

Mathematical Model for the Dynamics of Measles under the Combined Effect of Vaccination and Measles Therapy

Christopher Obumneke, Ibrahim Isa Adamu and Shamaki Timothy Ado

Department of Mathematics
Moddibo Adama University of Technology, Yola
P.M.B 2076, Yola Adamawa State Nigeria

ABSTRACT

The most important factor in the control of the spread of infectious disease is to understand the dynamics of the disease in a population; we can then develop strategies for the control of the disease. Available literature showed that; most authors worked on mathematical models for the dynamics of measles under the influence of Vaccination or other forms of therapies separately at the exposed class. In this work, we developed a mathematical model for the dynamics of measles under the combined effect of vaccination at the susceptible class, and administering measles drug therapy to screened infected individuals in the exposed class. In developing the model, we adopted compartmental modeling approach, where we partition the population into; Susceptible, Vaccinated, Exposed, Infected and Recovered subpopulations. The result of the model analysis showed that the model has a unique disease-free equilibrium which is locally asymptotically stable whenever the basic reproduction number, R_0 is less than one ($R_0 < 1$). We also carried out numerical experiment using data from Momoh et al. (2013), the results of the numerical experiments revealed that eradicating measles is more efficient if susceptible individuals are vaccinated and followed by drug therapy to screened infected individuals in the exposed class.

Keywords: Disease-Free Equilibrium, Infectious Disease, Jacobian Matrix, Reproduction Number, Vaccination, Dynamics, Population.

1. INTRODUCTION

Measles is a serious and highly infectious viral disease, which may lead to hospitalization or in some cases, death. It is caused by one serotype, classified as a member of the genus morbillivirus in the paramyxoviridae viral family. Humans are the only natural host for measles virus. (Chin, 2000). Individuals infected with Measles may develop complications like; diarrhea, pneumonia and encephalitis (i.e. infections of the brain) (Plotkin and Orenstein, 2004; Norrby and Oxman, 1990; Perry and Halsey, 2004; McLean and Carter, 1990; Miller, 1978).

Although immunization against measles using MMR (Measles Mump Rubella) vaccine has been the best preventive measures to eradicate the disease, yet in developed countries, 2 to 3 cases per 1,000 results in death and increases from 3 to 5 cases per 1,000 in developing countries (WHO, 2000). Measles has been reported to be the major cause of childhood morbidity and mortality in Nigeria; 212,183 and 168,107 cases were recorded in 2000 and 2001 respectively. For instance in 2005, Adamawa State, experienced 3,974 cases and 238 measles-deaths Ihekweazu et al., (2005).

Robert and Tobias (1999) developed a deterministic SIR mathematical model with varying immunization strategy in a population with size and age structure similar to that of New Zealand They used the model to investigate the prediction and prevention of measles in New Zealand. The model consists of two components, viz; predictive model component

and prevention model component. Robert and Tobias (1999) successfully predicted an epidemic in 1997 and their result was instrumental to the decision to carry out an intensive MMR immunization campaign in that year.

Kassem and Ndam (2010) in their work titled "A Stochastic Modeling of Recurrent Measles Epidemics", developed a simple stochastic Mathematical model for the dynamics of Measles with multidimensional diffusion process. In developing their model, they considered and partitioned the population into; susceptible, latent (exposed), infected and removed classes, they assumed, among other things that stochastic effects arise in the process of infection of susceptible individuals. The results of their simulation seemed to agree with the historical pattern of measles in Nigeria.

Momoh et al., (2013), developed a model that divides the total population (N) into four classes: Susceptible (S), Exposed (E), infected (I) and Recovered (R) classes, they incorporated testing and measles therapy into the dynamics at the latent (exposed) period to investigate the control of measles epidemiology at latent period. They assumed that both recovered individuals from exposed class as a result of testing and measles therapy and naturally recovered infected individuals becomes permanently immune, and developed a non-linear first order ordinary differential equation. The result of their stability analysis showed that the system is asymptotically stable.

Bolarin (2014), in his study, formulated a compartmental model by incorporating vaccination to examine the dynamics of measles to determined the required vaccination coverage and dosage that will guarantee eradication of measles within a population. He assumed that vaccinated individuals acquire

permanent immunity and move to recovered class. The model was expressed as a system of ordinary differential equations. Bolarin (2014) examined the stability of the equilibrium state as well as the basic reproductive number R_0 , and found out that the disease free equilibrium state is locally and globally stable when $R_0 \leq 1$, and the endemic equilibrium state is stable if $R_0 > 1$. It was also noted that the effective reproductive number R_{0v} under vaccination approaches zero as the proportion of successfully vaccinated individual increases. Their study suggested the required vaccination dosage and coverage that can lead to measles eradication.

Mose *et al.*, (2014) developed a mathematical Model for the dynamics of measles incorporating Vaccine at susceptible class. In developing their model they assumed a population with variable size, and that vaccinated individuals acquire permanent immunity and move to recovered class serve as framework for the study. Their model consists of a set of Ordinary Differential Equation (O.D.E) and Partial Differential Equations (P.D.E). They carried out numerical and qualitative analyses of the model by varying the values of the state variables. The result of their study showed that the model has the disease-free equilibrium which is locally asymptotically stable for $R_0 < 1$ and unstable for $R_0 > 1$.

From available literature, combined vaccination of susceptible individuals and testing /administering measles therapy as control strategy was not studied; also most authors assumed that vaccinated individuals acquire permanent immunity. However, the reality is Vaccines have efficacy period, after which a vaccinated individual loses immunity. In this paper, we consider the combine effect of vaccination of susceptible individuals and testing and administering measles therapy at latency period (exposed) by incorporating lost of immunity due to drop in efficacy of vaccine.

