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Article

Analysis of The Stochastic Model of Epidemic Malaria Transmission With Discrete Time Markov Chain in Gedebgie, Ethiopia

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Abstract: Malaria is an infectious disease caused by the Plasmodium parasite and transmitted between humans through bites of female Anopheles mosquitoes. This thesis modifies the SIR model to predict the spread of malaria in Gedebgie using the data from Gedebgie health station. A stochastic model describes the dynamics of malaria and human population compartments in terms of stochastic and deterministic equations and these equations represent the relations between relevant properties of the compartments. The aim of the study is to understand the important parameters in the transmission and spread of epidemic malaria disease. Our results show that the reproduction number R_0, is less than 1, so that the disease dies out and the probability of an outbreak is zero. Numerical simulations have been carried out applying the numerical software Matlab and python. These simulations show the behavior of the infected population in time. From the analysis and discussions of the model, SIR model is a good model to study the spread of malaria in Gedebgie.

Keywords: SIR model, stochastic and deterministic model, basic reproduction Number, Fokker plank equation, discrete time Markov chain

1. Introduction

Malaria is one of the diseases that have their presence constantly in human population. Malaria is widely spread in tropical and subtropical regions including Africa, Asia, Latin America, the Middle East and some parts of Europe [1]. The parasite is responsible for the greatest number of deaths and clinical cases in the tropics. Its infection can lead to serious complications affecting brain, lungs, kidneys and other organs [2]. It is predominantly present in the tropical countries. Even though the disease has been investigated for hundreds of years, it still remains a major public health problem with 109 countries declared as endemic to the disease in 2008. There were 243 million malaria cases reported, and nearly a million deaths - primarily of children under 5 years [3].

A stochastic model is preferable when studying a small community. Stochastic models have also shown to be advantageous when the contact structure in the community contains small complete graphs; households and other local social networks being common examples. Needless to say, both deterministic and stochastic epidemic models have their important roles to play and deterministic and stochastic models are used for epidemiological modeling. The stochastic model is a Markov population process with continuous time and discrete state space. Stochastic models incorporate discrete movements of individuals between epidemiological classes and not average rates at which individuals move between classes. A significant possibility is that the last infected individual can recover before the disease is transmitted and the infection can only reoccur if it is reintroduced from outside the population [4-6].

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A stochastic model is a tool for estimating probability distributions of potential outcomes by allowing for random variation in one or more inputs over time. The random variation is usually based on fluctuations observed in historical data for a selected period using standard time-series techniques [7]. Stochastic modeling of epidemics is important when the number of infectious individuals is small or when the variability in transmission, recovery, births, deaths, or the environment impacts the epidemic outcome. The variability associated with individual dynamics such as transmission, recovery, births or deaths is often referred to as demographic variability. The variability associated with the environment such as conditions related to terrestrial or aquatic settings is referred to as environmental variability. [8]. A Markov chain is a stochastic process with the Markov property.

A Markov chain is a stochastic model describing a sequence of possible events in which the probability of each event depends only on the state attained in the previous event [9]. In probability theory and related fields, a Markov process, named after the Russian mathematician Andrey Markov, is a stochastic process that satisfies the Markov property (sometimes characterized as "memorylessness"). In statistical mechanics, the Fokker–Planck equation is a partial differential equation that describes the time evolution of the probability density function of the velocity of a particle under the influence of drag forces and random forces, as in Brownian motion. The equation can be generalized to other observables as well. It is named after Adriaan Fokker and Max Planck and is also known as the Kolmogorov forward equation, after Andrey Kolmogorov, who independently discovered the concept in 1931 [10]. Kolmogorov gives a precise definition of stochastic processes. His point of view stresses the fact that a stochastic process is nothing else but a random variable valued in a space of functions (or a space of curves). For instance, if an economist reads a financial newspaper because he/she is interested in the price of a barrel of oil every day over the last year, then he/she will focus on the curve of these prices. According to Kolmogorov's point of view, saying that these prices form a stochastic process is then equivalent to saying that the curve that is seen is the realization of a random variable defined on a suitable probability space [11]. An early stochastic epidemic model was proposed by A.G. McKendrick in 1926, which precedes his work with Kermack on deterministic models [12]. A stochastic process has the Markov property if the conditional probability distribution of future states of the process (conditional on both past and present values) depends only upon the present state; that is, given the present, the future does not depend on the past. A process with this property is said to be Markovian or a Markov process. The most famous Markov process is a Markov chain. Brownian motion is another well-known Markov process [13]. In 1928 and 1931, Reed and Frost, and Greenwood proposed discrete time stochastic models, which proceeded by generations of infective, [14].

