

A DETERMINISTIC COMPARTMENTAL MODEL FOR TRANSMISSION AND CONTROL OF MEASLES INCORPORATING VACCINATION AND TREATMENT.

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Abstract:

In this study, we presented and analysed a deterministic compartmental model for transmission and control of measles incorporating vaccination and treatment. We obtained the positive invariant region for the model and the positivity of the solutions. We also established the existence of the equilibrium states and carried out the stability analysis of the equilibrium states. The result shows that both equilibrium states are stable.

Keywords: Measles, Positivity of solution, Invariant Region, Equilibrium State and Stability.

Introduction

Measles virus is a paramyxovirus, genus morbillivirus, measles (also called rubella) is a viral infectious disease highly contageneous through person-toperson transmission mode, with > 90% secondary attack rates among susceptible persons. It is the first and worst eruptive fever occurring during childhood. It produces also a characteristics fever, cough, runny nose 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 is now vaccine preventable, however in the pre-vaccine era, most people got infected by age 20 (Anderson and May, 1978), and the mean age of infection was much younger, approximately 4–5 years. After infection, there is a latent stage of the disease which lasts for approximately 10–12 days (Andrus, 2011). After, this stage individuals are usually infectious for approximately 8 days (Centers for Disease Control and Prevention, 2015).

There is no vertical transmission which means that newborns may not get the infection from their mothers. However a mother that has had the disease in the past passes temporary immunity to her offspring. This immunity wanes and lasts for approximately four months.

Although measles can be contracted by persons of any age, it is prevalent among children aged 5 years and below. Unvaccinated pregnant women are at high risk of complications if they contract the disease. The virus is spread when an infected person coughs, sneezes or breaths, it remains active in the air or an infected surface for up to two hours. There is no specific treatment for measles; however, people who recovered naturally from the disease confer lifelong immunity from further attacks.

One of the earliest written descriptions of measles as a disease was provided by an Arab physician in the 9th century who described differences between measles and smallpox in his medical notes. A Scottish physician, Francis Home, demonstrated in 1757 that measles was caused by an infectious agent present in the blood of patients. In 1954 the virus that causes measles was isolated in Boston, Massachusetts, by John F. Enders and Thomas C. Peebles. Before measles vaccine, nearly all children got measles by the time they were 15 years of age.

Worldwide, measles vaccination has been very effective, preventing an estimated 80 million cases and 4.5 million deaths annually and global incidence has been significantly reduced through vaccination, measles remains an important public health problem since vaccination coverage is not uniformly high worldwide, it is disheartening to mention that measles remains one of the leading causes of death among the children under-fives, especially in the Sub-Saharan African continent. The laboratory confirms measles when a blood sample taken from a suspected case within 30 days of onset of rash shows measles IgM antibodies. The caveat here with regards to IgM antibodies from suspected blood sample is that measles vaccination as well as measles infection both results in raised IgM antibodies; thus, presence of measles IgM in those vaccinated with the measles antigen 30 days before the sample is collected does not imply disease but rather vaccination against measles. Furthermore, an

outbreak of measles is said to occur when there are at least 3 measles IgM positive as confirmed by the laboratory in a health facility or district within 1-month.

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). developed a mathematical model on the dynamical analysis of a new model for measles infection. His study used SEIR model modified by adding vaccinated compartment. His model determined the required vaccination coverage and dosage that will guarantee eradication of measles disease within a population

(Bakare *et al.*, 2012). Studied modeling and simulation of the dynamics of the transmission of measles disease. They used SEIR model to discuss dynamics of measles infection and address the stability of disease free and endemic equilibrium states. The impact of vaccination in the control and elimination of measles was not considered in the work.

Ejima, (2012). developed a deterministic compartmental model to describe the transmission dynamics of measles. They divided the human population into susceptible, Exposed, infectious and Recover compartment. Stability Analysis and basic reproduction number R_0 were calculated and the results reveals that

the disease will die out if R_0 is less than one and the disease will persist if the R_0 is greater than one. On their study they didn't incorporate vaccination and treatment.

Ochoche and Gweryina (2014). developed a mathematical models of measles incorporating vaccination as a control strategy and capturing two phase of infectiousness ((i.e. asymptomatic infectives and symptomatic infectives). The basic reproduction Number R_0 was calculated using next generation matrix approach and proved that the system of Equations is locally asymptotically stable if R_0 is less than one. From their study they concluded that the disease will certainly be eliminated if all susceptible individual are vaccinated. But in their work they didn't incorporate screening and treatment of the measles disease.

