



Stochastic Modelling of the Transmission Dynamics of Measles with Vaccination Control

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Abstract: Measles is still endemic in many parts of the world including developed nations, despite the availability of the infectious disease vaccine since 1963. Elimination of measles requires maintaining the effective reproduction number by achieving and maintaining low levels of susceptibility $R_0 < 1$. In this project, we concentrate on the stochastic modelling of the transmission dynamics of measles with vaccination control. We have obtained the stochastic differential equations model from the deterministic model. Simulation of the stochastic differential equations model have been performed as well as the deterministic model. The stochastic differential equations model has described the transmission dynamics of measles with more information compared to the deterministic counterpart. Mathematical technique used in the simulation of the stochastic differential equations model is Euler-Maruyama numerical scheme and discussions of the model.

Keywords: Measles, Vaccination, Immunity, Stochastic Modeling

1. Introduction

In this chapter we discuss mathematical modelling, types of models and use of models.

Modelling is the process of producing a model; a model is the presentation of the construction and working of some system of interest. It is similar to but simpler than the system it represents. Mathematical modelling is the process of expressing real world phenomena or system using mathematical principles and formula. Mathematical Modelling can be classified into deterministic models and stochastic models based on certainty. In this study we will study stochastic model of dynamics of measles with vaccination by simulation of the transformed deterministic model into stochastic differential equations model.

Measles (also called rubeola) is a highly contagious viral infection that can be found around the world through person-to-person transmission mode, with over 90% attack rate among susceptible persons. The measles virus is a paramyxovirus, genus morbillivirus. Even though an effective vaccine is available and widely used, measles continues to occur even in developed countries. Children under five years are most at risk.

The main symptoms of measles are fever, runny nose,

cough and a rash all over the body, it also produces characteristics-red rash and can lead to serious and fatal complications including pneumonia, diarrhea and encephalitis. Many infected children subsequently suffer blindness, deafness or impaired vision. Measles confer lifelong immunity from further attacks [15].

Measles is a highly contagious virus that lives in the nose and throat mucus of an infected person. It can spread to others through coughing and sneezing. Also, measles virus can live for up to two hours in an airspace where the infected person coughed or sneezed. If other people breathe the contaminated air or touch the infected surface, then touch their eyes, noses, or mouths, they can become infected. Measles is so contagious that if one person has it, 90% of the people close to that person who are not immune will also become infected. Infected people can spread measles to others from four days before through four days after the rash appears. Measles is a disease of humans; measles virus is not spread by any other animal species.

There is no specific treatment for measles. People with measles need bed rest, fluids, and control of fever. Patients with complications may need treatment specific to their problem.

In the work [17] performed a study on mathematical modeling on the control of measles by vaccination. In their

study SEIR model was used to show control of measles by vaccination. Their study recommended introduction of mass vaccination programmer and improvement in early detection of measles cases to the minimize transmission.

In the work [18] performed a mathematical model of measles with vaccination and two phases of infectiousness. They followed the SIR modeling approach hence they partitioned the total population is into Susceptible, Infectious and Recovered compartments. Their study realized that the disease will certainly be eliminated if all susceptible are vaccinated. Achieving a 100% vaccination coverage is impractical but if the goal is set to 100% then we just might hit the $\geq 94\%$ vaccine coverage which is the herd immunity for measles. Since measles is predominantly found among children aged 5 years and below, they therefore suggested that the measles vaccine should be made compulsory such that no child is allowed to enter school without evidence of at least two dose measles vaccination.

In the work [12] performed a deterministic mathematical model for transmission dynamics of measles it shows that vaccination is an important control strategy for the transmission of this disease.

Despite the availability of the measles vaccine since 1963, the infectious disease is still endemic in many parts of the world including developed nations. The disease has continued causing both economic and health problems to large population worldwide mostly affecting children. Due to these impacts, this study aims to develop a stochastic model for control and elimination of the transmission dynamics of measles. This research in tends to achieve the following specific objectives; to formulate a stochastic model for control and elimination of the transmission dynamics of measles, to compare the stochastic and deterministic mathematical models for measles and to perform simulation and analysis of the stochastic mode. The significance of this research is to show the strength of stochastic methods in the analysis compared to deterministic methods and to emphasize on the importance of vaccination in the control of transmission dynamics of measles.

2. Stochastic Differential Equations

In this chapter we will discuss random variables, stochastic process, Markov process, transition pdf, time homogeneous, discrete random walk, diffusion process, wiener process and Ito formula ([13] and [2]).

Suppose $\{X_t\}$ is a collection of random variables defined on a probability space, a stochastic process that is continuous in time $t \in (-\infty, \infty)$ or $[0, \infty)$ or $[0, M]$ the associated pdf is denoted by $p(x, t)$ such that $P\{X_t \in [a, b]\} = \int_a^b p(x, t) dx$

If we assume $\{X_t\}$ is a stochastic process which is continuous in time and in state, then $\{X_t\}$ is a Markov Process if for any given sequence of times $t_0 < t_1 < t_2 \dots < t_{n-1} < t_n$ $P\{X_{t_n} \leq y | X_{t_0} = x_0, X_{t_1} = x_1, X_{t_2} = x_2, \dots, X_{t_{n-1}} = x_{n-1}\} = P\{X_{t_n} \leq y | X_{t_{n-1}} = x_{n-1}\}$

The transition pdf for a continuous time and state Markov process is the density function for a transition from state x at

time t to state y at time $t < s$, it is denoted by $p(y, s; x, t)$

The transition pdf is said to be homogeneous or time homogeneous if $p(y, s + \Delta t; t + \Delta t) = p(y, s; x, t)$ where $t_0 \leq t < s$ and $\Delta t > 0$ so the transitions only depend on the length of time between states $s - t$ and the transition pdf is denoted as $p(y, x, s - t) = p(y, s; x, t)$

If we consider a random walk on the set $\{0, \pm\Delta x, \pm 2\Delta x, \dots\}$, let a and b be the probabilities of moving to the right and to the left respectively such that $a + b = 1$, let $\{X_t\}$ be DTMC for this random walk where $t \in \{0, \Delta t, 2\Delta t, \dots\}$, $X_t \in \{0, \pm\Delta x, \pm 2\Delta x, \dots\}$ and $p_x(t) = P\{X_t = x\}$, it follows that $p(x, t + \Delta t) = ap(x - \Delta x, t) + bp(x + \Delta x, t)$ by using Taylor series expansion about the point (x, t) we obtain:

$$\begin{aligned} p(x, t + \Delta t) = & a \left[p(x, t) + \frac{\partial p(x, t)}{\partial x} (-\Delta x) \right. \\ & \left. + \frac{\partial^2 p(x, t)}{\partial x^2} \frac{(\Delta x)^2}{2} + O((\Delta x)^3) \right] \\ & + b \left[p(x, t) + \frac{\partial p(x, t)}{\partial x} (\Delta x) \right. \\ & \left. + \frac{\partial^2 p(x, t)}{\partial x^2} \frac{(\Delta x)^2}{2} + O((\Delta x)^3) \right] \end{aligned}$$

$$\begin{aligned} p(x, t + \Delta t) = & (a + b)p(x, t) + (b - a) \frac{\partial p(x, t)}{\partial x} (\Delta x) \\ & + (a + b) \frac{\partial^2 p(x, t)}{\partial x^2} \frac{(\Delta x)^2}{2} + O((\Delta x)^3) \\ & \frac{p(x, t + \Delta t) - p(x, t)}{\Delta t} \\ = & (b - a) \frac{\partial p(x, t)}{\partial x} \frac{\Delta x}{\Delta t} + \frac{1}{2} \frac{\partial^2 p(x, t)}{\partial x^2} \frac{(\Delta x)^2}{\Delta t} \\ & + O\left(\frac{(\Delta x)^3}{\Delta t}\right) \end{aligned}$$