2. METHODS

2.1. Assumptions

The following assumptions were made:

- i. Recruitment into the population is by birth only
- ii. Newly born (recruited) babies are free from the disease but susceptible
- iii. The parameters and variables used in the model are considered non-negative
- iv. The recruitment into the susceptible compartment is a constant
- v. Transition into and out of any compartment is governed by a specified rate
- vi. Individuals acquire permanently immunity only by natural recovery and are assumed to removed from the population to the population remain completely susceptible
- vii. Vaccinated individual acquires temporary immunity which may deteriorate due to drop in efficacy of Vaccine, hence the individual return to the susceptible class.
- viii. Exposed individual that has been tested and received measles therapy remain asymptomatic until they recover.

- ix. Natural death and death from Measles occur at a constant rates
- x. The members of the study population interacts freely
- xi. Immigration are not allowed.
- xii. Population is large, finite and panmictic

2.2. Notations

Variables

S (t) =Number of susceptible individuals at time t
 V (t) =Number of vaccinated individuals at time t
 E (t) = Number of exposed individuals at time t
 I (t) =Number of infectious individuals at time t
 R (t) =Number of recovered individuals at time t
 N (t) =Total population

Parameters

B = Birth rate
 μ = Natural death rate
 γ = Recovery rate
 σ = Rate of testing and administering Measles therapy
 α = Rate of becoming infectious
 β = Contact rate of susceptible class
 λ =Rate of vaccination
 ϕ = rate of immunity failure
 δ =Disease induced death rate

3. MODEL FORMULATION

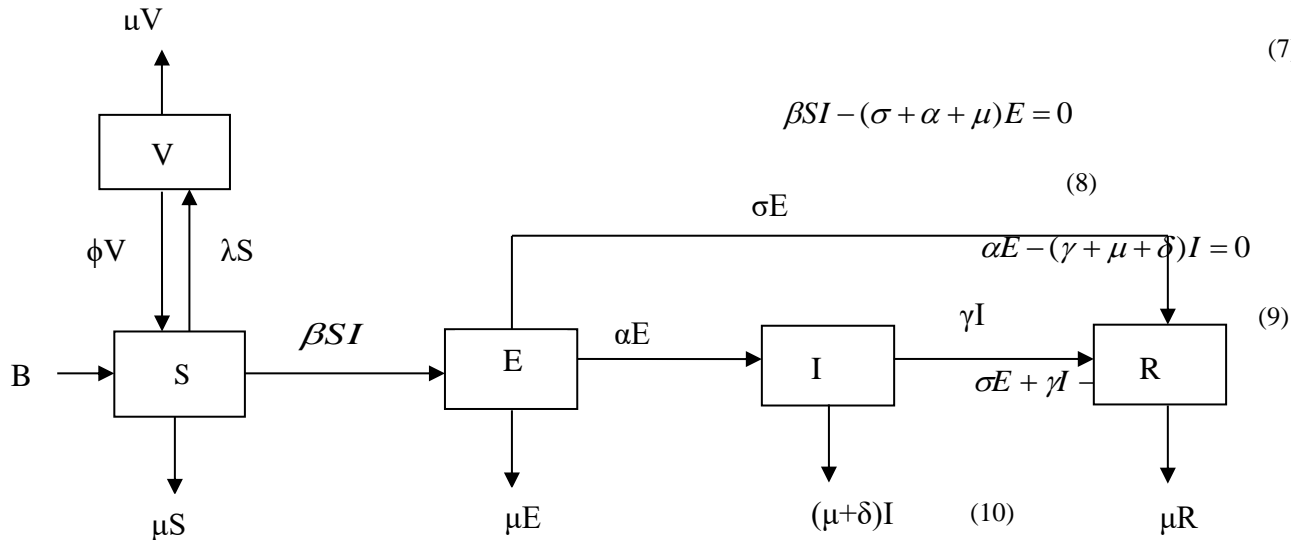
3.1. Compartmentalization of the Population

3.02. Natural History Dynamics of a Population In The Face Of

For the purpose of describing the natural history dynamics, we compartmentalized the Population into five compartments namely; Susceptible (S), Vaccinated (V), Exposed (E), Infectious (I) and Recovered (R). Now, Individuals are recruited into the susceptible compartment (S) at constant birth rate B, when a susceptible individual come into contact with the virus, he may be infected. The infected individual remains infected and infectious for some period before recovery (natural or through treatment) or die naturally or as result of the disease (Chin, 2000). Infected individuals may develop complications like; diarrhea, pneumonia and encephalitis (i.e. infections of the brain) (Plotkin and Orenstein, 2004; Norrby and Oxman, 1990; Perry and Halsey, 2004; McLean and Carter, 1990; Miller, 1978).

