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Mathematical Modelling of the Dynamics of Transmission of Measles

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Abstract: **In this paper, a deterministic, compartmental, mathematical model was formulated which described the transmission dynamics of measles with latency (exposed). The stability of the disease-free equilibrium is discussed. It is shown that if the basic reproduction number $R_o < 1$ measles can be eliminated and if $R_o > 1$ then there is a disease endemic equilibrium and the disease persists. Numerical Simulations are carried out in order to validate the analytical result.**

Keywords: **Mathematical Modelling, Measles, disease-free equilibrium, stability.**

1. INTRODUCTION

Measles is an infectious disease highly contagious through person-to-person transmission mode, with > 90% secondary attack rates among susceptible persons. It is a viral respiratory infection that attacks the immune system and is so contagious that any person not immunized will suffer from the disease when exposed. Measles virus causes rash, cough, running nose, eye irritation and fever [1][2],[3]. It can lead to ear infection, pneumonia, seizures, brain damage and death [4].

Mathematical modeling has been as a useful tool for studying disease transmission to gain a better understanding of the disease and help design control strategies [5], [6]. A mathematical model of the hand, foot, and mouth disease was proposed by [7] to investigate the transmission dynamics of the disease analytically. The standard $SEIR$ model was extended by adding two quarantine categories of susceptible and infected individuals [8]. Mathematical model for control of measles epidemiology has been developed by [9]. They used SEIR model to determine the impact of exposed individuals at latent period through the stability analysis and numerical simulation.

The purpose of this paper is to study the dynamic of measles transmission using deterministic model approach. The remaining of this paper is organized as follows: Section 2 introduces the formulation of model, the reproductive numbers are computed and the qualitative behavior of the disease-free steady state is also studied. In Section 3, we discuss the analysis of the model, in Section 4 we perform to numerical simulations and section 5 is devoted to discussions of our results.

2. MODEL FORMULATION

From the schematic diagram in Figure 1, we derive the equations of motion of the model, which capture the dynamics of the measles transmission. $SEIR$ model can then be represented by the following set of ordinary nonlinear differential equations as follows

$$\left.\begin{aligned}\frac{dS}{dt} &= \pi - \frac{\alpha SI}{N} - \mu S \\ \frac{dE}{dt} &= \frac{\alpha SI}{N} - (\beta + \mu)E \\ \frac{dI}{dt} &= \beta E - (\gamma + \mu)I \\ \frac{dR}{dt} &= \gamma I - \mu R\end{aligned}\right\} \qquad (1)$$

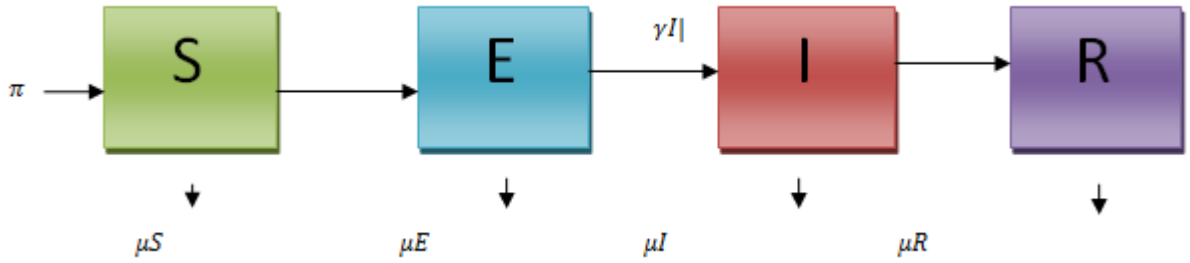

Figure 1: Schematic diagram of the model

Assumption

i. The population is homogeneously mixing and reflect the demography of a typical developing country

ii. All new born were susceptible

iii. Susceptible individual enters the exposed class E (class of those in latent period, who infected but not yet infectious) when there is adequate contact with an infective individual so that the transmission occurs.