A stochastic process has the Markov property if the conditional probability distribution of future states of the process (conditional on both past and present states) depends only upon the present state, not on the sequence of events that preceded it. A process with this property is called a Markov process. The term Markov assumption is used to describe a model where the Markov property is assumed to hold, such as a hidden Markov model. A Markov random field extends this property to two or more dimensions or to random variables defined for an interconnected network of items. A discrete-time stochastic process satisfying the Markov property is known as a Markov chain [15].

The SIR models the flows of people between three states: susceptible (S), infected (I), and recovered (R). Each of those variables represents the number of people in those groups. The SIR model is used where individuals infect each other directly (rather than through a disease vector such as a mosquito). Contact between people is also modeled to be random. The rate that people become infected is proportional to the number of people who are infected, and the number of people who are susceptible. The SIR model is a simple model, due to Kermack and McKendrick, of an epidemic of an infectious disease in a large population. The SIR Model is used in epidemiology to compute the amount of susceptible, infected, and recovered people in a population. It is also used to explain the change in the number of people needing medical attention during an epidemic. All these are functions

of the time t, and they change according to a system of differential equations. For simplicity, we assume a closed population (no births, deaths or migration) and thus we have only the transitions from susceptible to infected (S → I) and from infected to recovery (I → R). For a specific disease in a specific population, these functions may be worked out in order to predict possible outbreaks and bring them under control. For the full specification of the model, the arrows should be labeled with the transition rates between compartments. Between S and I, the transition rate is β, where β is the contact rate, which takes into account the probability of getting the disease in a contact between a susceptible and an infectious subject. Between I and R, the transition rate is γ (simply the rate of recovery or death). The parameters beta and gamma partially control how fast people move from being susceptible to infected (beta), and from infected to recover (gamma) [16, 17].

A stochastic model is a tool for estimating probability distributions of potential outcomes by allowing for random variation in one or more inputs over time. The random variation is usually based on fluctuations observed in historical data for a selected period using standard time-series techniques. Distributions of potential outcomes are derived from a large number of simulations (stochastic projections) which reflect the random variation in the input(s). Its application initially started in physics. It is now being applied in engineering, life sciences, social sciences, and finance [18]. The term stochastic is used in many different fields, particularly where stochastic or random processes are used to represent systems or phenomena that seem to change in a random way [19].

Deterministic system is a system in which no randomness is involved in the development of future states of the system. A deterministic model will thus always produce the same output from a given starting condition or initial state [20]

2. Materials and Methods

After complete the data is capture on malaria, the data enter into the python and matlab software preparation for analysis. Results are present in table and graphs. Then calculate the basic reproductive number to determine the distribution of malaria is high or low and also estimate the probability of an outbreak.

Stochastic simulation algorithm

Initial infected population, $i_0 = 2$ at time $t = 0$
Calculate the transmission and recovery rate
Consider only on the infected population
Generate random number r, $r \epsilon (0,1]$
Simulate the number of the infected
If $R_0 > 1$
Epidemic
else
Disease dies out
Go to step 2

SIR model and basic reproductive number

In SIR epidemic models, individuals in the population are classified according to disease status, susceptible, infectious and recovered. These three classifications are denoted by the variables S, I, and R, respectively. In SIR epidemic model, individuals become infected, but then develop immunity and enter the immune class R. In SIR model birth rate is zero (b=0). The basic reproductive number R_0, provides the expected number of new infections from one infectious individual over the duration of the infectious period given that all other members of the population are susceptible. The basic reproduction number is defined as follows:

$$R_0 = \frac{\beta}{\gamma} \qquad (3.1)$$

The fraction $\frac{1}{\gamma}$ is the length of the infectious period, adjusted for deaths. The fraction gamma (γ) of infected recovering in a given day can be estimated from observation of infected individuals. Specifically, γ is roughly the reciprocal of the number of days an

individual is sick enough to infect others. Let D is the average duration of infection [17]. Then

$$\gamma = \frac{1}{D} \quad (3.2)$$

If $R_0 < 1$, each individual produces on average less than one new infected individual and hence the disease dies out and if $R_0 > 1$, each individual produces more than one new infected individual and hence the disease is able to invade the susceptible population.

