascertain their similarities. They discovered that their model results had similar predictions to the ODE model based on the work of Ross and MacDonald [59].

In 2014, Mcleod et al.,[27] addressed the importance of using agent-based modeling (ABM) for studying malaria prevalence and transmission. The study consider malaria parasite life cycle within both human and mosquitoes as depicted in Figure 1.1 and explain it according to ABM perspective. For instance,

from Figure 1.1, an infectious mosquito inoculates sporozoites into the human host. According to ABM perspective, this is a probabilistic contact-based transmission. Also, Sporozoites infect human liver cells and mature into schizonts, which rupture and release merozoites. From an ABM perspective this is a latent period of time, where the individual remains in the exposed state for a latency period. A susceptible person move to exposed class after spending its latency period. According to Mcleod et al., a better understanding of prevention and control measures might be obtained through the use of technology and high-resolution modeling and simulation approaches.

In 2017, Jindal et al., [29] developed an Agent-Based Modeling and Simulation of Mosquito-Borne Disease Transmission. The authors consider temporal and spatial movement of infection, but do not account for the effect of clinical immunity in malaria transmission and Insecticide Treated Nets in reducing malaria transmission.

CHAPTER THREE

METHODOLOGY

3.1 Introduction

In this chapter, we formulate a stochastic ABM to address malaria transmission dynamics and is modeled using the SEIS ($susceptible \rightarrow exposed \rightarrow infectious \rightarrow susceptible$) framework. We first describe the current paradigms of malaria mathematical modeling, which drives the structure of our computational framework.

3.2 Model Formulation

The goal of our ABM is to extend the capabilities of the mathematical model of malaria transmission dynamics developed by Gimba and Bala in [21] with the addition of latency period in both human and mosquitoes population. The model underlies the ABM design presented during the next section. The basic features of the model are described as follows: we have two populations, humans and mosquitoes population. At any time t, the total human population denoted by

$N_h(t)$, is divided into six components of susceptible naive $S_n(t)$, susceptible clinically immune $S_c(t)$, exposed naive $E_n(t)$, exposed clinically immune $E_c(t)$, infectious naive $I_n(t)$, and infectious clinically immune $I_c(t)$. As defined in the work of ([21],[24],[30]) naive individuals are those who have never been infected with malaria or those who have been infected but do not develop clinical immunity or those who have lost all immunity. While clinically immune individuals are those with immunity to clinical symptoms. We define is exposed individuals as those infected with malaria but can not transmit the disease while infectious individuals transmits the malaria disease. Hence, the total population of human is given by

$$N_h = S_n + E_n + I_n + S_c + E_N + I_c \tag{3.2.1}$$

Also, at any time t, the mosquitoes population, denoted by $N_m(t)$, is sub-divided into three sub-population namely: susceptible mosquitoes S_m, exposed mosquitoes E_m, and infectious mosquitoes I_m. Therefore, the total population of mosquitoes is given by

$$N_m = S_m + E_m + I_m \tag{3.2.2}$$

From Figure 3.2 the population of susceptible naive individual is increased by naive infectious individuals that recovered without immunity at a rate γ_1, and clinically immune individuals that lost immunity at a rate α. The population of naive susceptible individuals is decreased by natural death rate μ, and following effective contact with infectious mosquito and probability of infection λ_k that pushed out susceptible naive into exposed naive class. Thus,

$$\frac{dS_N}{dt} = bN_h + (\gamma_1 + \gamma)I_N + \alpha S_C - (\lambda_h + \mu)S_N$$

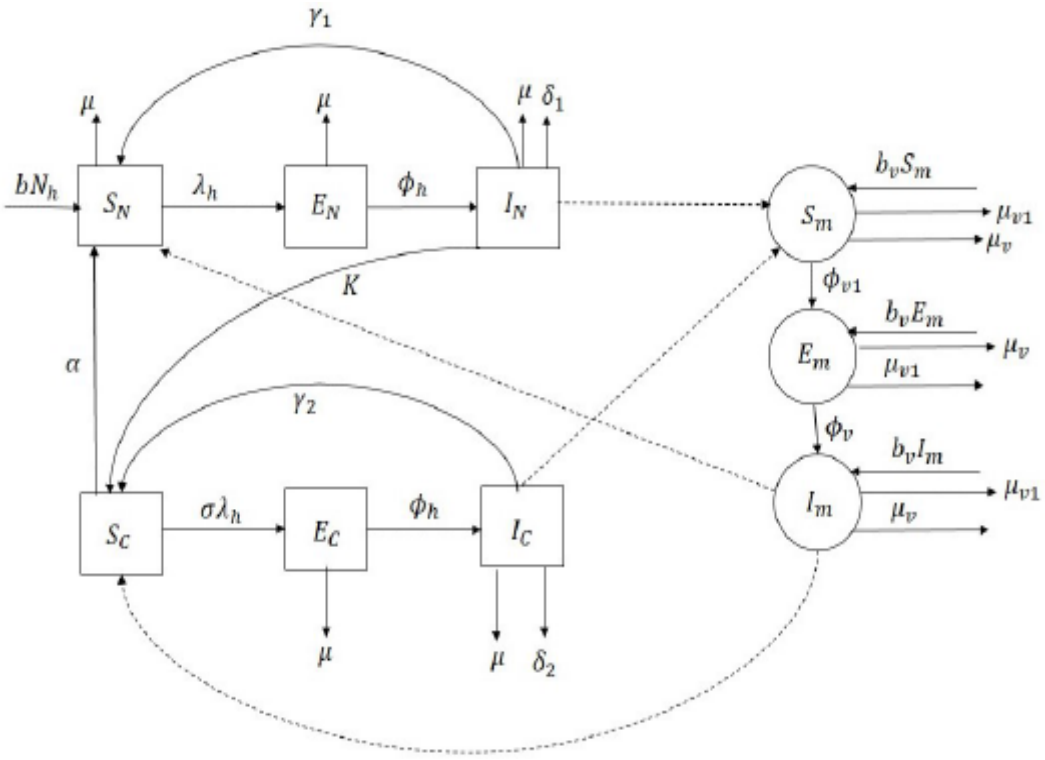

Figure 3.2: Schematic Diagram Representing the Dynamics of Malaria Transmission.

The population of susceptible clinically immune is generated by the infectious naive individuals that recovered with clinical immunity by the probability k, infectious clinically immune that recovered at a rate γ_2. It is decreased by susceptible clinically immune individuals that lose immunity at a rate α, natural death rate μ, and following effective contact with infectious mosquito which also depends on the probability of infection λ_k that pushed out susceptible clinically immune human into exposed clinically immune sub-population. We assume all recovered clinically immune individuals move only to clinically immune susceptible class. Thus,

$$\frac{dS_C}{dt} = (\gamma_2 + m_2)I_C + (m_1 + K)I_N - (\sigma\lambda_h + \alpha + \mu)S_C.$$

Exposed naive population is generated by the population of the infected susceptible naive human that become infected with Malaria and stay for their latency period. The exposed naive population is decreased when an exposed individual move to infectious class after reaching their latency period. Thus,

$$\frac{dE_N}{dt} = \lambda_h S_N - (\phi_h + \mu)E_N.$$

Also, clinically exposed population is generated from the population of the infected susceptible clinically immune. The exposed clinically immune population is decreased when an exposed individual move to infectious class after reaching their latency period. Thus,

$$\frac{dE_C}{dt} = \sigma\lambda_h S_C - (n\phi_h - \mu)E_C.$$

Infectious naive population is increased by infected naive individuals who become infectious and decrease by the recovered naive individuals who develop clinical immunity at a rate k, recovered naive individuals without clinical immunity λ_1 natural death rate μ and disease induced death rate δ_1. Thus

$$\frac{dI_N}{dt} = \phi_h E_N - (\gamma_1 + K + \delta_1 + \mu)I_N.$$

Clinically immune Infectious population are increased by infected Clinically immune individuals who become infectious and decrease by recovered Clinically immune individuals, medicated Clinically immune individuals, disease induced

death rate δ_1 and natural death rate μ

$$\frac{dI_C}{dt} = n\phi_h E_C - (\gamma_2 I_C + \delta_2 + \mu)I_C. \tag{3.2.3}$$

The population of susceptible mosquitoes is generated via birth by the probability b_v, and is reduce by the natural death rate μ_v, in contact death with ITN with probability μ_{v1}, and force of infection ϕ_{v1} when in contact with infectious human.

$$\frac{dS_m}{dt} = b_V S_m - (\phi_{v1} + \mu_v + \mu_{v1})S_m. \tag{3.2.4}$$

The population of exposed mosquitoes is increased with newborn by the probability b_v, susceptible mosquitoes that become infected but not infectious, and is reduced with mosquitoes that become infected and infectious, ITN induced death (if they are in contact) μ_{v1}, and natural death μ_v.

$$\frac{dE_m}{dt} = b_v E_m + \phi_{v1} S_m - (\phi_v + \mu_v + \mu_{v1})E_m. \tag{3.2.5}$$

The population of infectious mosquitoes is generated via birth by the probability b_v,and infected mosquitoes that become infectious, ITN induced death (if they are in contact) μ_{v1}, and natural death μ_v.

$$\frac{dI_m}{dt} = b_v I_m + \phi_v E_m - (\mu_v + \mu_{v1})I_m. \tag{3.2.6}$$

It follows that the model for the Malaria transmission dynamics is given by the following system of nonlinear differential equations

$$\begin{aligned}
\frac{dS_N}{dt} &= bN_h + (\gamma_1+\gamma)I_N + \alpha S_C - (\lambda_h+\mu)S_N,\\
\frac{dE_N}{dt} &= \lambda_h S_N - (\phi_h+\mu)E_N,\\
\frac{dI_N}{dt} &= \phi_h E_N - (\gamma_1+K+\delta_1+\mu)I_N,\\
\frac{dS_C}{dt} &= (\gamma_2+m_2)I_C + (m_1+K)I_N - (\sigma\lambda_h+\alpha+\mu)S_C,\\
\frac{dE_C}{dt} &= \sigma\lambda_h S_C - (n\phi_h-\mu)E_C,\\
\frac{dI_C}{dt} &= n\phi_h E_C - (\gamma_2 I_C+\delta_2+\mu)I_C,\\
\frac{dS_m}{dt} &= b_V S_m - (\phi_{v1}+\mu_v+\mu_{v1})S_m,\\
\frac{dE_m}{dt} &= b_{v1}E_m + \phi_{v1}S_m - (\phi_v+\mu_v+\mu_{v1})E_m,\\
\frac{dI_m}{dt} &= b_{v2}I_m + \phi_v E_m - (\mu_v+\mu_{v1})I_m.
\end{aligned} \tag{3.2.7}$$

The above system of equation describe the current paradigm of malaria mathematical modeling which derives the structure of our ABM. For the sake of simplicity, mathematical model of malaria transmission dynamics developed by Gimba and Bala in [21] fails to incorporate temperature as a time dependent variable, ITN efficacy as a function of time, and mosquito mortality rate as a function of temperature and ITN efficacy. This might be to reduce the number of equations or to ensure the equations are autonomous. Computer models promise an improvement in representing and understanding the complex social structure as well as the heterogenous patterns in the contact networks of real world populations determining

the transmission dynamics [10]. One of the most recent approaches of such sophisticated modeling is agent based modeling [17]. With ABM, we can model the non autonomous version of the Gimba and Bala model. Moreover, the limitation of mathematical flexibility is removed so we can start addressing problems that require models that are less simplified and include more characteristics of the real systems.

3.2.1 Formulation of the ABM model for malaria transmission

Our ABM consist of three types of agents, namely; environment, human, and mosquitoes. We formulated the ABM model in section 3.3, 3.4, 3.5 and the model codes is written in the Appendix. It is a modification of model developed by Gimba and Bala in [21] by incorporating exposed class both in human and mosquitoes population, influence of temperature in the development time of mosquitoes, effect of temperature and ITN decay in malaria transmission and effect of ITN efficacy and mortality rates of mosquitoes. The model assumptions are:

1. Time is discrete and measured in days. Each time step is considered as one day and a day is define as when people are asleep.

2. We assume that a month is thirty (30) days and a year is considered to be 360 days.

3. Disease transmission is from an infectious mosquito to a susceptible human or from an infectious human to a susceptible mosquito.