iv. Exposed individual enters the class I of infective after the latent period ends at the rate β

v. An infected individual recovered after infective period ends at the rate γ and acquired permanent immunity or otherwise die

vi. Death rate are assumed to be equal

Table 1: parameters of the model and their description

Parameter	Descriptions
π	Birth rate
μ	Death rate
α	Effective contact rate between the susceptible and infective
β	Rate of progression from exposed state to Infectious state
γ	Recovery rate

3. ANALYSIS OF THE MODEL

Since the model (1) monitor human populations, we assume all the variables and the associated parameters remain non negative all time. It is easy to show that the state variables of the model remain non – negative for all non – negative initial conditions.

$$\Omega = \left\{(S, E, I, R) \in R_+^4 : N \to \frac{\pi}{\mu}\right\}$$

Lemma 1. The closed Ω is positively invariant and attracting

Proof

Summing all the equations in (1), we obtained a total population N satisfy the differential equation

$$\frac{dN}{dt} = \pi - \mu N \qquad (2)$$

Thus, the total human (N) is bounded by $\frac{\pi}{\mu}$, so that $\frac{dN}{dt} = 0$ whenever $N(t) = \frac{\pi}{\mu}$. it can be shown that $N(t) = \frac{\pi}{\mu} + \left(N_o - \frac{\pi}{\mu}\right)e^{-\mu t}$. In particular $N(t) = \frac{\pi}{\mu}$, if $N(O) = \frac{\pi}{\mu}$

Hence, the Ω region is positively invariant and attracts all solution in R_+^4.

3.1 Disease-free equilibrium (DFE)

Disease-free equilibrium is a steady state solution where there is no disease spreading in the population. Thus, DFE of the system (1) is attained when all the variables and parameter related to measles are zero (i.e. $E^*, I^*, R^* = 0$). Thus, the model (1) has disease free equilibrium given by

$$E_o = (S^*, E^*, I^*, R^*) = \left(\frac{\pi}{\mu}, 0,0,0\right)$$

3.2 Basic Reproduction Number (R_o)

The basic reproduction denoted by R_o, is an important parameter which is used to study the bahaviour of epidemiological models. The basic reproduction number is defined as the number of newly infectious produced by a typical infected individual in a completely susceptible population. It is an important parameters threshold that determines whether or not, a disease will spread through a given population.

We apply the next generation matrix technique by [10] to calculate the R_o by considering the second and third equations of system (1). This is because at the disease free state, $S = R$. Thus the system has two spreading states; E and I

$$\left.\begin{aligned} \frac{dE}{dt} &= \frac{\alpha SI}{N} - (\beta + \mu)E \\ \frac{dI}{dt} &= \beta E - (\gamma + \mu)I \end{aligned}\right\} \qquad (3)$$

Let matrix F represent the rate of appearance of new infections into the compartment and V represent transfer into (out) of the compartment. Thus,

$$F = \begin{pmatrix} 0 & \frac{\alpha S^*}{N} \\ 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \gamma + \mu & \beta \\ 0 & \beta + \mu \end{pmatrix}$$

Therefore,

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

The NGM with largest domain is two dimensions and is given by FV^{-1}. Thus, it follows that the basic reproduction number of the model is given by

$$R_o = \frac{\alpha S^* \beta}{N(\beta + \mu)(\gamma + \mu)} = \frac{\alpha \beta \pi}{\mu N(\beta + \mu)(\gamma + \mu)}$$

3.3 Stability of disease free equilibrium

Theorem 1

The disease – free equilibrium of the model (1) given by E_o, is locally asymptotically stable if $R_o < 1$ and unstable if $R_o > 1$