The quantity $R_0\frac{S(0)}{N}$ is referred to as the initial replacement number the average number of secondary infections produced by an infected individual during the period of infectiousness at the outset of the epidemic. Since the infectious fraction changes during the course of the epidemic, the replacement number is generally defined as $R_0\frac{S(0)}{N}$. If $R_0\frac{S(0)}{N} > 1$, then there is an initial increase in the number of infected cases I(t) (epidemic) and the population experiences an outbreak, but if $R_0 S(0)/ N \leq 1$, then I(t) decreases monotonically to zero (disease-free equilibrium) and the disease eventually disappears from the population.

Model assumptions; The SIR Model is used in epidemiology to compute the amount of susceptible, infected, recovered people in a population. This model is an appropriate one to use under the following assumptions [30]:

The population is fixed.

The only way a person can leave the susceptible group is to become infected. The only way a person can leave the infected group is to recover from the disease. Once a person has recovered, the person received immunity.

Age, sex, social status, and race do not affect the probability of being infected.

There is no inherited immunity.

The member of the population mix homogeneously (have the same interactions with one another to the same degree).

The differential equations describing the dynamics of SIR epidemic model have the following form:

$$\frac{dS}{dt} = -\frac{\beta}{N}SI + b(I+R)$$

$$\frac{dI}{dt} = \frac{\beta}{N}SI - (b+\gamma)I$$

$$\frac{dR}{dt} = \gamma I - bR$$

$$N = S(t) + I(t) + R(t) \quad (3.3)$$

$$R(t) = N - S(t) - I(t) \quad (3.4)$$

By applying Euler's method of systems, we can solve the differential equations. The solutions to the differential equations are:

$$S_{n+1} = S_n - \beta S_n I_n \Delta t \quad (3.5)$$

$$I_{n+1} = I_n (1 + \beta S_n - \gamma)\Delta t \quad (3.6)$$

$$R_{n+1} = R_n + \gamma I_n \Delta t \quad (3.7)$$

Where, S_{n+1}, I_{n+1} and R_{n+1} are the number of susceptible, infected and recovered people at time (n+1). Δt is a small change in time, and will be equal to one [31]. These equations are primarily used to calculate β.

$$\beta = \frac{S_n - S_{n+1}}{S_n I_n} \quad (3.8)$$

Stochastic probability

The stochastic probability function of the stochastic process $\{I(t)\}_{t=0}^{\infty}$ has an associated probability function,

$p_i(t) = \text{Prob}\{I(t) = i\}$, for i = 0, 1, 2, . . . ,N and t = 0,Δt, 2Δt, . . . ,

Where $\sum_{i=0}^{N} p_i(t) = 1$

The stochastic process has the Markov property if

$$\text{Prob}\{I(t + \Delta t) \mid I(0), I(\Delta t), \ldots, I(t)\} = \text{Prob}\{I(t + \Delta t) \mid I(t)\}. \quad (3.9)$$

The Markov property means that the process at time t+Δt only depends on the process at the previous time step t. This relationship is determined by the underlying assumptions

in the epidemic model and is defined by the transition matrix. The probability of a transition from state I(t) = i to state I(t + Δt) = j, i → j, in time Δt, is denoted as

$p_{ji}(t + \Delta t, t) = \text{Prob}\{I(t + \Delta t) = j \mid I(t) = i\}$.

When the transition probability $p_{ji}(t + \Delta t, t)$ does not depend on t, $p_{ji}(\Delta t)$, the process is said to be time homogeneous. For the stochastic epidemic model, the process is time homogeneous because the deterministic model is autonomous. To reduce the number of transitions in time Δt, we make one more assumption. The time step Δt is chosen sufficiently small such that the number of infected individuals changes by at most one during the time interval Δt, that is,

i → i + 1, i → i − 1 or i → i.