4. There is no infection between an individual using efficient net and mosquito.

5. We assume that only mosquitoes move, while human agents do not human move.

6. Agent granularity is at the level of an individual human and individual mosquito.

3.3 Environment

Both human and individual agents live and interact in the same environment. The environment is heterogeneous, represented discretely by patches (square cells that represent space). The patches color as depicted in Table 3.2 determine weather a person is using efficient, inefficient or not using ITN.

Table 3.2: **Description of Patches**

Efficient ITN	Green
Inefficient ITN	Yellow
No ITN	Black

ITN Efficacy

According to WHO [55], the maximum life span of ITN is three (3) years and the minimum is one (1) year. We assume that the maximum life span of ITN is one (1) year and the minimum is six (6) months. Let T be the duration of ITN efficacy. That is, T is the replacement or distribution of ITNs. We also assume that ITN is 100% efficient at the distribution or replacement period. Let w(t) be the ITN

efficacy at any time t. Now, since perfect efficacy is decreasing daily and tends to no efficacy as

$$w(t) = 1 - \frac{t}{T}, \tag{3.3.1}$$

where $T > 0$ and $0 \leq t \leq T$. However, we incorporated periodic replacement of ITN in equation 3.3.1 by mod T and obtained a modified ITN efficacy model as

$$w(t) = 1 - (\frac{tmodT}{T})^s, \tag{3.3.2}$$

where w(t) is the ITN efficiency at time t, t is time measure in days, $T > 0$ is the ITN life span, and $s > 1$ is the shape parameter. Also, we assume ITN becomes inefficient when $w(t)$ is less than 0.5. In this case there is probability of contact between a person using inefficient ITN and a mosquito define by

$$\tau = 1 - 2w, \quad 0 \leq w < 0.5. \tag{3.3.3}$$

Furthermore, we assume that all ITN are distributed or replaced at the same time. See Figure 4.8 for a graphical illustration of the dynamics of the ITN efficacy.

3.4 Human Agents

Human agents are created and distributed randomly in space. Individuals are characterized by their states, reproduction, and death. Human agents are set to have different ages ranges from 0 to 70 years. The total human population is divided into six components of susceptible naive, exposed naive, infectious naive, susceptible clinically immune, exposed clinically immune, and infectious clinically

Table 3.3: **Description of Individual's Health Status**

Susceptible naive	White
Susceptible clinically immune	Pink
Exposed naive	Orange
Exposed clinically immune	Lime
Infectious naive	Red
Infectious clinically immune	Brown.

immune individuals as explained in section 3.2. Their states determine their health status which can easily be identified according to their colors as described in Table 3.3. Figure 3.4 presents flow chart which shows the sequence of the state chart of the model, while Table 3.5.7 is the description of the model parameters.

3.4.1 Reproduction in human population

According to WHO [56] reproductive age of are within the age of 15 to 50 years. We named the individual in this age range as matured people. Recruitment rate into human population is b. To determine wether an individual will reproduce during the current time step we proceed as follows, we randomly select 20% of the matured people (assume to be female). For each individual within the sample, we generate a uniform random number b_1 in [0 1], we then compare this number with the recruitment rate parameter b. If $b_1 < b$, then a new individual will be recruited into the human population at the current time step. Otherwise there will be no recruitment at this time step. Recruited individuals are distributed randomly in space. We set them to have random age range from 0 to 70 years and the same

probability of using or not using ITN. Recruited individuals are also randomly distributed to be in susceptible naive, exposed naive, infectious naive, susceptible clinically immune, exposed clinically immune, or infectious clinically immune population. This procedure is performed at each time step.

3.4.2 Natural death in human population

In this work, life span of human is assumed to be seventy (70) years. That is, no individual will live more than seventy (70) years of age. Human death rate is define as μ. To determine wether an individual will die naturally during the current time step we proceed as follows; we generate a uniform random number μ_1 in [0 1], we then compare this number with the natural rate parameter μ. We also calculates the individual current age. If $\mu_1 < \mu$, or current age is greater than 70 years, then the individual is said to die naturally and that individual will appear in the next time step. This procedure is performed for each human agent at each time step.

3.4.3 Susceptible naive population

At each time step, the population susceptible naive is increased through birth as explained in 3.4.1, naive infectious individuals that recovered without immunity as explained in 3.4.7 and clinically immune individuals that lost immunity as explained in 3.4.9. The population of susceptible naive is decreased by natural death as explained in 3.4.2, and following effective contact with an infectious mosquito that pushed out susceptible naive into exposed naive class as explained in 3.4.4.

3.4.4 Malaria transmission in a susceptible naive population

To determine wether an individual will be infected with malaria during the current time step we proceed as follows; we check if the susceptible naive individual is not using ITN or is using inefficient ITN. If the susceptible naive individual is not using ITN, we check whether the susceptible naive individual and an infectious mosquito are in contact. A susceptible naive and an infectious mosquito are said to be in contact if the distance between them is less than the parameter radius. If they are in contact, we generate a uniform random number λ_{hn} in [0 1], we then compare this number with the transmission probability from an infectious mosquito to susceptible naive individual not using ITN λ_h. If $\lambda_{hn} < \lambda_h$, then the individual is said to be infected with malaria and that individual will move from susceptible naive population to exposed naive population in the current time step. Otherwise, there is no transmission of malaria for this individual in the current time step. But if the susceptible naive individual is using inefficient ITN, we check whether the susceptible naive individual and an infectious mosquito are in contact. If they are in contact, we generate a uniform random number τ_1 in [0 1]. If $\tau_1 < \tau$, we then generate a uniform random number λ_{hn1} in [0 1]. We then compare this number with the transmission probability from an infectious mosquito to susceptible naive individual using inefficient ITN λ_{h1}. If $\lambda_{hn1} < \lambda_h$, then the individual is said to be infected with malaria and that individual will move from susceptible naive population to exposed naive population in the current time step. Otherwise, there is no transmission of malaria for this individual in the current time step. This procedure is performed for each susceptible naive individual at each time step.

3.4.5 Exposed naive population

The population of exposed naive individuals is increased through birth as explained in 3.4.1, infected naive individuals that became infected with malaria and stay for their latency period ϕ_h. The length of time an infected naive individual spends in the exposed class is infection length and denoted as ϕ_{iln}. The time is set to be 0 on the day at which the susceptible naive individual became infected and is increases by one at every time step. To determine wether an individual will become infected and infectious during the current time step we proceed as follows; we calculate the naive individual current infection length ϕ_{iln}. We then compare this number with the latency period parameter ϕ_h. If $\phi_{iln} > \phi_h$, then the individual is said to move from exposed naive population to infectious naive population in the current time step. Otherwise, the individual will remain in the exposed naive population. This procedure is performed for each infected naive individual at each time step. The latency period of each individual is determined by pulling from an approximately normal distribution with a mean and standard deviation of the average latency period. The exposed naive population is decreased when an exposed individual move to infectious class after reaching their latency period or due to natural death as explained in 3.4.2.

3.4.6 Infectious naive population

At every time step, the population susceptible naive is increased through birth as explained in 3.4.1, infected naive individuals who become infectious and decreased by the recovered naive with or without immunity as explained in 3.4.7

natural death as explained in 3.4.2, and disease induced death as explained in 3.4.7.

3.4.7 Recovery from Infection in a naive population

The recovery time for an infectious naive individual is γ_{hn}. The length of time an infected naive individual spends in the infectious class is infectious length and denoted as γ_{iln}. The time is set to be 0 on the day at which the infected naive individual became infectious and is increases by one at every time step. To determine wether an individual will recover during the current time step we proceed as follows; we calculate the naive individual current infectious length γ_{iln}. If $\gamma_{iln} > \gamma_{hn}$, then we generate a uniform random number γ_r in [0 1]. We then compare this number with the probability of an infectious naive individual to recover γ. If $\gamma_r < \gamma$, then we further generate a uniform random number K_1 in [0 1]. We then compare this number with the probability of an infectious naive individual to recover with immunity K. If $K_1 < K$, then the individual is said to recover with immunity. Otherwise, the individual recover with out immunity. But if $\gamma_r > \gamma$, then we further generate a uniform random number δ in [0 1]. We then compare this number with the disease induced death rate for a naive individual parameter δ_1. If $\delta < \delta_1$ then the individual is said to die due to disease and that individual will be taken out of the simulation, otherwise the individual will remain in an infectious naive class and will appear in the next time step. This procedure is performed for each infectious naive individual at each time step. We assume that an infectious naive person who gets medical attention will recover in one third of the recovery time. The recovery time of each naive individual is determined

by pulling from an approximately normal distribution with a mean and standard deviation of the recovery time. We set recovery time of each naive individual to lie between the minimum and maximum recovery time inclusive.

3.4.8 Susceptible clinically immune population

At each time step, the population susceptible clinically immune is increased through birth as explained in 3.4.1, naive infectious individuals that recovered with clinical immunity as explained in 3.4.7, and clinically immune individuals that recovered as explained in 3.4.13. The population of susceptible clinically immune is decreased by natural death as explained in 3.4.2, susceptible clinically immune that lost immunity as explained in 3.4.9 and following effective contact with an infectious mosquito that pushed out susceptible clinically immune into exposed clinically immune class as explained in 3.4.10.

3.4.9 Calculating lose of immunity in a susceptible clinically immune population

Susceptible clinically immune individual lose immunity as a rate α. To determine wether an individual will lost immunity during the current time step we proceed as follows; we generate a uniform random number α_1 in [0 1]. We then compare this number with the rate at which susceptible clinically immune individual lose immunity parameter α. If $\alpha_1 < \alpha$, then the individual is said to lose immunity and that individual will move to susceptible naive population. Otherwise, the individual will remain in a susceptible clinically immune population. This procedure is performed for each susceptible clinically immune individual at each time step.

3.4.10 Malaria transmission in a susceptible clinically immune population

To determine wether a susceptible clinically immune individual will be infected with malaria during the current time step we proceed as follows; we check if the susceptible clinically immune individual is not using ITN or is using inefficient ITN. If the susceptible clinically immune individual is not using ITN, we check whether the susceptible clinically immune individual and an infectious mosquito are in contact. A susceptible clinically immune and an infectious mosquito are said to be in contact if the distance between them is less than the parameter radius. If they are in contact, we generate a uniform random number λ_{hc} in [0 1], we then compare this number with the transmission probability from an infectious mosquito to susceptible individual not using ITN λ_h. If $\lambda_{hc} < \lambda_h$, then the individual is said to be infected with malaria and that individual will move from susceptible clinically immune population to exposed clinically immune population in the current time step. Otherwise, there is no transmission of malaria for this individual in the current time step. But if the susceptible clinically immune individual is using inefficient ITN, we check whether the susceptible clinically immune individual and an infectious mosquito are in contact. If they are in contact, we generate a uniform random number τ_1 in [0 1]. If $\tau_1 < \tau$, we then generate a uniform random number λ_{hc1} in [0 1]. We then compare this number with the transmission probability from an infectious mosquito to susceptible clinically immune individual using inefficient ITN λ_{h1}. If $\lambda_{hc1} < \lambda_{h1}$, then the individual is said to be infected with malaria and that individual will move from susceptible

clinically immune population to exposed clinically immune population in the current time step. Otherwise, there is no transmission of malaria for this individual in the current time step. This procedure is performed for each susceptible clinically immune individual at each time step.

3.4.11 Exposed clinically immune population

The population of exposed clinically immune individuals is increased through birth as explained in 3.4.1, infected clinically immune individuals that became infected with malaria and stay for their latency period ϕ_h. The length of time an infected clinically immune individual spends in the exposed class is infection length and denoted as ϕ_{ilc}. The time is set to be 0 on the day at which the susceptible naive individual became infected and is increases by one at every time step. To determine wether an individual will become infected and infectious during the current time step we proceed as follows; we calculate the clinically immune individual current infection length ϕ_{ilc}. We then compare this number with the latency period parameter ϕ_h. If $\phi_{ilc} > \phi_h$, then the individual is said to move from exposed clinically immune population to infectious clinically immune population in the current time step. Otherwise, the individual will remain in the exposed clinically immune population. This procedure is performed for each infected clinically immune individual at each time step. The latency period of each individual is determined by pulling from an approximately normal distribution with a mean and standard deviation of the average latency period. The exposed clinically immune population is decreased when an exposed individual move to infectious class after reaching their latency period or due to natural death as explained in 3.4.2.

3.4.12 Infectious clinically immune population

At every time step, the population susceptible clinically immune is increased through birth as explained in 3.4.1, infected clinically immune individuals who become infectious and decreased by the recovered clinically immune as explained in 3.4.13 natural death as explained in 3.4.2, and disease induced death as explained in 3.4.13.