Peter et-al (2018). Developed mathematical model of measles dynamics with vaccination by considering the total number of recovered individuals either from natural recovery or recovery due to vaccination. The population was divided into five compartments (Susceptible, Exposed, Infectious, Recover and Vaccination). The existence and uniqueness of solution for the model were tested using Lipchitz condition to ascertain the efficacy of the model and also the disease free equilibrium (DFE) and the endemic equilibrium (EE) for the Equation of the system were obtained and the basic reproduction Number R_0 were calculated which shows that is asymptotically stable. The numerical simulation of the model shows that vaccination is capable of reducing the number of exposed and infectious population. But in their work they didn't include screening and treatment.

In this study we present a mathematical recipe for transmission and control of measles incorporating vaccination and treatment.

MATERIAL AND METHODS Formulation of the Model

A mathematical model of transmission and control of measles is proposed by incorporating vaccination and treatment. We divided the population into six mutually-exclusive compartments namely; Susceptible Class (S), Vaccinated Class (V), Exposed Class (E), Exposed Receiving treatment Class (E_T), Infected and infectious Class (I) and Recovered Class (R).



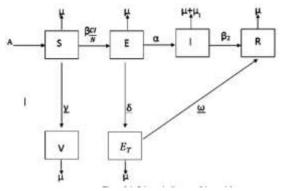


Figure 3.1: Schematic presentation of the model

Assumptions of the model

- i. The population is homogenous (population that shared similar characteristics and traits)
- ii. The natural death rate is constant
- iii. There is permanent immunity after recovery
- iv. The susceptible individuals enter the Exposed compartment at the rate λ which is a force of infection.
- v. The per capita recruitment rate A is constant,
- vi. Individuals can be infected through direct contact c, with an infectious individual.

This this can be represented by the following system of ordinary differential Equations;

Model Equations

$$\frac{dS}{dt} = A - (\mu + \gamma + \lambda)S$$

$$dV$$
(3.1)

$$\frac{dr}{dt} = \gamma S - \mu V \tag{3.2}$$

$$\frac{dL}{dt} = \lambda S - (\mu + \alpha + \delta)E$$
(3.3)

 $\frac{dE_T}{dt} = \delta E - (\mu + \omega) E_T \tag{3.4}$

$$\frac{dI}{dt} = \alpha E - (\mu_1 + \mu + \beta_2)I$$

$$\frac{dR}{dt} = \beta_2 I + \omega E_T - \mu R$$

$$\lambda = \frac{\beta cI}{\lambda E_T}$$
(3.6)

Where $\sqrt{N} = \frac{N}{N}$

Definition of variables and parameters

- N total population
- S number of susceptible (that is no infection but can be infected)
- V number of vaccinated individual (those who received vaccine)
- E number of exposed individual (infected individual but not yet infectious)
- E_T number of exposed individual receiving treatment
- I number of persons with active measles
- R number of persons recovered from measles
- A constant recruitment rate
- c per capita contact rate for measles
- δ Rate at which exposed individual move to exposed treated class
- μ Natural death rate
- α Rate at which exposed individuals becomes infectious
- ω Recovery rate for the exposed treated individual
- γ Rate at which susceptible individual receive vaccine
- β Probability of infectious individual infecting others
- β_2 Recovery rate for the infectious individuals
- μ_I death due to measles infection
- λ force infection

The Positive Invariant Region

The entire population size N can be determined from Equation (3.1) to (3.6)

The total population size is
$$N = S + V + E_T + E + I + R$$
(3.7)
$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE_T}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$$
(3.8)
(3.8)

The positive invariant region can be obtained using the following theorem.

Theorem 3.1

The solutions of the system Equation (3.1) to Equation (3.6) are feasible for t > 0 provided they enter the invariant region D.

Proof

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Let $D = (S, V, E, E_T, I, R) \in \mathbb{R}^{6_+}$

Be any solution of the system of Equations (3.1) to (3.6) with non-zero initial conditions.