Letting Δt and Δx approach zero, then $p(x, t)$ represents the pdf of the continuous time and state process X_t that satisfy the following partial differential equation which is also known as the forward kolmogorov equation:

$$\frac{\partial p(x, t)}{\partial t} = c \frac{\partial p(x, t)}{\partial x} - \frac{D}{2} \frac{\partial^2 p(x, t)}{\partial x^2}, x \in (-\infty, \infty)$$

where;

$c = \text{drift coefficient}$ and $D = \text{diffusion coefficient}$

$$\begin{aligned} \lim_{\Delta t, \Delta x \rightarrow 0} (p - q) \frac{\Delta x}{\Delta t} &= -c \\ \lim_{\Delta t, \Delta x \rightarrow 0} \frac{(\Delta x)^2}{\Delta t} &= D \\ \lim_{\Delta t, \Delta x \rightarrow 0} \frac{(\Delta x)^3}{\Delta t} &= 0 \end{aligned}$$

When the random walk is unbiased or symmetric, the limiting stochastic process is known as Brownian motion

where $c = 0$ since $p = q = \frac{1}{2}$ so that:

$$\frac{\partial p(x, t)}{\partial t} = \frac{D}{2} \frac{\partial^2 p(x, t)}{\partial x^2}, x \in (-\infty, \infty)$$

The standard Brownian motion with $X(0) = 0$ is also known as Wiener Process.

The assumptions on the limits in the random walk model were necessary to obtain the diffusion equation with drift. These assumptions are very important in obtaining the Kolmogorov Differential equations which are related to infinitesimal mean and variance of the process.

Let $\{X_t\}, t \geq t_0$ be a Markov Process with state space $(-\infty, \infty)$ having continuous sample paths and transition pdf given by $p(y, s; x, t), t < s$, then $\{X_t\}$ is a diffusion process if its pdf satisfy the following three assumptions in terms of the expectation:

$$\lim_{\Delta t \rightarrow 0^+} \frac{1}{\Delta t} E[|\Delta X_t|^\delta | X_t = x] = 0 \quad \delta > 2$$

$$\lim_{\Delta t \rightarrow 0^+} \frac{1}{\Delta t} E[\Delta X_t | X_t = x] = \mu(x, t)$$

$$\lim_{\Delta t \rightarrow 0^+} \frac{1}{\Delta t} E[\Delta X_t^2 | X_t = x] = \sigma(x, t)$$

where; $\Delta X_t = X_{t+\Delta t} - X_t = y - x$

$\mu(x, t)$ = drift coefficient and $\sigma(x, t)$ = diffusion coefficient

The backward Kolmogorov Differential Equation for a time homogeneous process is

$$\frac{\partial p(y, x, t)}{\partial t} = \mu(x) \frac{\partial p(y, x, t)}{\partial x} + \frac{1}{2} \sigma(x) \frac{\partial^2 p(y, x, t)}{\partial x^2}, x \in (-\infty, \infty).$$

The forward Kolmogorov Differential Equation for a time homogeneous process is

$$\frac{\partial p(y, x, t)}{\partial t} = \mu(y) \frac{\partial p(y, x, t)}{\partial y} - \frac{1}{2} \sigma(y) \frac{\partial^2 p(y, x, t)}{\partial y^2}, x \in (-\infty, \infty)$$

The pdf $p(x, t)$ with $p(x, 0) = \delta(x - x_0)$ is a solution of forward Kolmogorov equation and therefore, we can replace $p(y, x, t)$ by $p(x, t)$, it follows from the forward Kolmogorov differential equation

$$\frac{\partial p(x, t)}{\partial t} = \mu(x) \frac{\partial p(x, t)}{\partial x} - \frac{1}{2} \sigma(x) \frac{\partial^2 p(x, t)}{\partial x^2}, x \in (-\infty, \infty)$$

A solution of a stochastic differential equation is a sample path of a diffusion process, if $p(x, t)$ satisfies:

$$\frac{\partial p(x, t)}{\partial t} = \mu(x) \frac{\partial p(x, t)}{\partial x} - \frac{1}{2} \sigma(x) \frac{\partial^2 p(x, t)}{\partial x^2}, x \in (-\infty, \infty).$$

Then, the sample path of the process $\{X_t\}$ is a solution of the Itô SDE in the form

$dX_t = \mu(X_t, t)dt + \sqrt{\sigma(X_t, t)}dW_t$, where W_t is denoted by Wiener Process.

Then the differential equation is equivalent to the Itô stochastic integral equation

$$X_t = X_0 + \int_0^t \mu(X_t, t)dt + \int_0^t \sqrt{\sigma(X_t, t)}dW_t$$

where, the first integral is a Riemann integral and the second integral is an Itô stochastic integral.

If the drift and diffusion coefficient are $\mu(X_t, t) = 0$ and $\sigma(X_t, t) = 1$, then we obtain the following diffusion equation

$$\frac{\partial p(x, t)}{\partial t} = \frac{1}{2} \frac{\partial^2 p(x, t)}{\partial x^2}, x \in (-\infty, \infty) \text{ for } p(x, 0) = \delta(x),$$

which is the solution of the pdf in Wiener process W_t :

$p(x, t) = \frac{1}{\sqrt{2\pi t}} \exp\left(-\frac{x^2}{2t}\right)$, $x \in (-\infty, \infty)$ which is the pdf of normal distribution with mean zero and variance t .

Suppose X_t is a solution of the following Itô SDE: $dX_t = \mu(X_t, t)dt + \sigma(X_t, t)dW_t$, if $F(x, t)$ is a real valued function defined for $x \in \mathbb{R}$ and $t \in [a, b]$ with continuous partial derivatives, then

$$dF(X_t, t) = f(X_t, t)dt + g(X_t, t)dW_t$$

where;

$$f(x, t) = \frac{\partial F(x, t)}{\partial t} + \mu(x, t) \frac{\partial F(x, t)}{\partial x} + \frac{1}{2} \sigma^2(x, t) \frac{\partial^2 F(x, t)}{\partial x^2}$$

$$g(x, t) = \sigma(x, t) \frac{\partial F(x, t)}{\partial x}$$

3. Model Formulation and Analysis

In this chapter we discuss the modified SEIR model with control strategy of vaccination [12] in deterministic and its corresponding SDEs for measles transmission. Mathematical Models of Epidemics can be broadly classified into two main categories: deterministic models and stochastic models. These models often result into non-linear systems observed through partial noise data. After a deterministic system of ODEs has been formulated for the population dynamics it is possible to transform the system into various stochastic models such as DTMC, CTMC, MCMC, SDEs and others that take into account the uncertainties in the population.

There are many arguments for transforming deterministic to stochastic models. The following table shows the difference between deterministic and stochastic models [13]

Table 1. Difference between deterministic and stochastic approaches.

