Modeling the Transmission Dynamics of Measles in the Presence of Treatment as Control Strategy

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Abstract

We present in this research work, mathematical modeling of the transmission dynamics of measles using treatment as a control measure. We determined the Disease Free Equilibrium (DFE) point of the model after which we obtained the Basic Reproduction Number \( R_0 \) of the model using the next generation approach. The model Endemic Equilibrium (EE) point was also determined after which we performed Local Stability Analysis (LAS) of the Disease Free Equilibrium point and result shows that the Disease Free Equilibrium point of the model would be stable if \( R_0 < 1 \). Global Stability Analysis (GAS) result shows that, \( R_0 \leq 1 \) remains the necessary and sufficient condition for the infection to go into extinction from a population. We carried out Sensitivity Analysis of the model using the Basic Reproduction Number and we discovered that \( \delta, \mu, v, \theta \) are sensitive parameters that should be targeted towards control intervention strategy as an increase in these values can reduce the value of \( R_0 \) to a value less than unity and such can reduce the spread of measles in a population. Model simulation was carried out using mat lab software to support our analytical results.

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1 INTRODUCTION

Measles is sensitive and extremely infectious disease, which is greatly transmittable through contact with infected persons. Being a viral organism of the family Paramyxoviridae, it is an infection of the respiratory system caused by a virus known as Genus morbilivirus [1]. The symptom of the illness is high grade fever, in most cases, this is followed by cough, runny nose with red eyes and probably with tiny white spots in the mouth which appears at variably between 7 – 10 days of infection [1,2]. The later episode of the infection is the appearance of rashes all over the skin of the infected person, in severe cases, a child may develop pneumonia and encephalitis alongside other complications which may lead coma and death [3]. Children under five years are mostly affected by the disease. Rigorous cases are more possible among poorly nourished children, especially those with insufficient vitamins A or whose immune systems have been weakened by other diseases [1,3].

A susceptible person that is exposed to the measles virus has about 90 percent chance of becoming infected, while an infected person can go on to spread the virus to between 9 and 18 person. The average incubation period of the virus is 14 days, ranging from 7 to 18 days [1]. The causal organisms remain active in air and surfaces for more than an hour, whereas the period of greatest infectiousness has been closely observed to be 4 days before the onset of rash and 4 days after the rash has appeared [4].

Adapted from [1], Measles is responsible for approximately 2.6 million deaths each year before the introduction of measles vaccines in 1963 and widespread vaccination. Measles infects about 30 to 40 million children each year, causing mortality of over a million yearly. A reported case of 114 900 mortality resulting from measles was recorded against the year 2014 with over 95% of these deaths occurring in low income countries within Africa and Asia. Nigeria is rated among the countries significantly contributing to the mortality indices of measles [1,3,5].

As a management measure for measles infection [6] pointed out that accelerated immunization has had a significant impact on reducing measles deaths. Global measles mortality between 2000 and 2017 has decreased by 80%, from 545,000 cases to 110,000. To control this infectious disease from spreading among children, it was suggested that vaccination is a safe and cost effective measure [3,7]. A report by Nigeria Demographic and Health Survey published in 2013 finds that 42% of Nigerian children 12 to 23 months had received measles vaccination. To this end, a report published in [7] presents the fact that 85% of children globally received one dose of measles vaccine by their first birthday in 2014.

For elder people who are assumed to be infected by measles, the symptoms have to be treated without delay to prevent spreading the disease in the event of confirmation of measles infection. However, proper nutrition, adequate fluid intake and dehydration treatment with an oral rehydration solution recommended by WHO can prevent some complications of measles [1,3].