3.4.13 Recovery from Infection in a clinically immune population

We assume that recovery time for an infectious clinically immune individual is γ_{hc}. The length of time an infected clinically immune individual spends in the infectious class is infectious length and denoted as γ_{ilc}. The time is set to be 0 on the day at which the infected naive individual became infectious and is increases by one at every time step. To determine wether an individual will recover during the current time step we proceed as follows; we calculate the clinically immune individual current infectious length γ_{ilc}. If $\gamma_{ilc} > \gamma_{hc}$, then we generate a uniform random number γ_r in [0 1]. We then compare this number with the probability of an infectious clinically immune individual to recover γ_1. If $\gamma_r < \gamma_1$, then the individual is said to recover. But if $\gamma_r > \gamma_1$, then we generate a uniform random number δ in [0 1]. We then compare this number with the disease induced death rate for a clinically immune individual parameter δ_2. If $\delta < \delta_2$ then the individual is said to die due to disease and that individual will be taken out of the simulation, otherwise the individual will remain in an infectious clinically immune class and will appear in the next time step. This procedure is performed for each infectious

clinically immune individual at each time step. We follow the same assumption as in [29] that recovery time for a clinically immune individual is four times higher than that of naive individual. Also, recovered clinically immune individual recover from infection with immunity and move to susceptible clinically immune class only. We assume that an infectious clinically immune person who gets medical attention will recover in one third of the recovery time. The recovery time of each clinically immune individual is determined by pulling from an approximately normal distribution with a mean and standard deviation of the recovery time. We set recovery time of each clinically immune individual to lie between the minimum and maximum recovery time inclusive.

3.5 Mosquito Agents

Mosquito agents are created and distributed randomly in space and are characterized by their states, color, movements, reproduction, and death. Mosquito agents are set to have different ages ranges from 0 to 40 days. The total Mosquito population is divided into three (3) components of susceptible Mosquitoes, exposed Mosquitoes, and infectious mosquitoes as explained in section 3.2. Their states determine their health status which can easily be identified according to their colors as described in Table3.4.

Table 3.4: **Description of Mosquitoes Health Status**

susceptible Mosquitoes	White
Exposed Mosquitoes	Orange
Infectious mosquitoes	Red

Each mosquito is involved in a sequence of daily basis activities according to the mosquitoes status. These daily activities allow mosquitoes to interact with human. Mosquitoes move in space to search for blood meal. There appears to have been no study with definitive results to mathematically model mosquito movements. This study model mosquito movements as in [22]. The process of mosquito blood searching has two stages namely; the random movements and the directional movements. In the random movements, a mosquito has a sensory range which determines how far a mosquito is aware of a human nearby. When the distance between the mosquito and a person is greater than the sensory range, the mosquito can not detect the target person, it turns and move one step at a time, but if the distance between a mosquito and a person nearby is less than or equal to the sensory range, then it faces the target person and feeds. This is the only stage when the infection is transmitted between mosquitoes and people.

3.5.1 Recruitment in to mosquitoes population

For the reproduction of mosquitoes, we did not take their full life cycle in to consideration. But according to the study in [29], an adult female mosquito needs at least one meal after mating for the eggs to mature and three days is the time for the eggs to mature at an ideal temperature of 21^0C [6]. Hence, we assume that only mosquitoes of age greater than five (5) days can lay eggs. We named the mosquitoes in this age range as matured mosquitoes. To determine whether a mosquito will reproduce during the current time step we produce as follows; we randomly select 50% of the matured mosquitoes (assume to be female) each of

them to lay at least 100 eggs, because according to [13] mosquitoes generally lay 100 eggs at a time.

3.5.2 Development time of mosquitoes

We consider all the aquatic stages of mosquito life cycle (egg, larva and pupa) as eggs, and will be referred as such through out this work. The authors in [16] show the effect of temperature in the developmental time of mosquitoes from egg to adult. At least, in line with the report of [16], we modeled the development time of mosquitoes from egg to adult based on temperature influence. By considering Figure 2 of [16], we estimated the development time of mosquitoes from egg to adult as shown in Table 3.5.2. That is when the temperature is 16^0C, the development time of mosquitoes from egg to adult is 19 days. Similarly, when the temperature is 28^0C, the development time of mosquito from egg to adult is 11 days. Hence, using least square polynomial, we derived development time of mosquito from egg to adult as a linear function of temperature as

$$y = \frac{-13}{20} + \frac{146}{5}, \tag{3.5.1}$$

where y is the time for the development of mosquitoes from egg to adult measured in days, and x is the average monthly temperature. The values of the average monthly temperature used in this work is obtained from [18] and depicted in Table 3.6.

We assume that at most 100 eggs will turn into adult mosquitoes base on the favorable temperature conditions. We set 0 age to the newly adult mosquitoes. They are also distributed randomly in space having different health status. That is,

Table 3.5: **Estimated Development Time of Mosquitoes.**

Temperature	16	20	24	28	32
Days	19	17	12	11	9

Table 3.6: **Average Temperatuie of Kano State [16]**

Month	AverageTemperature(^0C)
January	21.5
February	24
March	27.9
April	30.9
May	30.3
June	28.4
July	26.4
August	24.9
September	25.9
October	26.4
November	24.5
December	22

they emerge as adult susceptible mosquitoes, exposed mosquitoes and infectious mosquitoes. This procedure is performed at each time step.

3.5.3 Mosquito mortality rate

According to [11], an adult female mosquito can survive up to a month or longer in captivity. We assume that life span of mosquito is 40 days. That is, no mosquito will live more than its life span. In this work, we model the mosquito mortality rate as a function of temperature and ITN efficacy as

$$\mu_{v1} = AN_m + d\beta_m, \qquad 0 \leq \mu_{v1} < 1, \tag{3.5.2}$$

where

$$\beta_m = \begin{cases} 1 - e^{\frac{-1}{-4.4+1.3x-0.03x^2}}, & \textit{mosquito not in contact with ITN} \\ 1 - e^{\frac{-1}{-4.4+1.3x-0.03x^2}} + w, & \textit{mosquito in contact with ITN} \end{cases} \tag{3.5.3}$$

is the mosquitoes death rate, d is the rate at which the mortality rate decreases or increases due to the combine effect of temperature and ITN usage, $0 < d \leq 1$, x is the average temperature, and A is the density dependent part of the death rate for mosquitoes. We assume that $d = 1, w(t) = 1 - (\frac{tmodT}{T})^s$ is the ITN efficacy. To determine wether a mosquito will die during the current time step we proceed as follows; we generate a uniform random number μ_v in [0 1], we then compare this number with the mosquito mortality rate μ_{v1}. We also calculates the mosquito current age. If $\mu_v < \mu_{v1}$, or current age is greater than 40 days, then the mosquito is said to die and that mosquito will be taken out from the simulation. Otherwise, the mosquito will appear in the next time step. This procedure is performed for each mosquito agent at each time step. See Figure 4.3.1 for a graphical illustration of the dynamics of the mortality rate of mosquitoes.

3.5.4 Susceptible mosquitoes population

At every time step, the population of susceptible mosquitoes is generated via birth as explained in 3.5.1. The population is reduced by mosquito mortality as explained in 3.5.3, and when infected by an infectious human as explained in 3.5.5.

3.5.5 Malaria transmission in a susceptible mosquitoes population

To determine wether a mosquito will be infected with malaria during the current time step we proceed as follows; we check whether the individual is an infectious naive or infectious clinically immune. Suppose is a naive individual, we then check if the infectious naive individual is not using ITN or is using inefficient ITN. If the infectious naive individual is not using ITN, we check whether the infectious naive individual and a susceptible mosquito are in contact. An infectious naive and a susceptible mosquito are said to be in contact if the distance between them is less than the parameter radius. If they are in contact, we generate a uniform random number λ_{vm} in [0 1]. We then compare this number with the transmission probability from an infectious naive individual to a susceptible mosquito not using ITN λ_v. If $\lambda_{vm} < \lambda_v$, then the susceptible mosquito is said to be infected with malaria and that mosquito will move from susceptible mosquito population to exposed mosquito population in the current time step. Otherwise, there is no transmission of malaria for this susceptible mosquito in the current time step. But if the infectious naive individual is using inefficient ITN, we check whether the susceptible naive individual and an infectious mosquito are in contact. If they are in contact, we generate a uniform random number τ_1 in [0 1]. If $\tau_1 < \tau$, we then generate a uniform random number λ_{vm} in [0 1]. We then compare this number with the transmission probability from an infectious individual using inefficient ITN to susceptible mosquito λ_{v1}. If $\lambda_{vm} < \lambda_v$, then the mosquito is said to be infected with malaria and that mosquito will move from susceptible mosquitoes population to exposed mosquitoes population in the current time step. Otherwise,

there is no transmission of malaria for this mosquito in the current time step. This procedure is performed for each susceptible mosquito at each time step.

3.5.6 Exposed mosquitoes population

At every time step, the population of exposed mosquitoes is generated through birth as explained in 3.5.1, and susceptible mosquitoes that become infected but not infectious as explained in 3.5.5. The population is reduced by mosquito mortality as explained in 3.5.3, mosquitoes that become infected and infectious after reaching their latency period ϕ_v. The latency period of each mosquito is determined by pulling from an approximately normal distribution with a mean and standard deviation of the mosquito latency period.

3.5.7 Infectious mosquitoes population

At every time step, the population of infectious mosquitoes is generated through birth as explained in 3.5.1, and susceptible mosquitoes that become infectious after reaching their latency period as explained in 3.5.6. The population is reduced by mosquito mortality as explained in 3.5.3. But once a mosquito is infectious, it does not recover from infection.

Table 3.7: **Simulation Parameters and their Initial Values**

Parameter	Initial Values	Reference
Susceptible naive	61%	Assumed
Exposed naive	5%	Assumed
Infectious naive	20%	[21]
Susceptible clinically immune	10%	[21]
Exposed clinically immune	3%	Assumed
Infectious clinically immune	1%	[21]
Susceptible mosquito	65%	Assumed
Exposed mosquito	5%	Assumed
Infectious mosquitoes	30%	[21]
Probability at which naive individual recovered with out immunity	0.5	Assumed

Table 3.8: **Description of State Variable of the Model**

Variable	Description
S_N	Susceptible Naive human population
E_N	exposed naive human population
I_N	infectious naive human population
S_C	susceptible clinically immune human
E_C	exposed clinically immune human
I_C	infectious clinically immune human
N_h	Total human population
S_m	Population of susceptible mosquitoes
E_m	Population of exposed mosquitoes
I_m	Population of infectious mosquitoes
N_m	Total vector population

Table 3.9: **Parameters and their Descriptions**

Parameters	Description and dimension
b	Recruitment rate into human population (human $\times$ day $^{-1}$).
γ_1	Probability at which naive individuals recovered without immunity (day^{-1})
γ	Probability at which medicated naive individuals recovered without immunity (day^{-1})
α	Rate at which clinically susceptible individuals lose immunity (day^{-1})
μ	Natural death rate for humans (day^{-1}).
ϕ_h	Time taken for an infected individual to become infectious (day^{-1})
ϕ_v	Time taken for an infected mosquito to become infectious (day^{-1})
γ_2	Probability at which clinically immune individuals recovered (day^{-1})
K	Probability at which naive individuals recovered with immunity
δ_1	Disease induced death rate in naive population
λ_h	probability of infection from infectious mosquito to susceptible human.
λ_v	probability of infection from infectious individual to susceptible mosquito.
δ_2	Disease induced death rate in clinically immune population
b_v	probability of recruitment into susceptible mosquito population (mosquito $\times$ day $^{-1}$)
b_{v1}	probability of recruitment into exposed mosquito population (mosquito $\times$ day $^{-1}$)
b_{v2}	probability of recruitment into infectious mosquito population (mosquito $\times$ day $^{-1}$)
μ_v	Natural death rate for mosquitoes (day^{-1})
μ_{v1}	Mosquito's mortality rate
σ	Relative susceptibility of clinically immune individuals
m_1	Probability of infectious naive individual to recover.
m_2	Probability of clinically immune individual to recover.