The above dynamics results into the following compartmental mass dynamics: The Susceptible population (S) diminishes by λS , βS , μS due to vaccination, exposure to Measles, and natural death, at the appropriate rates λ , β and μ respectively, it also increases by ϕS and B due to loss of vaccine immunity at a rate ϕ , and a birth rate respectively. The vaccinated compartment (V) increases by λS due to vaccination at a rate λ , and decreases by ϕV and μV due to loss immunity and natural death, at rates ϕ , and μ respectively. The exposed compartment (E) increases

by βS due to contact of susceptible individual(s) with infectious individual(s) at a rate β , and decreases by αE , μE and σE due to infection, natural death and drug therapy, at rates α , μ and σ respectively. The infected compartment (I) increases by αE due to infection at rate α , and diminishes by γI , μI and δI due to recovery, natural death, and death due to infection, at rates γ , μ and δ respectively. The recovered compartment (R) increases by γI , σI due to natural recovery and drug therapy, at rates γ and σ , respectively. R reduces by μR due to natural death. The above dynamics can be schematically represented as follows:



3.2. Model Equations

Based on the above assumptions and dynamics of Measles we obtained the following:

$$\frac{dS}{dt} = B + \phi V - \beta SI - (\lambda + \mu)S \tag{1}$$

$$\frac{dV}{dt} = \lambda S - (\phi + \mu)V \tag{2}$$

$$\frac{dE}{dt} = \beta SI - (\sigma + \alpha + \mu)E \tag{3}$$

$$\frac{dI}{dt} = \alpha E - (\gamma + \mu + \delta)I \tag{4}$$

$$\frac{dR}{dt} = \sigma E + \gamma I - \mu R \tag{5}$$

Where $\alpha, \beta, \gamma, \delta, \sigma, \mu, \phi, \lambda$ and S, E, V, R, I are rates and state variables as defined above

4. STABILITY ANALYSIS

4.1. The Existence of Disease Equilibrium State of the Model

At equilibrium point, the system becomes

$$B + \phi V - \beta SI - (\lambda + \mu)S = 0 \tag{6}$$

$$\lambda S - (\phi + \mu)V = 0 \tag{7}$$

$$\beta SI - (\sigma + \alpha + \mu)E = 0 \tag{8}$$

$$\alpha E - (\gamma + \mu + \delta)I = 0 \tag{9}$$

$$\sigma E + \gamma I - \mu R = 0 \tag{10}$$

4.2. Disease Free Equilibrium (DFE) Point of the Model

The disease free equilibrium state is given by;

$$B + \phi V - (\lambda + \mu)S = 0 \tag{11}$$

$$\lambda S - (\phi + \mu)V = 0 \tag{12}$$

$$E = 0 \tag{13}$$

$$R = 0 \tag{14}$$

Solving equation (11) – (14) simultaneously, we obtained the disease free equilibrium point

$$G_0 = (S_0, V_0, E_0, I_0, R_0) = G_0 = \left(\frac{B(\phi + \mu)}{((\lambda + \mu)(\phi + \mu) - \phi\lambda)}, \frac{\lambda B}{(\lambda + \mu)(\phi + \mu) - \phi\lambda}, 0, 0, 0 \right)$$

4.3. Endemic Equilibrium (EE) Point of the Model

The endemic equilibrium point is given as $G^* = \{S^*, V^*, E^*, I^*, R^*\}$, where;

$$S^* = \frac{(\sigma + \alpha + \mu)(\gamma + \mu + \delta)}{\alpha\beta}$$

$$V^* = \frac{\lambda(\sigma + \alpha + \mu)(\gamma + \mu + \delta)}{\alpha\beta(\phi + \mu)} \quad I^* = \frac{\alpha\beta B(\phi + \mu) + \phi\lambda(\sigma + \alpha + \mu)(\mu + \delta + \gamma)}{\beta(\phi + \mu)(\sigma + \alpha + \mu)(\mu + \delta + \gamma)} - \left(\frac{\lambda + \mu}{\beta} \right)$$

$$E^* = \frac{\alpha\beta B(\phi + \mu) + \phi\lambda(\sigma + \alpha + \mu)(\mu + \delta + \gamma)}{\beta(\phi + \mu)(\sigma + \alpha + \mu)} - \left(\frac{\lambda + \mu(\mu + \delta + \gamma)}{\alpha\beta} \right), \text{ and}$$

$$R^* = \frac{\sigma\alpha B}{\mu(\sigma + \alpha + \mu)(\mu + \delta + \gamma)} + \frac{\phi\lambda\sigma(\mu + \delta + \gamma)}{\mu\beta(\phi + \mu)} - (\lambda + \mu) \left(\frac{\sigma\alpha + \gamma(\mu + \delta + \gamma)}{\mu\alpha\beta} \right) + \frac{\alpha\gamma B}{\mu(\sigma + \alpha + \mu)}$$

4.4. Basic Reproduction Number of the Model

We compute the reproduction number of our model using the next generation matrix method. First of all, measles has two disease states namely; asymptomatic (exposed) and symptomatic (infectious). Therefore we focus on their equations only as follows:

$$\frac{dE}{dt} = \beta SI - (\sigma + \alpha + \mu)E$$

$$\frac{dI}{dt} = \alpha E - (\gamma + \mu + \delta)I$$

Transfer of susceptible individuals into exposed compartment as a result of new infection is given by βSI and transfer of susceptible individuals into infectious compartment as a result of new infection is 0. Thus the column matrix of new infections into compartment E, and I from S denoted by M is given as;

$$M = \begin{pmatrix} \beta SI \\ 0 \end{pmatrix}$$

Transfer of individuals into and out of the exposed compartment by any other means is given by $(\sigma + \alpha + \mu)E$ and transfer of individuals into and out of infectious compartment by any other means is given by $-\alpha E + (\gamma + \mu + \delta)I$. Thus, the

column matrix of transfer of individuals by any other means into compartment E, and I, denoted by N is given as;

$$N = \begin{pmatrix} (\sigma + \alpha + \mu)E \\ -\alpha E + (\gamma + \mu + \delta)I \end{pmatrix}$$