	DETERMINISTIC	STOCHASTIC
1	They are simple to analyse but give less information	They are difficult to analyse though they are preferred when the analysis is possible
2	Depends on the law of large numbers	There are cases where the law of large numbers is not satisfied
3	Difficult to analyse extinction	Extinction analysis is possible since it occurs when epidemic deviate from mean level
4	Hard to perform estimation because it is not probabilistic	The uncertainties makes it easier to perform estimations
5	Preferable for new phenomena	Not preferable for new phenomena
6	Repeated simulation from identical model result to one realization	Repeated simulation from identical model result to different realizations
7	Depends on the assumption of mass action to describe spread of the disease	Depends on the natural way to describe spread of the disease

3.1. Formulation of the Deterministic Mathematical Model

In this section we formulate a deterministic, compartmental mathematical model to describe the transmission dynamics of measles. We assume that the population is homogeneously mixing and reflects increasing dynamics such as birth and immigration, Per Capita birth rate is time constant, Per Capita natural mortality rate is time constant, individual can be infected through direct contact with an infectious individual, on recovery the individual obtains permanent infection-acquired immunity that is an individual cannot be infected again by measles and Individual who has attended first and second dose of vaccine consecutively receive permanent immunity to measles.

The total population is divided into the following epidemiological classes Susceptible, S (Individuals who may get the disease); Exposed or Latent, E (Individuals who are exposed to the disease); Infected, I (Individuals who have the disease and are able to transfer it to others); Recovered, R (Individuals who have permanent infection-acquired immunity and those who received the second dose of vaccine) and Vaccinated, V (Individuals who have received first dose of vaccine). In this study we assume that newborns and immigrants who received first dose of vaccine join the Vaccinated class, V at rate $\phi\pi N$ and ρA respectively. On the other hand newborns and immigrants who have not received first dose of vaccine join the Susceptible class, S at rate $(1-\phi)\pi N$ and $(1-\rho)A$ respectively. The Susceptible individuals who received the first dose of vaccine may join the Vaccinated class, V at rate ϵS . When there is an adequate contact of a Susceptible individual with an Infective individual so that transmission occurs, then the susceptible individual may join the Exposed class, E at the rate λS . After Latent period ends, exposed individuals may progress to the Infectious class, I at rate σE . When the infectious period ends, the individuals may join the recovery class, R at rate ηI otherwise they may die at rate $(\delta+\mu)I$ due to the disease or naturally. The recovery class, R consists of those with permanent infection-acquired immunity and those who received the second dose of vaccine at rate $\omega\theta V$. The Vaccinated individuals who did not receive second dose of vaccine may return to Susceptible class, S at rate $(1-\theta)\alpha V$ as

the first dose of vaccine is waning at rate α .

3.1.1. Description of Variables and Parameters

The following tables describe the variables and parameters used in our model:

Table 2. Variables used in the model.

VARIABLE	DESCRIPTION
S	The number of Susceptible individuals at time t
E	The number of Exposed individuals at time t
I	The number of Infected individuals at time t
R	The number of Recovered individuals at time t
V	The number of Vaccinated individuals at time t
N	The total population at time t

Table 3. Parameters used in the model

PARAMETER	DESCRIPTION
π	Per Capita birth rate
Λ	Constant Immigration rate
ϕ	Proportions of newborns who are vaccinated
$1-\phi$	Proportion of newborns who are not vaccinated
ρ	Proportions of immigrants who are vaccinated
$1-\rho$	Proportion of immigrants who are not vaccinated
a	Arrival rate
c	Per Capita contact rate
δ	Death due to disease
μ	Per Capita natural mortality rate
β	Probability of one infected individual to become infectious
λ	Force Of Infection, $\lambda=\frac{\beta c I}{N}$
σ	Progression rate from latent to infectious
η	Recovery rate of treated infectious individuals
α	The rate of waning of first dose of vaccine
ω	The rate of receiving second dose of vaccine
ϵ	Proportion of individuals who received a first dose of vaccine
θ	Proportion of individuals who received a second dose of vaccine at rate α
$1-\theta$	Proportion of individuals who are not vaccinated for a second time and return to Susceptible class

3.1.2. Compartmental Diagram

The description of measles dynamics can be summarized by compartmental diagram below:

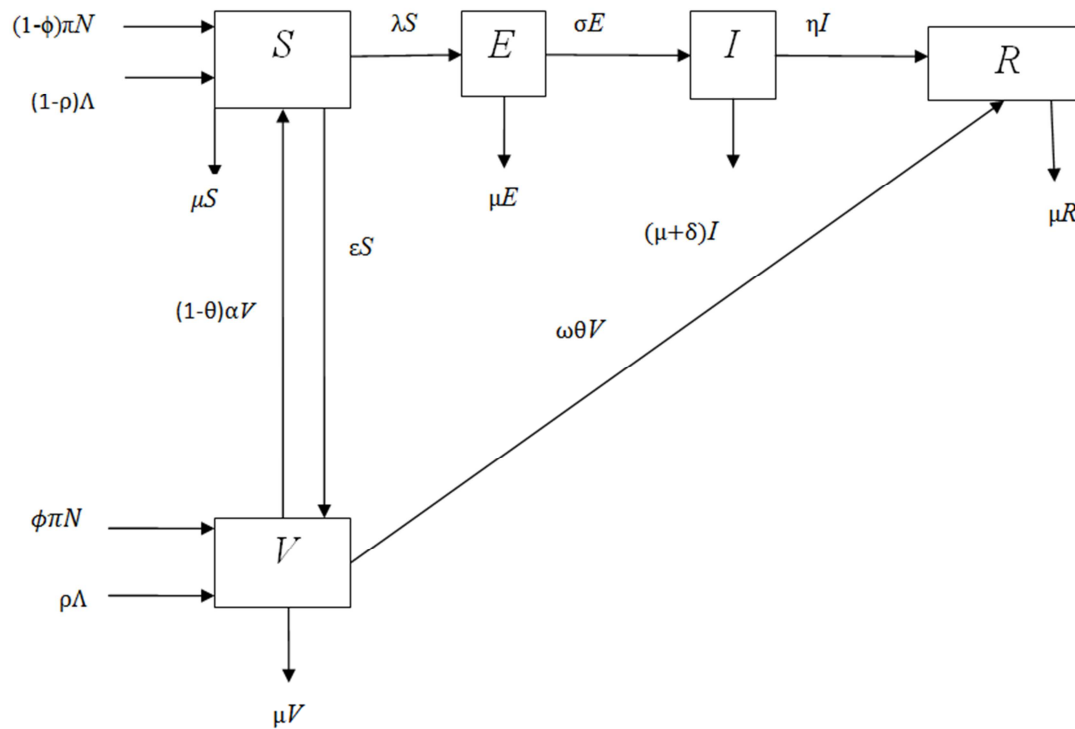


Figure 1. Compartmental Diagram of the Transmission Dynamics of Measles.