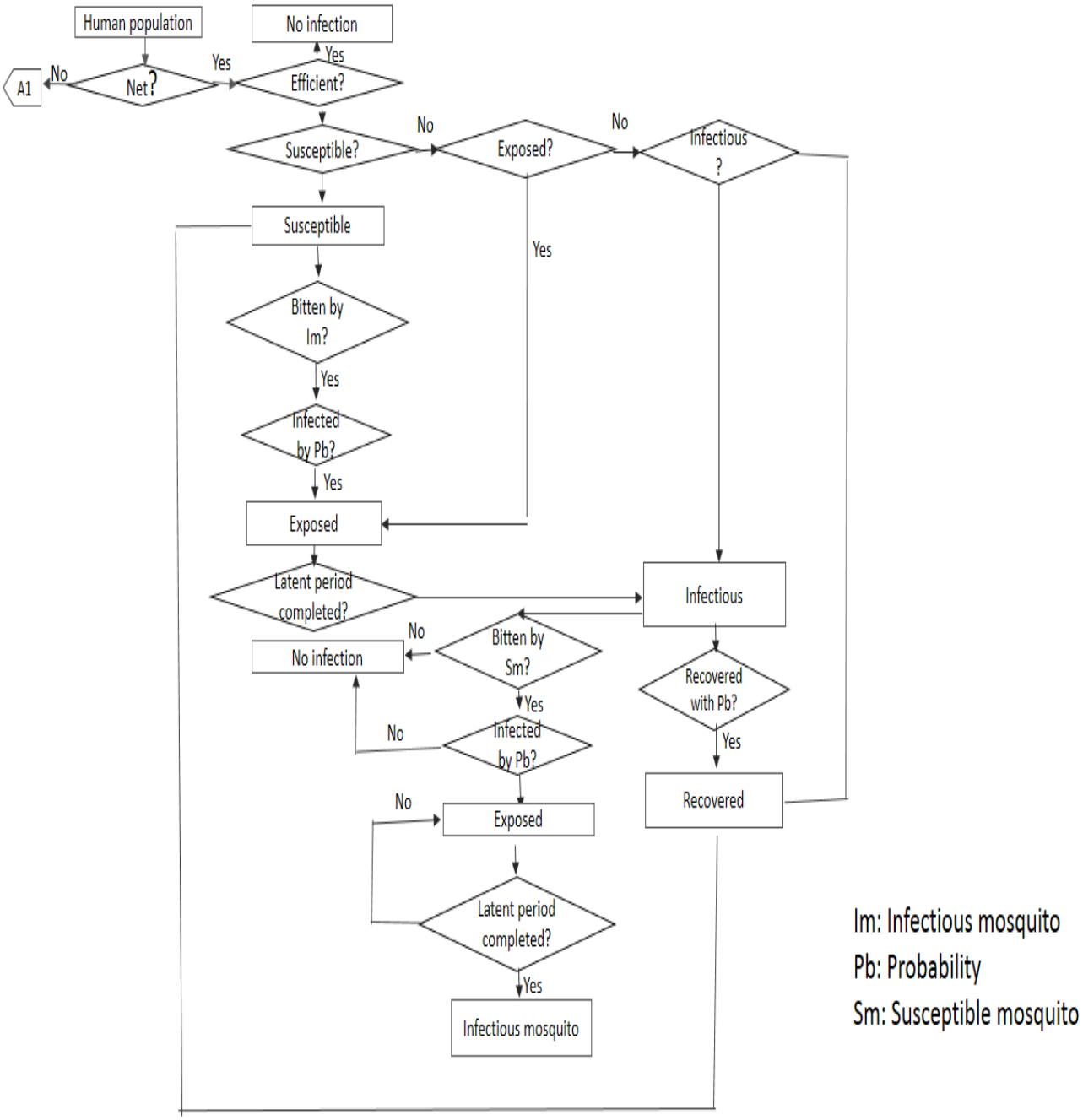

Figure 3.3: A Flow Chart Showing Malaria Transmission Dynamics in a Human Population Using ITN.

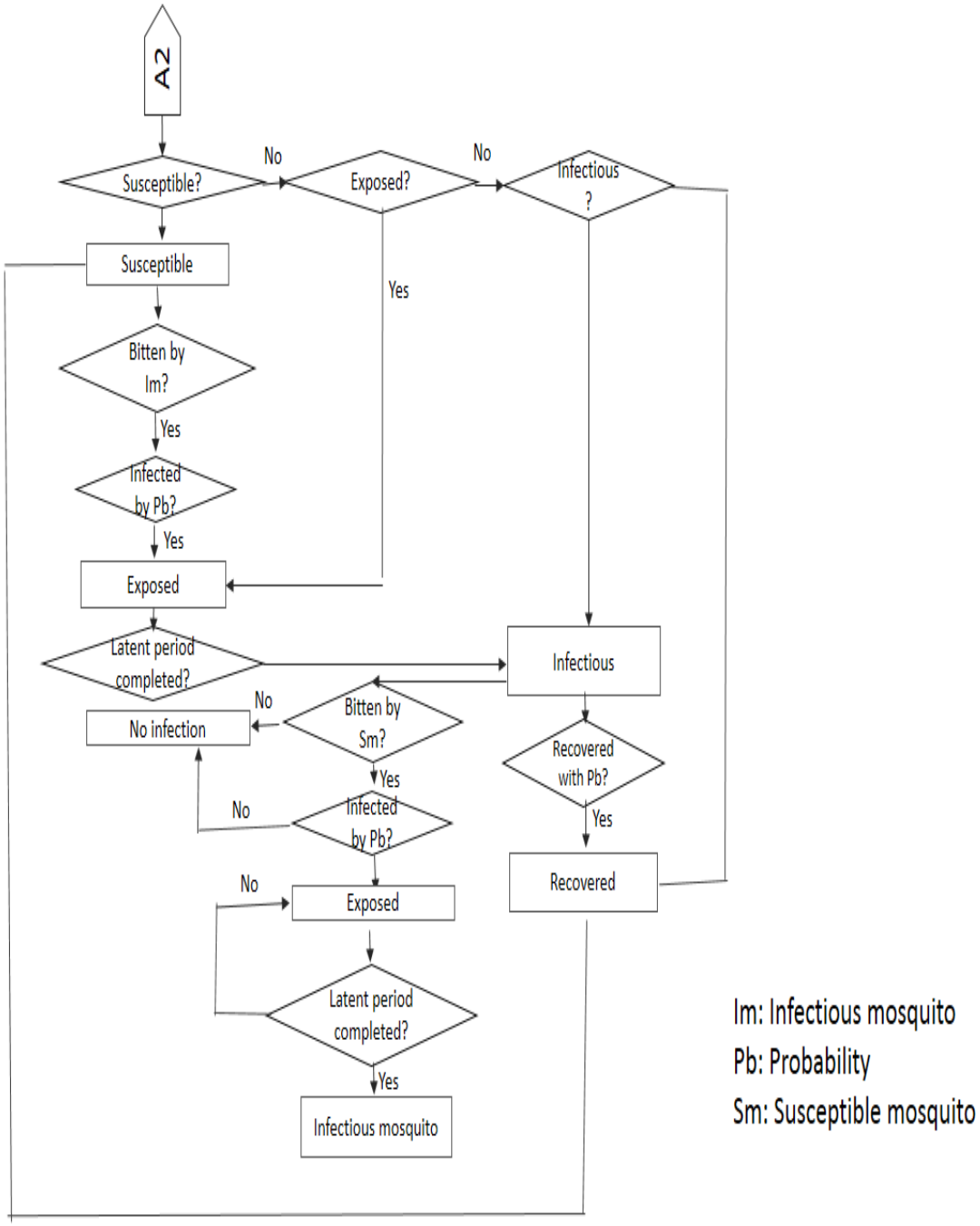

Figure 3.4: A Flow Chart Showing Malaria Transmission Dynamics in a Human Population not Using ITN.

CHAPTER FOUR

RESULTS AND DISCUSSION

4.1 Introduction

In this chapter, the developed method is validated, local sensitivity analysis is used to identify the effective method of malaria control and finally, impact of temperature and efficacy of ITN are accessed.

4.1.1 Visualization of our ABM

Our ABM is implemented using NetLogo software. World, plots and monitors are the major features to see consistent or logical outputs that are produced by the ABM. If themodel runs for a period of time then it is important to see the output. Output is important for scientists or modelers to check whether output flows the predictive behavior. If the predictive behavior seems to be okay then researchers may think to let the program run to its completion. If the predicted behavior is not perceived as acceptable then researchers may think to discontinue the program and change some parameters and then run the program again from the beginning.

Main view of our ABM

A snapshot of the Interface is depicted in Figure 4.5. We build in the left and right hand side of the interface different sliders, buttons, monitors, and plots. Monitors and plots show current statistics of the simulation program. On the left hand side of the Interface, there are six sliders, namely:

1. INITIAL-PEOPLE (initialized to vary between 100 - 1000) : Is use to initialize the total number of people the simulation begins with.

2. INITIAL-MOSQUITOES (initialized to vary between 500 - 5000): Is use to initialize the total number of mosquitoes the simulation begins with.

3. RECOVERY-CHANCE (1 - 100): Probability of an individuals recovery once the infection has lasted longer than the persons recovery time.

4. USE-NET (1-100) : Is use to set the percentage of people to wear ITN.

5. CHANCE OF-GETTING-MEDECINE-NAIVE (0-100): Probability of a naive individual to get treatment.

6. CHANCE OF-GETTING-MEDECINE-CLINICALLY (0-100): Probability of a clinically immune individual to get treatment.

To start up the ABM, the user is required to :

1. Press the SETUP. The SETUP button create the world containing square patches, human and mosquitoes population according to the parameter values chosen by the modeler/user. Some patches appear to be green while some are black which depend on the proportion of people using (ITN). Hence, the simulation has been setup.

2. To starts the simulation press the GO button. The GO button run the model for the agents to start practicing their natural daily activities. GO starts the simulation and runs it continuously until GO is pushed again or the simulation runs for a prespecified time-step.

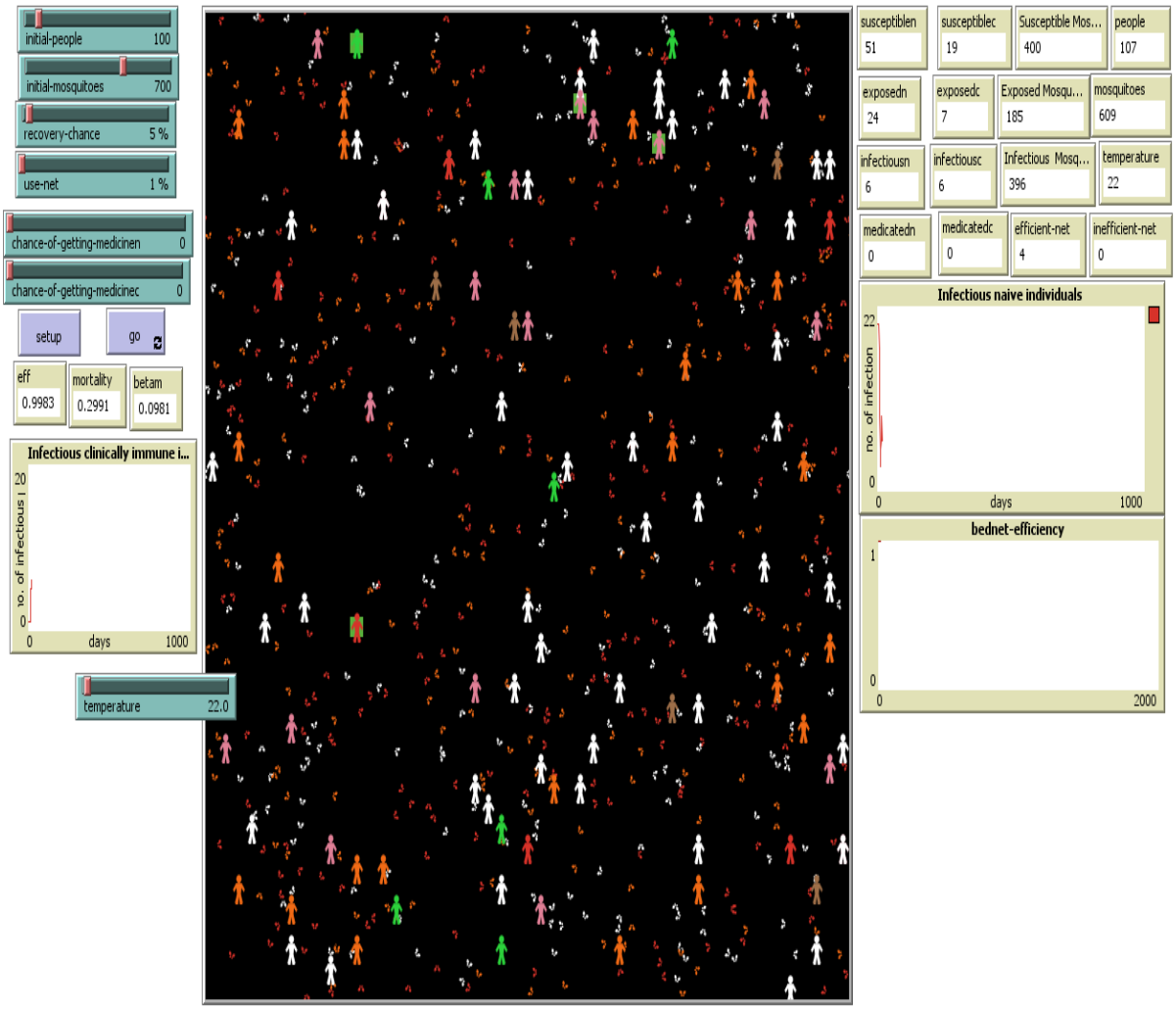

Figure 4.5: Snapshot Displays agents with Different Health States Mosquitoes Moving and Searching for Blood Meals from Humans.