Either there is a new infection a birth, a death, or a recovery during the time interval Δt. In the simplest case, with only three transitions possible, the transition probabilities are defined using the rates (multiplied by Δt) in the deterministic epidemic model. The transition probabilities for the DTMC epidemic model satisfy

$$P_{ji}(\Delta t) = \begin{cases} \frac{\beta i(N-i)}{N}(\Delta t) & j = i + 1 \\ (b + \gamma) i \Delta t & j = i - 1 \\ 1 - [\frac{\beta i(N-i)}{N} + (b + \gamma)]\,\Delta t & j = i \\ 0 & \text{other wise} \end{cases} \quad (3.10)$$

The probability of a new infection, i → i+1, is βi(N−i)Δt/N. The probability of a death or recovery, i → i − 1, is (b +γ)iΔt. Finally, the probability of no change in state, i → i, is 1 − [βi(N − i)/N + (b +γ)i]Δt. Since a birth of a susceptible must be accompanied by a death to keep the population size constant this probability is not needed in either the deterministic or stochastic formulations. To simplify the notation and relate to a birth and death process, the transition probability for a new infection is denoted as b(i)Δt and for a death or a recovery is denoted as d(i)Δt. Then

$$P_{ji}(\Delta t) = \begin{cases} b(i)\Delta t & j = i + 1 \\ d(i)\Delta t & j = i - 1 \\ 1 - [b(i) + d(i)]\Delta t & j = i \\ 0 & j \neq i + 1, i, i - 1 \end{cases} \quad (3.11)$$

The sum of the three transitions equal one because these transitions represent all possible changes in the state i during the time interval Δt. To ensure that these transition probabilities lie in the interval [0, 1], the time step Δt must be chosen sufficiently small such that

$\text{Max}\{[b(i) + d(i)]\Delta t\} \leq 1,\ i \in \{1,\ldots,N\}$

Where $b(i) = \frac{\beta i(N - i)}{N}$ and $d(i) = (b +\gamma)i$ and for i = 1, 2, . . . ,N (3.12)

A transition matrix is formed when the states are ordered from 0 to N. Denote the transition matrix as P(Δt). Matrix P(Δt) is a (N + 1) × (N + 1) matrix given by

$$P(\Delta t) = \begin{bmatrix} p_{00} & p_{01} & p_{02} & p_{03} & p_{04} & p_{05} & p_{06} & \cdots \\ p_{10} & p_{11} & p_{12} & p_{13} & p_{14} & p_{15} & p_{16} & \cdots \\ p_{20} & p_{21} & p_{22} & p_{23} & p_{24} & p_{25} & p_{26} & \cdots \\ p_{30} & p_{31} & p_{32} & p_{33} & p_{34} & p_{35} & p_{36} & \cdots \\ p_{40} & p_{41} & p_{42} & p_{43} & p_{44} & p_{45} & p_{46} & \cdots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \end{bmatrix} \quad (3.13)$$

$$\begin{bmatrix} 1 & d(1)\Delta t & 0 & \cdots & 0 & 0 \\ 0 & 1 - (b + d)(1)\Delta t & d(2)\Delta t & \cdots & 0 & 0 \\ 0 & b(1)\Delta t & 1 - (b + d)(2)\Delta t & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & 1 - (b + d)(90)\Delta t & d(91)\Delta t \\ 0 & 0 & 0 & \cdots & b(90)\Delta t & 1 - d(91)\Delta t \end{bmatrix}$$

$P(\Delta t) = p_{ji}(\Delta t)$ is known as the transition matrix. Where the notation (b+d)(i) = [b(i)+d(i)] for i = 1, 2, . . . ,N. Matrix P(Δt) is a stochastic matrix, i.e., the column sums equal one.