3.1.3. Ordinary Differential Equations

From the above explanation and compartmental diagram Figure 1, the transition between compartments can now be expressed by the following differential equations:

$$\frac{dS}{dt} = (1-\phi)\pi N + (1-\rho)\Lambda + (1-\theta)\alpha V - \lambda S - \varepsilon S - \mu S \quad (1)$$

$$\frac{dV}{dt} = \phi\pi N + \rho\Lambda + \varepsilon S - (1-\theta)\alpha V - \omega\theta V - \mu V \quad (2)$$

$$\frac{dE}{dt} = \lambda S - \sigma E - \mu E \quad (3)$$

$$\frac{dI}{dt} = \sigma E - \eta I - (\mu + \delta)I \quad (4)$$

$$\frac{dR}{dt} = \eta I + \omega\theta V - \mu R \quad (5)$$

The above system of equations (1)-(5) can be simplified into:

$$\frac{dS}{dt} = (1-\phi)\pi N + (1-\rho)\Lambda + (1-\theta)\alpha V - (\lambda + \varepsilon + \mu)S \quad (6)$$

$$\frac{dV}{dt} = \phi\pi N + \rho\Lambda + \varepsilon S - ((1-\theta)\alpha + \omega\theta + \mu)V \quad (7)$$

$$\frac{dE}{dt} = \lambda S - (\sigma + \mu)E \quad (8)$$

$$\frac{dI}{dt} = \sigma E - (\eta + \mu + \delta)I \quad (9)$$

$$\frac{dR}{dt} = \eta I + \omega\theta V - \mu R \quad (10)$$

where λ is the force of infection given by

$$\lambda = \frac{\beta c I}{N} \quad (11)$$

The total population size is:

$$N = S + V + E + I + R$$

Where by adding the system of equations (6)-(10) we get:

$$\begin{aligned} \frac{dN}{dt} &= \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\ \frac{dN}{dt} &= \Lambda + (\pi - \mu)N - \delta I \end{aligned} \quad (12)$$

3.1.4. The Basic Reproduction Number, R_0

Epidemiologists have always been interested in finding the basic reproduction number of an emerging disease because this threshold parameter can tell whether a disease will die out or persist in a population. Denoted by R_0 , this parameter is arguably the most important quantity in infectious disease epidemiology. It is defined as the average number of new cases (infections) produced by a single infective when introduced into a susceptible population. It is one of the first quantities estimated for emerging infectious diseases in outbreak situations (Diekmann et al, 2009). It is a key

epidemiological quantity, because it determines the size and duration of epidemics and is an important factor in determining targets for vaccination coverage (Graiss et al, 2006). The basic reproduction number is sought after principally because:

If $R_0 < 1$, then throughout the infectious period, each infective will produce less than one new infective on the average. This in turn implies that the disease will die out as the DFE is stable.

If $R_0 > 1$, then throughout the infectious period, each infective will produce more than one new infective on the average. This in turn implies that the disease will persist as the DFE is unstable. In other words, there will be an outbreak.

If R_0 can be determined, then the transmission parameters which will force R_0 to be less than or greater than 1 can easily be identified and control measures effectively designed.

Next, we shall find the Basic Reproduction Number of the system using the next generation method [6] and we obtain the basic reproduction number denoted by R_0 equation (13) below:

$$R_0 = \frac{\beta c \sigma (\pi + a)}{\mu (\sigma + \mu) (\eta + \delta + \mu)} \quad (13)$$

3.2. Formulation of Stochastic Mathematical Model

In this section we will transform the deterministic model to stochastic model. The corresponding Stochastic Differential Equations model for control of the transmission dynamics of measles with vaccination will be formulated by construction of equivalent Stochastic Differential Equations Models [13].

Let X_1, X_2, X_3, X_4, X_5 denote the number of individuals for S, E, I, R and V respectively

Thus we can have

$$\frac{dX_1}{dt} = (1 - \phi)\pi N + (1 - \rho)\Lambda + (1 - \theta)\alpha X_5 - \lambda X_1 - \varepsilon X_1 - \mu X_1 \quad (14)$$

$$\frac{dX_2}{dt} = \lambda X_1 - \sigma X_2 - \mu X_2 \quad (15)$$

$$\frac{dX_3}{dt} = \sigma X_2 - \eta X_3 - (\mu + \delta) X_3 \quad (16)$$

$$\frac{dX_4}{dt} = \eta X_3 + \omega \theta X_5 - \mu X_4 \quad (17)$$

$$\frac{dX_5}{dt} = \phi \pi N + \rho \Lambda + \varepsilon X_1 - (1 - \theta)\alpha X_5 - \omega \theta X_5 - \mu X_5 \quad (18)$$

Define $X = [X_1 \ X_2 \ X_3 \ X_4 \ X_5]$, to transform the above deterministic model we need to compute the expectations $E[\Delta X]$ and $E[\Delta X \Delta X^T]$. The table below contains the possible changes of the process together with their associated transition probabilities.

Table 4. Possible changes of processes and their associated transition probabilities.

POSSIBLE CHANGES	PROBABILITIES
$(\Delta X)_1 = [1 \ 0 \ 0 \ 0 \ 0]^T$	$p_1 = ((1 - \phi)\pi N + (1 - \rho)\Lambda)$
$(\Delta X)_2 = [-1 \ 0 \ 0 \ 0 \ 0]^T$	$p_2 = \mu X_1$
$(\Delta X)_3 = [-1 \ 1 \ 0 \ 0 \ 0]^T$	$p_3 = (\beta X_3 X_1 / N)$
$(\Delta X)_4 = [0 \ -1 \ 0 \ 0 \ 0]^T$	$p_4 = \mu X_2$
$(\Delta X)_5 = [0 \ -1 \ 1 \ 0 \ 0]^T$	$p_5 = \sigma X_2$
$(\Delta X)_6 = [0 \ 0 \ -1 \ 0 \ 0]^T$	$p_6 = (\mu + \delta) X_3$
$(\Delta X)_7 = [0 \ 0 \ -1 \ 1 \ 0]^T$	$p_7 = \eta X_3$
$(\Delta X)_8 = [0 \ 0 \ 0 \ -1 \ 0]^T$	$p_8 = \mu X_4$
$(\Delta X)_9 = [0 \ 0 \ 0 \ 0 \ 1]^T$	$p_9 = (\phi \pi N + \rho \Lambda)$
$(\Delta X)_{10} = [-1 \ 0 \ 0 \ 0 \ 1]^T$	$p_{10} = \varepsilon X_1$
$(\Delta X)_{11} = [0 \ 0 \ 0 \ 1 \ -1]^T$	$p_{11} = \omega \theta X_5$
$(\Delta X)_{12} = [1 \ 0 \ 0 \ 0 \ -1]^T$	$p_{12} = (1 - \theta)\alpha X_5$
$(\Delta X)_{13} = [0 \ 0 \ 0 \ 0 \ -1]^T$	$p_{13} = \mu X_5$

From the table above we formulate three systems of SDEs that have the same Forward Kolmogorov Differential equation and sample paths:

First SDE model:

$$\begin{cases} dX_t = f(t, X_t)dt + B(t, X_t)dW_t^* \\ X(0) = [X_1(0), X_2(0), X_3(0), X_4(0), X_5(0)]^T \end{cases}$$

where $W_t^* = [W_1^*(t), W_2^*(t), W_3^*(t), W_4^*(t), W_5^*(t)]^T$

is a vector of five independent wiener processes

The drift part $f(t, X_t)$ and the diffusion part $B(t, X_t)$ are computed by the following neglecting higher orders of Δt (Yuan and Allen, 2011)

If we define

$$f(t, X_t) = \frac{E[\Delta X]}{\Delta t} \text{ and } B(t, X_t) = V^{\frac{1}{2}} = \sqrt{\frac{E[\Delta X \Delta X^T]}{\Delta t}}$$

where; $E[\Delta X] = \sum_{i=1}^{13} p_i(\Delta X)_i \Delta t$ and

$$E[\Delta X \Delta X^T] = \sum_{i=1}^{13} p_i(\Delta X)_i (\Delta X)_i^T \Delta t$$