Taking the partial derivatives of M and N with respect to E and I to form a square matrices F and V as follows;

$$F = \begin{pmatrix} \frac{\partial(\beta SI)}{\partial E} & \frac{\partial(0)}{\partial E} \\ \frac{\partial(\beta SI)}{\partial I} & \frac{\partial(0)}{\partial I} \end{pmatrix}$$

And

$$V = \begin{pmatrix} \frac{\partial(\sigma + \alpha + \mu)E}{\partial E} & \frac{\partial(-\alpha E + (\gamma + \mu + \delta)I)}{\partial E} \\ \frac{\partial(\sigma + \alpha + \mu)E}{\partial I} & \frac{\partial(-\alpha E + (\gamma + \mu + \delta)I)}{\partial I} \end{pmatrix}$$

Hence,
$$F = \begin{pmatrix} 0 & 0 \\ \beta S & 0 \end{pmatrix}$$

And

$$V = \begin{pmatrix} (\sigma + \alpha + \mu) & -\alpha \\ 0 & (\gamma + \mu + \delta) \end{pmatrix}$$

Now, taking the inverse of matrix V; leads to

$$V^{-1} = \frac{1}{(\sigma + \alpha + \mu)(\lambda + \mu + \delta)} \begin{pmatrix} (\gamma + \delta + \mu) & \alpha \\ 0 & (\sigma + \alpha + \mu) \end{pmatrix}$$

Hence

$$FV^{-1} = \begin{pmatrix} \frac{\alpha\beta S}{(\sigma + \alpha + \mu)(\gamma + \mu + \delta)} & 0 \\ \frac{\beta S}{(\gamma + \mu + \delta)} & 0 \end{pmatrix}$$

Evaluating $Det(FV^{-1} - mI) = 0$, we have the characteristic equation given as

$$m^2 - \frac{\alpha\beta S}{(\sigma + \alpha + \mu)(\gamma + \mu + \delta)} m = 0, \Rightarrow$$

$$m_1 = \frac{\alpha\beta S}{(\sigma + \alpha + \mu)(\gamma + \mu + \delta)} \text{ or } m_2 = 0.$$

Thus, the spectral radius (dominant Eigen value) of the matrix is m_1 . Hence the basic reproduction number in the presence of supportive treatment at exposed class and vaccination of susceptible class is given by,

$$\mathfrak{R}_0 = \frac{\alpha\beta B(\phi + \mu)}{(\lambda + \mu)(\phi + \mu) - \phi\lambda[(\sigma + \mu + \alpha)(\gamma + \mu + \delta)]}$$

$$J(S_0, V_0, E_0, I_0, R_0) = \begin{vmatrix} -(\lambda + \mu) & \phi & 0 & \frac{-\beta B(\phi + \mu)}{(\lambda + \mu)(\phi + \mu) - \phi\lambda} & 0 \\ \lambda & -(\phi + \mu) & 0 & 0 & 0 \\ 0 & 0 & -(\sigma + \mu + \alpha) & \frac{\beta B(\phi + \mu)}{(\lambda + \mu)(\phi + \mu) - \phi\lambda} & 0 \\ 0 & 0 & \alpha & -(\gamma + \mu + \delta) & 0 \\ 0 & 0 & \sigma & \gamma & -\mu \end{vmatrix}$$

4.5. Stability Analyses of the Disease-Free Equilibrium Point of the Model

Let

$$F_1 = B + \rho V - \beta SI - (\lambda + \mu)S \tag{15}$$

$$F_2 = \lambda S - (\phi + \mu + \rho)V \tag{16}$$

$$F_3 = \beta SI - (\sigma + \alpha + \mu)E \tag{17}$$

$$F_4 = \alpha E - (\gamma + \mu + \delta)I \tag{18}$$

$$F_5 = \phi V + \sigma E + \gamma I - \mu R$$

To examine the local stability of the disease-free equilibrium of the model, we obtain the Jacobian matrix of the system above given by;

$$J(S, V, E, I, R) = \begin{vmatrix} \frac{\partial F_1}{\partial S} & \frac{\partial F_1}{\partial V} & \frac{\partial F_1}{\partial E} & \frac{\partial F_1}{\partial I} & \frac{\partial F_1}{\partial R} \\ \frac{\partial F_2}{\partial S} & \frac{\partial F_2}{\partial V} & \frac{\partial F_2}{\partial E} & \frac{\partial F_2}{\partial I} & \frac{\partial F_2}{\partial R} \\ \frac{\partial F_3}{\partial S} & \frac{\partial F_3}{\partial V} & \frac{\partial F_3}{\partial E} & \frac{\partial F_3}{\partial I} & \frac{\partial F_3}{\partial R} \\ \frac{\partial F_4}{\partial S} & \frac{\partial F_4}{\partial V} & \frac{\partial F_4}{\partial E} & \frac{\partial F_4}{\partial I} & \frac{\partial F_4}{\partial R} \\ \frac{\partial F_5}{\partial S} & \frac{\partial F_5}{\partial V} & \frac{\partial F_5}{\partial E} & \frac{\partial F_5}{\partial I} & \frac{\partial F_5}{\partial R} \end{vmatrix} = 0$$

Now evaluating the derivatives at the disease free equilibrium point we obtain.