Applying the Markov property and the preceding transition probabilities, the probabilities $p_i(t + \Delta t)$ can be expressed in terms of the probabilities at time t. At time $t + \Delta t$,

$p_i(t+\Delta t) = p_{i-1}(t)b(i-1)\Delta t+p_{i+1}(t)d(i+1)\Delta t+p_i(t)(1-[b(i)+d(i)]\Delta t)$

$\frac{Pi(t+\Delta t)-pi(t)}{\Delta t} = p_{i-1}(t)b(i-1)+p_{i+1}(t)d(i+1)-p_i(t)[b(i)+d(i)]$

$\frac{dp_i}{dt} = p_{i-1}(t)b(i-1)+p_{i+1}(t)d(i+1)-p_i(t)[b(i)+d(i)]$ (3.14)

The stochastic process is referred to as a diffusion process if it is a Markov process in which the infinitesimal mean and variance exist. The probability distribution equation satisfies a forward Kolmogorov differential equation (Fokker plank equation). This equation is a second order partial differential equation [27, 32]. Assume Prob{I(0) = i_0} = 1 and let p(i, i_0; t) = p(i, t) = $p_i(t)$. Then the system of differential equations in (3.14) can be expressed as a finite difference scheme in the variable i with $\Delta i = 1$,

$\frac{dp_i}{dt} = p_{i-1}b(i-1)+p_{i+1}d(i+1)-p_i[b(i)+d(i)]$

$=-\frac{\{p_{i+1}[b(i+1)-d(i+1)]-\{p_{i-1}[b(i-1)-d(i-1)]\}}{2\Delta i}+\frac{1}{2}\frac{p_{i+1}[b(i+1)+d(i+1)]-2p_i[b(i)+d(i)]+p_{i-1}[b(i-1)-d(i-1)]\}}{(\Delta i)^2}$

Let $i = x$, $\Delta i = \Delta x$ and $p_i(t) = p(x, t)$. The limiting form of the preceding equation (as $\Delta x \to 0$) is the forward Kolmogorov differential equation for p(x, t):

$\frac{\partial p(x,t)}{\partial t} = -\frac{\partial}{\partial x}\{[b(x)-d(x)]p(x,t)\}+\frac{1}{2}\frac{\partial^2}{\partial x^2}\{[b(x)+d(x)]p(x,t)\}$

Substituting $b(x) = \frac{\beta x(N-x)}{N}$ and $d(x) = (b+\gamma)x$ yields

$\frac{\partial p(x,t)}{\partial t} = -\frac{\partial}{\partial x}\{[\frac{\beta x(N-x)}{N} - (b+\gamma)x]p(x,t)\}+\frac{1}{2}\frac{\partial^2}{\partial x^2}\{[\frac{\beta x(N-x)}{N} +(b+\gamma)x]p(x,t)\}$ $\frac{\partial p(x,t)}{\partial t} = -\frac{\partial}{\partial x}\{[b(x) - d(x)]p(x,t)\}+\frac{1}{2}\frac{\partial^2}{\partial x^2}\{[b(x)+d(x)]p(x,t)\}$ (3.15)

This equation is called forward Kolmogorov differential equations (Fokker Plank equation).

The coefficient in the first term on the right side of the preceding equations $[\frac{\beta x(N-x)}{N} - (b+\gamma)x]$, is the infinitesimal mean and the coefficient in the second term, $[\frac{\beta x(N-x)}{N} + (b+\gamma)x]$, is the infinitesimal variance. More generally, the forward Kolmogorov differential equations (Fokker Plank equation) are expressed in terms of the transition probabilities. To solve the differential equation requires boundary conditions for x = 0, N and initial conditions for t = 0. An explicit solution is not possible because of the nonlinearities. We derive a SDE that is much simpler to solve numerically and whose solution is a sample path of the stochastic process [33].

In addition, assume that ΔI has an approximate normal distribution for small Δt. The expectation and the variance of ΔI are computed.

$E(\Delta t) = b(I)\Delta t-d(I)\Delta t$

$= [b(I)-d(I)]\Delta t = \mu(I)\Delta t, \quad \mu(I) = b(I)-d(I)$ (3.16)

$Var(\Delta t) = E(\Delta I)^2 - [E(\Delta I)]^2$

$= [b(I) + d(I)]\Delta t$

$= \sigma^2(I)\,\Delta t, \quad \sigma^2(I) = b(I) + d(I)$ (3.17)

where the notation means $b(I) = \beta i(N - i)/N$ and $d(I) = (b + \gamma)i$ given that I(t) = i. Because the random variable ΔI is approximately normally distributed, $\Delta I(t) \sim N(\mu(I)\Delta t, \sigma^2(I)\,\Delta t)$,