Thus computing from the table we obtain:

$$E[\Delta X] = p_1 \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \Delta t + p_2 \begin{bmatrix} -1 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \Delta t + p_3 \begin{bmatrix} -1 \\ 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \Delta t + \dots + p_{13} \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ -1 \end{bmatrix} \Delta t$$

$$E[\Delta X] = \begin{bmatrix} p_1 - p_2 - p_3 - p_{10} + p_{12} \\ p_3 - p_5 - p_4 \\ p_5 - p_7 - p_6 \\ p_7 + p_{11} - p_8 \\ p_9 + p_{10} - p_{12} - p_{11} - p_{13} \end{bmatrix} \Delta t$$

$$E[\Delta X] = \begin{bmatrix} \Lambda(1-\rho) + N\pi(1-\phi) - \mu X_1 - \frac{\beta X_1 X_3}{N} - \square X_1 + \alpha(1-\theta)X_5 \\ \frac{\beta X_1 X_3}{N} - \sigma X_2 - \mu X_2 \\ \sigma X_2 - \eta X_3 - (\delta + \mu)X_3 \\ \eta X_3 + \theta \omega X_5 - \mu X_4 \\ \Lambda\rho + N\pi\phi + \square X_1 - \alpha(1-\theta)X_5 - \theta \omega X_5 - \mu X_5 \end{bmatrix} \Delta t$$

This is the same as the RHS of the deterministic model.

$$E[\Delta X \Delta X^T] = p_1 \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} [1 \ 0 \ 0 \ 0 \ 0] \Delta t + p_2 \begin{bmatrix} -1 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} [-1 \ 0 \ 0 \ 0 \ 0] \Delta t + p_3 \begin{bmatrix} -1 \\ 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} [-1 \ 1 \ 0 \ 0 \ 0] \Delta t$$

$$+ p_4 \begin{bmatrix} 0 \\ -1 \\ 0 \\ 0 \\ 0 \end{bmatrix} [0 \ -1 \ 0 \ 0 \ 0] \Delta t + \dots + p_{13} \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ -1 \end{bmatrix} [0 \ 0 \ 0 \ 0 \ -1] \Delta t$$

$$E[\Delta X \Delta X^T] = \begin{bmatrix} (p_1 + p_2 + p_3 + p_{10} + p_{12}) & -p_3 & 0 & 0 & -p_{10} - p_{12} \\ -p_3 & p_3 + p_5 + p_2 & -p_5 & 0 & 0 \\ 0 & -p_5 & p_5 + p_6 + p_7 & -p_7 & 0 \\ 0 & 0 & -p_7 & p_7 + p_8 + p_{11} & -p_{11} \\ -p_{10} - p_{12} & 0 & 0 & -p_{11} & (p_9 + p_{10} + p_{11} + p_{12} + p_{13}) \end{bmatrix} \Delta t$$

$$\frac{E[\Delta X \Delta X^T]}{\Delta t} = V = \begin{bmatrix} V_{11} & -\frac{\beta X_1 X_3}{N} & 0 & 0 & -\square X_1 - \alpha(1-\theta)X_5 \\ -\frac{\beta X_1 X_3}{N} & V_{22} & -\sigma X_2 & 0 & 0 \\ 0 & -\sigma X_2 & V_{33} & -\eta X_3 & 0 \\ 0 & 0 & -\eta X_3 & V_{44} & -\theta \omega X_5 \\ -\square X_1 - \alpha(1-\theta)X_5 & 0 & 0 & -\theta \omega X_5 & V_{55} \end{bmatrix}$$

where;

$$V_{11} = \Lambda(1-\rho) + N\pi(1-\phi) + \square X_1 + \mu X_1 + \frac{\beta X_1 X_3}{N} + \alpha(1-\theta)X_5$$

$$V_{22} = \sigma X_2 + \mu X_2 + \frac{\beta X_1 X_3}{N}$$

$$V_{33} = \sigma X_2 + \eta X_3 + (\delta + \mu)X_3$$

$$V_{44} = \eta X_3 + \mu X_4 + \theta \omega X_5$$

$$V_{55} = \Lambda\rho + N\pi\phi + \square X_1 + \alpha(1-\theta)X_5 + \mu X_5 + \theta \omega X_5$$

The resulting SDE is a multidimensional and multiplicative, hence it is hard to simulate. Also, the diffusion coefficient of the formed SDE is a square root of a matrix, that is $B = V^{\frac{1}{2}}$

Second SDE model:

$$\begin{cases} dX_t = f(t, X_t)dt + G(t, X_t)dW_t' \\ X(0) = [X_1(0), X_2(0), X_3(0), X_4(0), X_5(0)]^T \end{cases}$$

where

$$W_t^* = [W_1'(t), W_2'(t), W_3'(t), W_4'(t), W_5'(t), W_6'(t), W_7'(t), W_8'(t), W_9'(t), W_{10}'(t), W_{11}'(t), W_{12}'(t), W_{13}'(t)]^T$$

is a vector of thirteen (13) independent wiener processes

Since matrix V is hermitian (symmetric) and positive definite, cholesky decomposition can be applied obtain matrix G such that; $GG^T = V$

The diffusion matrix G is a 5×13 matrix of the form:

$$G = \begin{bmatrix} \sqrt{\Lambda(1-\rho) + N\pi(1-\phi)} & -\sqrt{\mu X_1} & -\sqrt{\frac{\beta X_1 X_3}{N}} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\sqrt{\square X_1} & 0 & \sqrt{\alpha(1-\theta)X_5} & 0 \\ 0 & 0 & \sqrt{\frac{\beta X_1 X_3}{N}} & -\sqrt{\mu X_2} & -\sqrt{\sigma X_2} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sqrt{\sigma X_2} & -\sqrt{(\delta + \mu)X_3} & -\sqrt{\eta X_3} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \sqrt{\eta X_3} & -\sqrt{\mu X_4} & 0 & 0 & 0 & \sqrt{\theta \omega X_5} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sqrt{\Lambda\rho + N\pi\phi} & \sqrt{\square X_1} & -\sqrt{\theta \omega X_5} & -\sqrt{\alpha(1-\theta)X_5} & -\sqrt{\mu X_5} \end{bmatrix}$$

Third SDE model:

$$\begin{cases} dX_t = f(t, X_t)dt + H(t, X_t)dW_t' \\ X(0) = [X_1(0), X_2(0), X_3(0), X_4(0), X_5(0)]^T \end{cases}$$

where $W_t^* = [W_1(t), W_2(t), W_3(t), W_4(t), W_5(t)]^T$

is a vector of five independent wiener processes

Column reduction can be performed on the matrix ΔX to obtain matrix H such that; $HH^T = V$

The diffusion matrix H is a 5×5 matrix of the form:

$$H = \begin{bmatrix} H_{11} & 0 & 0 & \sqrt{\square X_1} & \sqrt{\alpha(1-\theta)X_5} \\ -\sqrt{\frac{\beta X_1 X_3}{N}} & H_{22} & 0 & 0 & 0 \\ 0 & \sqrt{\sigma X_2} & H_{33} & 0 & 0 \\ 0 & 0 & -\sqrt{\eta X_3 + \mu X_4} & H_{44} & \sqrt{\theta \omega X_5} \\ 0 & 0 & 0 & -\sqrt{\Lambda\rho + N\pi\phi + \square X_1} & H_{55} \end{bmatrix}$$

where;

$$H_{11} = \sqrt{\Lambda(1-\rho) + N\pi(1-\phi) + \mu X_1 + \frac{\beta X_1 X_3}{N}}$$

$$H_{22} = -\sqrt{\mu X_2 + \sigma X_2}$$

$$H_{33} = \sqrt{\eta X_3 + (\delta + \mu)X_3}$$

$$H_{44} = 0$$

$$H_{55} = -\sqrt{\alpha(1-\theta)X_5 + \mu X_5 + \theta \omega X_5}$$

4. Simulation and Discussion

In this chapter we simulate the deterministic and stochastic models formulated.