An extension of Susceptible, Infected and Recovered (SIR) models for measles came in the form describes in [8, 9], where an incubation period was considered [8] Present a model that reflected the typical demographical property of a developing country and a homogeneous mixed population. The dynamics of the disease was modeled by Susceptible, Exposed, Infected and Recovered (SEIR) compartmental model which found that when the basic reproduction number \( R_0 \) of the system is smaller than one, the disease-free equilibrium will be globally asymptotically stable and when \( R_0 \) is larger than one, the endemic equilibrium will be locally asymptotically stable. Communicated in [10-12] is a compartmental modeling of measles where a Susceptible-Infected-Recovered schematic approach was presented. Accessible in [11] also was the numerical solution of SEIR compartmental epidemic model of measles with non – integer time fraction using Laplace Adomian Decomposition Method, [LADM]. Control measure of measles infection was also investigated, it was concluded that the fractional model approach gave better simulation results compared to models addressed via differential transform methods. Improvement to the epidemiological model of measles is evident from the works of [13-14] where vaccination was incorporated into their models. Vaccine efficaciousness was used to measure the effect of vaccines while the sensitivity of \( R_0 \) is used to measure the spread of the infection. Introduced in [14] is the
vaccinated class as a compartment of the described model as well as 2-dose vaccination for infants. It was assumed that individuals who have been vaccinated twice will have lifelong immunity, while those who receive one dose vaccination can still possible to be infected with measles. Dimensionless transformation was employed in analyzing the model from the perspective of vaccination on newborns and immigrants while omitting susceptible individuals as well as all individuals in a given population. They found that the disease-free equilibrium is locally stable if the basic reproduction number is smaller than one and vice versa. From [13] and [14], it was concluded that vaccines can reduce the spread of measles.

In this present work, we introduce the Treatment as a control variable so as to gain insight into the transmission dynamics and control of measles in a population. We present (SEITR) model, which is an extension of (SEIR) model with Treatment class \((T)\) incorporated, since this has not been discussed much in the literature. The treatment of infected individuals suggests that exposed individual’s do not all get automatically healed of measles after being infected.

### 2 MODEL ASSUMPTIONS AND EQUATIONS

(i) The proposed model is considered in a heterogeneous population with the dynamics of a typical developing country, described with respect to time \(t\). The total population \(N\) is divided into five classes; Susceptible Individuals \((S)\), Exposed Individuals \((E)\), Infected Individuals \((I)\), those undergoing treatment \((T)\) and Recovered Individuals \((R)\).

(ii) The Susceptible populations is generated by birth

(iii) Susceptible individuals are infected at a contact rate of \(\beta\)

(iv) The Susceptible individuals progress to the Infected class at the rate of \(\gamma\)

(v) The Infected recovers naturally at the rate of \(\nu\)

(vi) The Infected recovers due to treatment at the rate of \(\sigma\)

(vii) The infectious classes die at same rate of \(\delta\)

(viii) The Recovered develops permanent immunity

(ix) All class die naturally

The mathematical model that incorporates the above assumptions is given below:

\[
\frac{dS}{dt} = \pi - (\beta I + \mu)S \\
\frac{dE}{dt} = \beta IS - (\gamma + \mu)E \\
\frac{dI}{dt} = \gamma E - (\delta + \nu + \theta + \mu)I \\
\frac{dT}{dt} = \theta I - (\gamma + \sigma + \mu)T \\
\frac{dR}{dt} = \nu I + \sigma T - \mu R
\]

Where the total population is given by:

\[N(t) = S(t) + E(t) + I(t) + T(t) + R(t).\]

### 2.1 Qualitative Analysis

#### 2.1.1 Invariant region

It is expected that at \(t = 0\), all state variables and parameters are non-negative, since the model describes human population dynamics. This is determined by considering a feasible region:
\[ \Omega = \left\{ (S, E, I, T, R) \in \mathbb{R}_+^5 : N \rightarrow \frac{\mu}{\mu} \right\} \]  

To prove that all state variables remain positive for non-negative initial conditions, where \( \frac{dN}{dt} \leq \pi - \mu N \) is obtained by adding all components on the left and right hand side of (1).

Following the argument of Lemma 1 contained in [9], and by the structure of the proof therein, we have that

\[ N(t) = \frac{\pi}{\mu} + \left( N_0 - \frac{\pi}{\mu} \right) e^{-\mu t} \]  

and in particular, if \( N(0) = \frac{\pi}{\mu} \), then \( N(t) = \frac{\pi}{\mu} \).