$I(t + \Delta t) = I(t) + \Delta I(t) \approx I(t) + \mu(I)\Delta t + \sigma(I)\sqrt{\Delta t}\,\eta, \quad$ where $\eta = N(0,1)$

The difference equation $I(t+\Delta t) = I(t) + \mu(I)\Delta t + \sigma(I)\sqrt{\Delta t}\,\eta$ is Euler's method applied to the following Itô SDE: $\frac{dI}{dt} = \mu(I) + \sigma(I)\frac{dW}{dt}$ (3.18)

Where W is the Wiener process, $W(t + \Delta t) - W(t) \sim N(0,\Delta t)$ [34].

Euler's method converges to the Itô SDE provided the coefficients, $\mu(I)$ and $\sigma(I)$, satisfy certain smoothness and growth conditions [25]. The coefficients for the stochastic epidemic model are

$\mu(I) = b(I) - d(I) = \frac{\beta}{N}I(N-I)-(b+\gamma)I$ (3.19)

$\sigma(I) = \sqrt{b(I) + d(I)} = \sqrt{\frac{\beta}{N}I(N - I) + (b + \gamma)I}$ (3.20)

$b(I) = \frac{\beta}{N}I(N-I)$ and $d(I) = (b+\gamma)I$

Substituting these values into the Itô SDE gives the SDE epidemic model,

$$\frac{dI}{dt} = b(I)-d(I) +\sqrt{b(I) + d(I)}\ \frac{dW}{dt} = \text{drift} + \text{diffusion} \quad (3.21)$$

The drift and diffusion term determine the change in number of infections over time. From the Itô SDE, it can be seen that when I(t) = 0, dI/dt = 0. The disease free equilibrium is an absorbing state for the Itô SDE. The notation $\frac{dW}{dt}$ is only for convenience because sample paths of W (t) are continuous but nowhere differentiable [32, 35].

The Wiener process is the stochastic processes with a stationary independent increment that is the increments ΔW depend only on Δt and it is independent of the past values. They are independent of t and the value of W (t): $\Delta W = W(t+\Delta t) - W(t) \sim N(0,\Delta t)$

The probability of an outbreak is

$$\text{Probability of an Outbreak} \approx \begin{cases} 0 & \text{if } R_0 \leq 1 \\ 1 - (\frac{1}{R_0})^{i_0} & \text{if } R_0 > 1 \end{cases}$$

3. Results

This presents the result of the study in the form of tables, graphs and matrix's and discussion of the finding arising from the analysis of the result.

Table 1: The number of cases in each state per period

Period	States		
	S	I	R
0	89	2	0
1	85	6	0
2	79	6	6
3	57	22	12
4	40	17	34
5	27	13	51
6	16	11	64
7	10	6	75
8	6	4	81
9	0	6	85

Since the disease is infectious everyone will eventually become infected. In Tables 1 we can see how many people will be in each state at a given period of time. We start with everyone being susceptible to the disease, and then two persons suddenly become infected. From Tables 1, we can calculate β using Euler method from the equation $\beta = \frac{S_n - S_{n+1}}{S_n I_n}$

We obtain the following table from the calculation

Table 2: The parameters values of malaria model

Period	beta(β)
0	0
1	0.0225
2	0.0118
3	0.0464
4	0.0136
5	0.012

6	0.0313
7	0.0341
8	0.0667
9	0.25
Average	0.05

To find the recovery rate (γ) from the average duration of infection from the equation, then from the study the average duration of infection (D) is 10 days. From these D = 10

$$\gamma = \frac{1}{D} = \frac{1}{10} = 0.1$$

Therefore, the recovery rate (γ) = 0.1

To find the basic reproductive number using equation

The basic reproductive number (R_0) = $\frac{\beta}{\gamma}$ from these

$\beta = 0.05$ and

$\gamma = 0.1$

There for, $R_0 = \frac{0.05}{0.1} = \frac{0.05}{0.1} = 0.5$

This number is less than one. So, the distribution of the malaria disease in Gedebge is small. To determine the initial displacement number ($\frac{R_0 S_0}{N}$),

$$\frac{R_0 S_0}{N} = \frac{0.5 \times 89}{91} = 0.49 < 1$$

Then this show that I(t) decrease monotonically to zero (disease-free equilibrium) and the disease eventually disappears from the population.