Monitors include:

1. Betam: It displays the efficacy of ITNs at every time step.
2. Mortality : Is use to report mosquitoes mortality rate at every time step.
3. eff: Is use to report the efficiency of ITN at every time step.
4. Susceptiblen: Is use to report the number of susceptible naive at every time step.
5. Susceptiblec: Is use to report the number of susceptible clinically immune at every time step.
6. Exposedn: Is use to report the number of infected naive at every time step.
7. Exposedc: Is use to report the number of infected clinically immune at every time step.
8. Infectiousn: Is use to report the number of infected and infectious naive at every time step.
9. Infectiousc: Is use to report the number of infected and infectious clinically immune at every time step.
10. medicatedn: Is use to report the number of infected and infectious naive individuals that are receiving medicine at every time step.
11. medicatedc: Is use to report the number of infected and infectious clinically immune individuals that are receiving medicine at every time step.
12. Susceptible-mosquitoes: Is use to report the number of susceptible mosquitoes at every time step.

13. Exposed-mosquitoes: Is use to report the number of infected but not infectious mosquitoes at every time step.

14. Infectious-mosquitoes: Is use to report the number of infected and infectious mosquitoes at every time step.

15. People: Is use to count total number of people at every time-step.

16. Mosquitoes: Is use to count total number of mosquitoes at every time-step.

17. Efficient-net: Is use to report total number of people using efficient net.

18. Ineficient-net: Is use to report total number of people using inefficient net.

19. Temperature: Is use to report the value of temperature at every time step.

There are also three graphs:

- Population of infectious naive: This plots the number of infectious naive people.

- Population of infectious clinically immune: This plots the number of infectious clinically immune people.

- Bednet-efficiency: This plots the ITN efficacy.

4.2 Our ABM Validation

Model validation is essential for ensuring that there is a correspondence between the proposed model and the reality. It is often very difficult to validate epidemiological simulation models due to the lack of reliable field data. According to

[57], docking also known as alignment, model-to-model comparison, cross model validation is a verification and validation method which aligns multiple models in order to investigate whether they produce similar result. While in this research, we adopt docking method of validation and verification by aligning our proposed model against Gimba and Bala model. To do this, the ABM was simulated over five years to measure the number of infectious naive and infectious clinically immune individuals. Simulation parameters and their initial values is depicted in Table3.5.7 and description of the model parameters and their values is depicted in Table3.5.7. The output of numbers of the infectious naive and infectious clinically immune individuals are plotted using Matlab and the graphs are shown in Figure 4.6. The corresponding output of the infectious naive and infectious clinically immune individuals of the Gimba and Bala model is also presented in Figure4.2. The two graphs show similar pattern. It is observed that noise and variation are apparent in the ABM simulation, and this happen due to the following factors:

a. the heterogeneous structure of the population,

b. temperature as a variable,

c. Stochasticity of the ABM model,

d. and the usage of random variable for infection time instead of deterministic values in Gimba model.

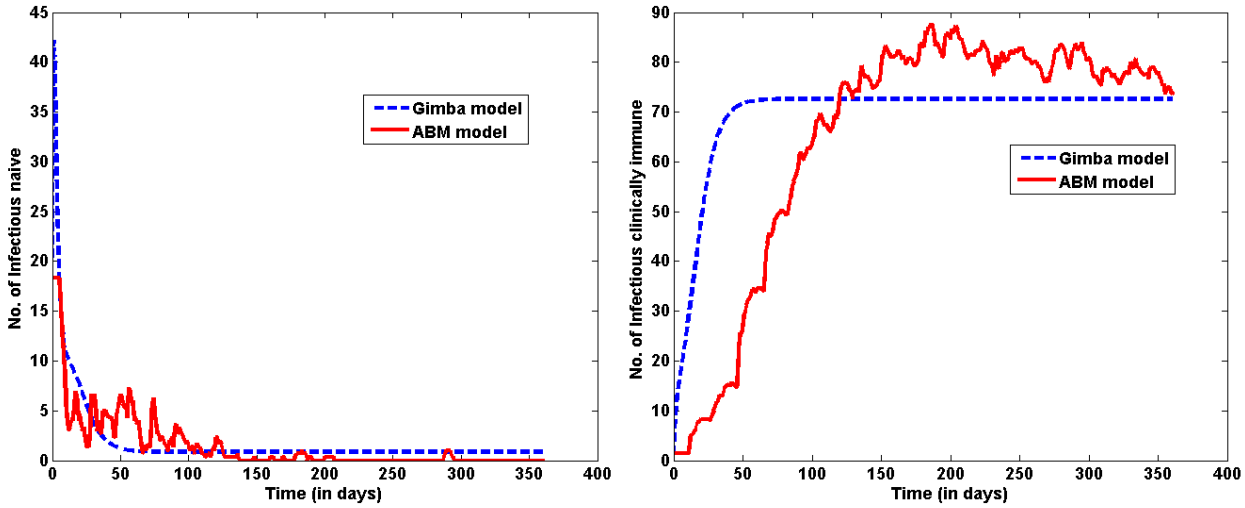

Figure 4.6: Our ABM Validation Using Gimba and Bala Model. The ABM Model is Shown by the zig-zag, while Gimba and Bala model is the dashes . The first Figure from the left hand side plots the number of infectious naive individuals versus time and the second Figure plots the number of infectious clinically immune individuals versus time.

4.3 Control Strategy

Control strategies are important for the development of an action plan to control Malaria disease burden. The model developed in this work, incorporates three (3) interventions, namely:

1. treatment of infectious naive individuals,
2. treatment of infectious clinically immune individuals,
3. and use of ITN.

In order to reduce or curtail the transmission of malaria, the interventions mentioned above are implemented in single or in combination to identify the most

effective control strategy. The most effective strategy is characterized by least number of infectious individual and will be identified through sensitivity analysis. The control strategies are:

A. 1 only,

B. 2 only,

C. 3 only,

D. 1 and 2 only,

E. 1 and 3 only,

F. 2 and 3 only,

G. All interventions,

H. No interventions.

Table 4.10: Intervention Parameters and their Values [7]

Parameter	Description	Value
P_{nm}	Chance of treating naive individual	50%
P_{cm}	Chance of treating clinically immune individual	20%
P_{itn}	Proportion of people using ITN	90%

4.3.1 Sensitivity analysis

Sensitivity analysis is a measure of change in model output associated with a change in model input. It provides insight into the robustness of model results for decision making. In our ABM, local sensitivity analysis of parameters depicted in Table 4.10 is conducted using BehaviorSpace. The ABM model was run for a period of one (1) year. The model was set to repeat three (3) times due to the stochastic nature of the ABM. The average of the total number of infectious human was taken and plotted as shown in Figure 4.7. The model was set to repeat three (3) times and the average of the total number of infectious human was taken and plotted as shown in Figure 4.7. The shape of the distribution of strategy B is roughly symmetric except for the outliers, srategy A, D and H are skewed left, while those of strategy C, G, and E are skewed right. It can be observed that strategy G is strongly skewed right because the left whisker is shorter than the right whisker. Each of strategy A, B, D, F and H has outliers. The appearance of outliers in the five (5) strategies guarantees us to use median as the measure of center. As depicted in Figure 4.7, control strategy G has the lowest median followed by F, where as control strategy C and E have almost the same median. Control strategy H has the highest median, followed by A, while B and D have almost the same median. Table 4.11 shows the summary statistics of Figure 4.7. The control strategy G appears to be the most effective method of Malaria prevention and control. It is characterized by low median. The control strategy F is the better option after G as compared with other strategies. It can easily observed

Table 4.11: Summary Statistics of Control Strategies

Control Strategy	Median
A	65
B	59
C	20
D	59
E	21
F	19
G	15
H	68

that any intervention which contains ITN use is effective. This shows that reducing contacts between humans and mosquitoes and treatment of clinically immune individuals is important in controlling the size of the infectious human population.

4.4 Discussion

Malaria is world wide considered as the most devastating and the most prevalent human vector borne disease, with one half of the world population living in areas where there is risk of infection [49]. Understanding the impact of control strategies such as use of ITN can help us inform policy health makers. We developed an ABM model that describes malaria transmission dynamics between individual humans and individual mosquitoes, and investigated the impactof ITN and temperature on malaria transmission and control. The ABM used to model personal protection through ITN captures the decrease in ITN efficacy due to physical decay and human behavior, influence of temperature in the mosquito development time, as well as mosquito mortality rate as a function of temperature and ITN efficacy.

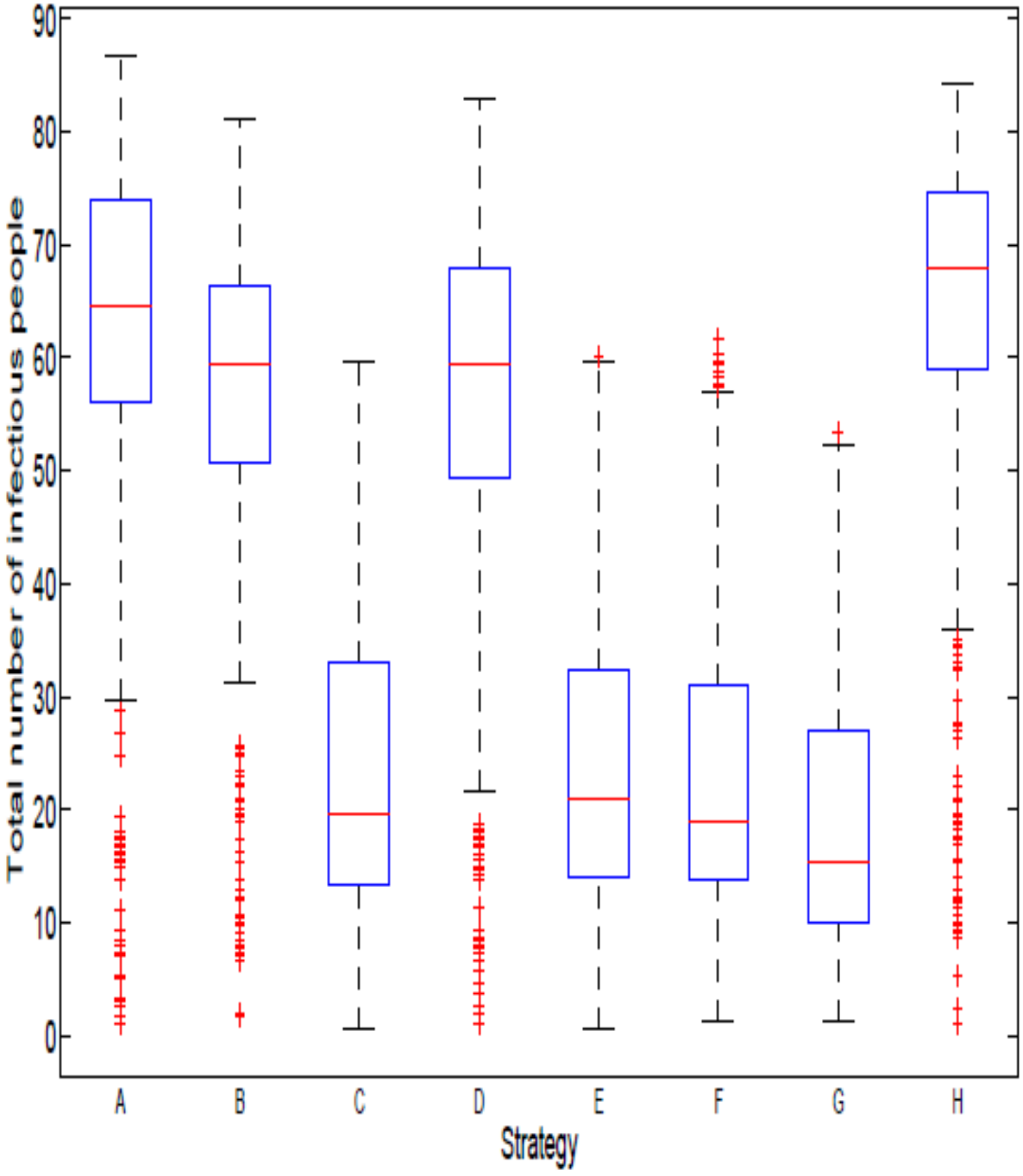

Figure 4.7: **Box Plots Showing Number of Infectious Human Populations Subjected to Different Control Strategies.**