Thus, (2) is positively invariant and attracts all solutions in \( \mathbb{R}_+^5 \), otherwise all solution to (1) is bounded in (2)

### 2.1.2 Positivity of solution

Each of the equations in (1) is such that

\[
\begin{align*}
\frac{dS}{dt} & \geq -(\beta I + \mu)S, \\
\frac{dE}{dt} & \geq -(\gamma + \mu)E, \\
\frac{dI}{dt} & \geq -(\delta + \nu + \theta + \mu)I \\
\frac{dT}{dt} & \geq -(\delta + \sigma + \mu)T \quad \text{and} \quad \frac{dR}{dt} \geq -\mu R.
\end{align*}
\]

Hence, the solution to each of the inequality above suggests that

\[
S(t) \geq S_0 e^{-(\beta I + \mu)t} , \quad E(t) \geq E_0 e^{-(\gamma + \mu)t} , \quad I(t) \geq I_0 e^{-(\delta + \nu + \theta + \mu)t} , \quad T(t) \geq T_0 e^{-(\delta + \sigma + \mu)t} \quad \text{and} \quad R(t) \geq R_0 e^{-\mu t}.
\]

Therefore, it is concluded that the solution to the model equation remains positive for all positive time \( t \).

### 2.2 Disease Free Equilibrium (DFE)

With the individual equations of (1) set to 0, it is evident that for \( I = 0 \), the model has a disease free equilibrium \( E_0 = (S^*, 0, 0, 0, 0) = \left( \frac{\pi}{\mu}, 0, 0, 0, 0 \right) \).

**Remark 1:** \( R_0 < 1 \) suggests that the disease will be under control, since there would be no case of erratic spread of the infection. In the contrast, \( R_0 > 1 \) will lead to the infection thriving in the population.

### 2.3 Basic Reproduction Number \( R_0 \)

\( R_0 \) is defined as the average number of secondary infections produced when a single infected person is introduced into a totally susceptible population. The next generation matrix method used in [13-14] is adopted in finding the Basic Reproduction Number of this model.

We take \( U \) to be the matrix of new infectious terms and \( V \) to be the matrix of transfer terms in the infectious classes only, thus we have
\[ R_0 = \rho(UV^{-1}) = \frac{\beta SI}{q_1q_2} = \frac{\beta \pi \gamma}{\mu q_1q_2} \] (4)

Where \( \rho \) is the spectral radius that is the largest eigenvalue of the matrix product.

\[ q_1 = \gamma + \mu \text{ and } q_2 = \delta + \nu + \theta + \mu \]

### Table 1. Description of state variables and parameters

| State Variables          | Description                                                                 |
|--------------------------|-----------------------------------------------------------------------------|
| \( N(t) \)               | Total population                                                            |
| \( S(t) \)               | Population of susceptible individuals                                       |
| \( E(t) \)               | Population of exposed individuals                                           |
| \( I(t) \)               | Population of infected individuals                                          |
| \( T(t) \)               | Population of individuals undergoing treatment                               |
| \( R(t) \)               | Population of individuals who recovered either naturally or after being treated |
| Parameters               |                                                                             |
| \( \tau \)               | Time                                                                        |
| \( \beta \)              | Birth rate                                                                  |
| \( \gamma \)             | Rate at which individuals progresses from susceptible class to exposed class |
| \( \theta \)             | Rate at which individuals progress from being exposed to getting infected    |
| \( \sigma \)             | Progression rate of infected individuals to treatment class                 |
| \( \nu \)                | Rate at which individuals recover after being treated                       |
| \( \delta \)             | Rate at which individuals recover naturally from the diseases without going through treatment |
| \( \mu \)                | Disease induced death rate in the infected and treatment classes            |
| \( \mu \)                | Natural death rate                                                          |

#### 2.4 Local Stability of DFE

**Theorem 1:** The disease free equilibrium is locally asymptotically stable if \( R_0 < 1 \) and unstable if \( R_0 > 1 \).

**Proof:**

A proof to the theorem suggests differentiating the right hand side of class \( I(t) \) partially with respect to \( I \), for

\[ \dot{I}(t) = 0, \quad E = \frac{\beta SI}{(\gamma + \mu)} \quad \text{and} \quad S = \frac{\pi}{\mu} \]

Thus

\[ \gamma E - (\delta + \nu + \theta + \mu) I = \frac{\beta I \pi \gamma}{\mu(\gamma + \mu)} - (\delta + \nu + \theta + \mu) I \]

\[ \frac{\partial}{\partial I} \left( \frac{\beta I \pi \gamma}{\mu(\gamma + \mu)} - (\delta + \nu + \theta + \mu) I \right) \left|_{\left( \pi \frac{\beta \gamma}{\mu(\gamma + \mu)} \right)} \right. = \frac{\beta \pi \gamma}{\mu(\gamma + \mu)} - (\delta + \nu + \theta + \mu) \]