The probability of an outbreak can be determining using equation

$$\text{Prob}(I(t) = 0) \approx \begin{cases} 1 & \text{if } R_0 \leq 1 \\ (\frac{1}{R_0})^{i_0} & \text{if } R_0 > 1 \end{cases}$$

Based on the calculation we obtain $R_0 = 0.5$. This number is less than one.

$$\text{Prob}(I(t) = 0) \approx 1$$

To estimate the probability of an outbreak is using the equation

$$\text{Probability of an Outbreak} \approx \begin{cases} 0 & \text{if } R_0 \leq 1 \\ 1 - (\frac{1}{R_0})^{i_0} & \text{if } R_0 > 1 \end{cases}$$

Based on the calculation we obtain $R_0 = 0.5$. This number is less than one. Therefor the probability of an outbreak is zero.

The transition matrix and the stochastic matrix can be obtained by using python program simulation based on equation (3.13). The following matrix will be the result of the stochastic matrix (see the program in appendix python program 1).

$$P(\Delta t) = p_{ji}(\Delta t) = \begin{bmatrix} 1 & 0 & 0 & \cdots & 0 & 0 & 0 \\ 0 & 1 & 0 & \cdots & 0 & 0 & 0 \\ 0 & 0 & 1 & \cdots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & 1 & 0 & 0 \\ 0 & 0 & 0 & \cdots & 0 & 1 & 0 \\ 0 & 0 & 0 & \cdots & 0 & 0 & 1 \end{bmatrix}$$

$P(\Delta t) = p_{ji}(\Delta t)$ is known as the transition matrix. Matrix $P(\Delta t)$ is a stochastic matrix, i.e., the column sums equal one because $p_{ji} \geq 0$ and $\sum_{j=1}^{N} p_{ji} \approx 1$, for all $i \in N$. Therefor this transition matrix satisfies the stochastic matrix.

4. Discussion

Our numerical simulation result examines the effect of different combination of treatment and preventions on the transmission of the malaria disease using Matlab and python program. The main strategy to be considered for controlling malaria is the reduction in the number of infected humans through a program preventive measure. In our model, the interaction coefficient, β, between susceptible and infected humans, and the interaction coefficient, γ, between infected and recovered humans are more sensitive parameters.

In Fig. 3, the fractions of the populations, S, I, and R versus time are plotted. Blue represents the number of susceptible people. At the beginning of the epidemic, the number of susceptible people decreases as the number of infected people increases. Gradually the number of recovered people increases. In this particular model, after the epidemic is over, most of the people have been infected and recovered. With increasing time, the infected human decrease.