To support our stability analysis, we state and prove the following proposition

Proposition 4.1.

let $\Omega = (S_0, V_0, E_0, I_0, R_0)$, the disease free equilibrium, then Ω is locally asymptotically stable if $\text{Re}(m_i) \leq 0$ (real part)

$$|J - mI| = \begin{vmatrix} -x - m & \phi & 0 & \frac{-\beta B y}{xy - \phi \lambda} & 0 \\ \lambda & -y - m & 0 & 0 & 0 \\ 0 & 0 & -z - m & \frac{\beta B y}{xy - \phi \lambda} & 0 \\ 0 & 0 & \alpha & -q - m & 0 \\ 0 & 0 & \sigma & \gamma & -\mu - m \end{vmatrix} = 0$$

for all $i=1, 2, 3, \dots$ Where m_i is the eigenvalues of the Jacobian matrix above

Proof

For simplicity we let $x = (\lambda + \mu)$, $y = (\phi + \mu)$, $z = (\sigma + \alpha + \mu)$ and $q = (\gamma + \mu + \delta)$ So that the matrix can be simply as:

Where m is the eigenvalue, computing the determinant we obtained the characteristic equation as follows:

$$(-\mu - m)((-x - m)(-y - m) - \phi \lambda) \left((-z - m)(-q - m) - \frac{\alpha \beta B y}{xy - \phi \lambda} \right) = 0$$

Hence either $-\mu - m = 0$, $(-x - m)(-y - m) - \phi \lambda = 0$ or

$$(-z - m)(-q - m) - \frac{\alpha \beta B y}{xy - \phi \lambda} = 0$$

This implies that $m_1 = -\mu$, $m_2 = -\mu$, $m_3 = -(\lambda + \phi + \mu)$

$$, m_4 = \frac{-(z + q) - \sqrt{(z + q)^2 + 4zqR_0}}{2}$$

$$\text{and } m_5 = \frac{-(z + q) + \sqrt{(z + q)^2 - 4zq(1 - R_0)}}{2}$$

Now m_1, m_2, m_3, m_4 obviously have negative real parts for the eigenvalues for all finite values of $\lambda, \sigma, \mu, \gamma$, and R_0 .

However, $m_5 = \frac{-(z + q) + \sqrt{(z + q)^2 - 4zq(1 - R_0)}}{2}$

will be negative if;

$$\frac{-(z + q) + \sqrt{(z + q)^2 - 4zq(1 - R_0)}}{2} < 0$$

$$\Leftrightarrow (z + q)^2 - 4zq(1 - R_0) < (z + q)^2$$

$$\Leftrightarrow -4zq(1 - R_0) < 0 \Rightarrow 1 - R_0 > 0$$

Therefore, we must have that $R_0 < 1$ for m_5 to be negative; hence the system 15 - 18 is locally and asymptotically stable.

4.6. Numerical Experiment

We showed analytically that the developed model equation is locally and asymptotically stable at the disease free equilibrium point. In this sub-section, we carry out the following two phase numerical experiment of the Model using MATLAB, viz:

1. We show numerically the combine effect of testing and administering measles therapy to exposed individuals and vaccination of susceptible individuals.

2. We compare the results of our developed model with that of Momoh *et al.*, (2013).

INITIAL DATA

Table 1:Initial Values for the Numerical Experiments

Variables	First simulation	Second simulation	Third simulation	Source of Data
S(0)	600	600	600	Estimated
V(0)	400	400	400	Estimated
E(0)	250	250	250	Estimated
I(0)	100	100	100	Estimated
R(0)	50	50	50	Estimated
Parameters				
Values				
B	0.32	0.32	0.32	Momoh <i>et al.</i> , (2013)
α	0.01	0.01	0.01	Momoh <i>et al.</i> , (2013)
β	0.01	0.01	0.01	Momoh <i>et al.</i> , (2013)
σ	0.25	0.5	0.75	Momoh <i>et al.</i> , (2013)
γ	0.2	0.2	0.2	Momoh <i>et al.</i> , (2013)
μ	0.2	0.2	0.2	Momoh <i>et al.</i> , (2013)
λ	0.5	0.75	0.95	Estimated
ϕ	0.05	0.05	0.05	Estimated
δ	0.2	0.2	0.2	Ochoche <i>et al.</i> , (2014)
R_0	0.00019	0.000094	0.000058	

5. RESULT AND DISCUSSION

5.1. Results

In this work, we have developed a mathematical model for the dynamics of Measles under the combined effect of

Vaccination at the susceptible class and drug therapy at the exposed class given by equations (1) to (5) above. We present simulation results and discussion on results as follows;

5.1.1Simulation Results

We give a graphical representation of our experimental results with varying rates λ and σ of vaccination and testing & administering Measles therapy respectively as follows;

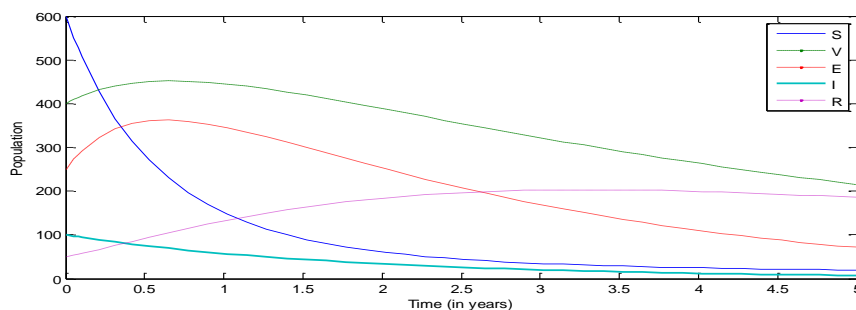


Figure 1: Graph showing the dynamics of measles with 0.5 rate of vaccination and 0.25 rates of testing and administering Measles therapy.