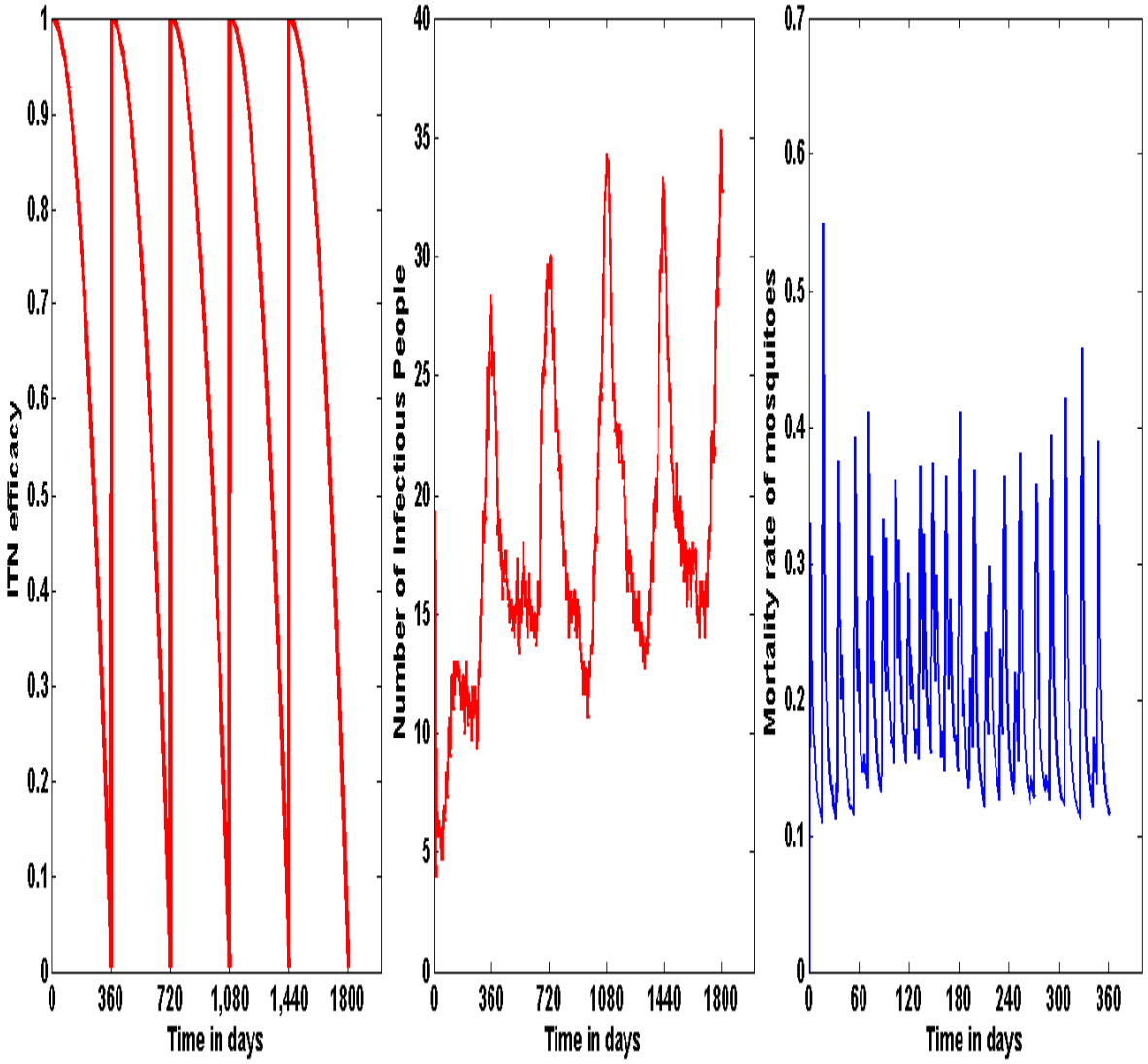

Figure 4.8: Graphical Illustration of the Dynamics of ITN Efficacy, Number of Infectious Individuals and Mosquito Mortality Rate. The results reveal that, when the effectiveness of the ITN is high, then the number of infectious individual is low, while mosquito mortality rate is high. However, as the effectiveness of ITN is reducing the mosquito mortality rate reduces and the number of infectious people increses.

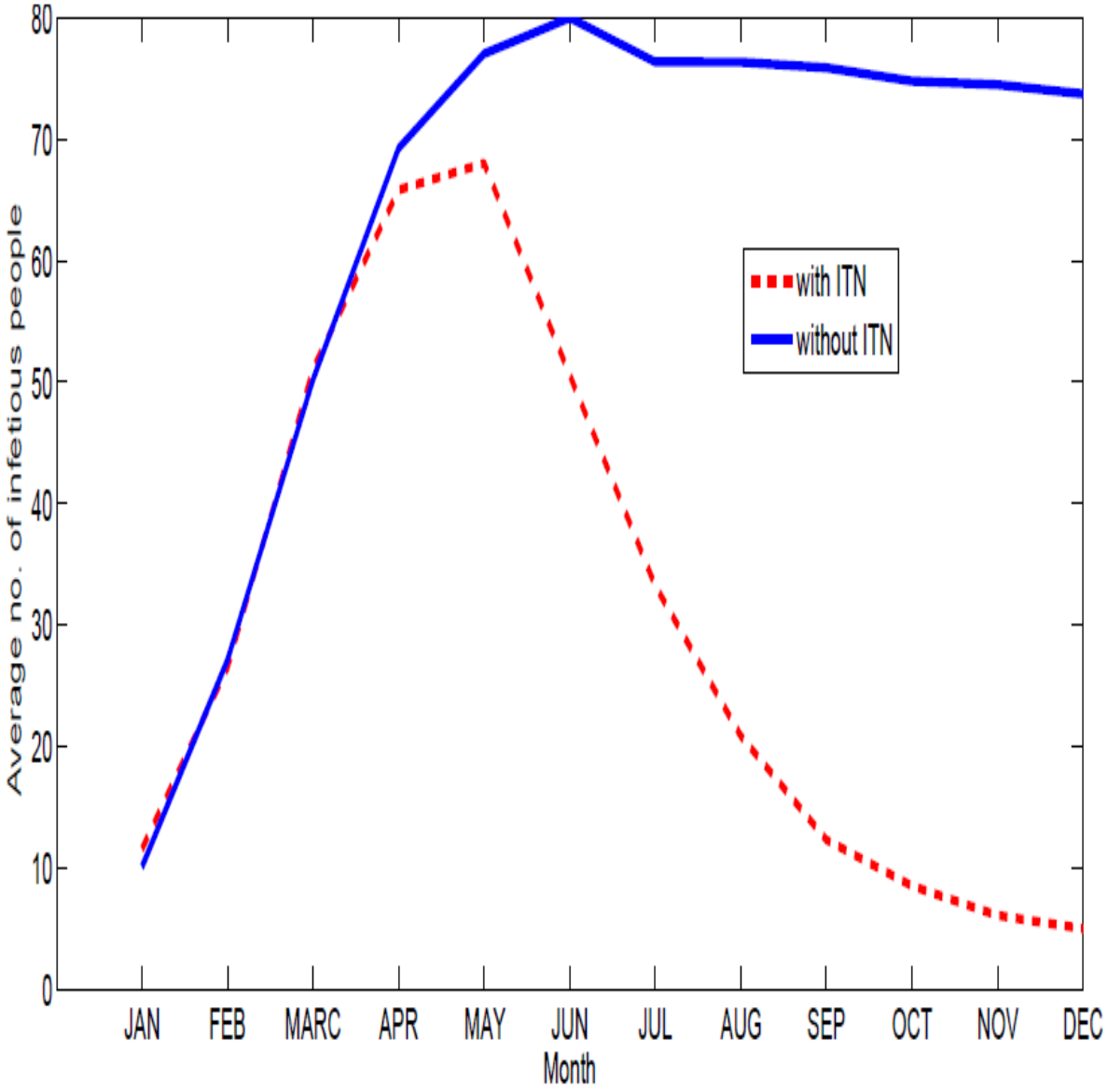

Figure 4.9: Graphical Illustration of the Effect of Temperature and ITN in Malaria Transmission. The results reveal that malaria is peak in certain month of the year. Initially, only 5% of the population are using ITN. But if at least 50% of the population are to use ITN, two months before the epidemics malaria could be eliminated.

Our simulations result show that ITN efficacy decreases number of infected humans and increases mosquito mortality rates. That is, if ITN are replaced regularly malaria could be eliminated. However, there will be cost associated with the replacement of ITN, which may not be possible in many malaria endemic regions. Hence, increasing ITN efficacy will reduce the cost associated with regular replacement.

The ABM of malaria transmission dynamics makes similar predictions to the equation based model based on the work of Gimba and Bala. The ABM model provides a convenient way to add complexity in modeling malaria transmission, such as incorporating the effects of decay and variability in temperature. By aligning our ABM with Gimba and Bala model shows that ABM can be used in modeling malaria transmission.

The analysis on control strategies such as treatment of both naive and clinically immune individual might be necessary to reduce malaria burden. Though, the development of clinical immunity by individuals will result in such individuals not seeking treatment for a long time. Thus, they will harbor the disease and can transmit it when bitten by mosquitoes. From our model results, the infectivity of the clinically infectious individual does not wane with time. To eradicate malaria transmission in malaria endemic regions, we need to make treatment of infectious clinically immune possible. This can be achieved by considering strategies that can be use to examine individuals not seeking treatment.

The local sensitivity analysis results show that we need to embark on combination of strategies that will decrease the possibilities of immune individuals becoming infective and treating them in order to effectively reduce malaria transmission. This is quite difficult because clinically immune population are not likely to seek treatment for along period of time. Moreover, failing to detect the parasite in them may not necessarily mean the absence of the disease. In view of these difficulties, the best thing to do is to embark on maximum ITN usage.

Other metrics that will assist significantly in this direction are the increase in mosquitoes death rates and temperature. In some African countries such as Nigeria where malaria is endemic and electricity supply is erratic, improved supply of electricity will enable people to use fans and air conditioning system to provide relatively colder environment in their houses. It will also help to provide enabling environment for effective usage of ITN and also reduces human-mosquitoes contacts [21].

Furthermore, we have that temperature changes have great influence on malaria transmission which is essential in order to predict future malaria intensity accurately. That is, malaria transmission is peak in certain period of the year. For instance, according to our model malaria is peak in the month of June up to December. The public health interpretation of this result is that, understanding the month at which an epidemic occur can help us inform policy health makers to make a massive campaign especially two or three month before malaria epidemics, on the use of preventive measures such as use of ITN in order to prevent the occurrence of malaria epidemics.

CHAPTER FIVE

SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

5.1 Summary

An ABM model is developed to investigate the impact of bed net use and temperature in Malaria transmission dynamics through simulated random interactions of population agents which is related to the mathematical model for malaria transmission dynamics developed by Gimba and Bala in [7] with the addition of exposed class in both human and vector populations. The developed ABM is validated with Gimba and Bala model. Furthermore, local sensitivity analysis of the intervention strategies reveals that any intervention which include use of ITN is found to be effective. Our ABM model results show that temperature and ITN efficacy play a vital role in malaria transmission dynamics.