For simplicity this study will perform simulation the Third SDE model at $\pi = \mu = \delta = \Lambda = 0$ thus we have the following system of non-linear equations:

$$\begin{cases} dX_t = f(t, X_t)dt + H(t, X_t)dW_t \\ X(0) = [X_1(0), X_2(0), X_3(0), X_4(0), X_5(0)]^T \\ \text{where } W_t^* = [W_1(t), W_2(t), W_3(t), W_4(t), W_5(t)]^T \end{cases}$$

is a vector of five independent wiener processes

$$\begin{aligned} \begin{bmatrix} dX_1 \\ dX_2 \\ dX_3 \\ dX_4 \\ dX_5 \end{bmatrix} &= \begin{bmatrix} -\frac{\beta X_1 X_3}{N} - \square X_1 + \alpha(1-\theta)X_5 \\ \frac{\beta X_1 X_3}{N} - \sigma X_2 \\ \sigma X_2 - \eta X_3 \\ \eta X_3 + \theta \omega X_5 \\ \square X_1 - \alpha(1-\theta)X_5 - \theta \omega X_5 \end{bmatrix} dt + \\ &\begin{bmatrix} \sqrt{\frac{\beta X_1 X_3}{N}} & 0 & 0 & \sqrt{\square X_1} & \sqrt{\alpha(1-\theta)X_5} \\ -\sqrt{\frac{\beta X_1 X_3}{N}} & -\sqrt{\sigma X_2} & 0 & 0 & 0 \\ 0 & \sqrt{\sigma X_2} & \sqrt{\eta X_3} & 0 & 0 \\ 0 & 0 & -\sqrt{\eta X_3} & 0 & \sqrt{\theta \omega X_5} \\ 0 & 0 & 0 & -\sqrt{\square X_1} & -\sqrt{\alpha(1-\theta)X_5 + \theta \omega X_5} \end{bmatrix} \begin{bmatrix} dW_1 \\ dW_2 \\ dW_3 \\ dW_4 \\ dW_5 \end{bmatrix} \\ dX_1 &= \left(-\frac{\beta X_1 X_3}{N} - \square X_1 + \alpha(1-\theta)X_5 \right) dt + \left(\sqrt{\frac{\beta X_1 X_3}{N}} dW_1 + \sqrt{\square X_1} dW_4 + \sqrt{\alpha(1-\theta)X_5} dW_5 \right) \\ dX_2 &= \left(\frac{\beta X_1 X_3}{N} - \sigma X_2 \right) dt - \left(\sqrt{\frac{\beta X_1 X_3}{N}} dW_1 + \sqrt{\sigma X_2} dW_2 \right) \\ dX_3 &= (\sigma X_2 - \eta X_3) dt + (\sqrt{\sigma X_2} dW_2 + \sqrt{\eta X_3} dW_3) \\ dX_4 &= (\eta X_3 + \theta \omega X_5) dt + (-\sqrt{\eta X_3} dW_3 + \sqrt{\theta \omega X_5} dW_5) \\ dX_5 &= (\square X_1 - \alpha(1-\theta)X_5 - \theta \omega X_5) dt - (\sqrt{\square X_1} dW_4 + \sqrt{\alpha(1-\theta)X_5 + \theta \omega X_5} dW_5) \end{aligned}$$

Table 5. Value of Parameters Used in Model.

PARAMETER	DESCRIPTION	VALUE/RANGE	SOURCE
π	Per Capita birth rate	0.02755 per year	[9]
ϕ	Proportions of newborns who are vaccinated	0.5 also varies with scenario (0.0 – 1.0)	[10]
ρ	Proportions of immigrants who are vaccinated	0.7 also varies with scenario (0.0 – 1.0)	[10]
a	Arrival rate	0.02755 per year	[9]
c	Per Capita contact rate	0.09091 per year	[9]
δ	Death due to disease	0.125 per year	[4]
μ	Per Capita natural mortality rate	0.00875 per year	[9]
β	Probability of one infected individual to become infectious	varies with scenario (0.08 – 0.7)	[5]
λ	Force Of Infection, $\lambda = \frac{\beta c I}{N}$	0.096 per year	[10]
σ	Progression rate from latent to infectious	0.125 per year	[9]
η	Recovery rate of treated infectious individuals	0.14286 per year varies with scenario (0.0 – 1.0)	[9]
α	The rate of waning of first dose of vaccine	0.167 per year	[10]
ω	The rate of receiving second dose of vaccine	0.8 per year	[10]
ε	Proportion of individuals who received a first dose of vaccine	0.7 per year varies with scenario (0.0 – 1.0)	[10]
θ	Proportion of individuals who received a second dose of vaccine	0.5 varies with scenario (0.0 – 1.0)	[10]

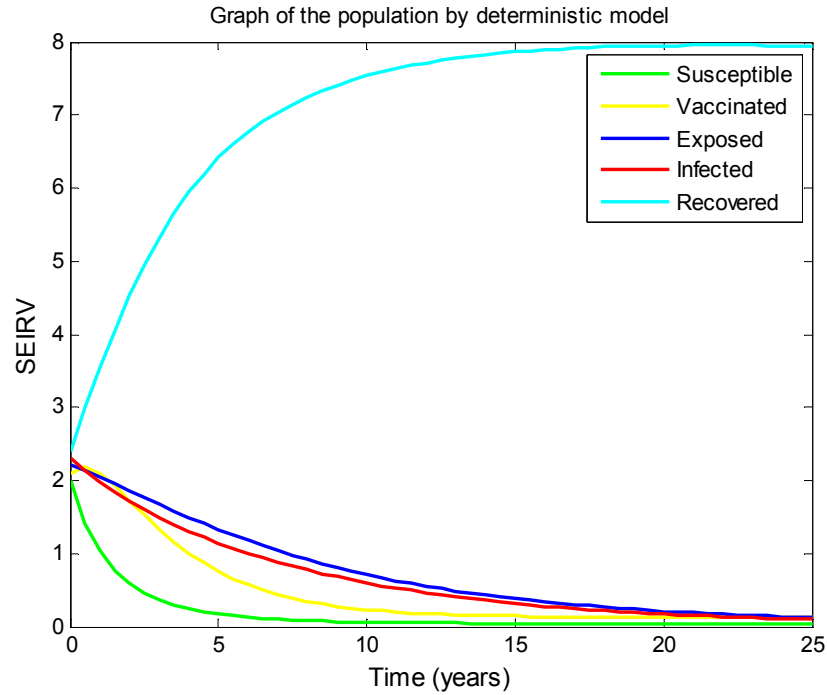


Figure 2. Graph of the population by deterministic model.

From Figure 2 we observe that individuals who have received first and second dose of vaccine and those who have been treated which comprise the recovered population in the sense that they can't be infected is increasing hence the infectious disease is controlled in the population.