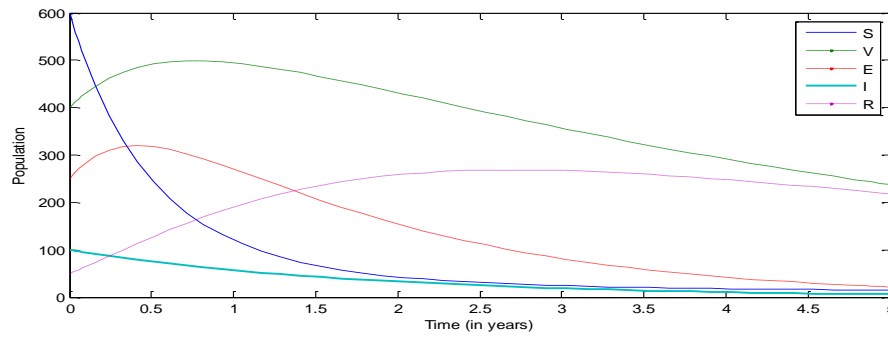


Figure 2: Graph showing the dynamics of measles with 0.75 rate of vaccination and 0.5 rates of testing and administering Measles therapy.

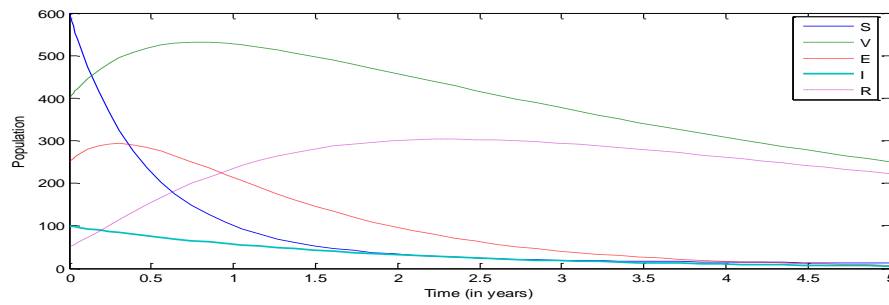


Figure 3: Graph showing the dynamics of measles with 0.95 rate of vaccination and 0.75 rates of testing and administering Measles therapy.

COMPARISON: We compare the existing model dynamics of measles by Momoh *et al.*, (2013) and our developed model

Table 3: Initial Values for the Numerical Experiments of Existing (Momoh *et al.*, (2013)) Model

Variables	Fourth simulation	Fifth Simulation	Sixth Simulation	Seventh simulation
S(0)	600	600	600	600
E(0)	250	250	250	250
I(0)	100	100	100	100
R(0)	50	50	50	50
Parameters				
B	0.32	0.32	0.32	0.32
α	0.01	0.01	0.01	0.01
β	0.01	0.01	0.01	0.01
γ	0.2	0.2	0.2	0.2
μ	0.2	0.2	0.2	0.2
σ	0.25	0.5	0.75	0.5

Source: Momoh *et al.*, (2013)

Table3:Initial Values for the Numerical Experiments of our new Model

Variables	Fourth Simulation	Fifth Simulation	Sixth Simulation	Seventh simulation
S(0)	600	600	600	600
V(0)	400	400	400	400
E(0)	250	250	250	250
I(0)	100	100	100	100
R(0)	50	50	50	50
Parameters				
B	0.32	0.32	0.32	0.32
α	0.01	0.01	0.01	0.01
β	0.01	0.01	0.01	0.01
γ	0.2	0.2	0.2	0.2
μ	0.2	0.2	0.2	0.2
σ	0.25	0.5	0.75	0.5
λ	0.25	0.5	0.75	0.95
ϕ	0.05	0.05	0.05	0.05
δ	0.2	0.2	0.2	0.2

Graphical Comparison between model by Momoh *et al.*,(2013) and our new Model

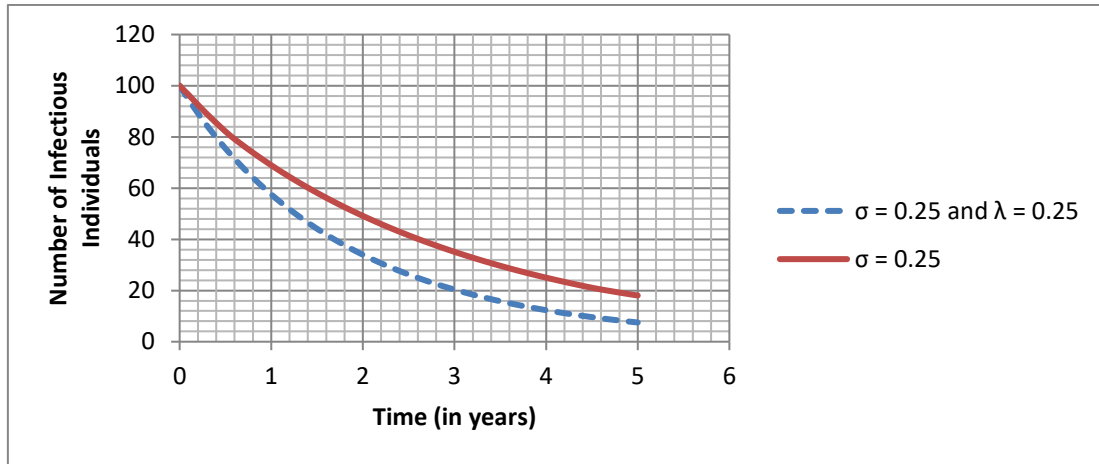


Figure 4: Solid line shows the dynamics of measles by Momoh *et al.*,(2013)'s model with 0.25 rate of testing and administering Measles therapy, while the dotted line shows the dynamics of measles by our model with 0.25 rate of vaccination and 0.25 rate of testing and administering Measles therapy.