5.2 Conclusion

The field of computational epidemiology has arisen as a new branch of epidemiology to understand epidemic transmission patterns, and to help in planning precautionary measure. In this research work, we modify Gimba and Bala model by incorporating latency period in both human and vector populations using ABM approach. The main findings of the study show the followings:

a. Bed-net efficacy has a positive impact on reducing malaria burden.

b. Any intervention which contain ITN is effective.

c. Increase in ITN efficacy reduces Malaria burden, and vice versa.

d. Temperature has a great influence on malaria transmission dynamics. That is, malaria transmission increases when the temperature is relatively high.

5.3 Recommendations

During model creation and development, several things are assumed for several reasons (such as unavailability of real life field data and computational limitation, etc.). The following recommendations are raised for further research:

1. Consideration of other environmental factors such as rainfall, humidity, e.t.c.

2. Consideration of other vector control interventions such as Indoor Residual Spray (IRS).

3. Consideration of full life cycle of mosquitoes.

5.4 Contributions

This study makes the following contributions:

- We designed and developed an ABM model of malaria transmission to investigate malaria transmission, which is a shift from the usual traditional approach which makes simplified assumptions.

- We perform verification & validation (V&V) of ABM using the basic techniques and by docking ABM with an existing model developed by Gimba and Bala.

- We have shown that temperature changes have a great influence on malaria transmission. From the ABM model, malaria is peak in a certain period of the year. The public health interpretation of this result is that understanding the month at which malaria epidemic occur can help us inform policy makers to make a massive campaign, especially two or three months before the epidemic on the use of preventive measures such as use of ITN in order to prevent the occurrence of the epidemic.

- We have shown that increase in ITN efficacy reduces malaria transmission and increases mosquito mortality rate.

- We designed and developed a model using ABM approach that modeled complex system which is difficult to handle using deterministic approach.

- This work serves as a guide to a new modeling approach on the extensive use of computational resources to study the behavior of a complex system by computer simulation.

- In this work, we have shown that treatment of infectious clinically immune individuals is one of the effective method of malaria control. This can be achieved by considering strategies that can be used to examine individuals not seeking treatment.