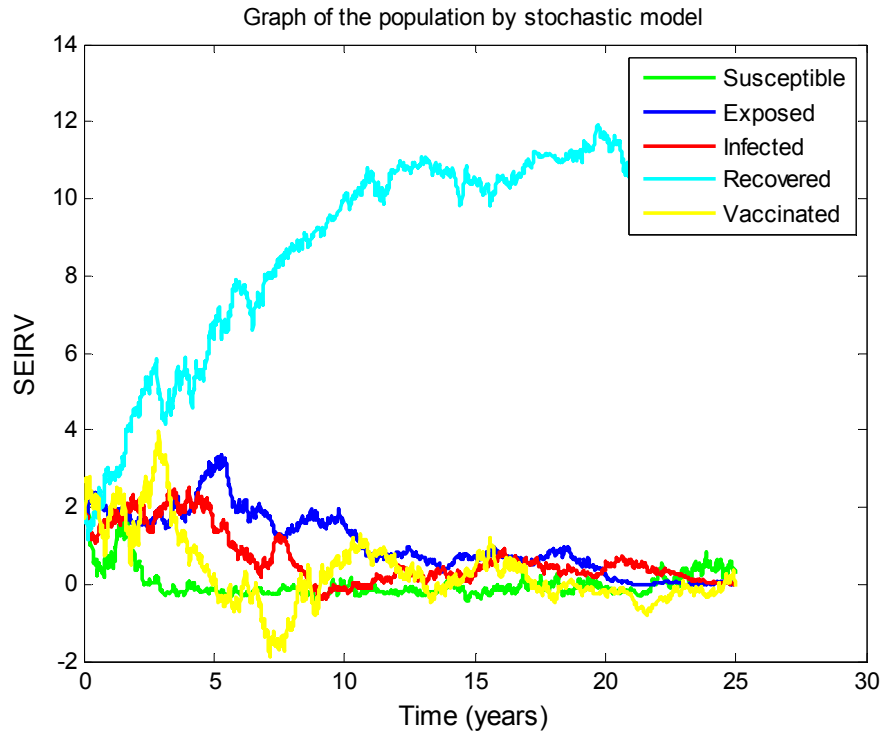


Figure 3. Graph of the population by stochastic model.

The Figure 3 shows that Susceptible population is decreasing while the exposed and infected ones are increasing from the beginning till a certain time, t where it starts decreasing to be zero. This means that vaccination is controlling the infectious disease and eradicated to die out from the population hence the recovered population is increasing.

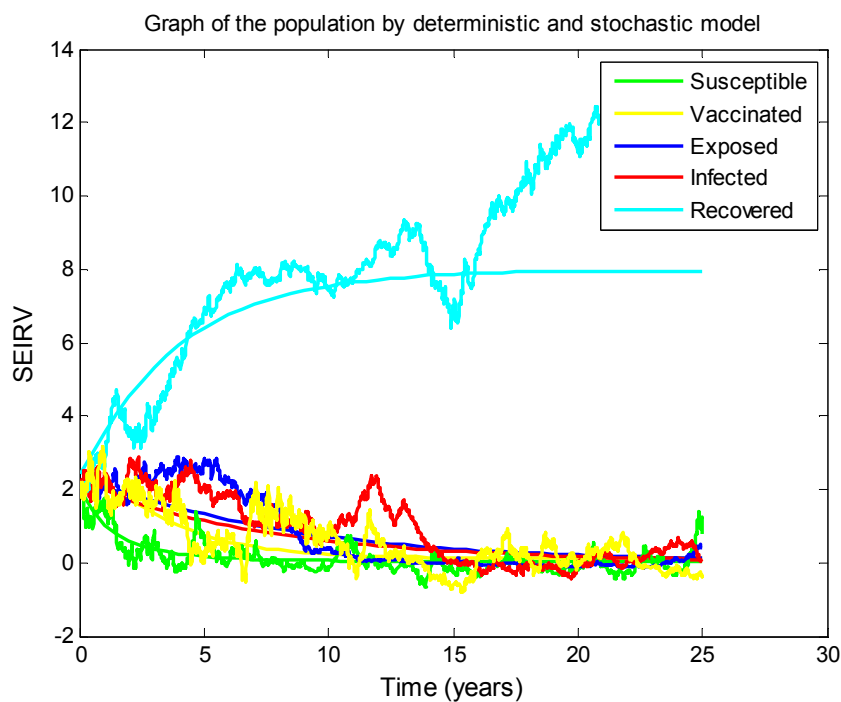


Figure 4. Graph of the population by deterministic and stochastic model.

Figure 4 shows that the stochastic model describe the dynamics of measles transmission more effectively.

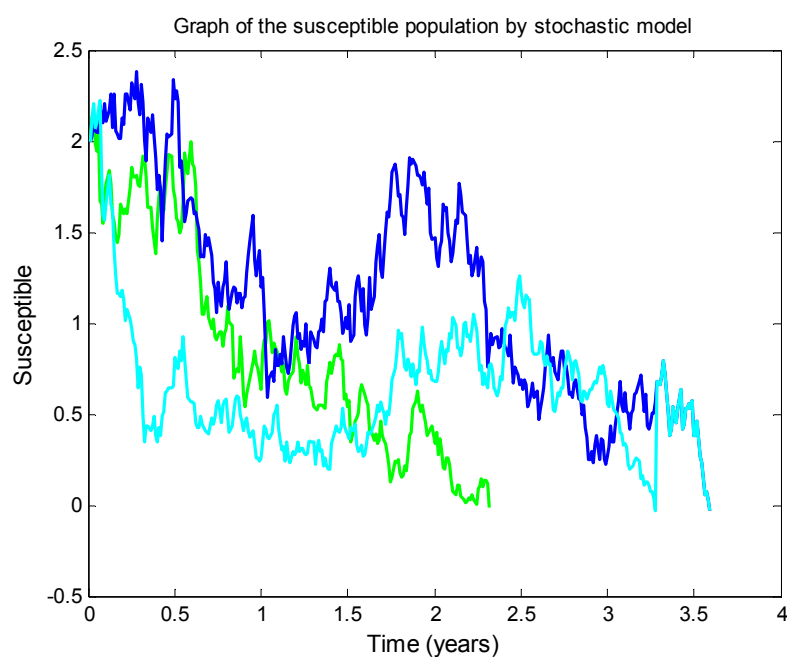


Figure 5. Graph of the susceptible population by stochastic model.

Figure 5 shows that the Susceptible population varies as time goes on but eventually decreases hence the disease is controlled in the population.

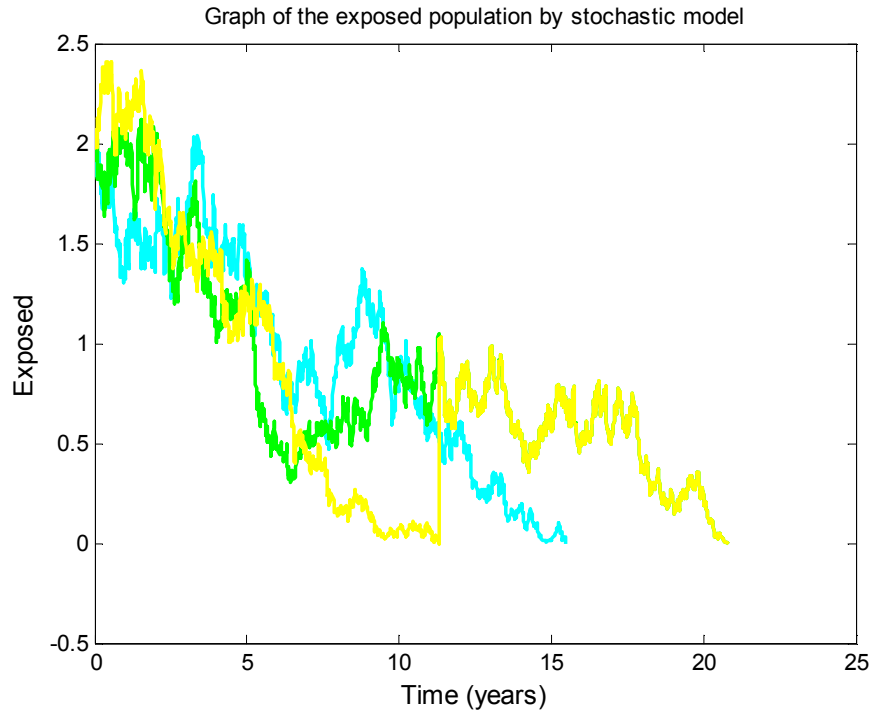


Figure 6. Graph of the exposed population by stochastic model.