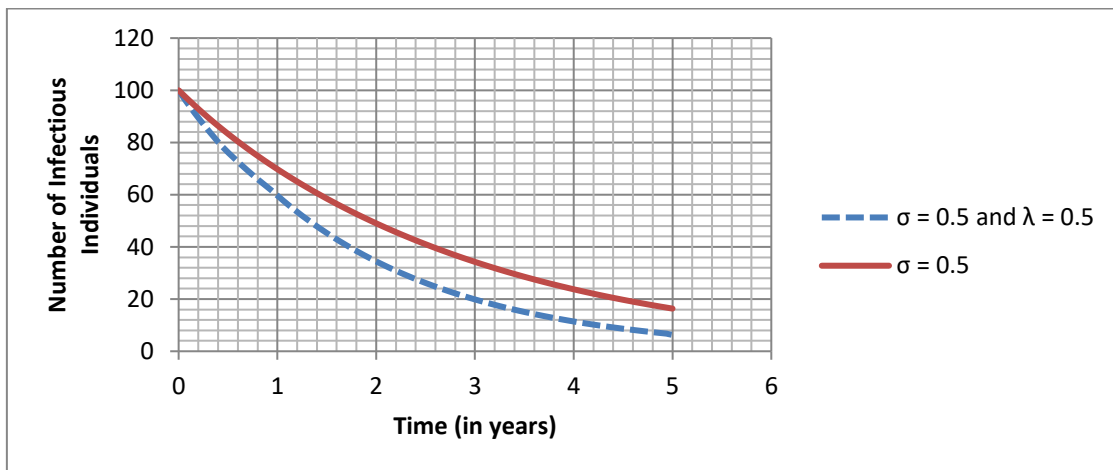


Figure 5: Solid line shows the dynamics of measles by Momoh *et al.*,(2013)'s model with 0.5 rate of testing and administering Measles therapy, while the dotted line shows the dynamics of measles by our developed model with 0.5 rate of vaccination and 0.5 rates of testing and administering Measles therapy.

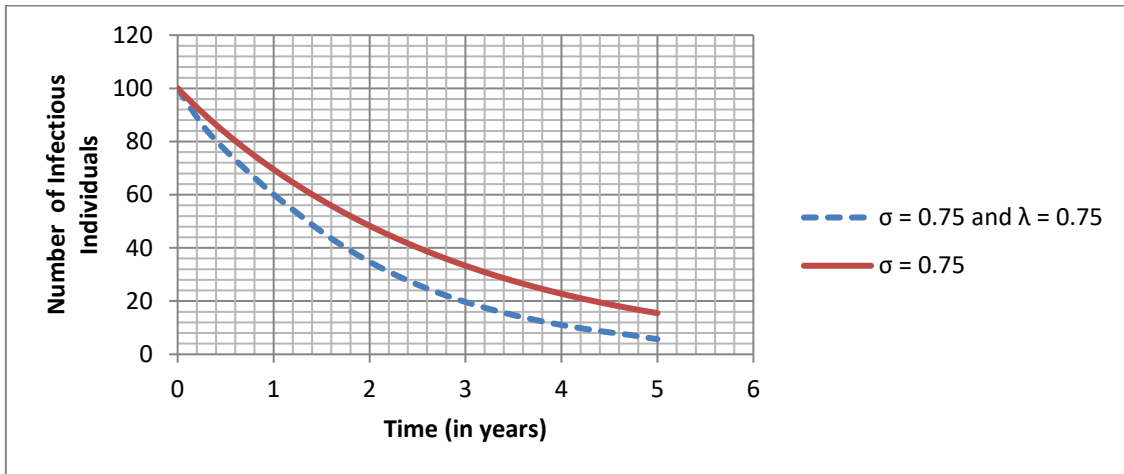


Figure 6: Solid line shows the dynamics of measles by Momoh *et al.*, (2013)'s model with 0.75 rate of testing and administering Measles therapy and our model, while dotted line shows the dynamics of our developed model with 0.75 rate of vaccination and 0.75 rates of testing and administering Measles therapy.

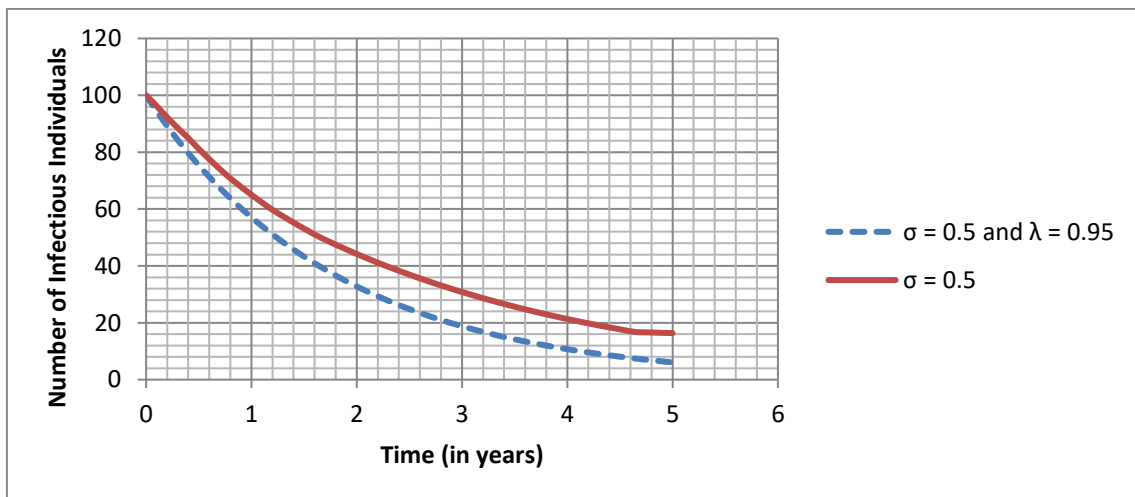


Figure 7: Solid line shows the dynamics of measles by Momoh *et al.*, (2013)'s model with 0.5 rate of testing and administering Measles therapy and our model, while dotted line shows the dynamics of our developed model with 0.95 rate of vaccination and 0.5 rate of testing and administering Measles therapy.