Proof

The Jacobian of (1)

$$J(S^*, E^*, I^*, R^*) = \begin{pmatrix} -\frac{\alpha I^*}{N^*} - \mu & 0 & -\frac{\alpha S^*}{N^*} & 0 \\ \frac{\alpha I^*}{N^*} & -(\beta+\mu) & \frac{\alpha S^*}{N^*} & 0 \\ 0 & 0 & -(\gamma+\mu) & 0 \\ 0 & 0 & \gamma & -\mu \end{pmatrix}$$

at equilibrium point $E_o = \left(\frac{\pi}{\mu}, 0,0,0\right)$ is

$$J_{(E_o)} = \begin{pmatrix} -\mu & 0 & -\frac{\alpha\pi}{N} & 0 \\ 0 & -(\beta+\mu) & \frac{\alpha\pi}{N} & 0 \\ 0 & 0 & -(\gamma+\mu) & 0 \\ 0 & 0 & \gamma & -\mu \end{pmatrix} \qquad (4)$$

Now, the eigenvalue of (4) is obtained by applying the characteristic equation $\left|J_{(E_o)} - \lambda I\right| = 0$

$$\begin{vmatrix} -\mu-\lambda & 0 & -\frac{\alpha\pi}{N} & 0 \\ 0 & -(\beta+\mu)-\lambda & \frac{\alpha\pi}{N} & 0 \\ 0 & 0 & -(\gamma+\mu)-\lambda & 0 \\ 0 & 0 & \gamma & -\mu-\lambda \end{vmatrix} = 0 \qquad (5)$$

$\lambda_1 = -\mu, \quad \lambda_2 = -(\beta+\mu), \quad \lambda_3 = -(\gamma+\mu), \quad \lambda_4 = -\mu$

Since all the eigenvalues of (5) have negative real parts when $R_o < 1$, it implies that, the disease – free equilibrium is locally asymptotically stable. Thus, it implies that measles can be eliminated from human population when the basic reproduction number, R_o, is less than 1.

4. NUMERICAL SIMULATION

In this section, we present a computer simulation of some solution of the system (1) to validate the analytical study.

At time t=0, over the time interval of [0, 10], we take (S(0), E(0), I(0), R(0)) = (400, 30, 5, 1) and the parameters used in the simulation are shown in table 2 below

Table 2: parameters value used in the simulation

Parameter	Value
π	7.5
α	16
β	2.5
γ	3.0
μ	4.5

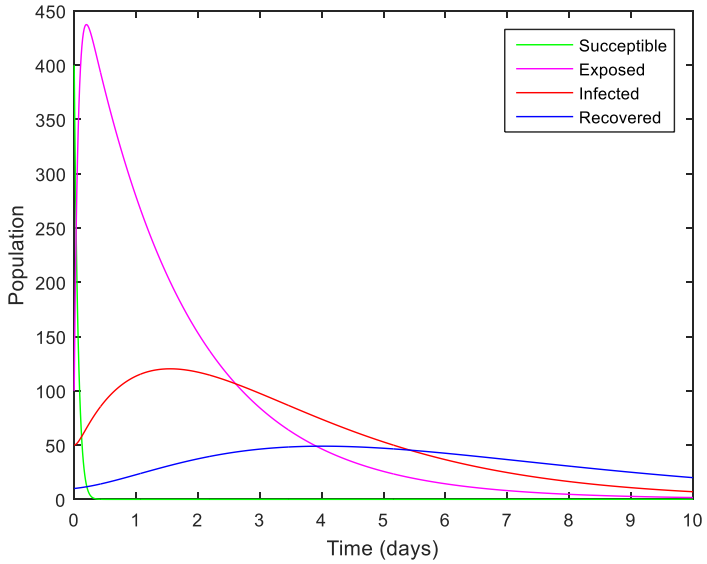

Figure 2

5. DISCUSSION

In this study we developed a system of differential equations to model diverse dynamics of measles transmission. To accomplish this, a four compartmental model was developed. In our analysis, we derived mathematically and proved the stability of the equilibrium point. The numerical simulations showed that the spread of measles in the population depends on how the susceptible individuals come into contact with the infected people.

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