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Appendix

```
globals [ steps
  ;temperature                    ;; we use kano state average temperature
  mosquitoes-biting-rate          ;; number of bites per mosquito per day
                                     which depend on
                                     bednet use and its efficiency
  beta                            ;; contact rate between mosquitoes and
                                     individuals which
                                     depend on ITN efficacy
  betam                           ;; betam measures the efficacy of ITNs in
                                      killing mosquitoes
                                     that land on them.
  mosquitoes-mortality-rate       ;; Measure the mosquitoes death rate per day
  no-of-bites                     ;;  all mosquitoes have the same number of bite
  max-mosquitoes                  ;; we limited the number of mosquitoes not
                                     to exceed certain number
  efficiency-length               ;; represent the replacement or distribution
                                      period of ITNs
  no-of-days
  net-life-span
  shape-parameter
;
mylist
  counta
  tica
```

```
n-eggs
radius
bednet-efficiency]

people-own
[ susceptiblen?                    ;; if true, the person is susceptible
                                      ( susceptible naive individuals ar
                                     who have never been infected with m
                                   ;; or have been infected but have not
                                      clinical immunity or those who hav
  exposedn?                        ;; if true, the person is infected na
                                       infectious naive
  infectiousn?                     ;; if true, the person can infect a s
  medicatedn?                      ;; if true. the peron is receiving me
                                      recover in half the average-recove


  susceptiblec?                    ;; if true, the person is susceptible
                                    immune ( susceptible clinically immu
                                     with immunity to clinical symptoms
                                   ;;  )
  exposedc?                        ;; if true, the person is infected bu
  infectiousc?                     ;; if true, the person can infect sus
  medicatedc?                      ;; if true. the peron is receiving me
```

```
                                        recover in half the average-recover

  latent-period                        ;; time ( in days ) an infected individ
                                        in exposed class before moving to infe
  recovery-time                        ;; Time (in days) it takes before the p
                                          has a chance to recover from the inf
  infection-lengthn                     ;; How long the naive person has been
  infection-lengthc                     ;; How long the clincally immune perso
                                          infected


  chance-of-getting-medicine              ;; how individual go to hospital
  chance-of-infectious-naive-to-recover-without-immunity
  chance-of-infectious-naive-to-recover-with-immunity
  chance-of-infectious-clinically-immune-to-recover
  chance-of-clinically-immune-susceptible-to-lose-immunity
   nb-recoverd
   nb-medicated
   nb-infected
  people-life-span               ; we assume people will not live more
                                   than 70yrs ( 365 x 70 = 25550)
  people-age
]
```

```
mosquitoes-own [
 susceptible?                ;; if true, the mosquito is susceptible and carryi
 exposed?                    ;; if true, the mosquito is infected  but not infe
 infectious?                 ;; if true, the mosquito is infected  but not infe

ticky
 infection-length            ;; time taken for an infected mosquito  to become
age
 life-span                   ;; mosquitoes can not live more than its life span
 target
]
                             ;; green patches represent efficient net
patches-own [ efficient-net?   ;; yellow patches represent in-efficient net whil
in-efficient-net?             ;; black patches represent no net
              no-net?
     ]


;; people and mosquitoes are both breeds of turtle.


breed [ mosquitoes mosquito ]
breed [ people person ]
```

```
to setup
  ca
 set max-mosquitoes 50000        ;;clear all ( ca ) is used to clean model's his
  setup-people
  setup-mosquitoes
  setup-world
set mylist (list  21.5 24 27.9 30.9 30.3 28.4 26.4 26 24.9 26.4 24.5 22);
    set counta 0
    set tica 0
  set n-eggs 4

  reset-ticks
 end




to setup-people
  create-people  initial-people        ;; create the people, then initialize the
  [ setxy random-pxcor random-pycor         ;; to distribute people in space ran
                                          and at the centre of the patch they ar
     ;; Initially, we set percentage  of the population to be susceptible naive
    set susceptiblen? true            ;; susceptible naive have white color
```

```
    set color white
    set exposedn? false
    set infectiousn? false
    set medicatedn? false
     set medicatedc? false
    set susceptiblec? false
    set exposedc? false
    set infectiousc? false
    set medicatedc? false
  if random-float  100 <= 10
[
    set susceptiblec? true                ;; the remaining percentage of the po
                                               to be susceptible clincal
    set color pink                        ;; A susceptible clinical has pink co
    set exposedn? false
    set infectiousn? false
    set medicatedn? false
    set susceptiblen? false
    set exposedc? false
    set infectiousc? false
    set medicatedc? false ]

if random-float  100 <= 20
[
    set susceptiblec? false            ;; the remaining percentage of the popul
```

```
                                        to be susceptible clincal
    set color red                      ;; A susceptible clinical has pink col
    set exposedn? false
    set infectiousn? true
    set medicatedn? false
    set susceptiblen? false
    set exposedc? false
    set infectiousc? false
    set medicatedc? false ]

    if random-float  100 <= 1
[
    set susceptiblec? false              ;; the remaining percentage of the
                                           to be susceptible clincal
    set color brown                       ;; A susceptible clinical has pin
    set exposedn? false
    set infectiousn? false
    set medicatedn? false
    set susceptiblen? false
    set exposedc? false
    set infectiousc? true
    set medicatedc? false ]
    set shape "person"
    set size 1.5                          ;;visible to see
```

```
    if ( random 100 <= 5 ) [            ;; we arbitrarily assume  each naive ind
                                           has a 5% chance of starting out infec
      set susceptiblen? false
      set exposedn? true
      set infectiousn? false
      set medicatedn? false
      set color orange                      ;; An infectious naive has red color

      set susceptiblec? false
      set exposedc? false
      set infectiousc? false
      set medicatedc? false
                           ]


if ( random 100 <= 3 ) [            ;; we arbitrarily assume  each naive individ
                                       has a 5% chance of starting out infected
      set susceptiblen? false
      set exposedn? false
      set infectiousn? false
      set medicatedn? false
      set color lime                     ;; An infectious naive has red color
```

```
      set susceptiblec? false
      set exposedc? true
      set infectiousc? false
      set medicatedc? false
                           ]


;; Set the  infection-length  for each person to be zero

      set infection-lengthn 0
      set infection-lengthc 0

 ; we assume people will not live more than 70yrs ( 365 x 70 = 25550)

     set people-life-span 25550
     set people-age random 25550


     ;; Set the latent-period for each person to fall on a
     ;; normal distribution around mean
    set latent-period random-normal 10.5 3.5353
    if latent-period > 15 [ set latent-period 15 ]
```

```
    if latent-period < 10 [ set latent-period 10 ]

     ;; Set the recovery time for each person to fall on a
     ;; normal distribution around mean
    set recovery-time random-normal 5.5 2.1213
    if recovery-time > 7 [

    set recovery-time 7 ]
    if recovery-time < 4 [ set recovery-time 4 ]




  ; set temperature  21.5           ;; set temperature to be average from
                                       the month of january 21.5 from 30

   set radius 0.5
    set shape-parameter 2




  ]
end
```

```
;;create the mosquitoes, then initialize their variables
to  setup-mosquitoes
  create-mosquitoes initial-mosquitoes
  [ setxy random-xcor random-ycor


   ;; we assume 50% of the inital mosquitoes are susceptible and carrying eggs
   set susceptible? true
    set color white                  ;; they have white color
     set exposed? false
     set infectious? false
       set shape "butterfly"
    set size 0.5
     set ticky 0
           set life-span 40
    set age random 40
    set no-of-bites 0
      if ( random-float 100 < 30 )    ;; 10% of the susceptible carrying eggs ha
                                        chance of starting out infections
    [   set susceptible? false        ;; and they have red color
    set color red
     set exposed? false
     set infectious? true
```

```
            ]

        if ( random-float 100 < 5 )  ;; 5% of the susceptible carrying eggs have
                                     chance of starting out infections
    [   set susceptible? false        ;; and they have orange color
    set color brown
      set exposed? true
        set infectious? false
            ]
  ]



end

;; set some percentage of people to enter bed-net

;; green patches represent efficient bed net
to setup-world
  ask n-of ( use-net * initial-people / 100 ) people [
    set pcolor green
    set efficient-net? true
    set in-efficient-net? false
    set no-net? false
    set bednet-efficiency 1
```

```
  set net-life-span 360]




end









;; Different people are displayed in  different
colors depending on their health status
;; White is set at beginning as susceptible naive person
;; orange is an exposed naive person
;; Red is an infectious naive person
;; pink is also set at beginning as susceptible clinical person
;; lime is an exposed clinical person
;; brown is an infectious clinical person


;; Different mosquitoes are displayed in 3 different colors
```

```
depending on health
;; White is neither infected nor infectious (set at beginning as susceptible )
;; ornge is an exposed mosquito
;; Red is an infectious mosquito



;; Different patches are displayed in 3 different colors depending on net use
;;  people on green patches are using  efficient net
;;  people on yellow patches are using inefficient net
;;  people on black patches are not using net



;;;
;;; GO PROCEDURES
;;;



to go

;    export-interface(word "Film-"(0 + ticks)".png")
;;;
```

```
;  ;;-------------------------------------------------------------------
;ifelse counta <= 11 [
;  ifelse tica <= ( counta + 1 ) * 30 [set temperature item counta mylist
;   set tica tica + 1
;   ] [set counta counta + 1]
;  ][set counta 0
;  set tica 0]
;;-------------------------------------------------------------------


    ;if not any? mosquitoes or
  if count mosquitoes > max-mosquitoes or ticks >= 360 [ stop ]


   ask people with [  exposedn? ]
    [ become-infectiousn ]
  ask people with [ infectiousn? ]
    [   recovern infectm1  ]
   ask people with [ infectiousn? ]
    [ if random 100 < chance-of-getting-medicine [ medicatedn ]]
 ask people with [ infectiousc? ]
    [ if random 100 < chance-of-getting-medicine [ medicatedc ]]
  ask people with [ medicatedn? ]
    [  recovern ]
 ask people with [ medicatedc? ]
    [  recoverc ]
```

```
   ask people with [  susceptiblec? ]
    [ become-susceptiblen1  ]
   ask people with [  exposedc? ]
    [ become-infectiousc ]
   ask people with [ infectiousc? ]
    [ recoverc  infectm2  ]


   ask people [  reproduce-people  death]
  ask people [cal-bed-net-efficiency]
  ask people [ set people-age ( people-age + 1 ) ]

ask mosquitoes [ set age (age + 1) ]

  ask mosquitoes [ move-mosquitoes ]
  ask mosquitoes with [age > 5] [reproduce-mosquitoes ]

 ask mosquitoes [  deathm ]
  ask mosquitoes with [ exposed? ]  [ become-infectious ]


  ask mosquitoes with [ ( infectious?) ]
             [ infectn infectc  ]
```

```
  ask patches with [ pcolor = green ] [ become-inefficient ]
  ask patches with [ pcolor = yellow ] [ become-efficient ]


  ask mosquitoes [cal-mortality-rate]

  tick
end
to move-mosquitoes
  set target one-of people
  face target
  ifelse distance target <= 2
  [move-to target]
  [lt 90 fd 1 ]
end


to  become-inefficient

  if bednet-efficiency < 0.5
  [ set in-efficient-net? true
    set efficient-net? false
```

```
    set pcolor yellow
  ]
end

to become-efficient

  if bednet-efficiency >= 0.5
  [ set efficient-net? true
    set in-efficient-net? false
    set pcolor green
  ]
end

 ;; The susceptible individual may be infected, if bitten by
 infected mosquito.
 ;;  We assume that,  there will be no contact between
 mosquito(es) and a person using efficient bednet.
 ;; but, if the bednet is ineffecient, then there may
 be contact.
 ;; Since distance is measured from the centre of the
  patches, we use a radius  of  0.4.
 ;; On the other hand, a mosquito has 100% chance to
 have contact with a nearby person not using bednet.
 ;; Therfore, effeciency of bednet define the probability
  of contact between a mosquito and a person in thesame neighbourhood.
```

```
 ;; Transmission probability from infectious mosquito  to
 susceptible individual (naive or clinically immune) is 0.8
 ;; baseline value is 0.8 and range is [0.1, 0.8]
 ;; Transmission probability from infectious naive to
  susceptible mosquito is 0.2299
 ;; baseline value is [0.1, 0.7] from 12
 ;; Transmission probability from infectious clinically
  immune to susceptible mosquito is 0.5342
 ;; baseline value is 0.5342 and range is [0.072, 0.64]
to infectn
  let closer-uninfected ( people in-radius radius )

  with [  susceptiblen? ]
  if closer-uninfected != nobody
    [ask closer-uninfected
    [ifelse pcolor = black
    [if random-float 1 < 0.8
    [set exposedn? true
     set susceptiblen? false
           set color orange
]
]
      [ ifelse pcolor = yellow
      [ if random-float 100 < ( 1 - bednet-efficiency * 2 )
      [ if random-float 1 < 0.4
```

```
      [ set susceptiblen? false
        set exposedn? true
        set color orange
]
]
]

                [  ]
]
]
]
end


to infectc
  let closer-uninfected ( people in-radius radius )

  with [  susceptiblec? ]
  if closer-uninfected != nobody
    [ ask closer-uninfected
    [ ifelse pcolor = black

    [ if random-float 1 < 0.8
    [ set exposedc? true
      set susceptiblec? false
```

```
      set color lime


       ]
      ]
      [ ifelse pcolor = yellow
    [ if random-float 1 < ( 1 - bednet-efficiency * 2 )
    [ if random-float 1 < 0.4
   [ set exposedc? true
     set color lime
     set susceptiblec? false

      ]
          ]
        ]

        [ ]
    ]
    ]
  ]
end


;;  As in [2], the time taken for an infected mosquito (not infectious)
;;to become infectious (begin to transmit the disease)
;; is 7 days from [47].
```

```
to become-infectious
   set infection-length ( infection-length + 1 )
   if infection-length > 7
  [ set exposed? false
    set infectious? true
     set color red ]
end

    ;; procedure of how mosquitoes die

to deathm

  if  random-float 1 <  mosquitoes-mortality-rate or age > life-span
         [ die ]
end




to infectm1
  let closer-uninfected ( mosquitoes in-radius radius )

  with [  susceptible? ]
  if closer-uninfected != nobody
  [ ask closer-uninfected
```

```
    [ ifelse pcolor = black

   [ if random-float 1 < 0.2299
   [ set exposed? true
     set susceptible? false
           set color orange

      ]
     ]
      [ ifelse pcolor = yellow
    [ if random-float 1 < (1 - bednet-efficiency * 2 )
    [ if random-float 1 < 0.2299
   [ set exposed? true
     set color orange
     set susceptible? false

      ]
         ]
       ]

        [ ]
    ]
    ]
  ]
end
```

```
to infectm2
  let closer-uninfected ( mosquitoes in-radius radius )
  with [  susceptible? ]
  if closer-uninfected != nobody
  [ ask closer-uninfected
    [ ifelse pcolor = black



   [ if random-float 1 < 0.5342
   [ set exposed? true
     set susceptible? false
           set color orange


      ]
     ]
      [ ifelse pcolor = yellow
    [ if random-float 1 < ( 1 - bednet-efficiency * 2 )
    [ if random-float 1 < 0.5342
   [ set exposed? true
     set color orange
     set susceptible? false
        ]]]
        [ ]
    ]
```

```
    ]
  ]
end


;;time taken for an infected naive person to become
;;infectious (latency period of human from 3 )
to become-infectiousn
  set infection-lengthn ( infection-lengthn + 1 )
   if infection-lengthn > latent-period
  [ set exposedn? false
    set infectiousn? true
     set color red
   ]
end
to medicatedn
  set medicatedn? true
  set infectiousn? false
  set color red + 3
end
to medicatedc
  set medicatedc? true
  set infectiousn? false
  set color brown + 3
end
```

```
;  An infected naive individual has a probability of recovering
naturally after reaching their
;  recovery period. From [3], the recovery period of naive
person fall within 4 to 7 days
;  and determined by pulling from an approximate normal distribution
 with mean  5.5 and
;;standard deviation 2.1213.
;  We assume that a person who gets medical attention will recover
in half  of the recovery period. Also,
;  If an infected naive individual remain infected  for more than
the recovery-time, then there is a
;;chance for recovery or die due to the desease.
;  a recovered naive person moves to either a susceptible naive or
 clinically immune class.
to recovern
  set infection-lengthn ( infection-lengthn + 1 )

 ifelse not medicatedn? [
  if infection-lengthn > recovery-time [
   ifelse random-float 100 <  recovery-chance * 6 [
    ifelse random-float 100 <  50 [
    set infectiousn? false
    set color white
    set susceptiblen? true
   ][
```

```
 set infectiousn? false
 set color pink
 set susceptiblec? true
]
   ][ if random-float 1 < 0.000057341 [
    ;; disease induced death rate for a naive individual from 1
set pcolor black
  die
  ;; if the individual is wearing efficient or inefficient net

  ;;and died then the patch color turn to black i.e no net
]]
]
]
[ if infection-lengthn > ( recovery-time / 3 )  [

   ifelse random-float 100 <  50 [
 set medicatedn? false
 set color white
 set susceptiblen? true
][
 set medicatedn? false
 set color pink
 set susceptiblec? true
]
```

```
  if random-float 1 < 0.000057341 [
  ;; disease induced death rate for a naive individual
   set pcolor black
     die
     ;; if the individual is wearing efficient or inefficient net

     ;;and died then the patch color turn to black i.e no net
  ]]]
end

;  Similarly, an infected clinically immune  individual has a
 probability of recovering naturally
;after reaching their
;  recovery period. From [24], the recovery period of clinically
 immune person is four times
;than that for naive individual  and determined by pulling from
an approximate normal distribution.
;  We assume that a person who gets medical attention will recover
in half  of the recovery period. Also,
;  if an infected clinically immune individual remain infected
for more than the recovery-time,
;then there is a chance for recovery or die due to the desease.
;  A recovered clinically immune person moves to clinically immune
class only.
```

```
to recoverc
 set infection-lengthc ( infection-lengthc + 1 )



 ifelse not medicatedc? [
  if infection-lengthc > recovery-time * 4 [
   ifelse random-float 100 < recovery-chance / 4 [
    set infectiousc? false
    set color pink
    set susceptiblec? true
   ]
      [ if random-float 1 < 0.00032084 [
       ;; disease induced death rate for a clinically immune individual
       ;; if the individual is wearing efficient or inefficient net
        ;; and died then the patch color turn to black i.e no net
   set pcolor black
     die


  ]]
  ]
  ]
  [ if infection-lengthc > ( recovery-time / 3 )  [
    set medicatedc? false
    set color pink
```

```
    set susceptiblec? true
   ]
  if random-float 1 < 0.00032084 [
   set pcolor black
     die
  ]]
end

; Susceptible clinically immune can loose immunity with the probability 0.0001
to  become-susceptiblen1
  if random-float 1 < 0.0001   [
  set  susceptiblec? false
  set  susceptiblen? true
    set color white ]
end




to become-infectiousc

   set infection-lengthc ( infection-lengthc + 1 )
   if infection-lengthc > latent-period
  [ set exposedc? false
    set color brown
```

```
    set infectiousc? true
   ]
end


; Recruitment into human population is either by birth
or immigration. Human population is
; increased at a rate of 0.000027 as in [1] and only 10%
of the human population reproduce.
;We assume that all recruitment into human population
; go to susceptible population with random age between 0 to 70yrs.
 Also, we assume the recruits
; either use efficient or inefficient bednet depending on the
 bednet that population are using
;or may not use bednet at all.



to reproduce-people
  let matured-people ( people with [people-age > 15 * 360 and people-age <= 50 *
  if matured-people != nobody [

  if random-float 1 < ( 0.000027 )  [
     ;; recruitment into human population either by birth or immigration
```

```
  ask n-of ( floor (random-float 20 / 100 * count matured-people)) matured-peo

hatch 1 [setxy random-pxcor random-pycor
    set people-age random people-life-span
    set color one-of [white brown pink red orange lime]
    if color = white
    [set susceptiblen? true ]
    if color = pink
    [set susceptiblec? true ]

    if color = red
    [set infectiousn? true ]
    if color = brown
    [set infectiousc? true ]

    if color = orange
    [set exposedn? true ]

    if color = lime
    [set exposedc? true ]

 ifelse bednet-efficiency >= 50;;
[ set efficient-net? true
  set in-efficient-net? false
      set pcolor one-of [green black ]
```

```
  ]
   [ set efficient-net? false
    set in-efficient-net? true
        set pcolor one-of [ yellow black ]
  ]]]]
  ]
end


; Individual dies naturally. we assume average life expectancy
of human to be 70yrs
; which implies human death rate is ( 1/ 70 x 365 = 3.913894 x 10^-5).
 where 365 is the number of days of the year.



to death
  if random-float 1 < 1 / 25550 or people-age > people-life-span
 [  set pcolor black
   die ]
end


; we assume that only 3% of the mosquitoes population reproduce and mosquitoes
; emerge as a susceptible, exposed or infectious adult mosquitoes
```

```
; after some days depending on the average temperature.

;

to reproduce-mosquitoes
  set ticky ticky + 1
  let matured-mosquitoes ( mosquitoes with [age > 5] )


ask n-of ceiling ( 0.5 * count matured-mosquitoes) matured-mosquitoes [

  if ticky >= (- 13 / 20 * temperature + 146 / 5)

     [set ticky 0 hatch random 100 [setxy random-xcor random-ycor
      set color one-of [white orange red ]
      if color = white [set susceptible? true]
      if color = orange [set exposed? true]
      if color =  red [set infectious? true]
     set age 0 ]

  ]

  ]

end
```

```
to cal-bed-net-efficiency
set bednet-efficiency ( 1 -  (ticks mod net-life-span  / ( net-life-span ))  ^ s
end
to cal-mortality-rate

let closer-mosquitoes ( mosquitoes in-radius radius )


if closer-mosquitoes != nobody
[ ask closer-mosquitoes
[ ifelse pcolor = black



[ set betam (1 - exp( - 1 / (- 4.4 + 1.3 * temperature - .03 * temperature * tem
[ if pcolor = green or pcolor = yellow

[set betam (1 - exp( - 1 / (- 4.4 + 1.3 * temperature - .03 * temperature * temp
+ ( 1 -  (ticks mod net-life-span  / ( net-life-span ))  ^ shape-parameter)  * 0
]
]
]
 set mosquitoes-mortality-rate  ( 3.3 * 10 ^ (- 4) * count mosquitoes + ( betam
end
```