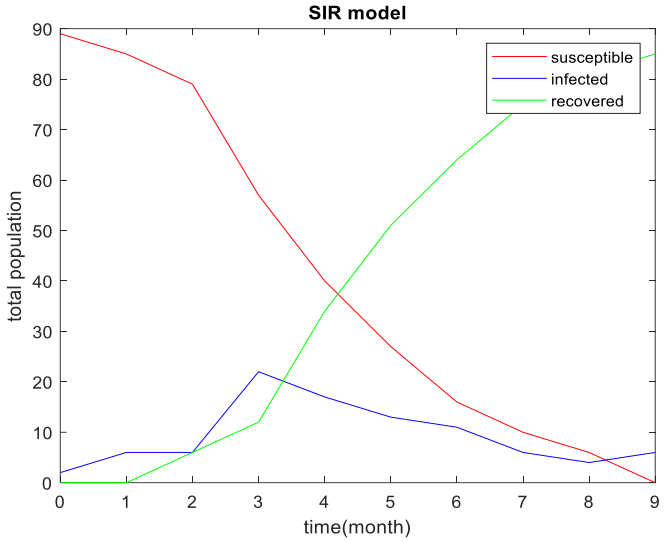

Figure 3: Susceptible, infection and recovered population in each period

Figure 4.below shows for the stochastic model of the probability distribution function for the initial condition is $p(x, 0) = \delta(x - 2)$, where $\delta(x)$ is the Dirac delta function. The basic reproduction number is $R_0 = 0.5$, so that the deterministic solution approaches the disease free equilibrium (the infectious approaches zero) and it is not random but the stochastic solution shows random motion Three sample paths of the DTMC SIR model are compared to the solution of the deterministic model in Figure below $\Delta t = 0.01$, $N = 91$, $\beta = 0.05$, $b = 0$, $\gamma = 0.1$, and $(S(0), I(0)) = (89, 2)$. In the stochastic model, $Prob\{(S(0), I(0)) = (89, 2)\} = 1$.

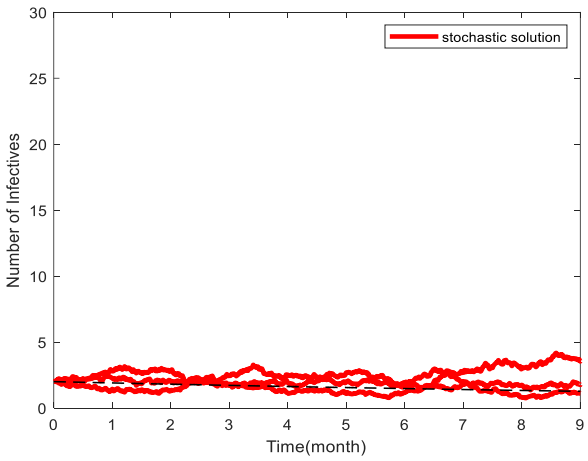

Fig4. Three sample paths of the DTMC SIR epidemic model are graphed with the deterministic solution (dashed curve). The parameter values are $\Delta t = 0.01$, $N = 91$, $\beta = 0.05$, $b = 0$, $\gamma = 0.1$, $S(0) = 89$, and $I(0) = 2$.

Fig5.below shows the Wiener process has a stationary independent increment that is the increments ΔW depend only on Δt. They are independent of t. Two sample paths of a Wiener process are graph (shown in the figure below). The notation $\frac{dW}{dt}$ is only for convenience because sample paths of W (t) are continuous but nowhere differentiable.

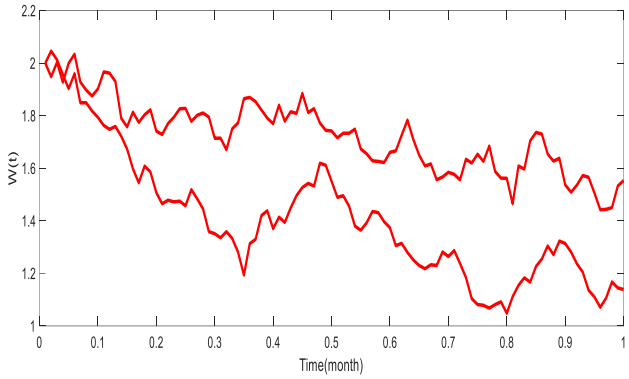

Figure5. Two sample paths of a Wiener process. The parameter values are $\beta = 0.05$, $\gamma = 0.1$, b= 0, N = 91, I(0) = 2. The sample paths of W (t) are continuous but nowhere differentiable

5. Conclusion

The study has been derived and analyzed the stochastic model in order to better understand the transmission and spread of the malaria disease, and tried to find an effective parameter (β, γ) and the basic reproductive number (R_0). The study has been shown that the simulation of the infected population with a given period of time using matlab and python program. The stochastic model is random but the deterministic is not random and the stochastic matrix satisfies the column sum equal to one. The basic reproductive number (R_0) provides the disease is an epidemic or the disease dies out. In this study, we demonstrated that $R_0 < 1$, so that the disease dies out. Therefore, the probability of an outbreak is zero. The numerical simulation has shown that the disease-free equilibrium is occurring when the reproduction number lies below 1. We notice that in order to reduce the basic reproduction number below 1, intervention strategies need to be focused on treatment and reduction of the parameters. From this study we can also conclude that the probability of the disease is zero. From the analysis and discussions of the model, SIR epidemiological model is a good model to study the spread of malaria in Gedebgie.

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