Figure 6 shows that the exposed population is decreasing since vaccination is controlling the spread of the disease.

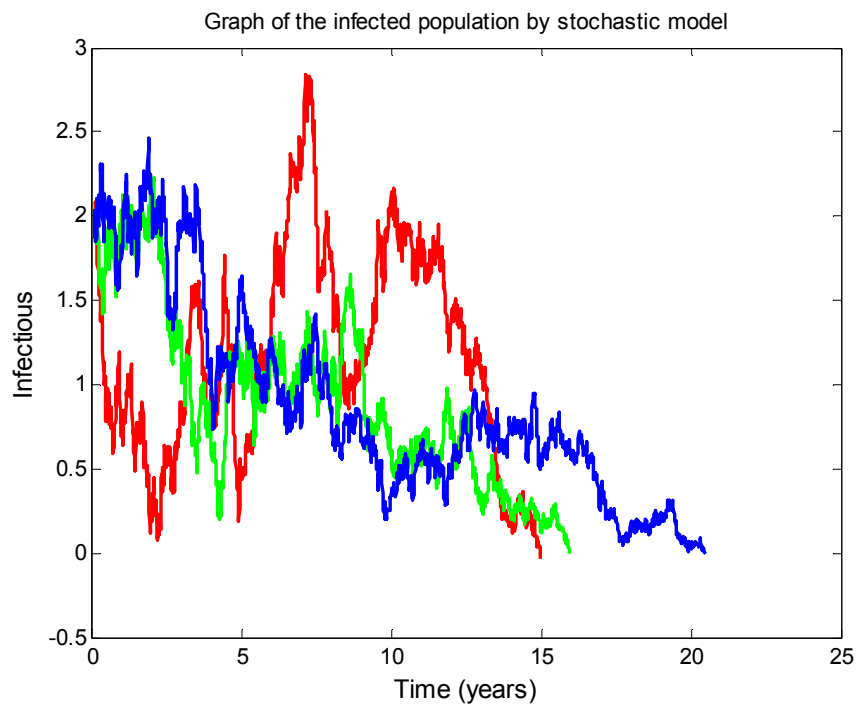


Figure 7. Graph of the infected population by stochastic model.

Figure 7 shows that the infectious population increasing and decreasing in the population till a certain time where it starts decreasing to be zero because of vaccination control strategy.

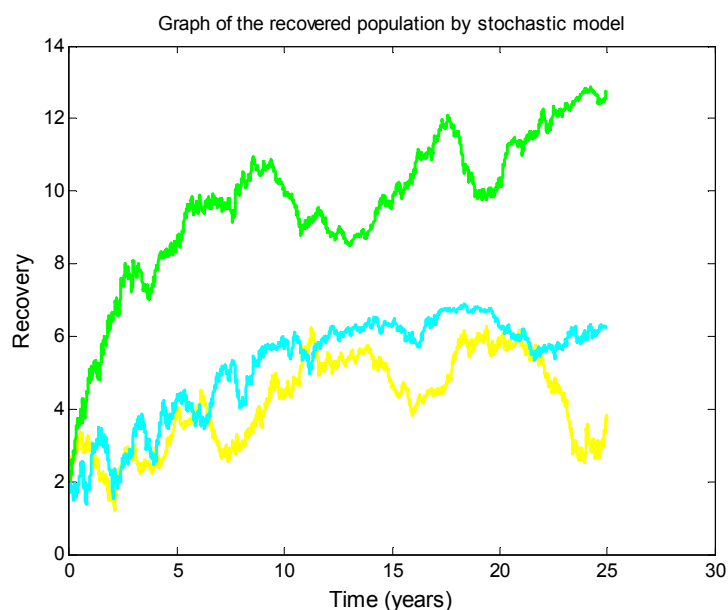


Figure 8. Graph of the recovered population by stochastic model.

Figure 8 shows the variation of the recovered population which shows the vaccination strategy is controlling the disease, since as time goes on the recovered population is increasing.

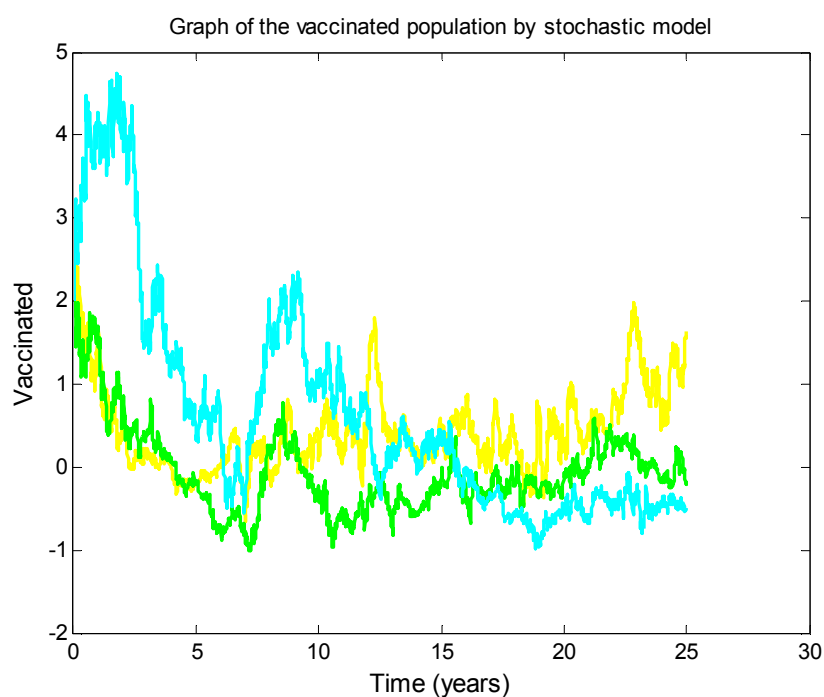


Figure 9. Graph of the vaccinated population by stochastic model.

Figure 9 shows that the variation of the vaccinated population

5. Conclusion, Recommendation and Future Work

In this chapter we provide conclusion and recommendation of the project.

5.1. Conclusion

The study has shown the effectiveness of stochastic analysis in studying the dynamics of measles compared to deterministic analysis.

5.2. Recommendation

This study recommend the use of stochastic analysis in studying dynamics of infectious diseases.

5.3. Future Work

Based on the model of this study, it is proposed that future work should consider the following:

- i. Application of other stochastic approaches such as Monte Carlo Markov Chains
- ii. Use of more accurate numerical schemes like Runge-kutta and others

List of Abbreviations and Symbols

AIDS	Acquire Immune Deficiency Syndrome
CFRs	Case- Fatality Ratios
CTMC	Continuous Time Markov Chain
DTMC	Discrete Time Markov Chain
HIV	Human Immunodeficiency Virus
MCC	Measles Control Campaign
MCMC	Monte Carlo Markov Chain
MCV1	First Dose of Measles Containing Vaccine
MCV2	Second Dose of Measles Containing Vaccine
MMR	Measles Mumps-Rubella
ODEs	Ordinary Differential Equations
Pdf	Probability Density Function
SEIR	Susceptible Latent Period Infectious Recovery
SIA	Supplemental Immunization Activity
SDEs	Stochastic Differential Equations
SIR	Susceptible Infectious Recovery
U.S	United States
UNICEF	United Nation Children's Fund
WHO	World Health Organization

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