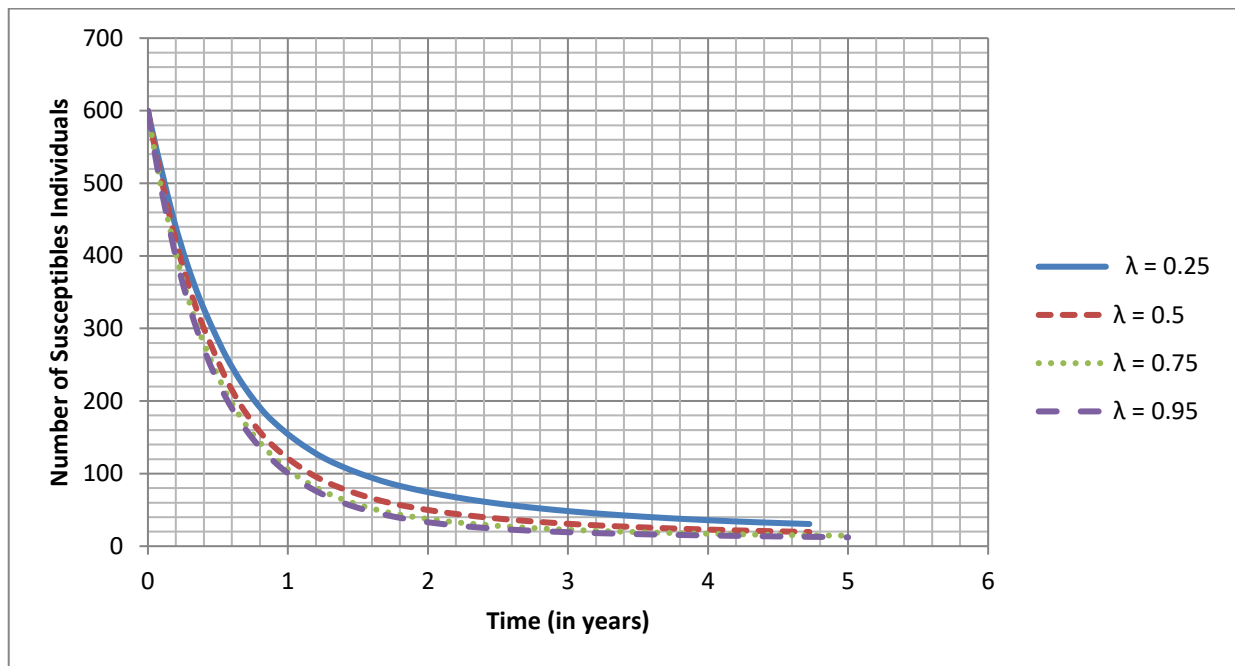


Figure 8: Graph showing the dynamics of the susceptible class with 0.25, 0.5, 0.75 and 0.95 rates of vaccinations using our developed model

5.1.2. DISCUSSION

Analytical Results: We established the Disease-free Equilibrium point (DFE) and analyze the stability of our model at disease free equilibrium point, the analytical results showed that our model is locally and asymptotically stable (LAS), provided that $R_0 < 1$, this was further demonstrated numerically to be true in experiment 1-3 with corresponding Reproduction numbers as 0.00019, 0.000095 and 0.000058 respectively. Meaning that the disease can be eradicated by

vaccination, testing and administering measles therapy as a strategy

Numerical Results: Experiment one, two and three affirms the theoretical results; that vaccination plays a vital role in the epidemiology of measles, and that, when 95% of susceptible individuals are vaccinated in a given host population the exposed class will reduce which will inturn infectious class reduces, this will affect other compartments with time.

Experiment four, five, six and seven is the comparison between the model by Momoh *et al.*, (2013) and our developed model. The result showed that combining testing and administering measles therapy to exposed individuals and vaccination of susceptible eradicates Measles faster than just Testing and administrating drug therapy as suggested by Momoh *et al* (2013). That is, eradication of the disease is possible with combination of treatment rates ranging from $\sigma = 0.25$ to $\sigma = 0.5$ and vaccination rates from $\lambda = 0.75$ to $\lambda = 0.95$ respectively.

Experiment eight shows a decline of susceptible population at different rates of vaccination, it showed that; vaccinating 95% of susceptible individuals will lead to decrease in the number of susceptible individuals and hence reduces the chance for the disease to persist

6. CONCLUSION

This study incorporated vaccination of susceptible individuals into the model by Momoh *et al* (2013) for the dynamics of measles. Analytical study was carried out using linearized stability, the results showed that the disease-free equilibrium points (DFE) are locally asymptotically stable (LAS) whenever $R_0 < 1$. Numerical experiments were also carried out, the result of the experiment revealed that eradication is possible and more efficient if 50% of exposed individuals receive measles therapy and 95% of the susceptible individuals are vaccinated.

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