However, stability of the disease free equilibrium implies
\[
\frac{\beta \pi y}{\mu (\gamma + \mu)} - (\delta + \nu + \theta + \mu) < 0
\]

\[
(\delta + \nu + \theta + \mu) \left( \frac{\beta \pi y}{\mu (\gamma + \mu)(\delta + \nu + \theta + \mu)} - 1 \right) < 0
\]

that is

\[
(\delta + \nu + \theta + \mu)(R_0 - 1) < 0
\]

Clearly, (5) holds for \( R_0 < 1 \), hence the stability of the disease free equilibrium

2.5 Global Stability DFE

**Theorem 2:** The disease free equilibrium is globally asymptotically stable if \( R_0 < 1 \)

**Proof:** We systematically define a Lyapunov \( L \) function as

\[
L = \frac{1}{(\delta + \nu + \theta + \mu)} I
\]

The derivative of (6) is such that

\[
\frac{dL}{dt} = \frac{1}{(\delta + \nu + \theta + \mu)} \frac{dl}{dt}
\]

\[
= \frac{1}{(\delta + \nu + \theta + \mu)} (\gamma E - (\delta + \nu + \theta + \mu)I)
\]

\[
\leq \frac{1}{(\delta + \nu + \theta + \mu)} \left( \frac{\beta \pi y}{\mu (\gamma + \mu)} - (\delta + \nu + \theta + \mu)I \right) \left( \frac{\beta \pi y}{\mu (\gamma + \mu)(\delta + \nu + \theta + \mu)} - 1 \right) I
\]

\[
\Rightarrow \frac{dL}{dt} \leq (R_0 - 1) I
\]

From (7), it is can be deduced that \( L \leq 0 \) for \( R_0 \leq 1 \), where \( L = 0 \) if and only if \( I = 0 \). Hence, \( L \) is found to be a Lyapunov function in the invariant region. Thus, by [15-16], \( R_0 \leq 1 \) is the necessary and sufficient condition for the infection to go into extinction from the population.

2.6 Endemic Equilibrium (EE)

The endemic equilibrium \((S^*, E^*, I^*, T^*, R^*)\) exist when the infection is out broken at large scale in the population. To check for the existence of this equilibrium, we set the equations of model (1) to zero, as such, we have

\[
S^* = \frac{\pi}{\beta I + \mu} \quad E^* = \frac{\beta IS}{\gamma + \mu} \quad I^* = \frac{\gamma E}{\delta + \nu + \theta + \mu}
\]
Equation (8) is solved qualitatively in terms of the endemic equilibrium points, after rigorous substitution and simplification with \( q_1 = \gamma + \mu \) and \( q_2 = \delta + \nu + \theta + \mu \), we have

\[
E^* = \frac{\beta \pi \gamma - \mu q_1 q_2}{\beta q_1}, \text{ which is leads to } I^* = \frac{\beta \pi \gamma - \mu q_1 q_2}{\beta q_1 q_2}
\]

Hence, \( I^* \) is substituted in \( \lambda^* = \beta I^* \), which is simplified to give

\[
\lambda^* = \mu (R_0 - 1)
\]

Clearly from (9), it is apparent that \( \lambda^* \) will take a unique value when \( R_0 > 1 \), confirming an endemic equilibrium of the infection in the population.

### 2.7 Sensitivity Analysis

The sensitivity analysis of \( R_0 \) is performed to identify the most influential parameters which may be of importance in the escalation as well as control of measles infection in the population of interest as described in [15]. The sensitivity index of \( R_0 \) with respect to a parameter, say \( z \), is given by

\[
\Delta R_0^z = \frac{\partial R_0}{\partial z} \frac{z}{R_0}
\]

(10)

to check if this outcome is positive or negative. If (10) turns out positive, the parameter \( z \) tends to escalate the outbreak; however, if negative, the parameter tends to control the epidemic.

Thus, all parameters of \( R_0 \) shall be treated as in (10).

\[
\Delta R_0^\pi = \frac{\partial R_0}{\partial \pi} \frac{\pi}{R_0} = 1 > 0, \quad \Delta R_0^\gamma = \frac{\partial R_0}{\partial \gamma} \frac{\gamma}{R_0} = \frac{\mu}{q_1} > 0, \quad \Delta R_0^\delta = \frac{\partial R_0}{\partial \delta} \frac{\delta}{R_0} = -\frac{\delta}{q_2} < 0
\]

, \[
\Delta R_0^\mu = \frac{\partial R_0}{\partial \mu} \frac{\mu}{R_0} = -\frac{\mu(q_1 + q_2)}{q_1 q_2} < 0, \quad \Delta R_0^\nu = \frac{\partial R_0}{\partial \nu} \frac{\nu}{R_0} = -\frac{\nu}{q_2} < 0 \quad \text{and}
\]
\[
\Delta R_0^\theta = \frac{\partial R_0}{\partial \theta} \frac{\theta}{R_0} = -\frac{\theta}{q_2}
\]

We summarize the sensitivity test for the parameters of \( R_0 \) in Table (2).

### 3. NUMERICAL SIMULATION

The derived model is numerically simulated with parameter values and data, to determine the dynamics of the disease under variable instances. The following model variables and parameters were assumed and used for the model simulation.
$S = 6000, E = 3000, I = 2500, T = 2000, R = 1000, \pi = 0.8, \beta = 0.058, \mu = 0.0008, \gamma = 0.4, \delta = 0.05, \nu = 0.1, \theta = 0.6, \sigma = 0.05$

Table 2. Sensitivity Indices for the Parameters of $R_0$

| Parameter | Description                                                                 | Indices |
|-----------|------------------------------------------------------------------------------|---------|
| $\pi$    | Birth rate                                                                   | $+ve$   |
| $\gamma$ | Rate at which individuals progress from being exposed to getting infected     | $+ve$   |
| $\delta$ | Disease induced death rate in the infected and treatment classes             | $-ve$   |
| $\mu$    | Natural death rate                                                           | $-ve$   |
| $\nu$    | Rate at which individuals recover naturally from the diseases without going through treatment | $-ve$   |
| $\theta$ | Progression rate of infected individuals to treatment class                  | $-ve$   |

Fig. 1. Dynamics of susceptible individuals

The Susceptible individuals’ population reduces significantly due to the high rate at which the susceptible becomes exposed to the disease as shown in figure 1 above.

Fig. 2. Dynamics of Exposed Individuals

The Exposed individuals’ population reduces significantly also due to the high rate at which the Exposed individuals become fully infectious after some days as depicted in figure 2.

83
Fig. 3. Dynamics of Infected population with time
The Infected individuals' population reduces significantly due to the effectiveness of the treatment received by the infected population as depicted in figure 3.

Fig. 4. Dynamics of individuals undergoing treatment
Individuals on treatment population increase sharply and later decreases, and this may be as a result of treatment failure over time, this is seen in figure (4).

Fig. 5. Dynamics of Recovered Individuals
As seen also in figure 5, the Recovered individuals population increase sharply over time, and this shows that treatment as a control measure is sufficient enough to reduce the spread of measles in a population.
4. DISCUSSION OF RESULTS AND CONCLUSION

Fig. (1) shows the dynamics of susceptible population with time, it is evident from the graph that the population reduces significantly. Similar dynamics is obtained in Fig. (2) where theExposed population decreases significantly as a result of reduction in the exposure rate of the susceptible individuals. In Fig. (3), the infected population reduces with time as a result of treatment. Individuals on treatment population increase sharply and later decreases, and this may be as a result of treatment failure over time, this is seen in Fig. (4). The Recovered individuals’ increases significantly as evident in Fig. (5), this implies that treatment as a control measure is sufficient enough to reduce the spread of measles in a population.

The Local Stability Analysis of the Disease Free Equilibrium point and the Global Stability Analysis of the Disease Free Equilibrium point show that the disease would be eradicated from the population with respect and irrespective of the initial conditions (population) under consideration. Sensitivity Analysis result shows that; Disease induced death rate in the infected and treatment classes ($\delta$ ), Natural death rate ($\mu$), Rate at which individuals recover naturally from the diseases without going through treatment ($\nu$) and Progression rate of infected individuals to treatment class ($\theta$) should be targeted towards control intervention measure.

Competing Interests

Authors have declared that no competing interests exist.

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