Assuming there is no disease-induced deaths, Equation (3.9) now becomes

$$\frac{dN}{dt} \le A - \mu N \tag{3.10}$$

$$\frac{dN}{dt} + \mu N \le A \tag{3.11}$$
The integrating factor for (3.11) is $e^{\mu t}$
Multiply both sides of (3.11) by $e^{\mu t}$ gives
$$\frac{d(Ne^{\mu t}) \le A e^{\mu t} dt}{(3.12)}$$
Integrating both sides we have
$$N(t)e^{\mu t} = \frac{Ae^{\mu t}}{\mu} + D \tag{3.13}$$

$$N(t) = \frac{A}{\mu} + D e^{-\mu t} \tag{3.14}$$
Applying the initial condition $t = 0$; $N_h(0) = N_0$ (3.15)
$$N_0 \le \frac{A}{\mu} + D \Rightarrow N_0 - \frac{A}{\mu} \le D \tag{3.16}$$

$$\Rightarrow N(t) \le \frac{A}{\mu} + (N_0 - \frac{A}{\mu}) e^{-\mu t} \tag{3.17}$$

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$$K = \frac{A}{C}$$

Therefore, as $t \rightarrow \infty$ in (3.17) the human population N approaches μ (That

 $K = \frac{A}{\mu}$ is called the carrying capacity. Hence all feasible solution set of the human population of the model Equations (3.1) to (3.6) enter the region

$$D = \left\{ \left(S, V, E, E_T, I, R \right) \in R^6 : S > 0, V \ge 0, E \ge 0, E_T \ge 0, I \ge 0, R \ge 0, N \le \frac{A}{\mu} \right\}$$

Therefore, in this region it is appropriate to consider the dynamics of flow generated by the model Equations (3.1) to (3.6).

Positivity of Solutions

Since Equations (3.1) - (3.6) represent the population in each compartment and all model parameters are all positive, then it lies in a region D.

Theorem 3.2 Let the initial data for the model Equations be given as $\{(S(0) > 0, (V(0), E(0), E_T(0), I(0), R(0) > 0)\} \in D$

Then the solution set $\{S, V, E, E_T, I, R\}(t)$ of the system of Equations (3.1) to (3.6) is positive for all t > 0

Proof

From Equation (3.1), we have

$$\frac{dS}{dt} = A - (\mu + \gamma + \lambda)S \ge -(\mu + \gamma + \lambda)S \qquad (3.18)$$

$$\frac{dS}{dt} \ge -(\mu + \gamma + \lambda)S \qquad (3.19)$$

Separating the variables we have

$$\frac{dS}{S} \ge -(\mu + \gamma + \lambda)dt$$

By integration we have $InS \ge -(\mu + \gamma + \lambda)t + C_2$

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$\Rightarrow e^{In}S \ge e^{-(\mu+\gamma+\lambda)t} + e^{C_2}$	(3.21)
$S(t) \ge K_1 e^{-\left(\mu + \gamma + \lambda\right)t}$	(3.22)
Where $K_1 = e^{C_2}$	
Using the initial condition $t=0 \Rightarrow S(0) \ge K_1$	
Therefore, $S(t) \ge S(0)e^{-(\mu+\gamma+\lambda)t} \ge 0$	(3.23)
From Equation (3.2)	
$\frac{dV}{dt} = \gamma S - \mu V \ge -\mu V$	(3.24)
$\frac{dV}{dt} \ge -\mu V$	(3.25)
$\frac{dV}{V} \ge -\mu dt$	(3.26)
$InV \ge -\mu t + C_3$	(3.27)
$V(t) \ge K_2 e^{-\mu t}$	(3.28)
Applying the initial condition $t=0 \Rightarrow V(0) \ge K_2$ Therefore $V(t) \ge V(0)e^{-\mu t}$	
Therefore, $V(t) \ge V(0)e^{-\mu t}$	(3.29)
Similarly, it can be verified that the rest of the Equation	ns are positive for all t >
0 since	
$e^{\omega} > 0_{\text{For all }} \omega \in R$	
3.4 Equilibrium States of the Model	
At equilibrium, $\frac{dS}{dt} = \frac{dV}{dt} = \frac{dE}{dt} = \frac{dE_T}{dt} = \frac{dE}{dt} = \frac{dR}{dt} = 0$	
At equilibrium, $dt dt dt dt dt dt$ From Equation (3.1) to (3.6)	(3.30)
Let $S = x_1$, $V = x_2$, $E = x_3$, $E_T = x_4$, $I = x_5$ and $R = x_4$	⁶ (3.31)
$A - \left(\mu + \gamma + \frac{\beta c x_5}{N}\right) x_1 = 0$	(3.32)
$\gamma x_1 - \mu x_2 = 0$	(3.33)
	(2.22)

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$\frac{\beta c x_5 x_1}{N} - (\mu + \alpha + \delta) x_3 = 0$	(2,24)
$\delta x_3 - (\mu + \omega) x_4 = 0$	(3.34) (3.35)
$\alpha x_3 - \left(\mu_1 + \mu + \beta_2\right) x_5 = 0$	(3.36)
$\beta_2 x_5 + \omega x_4 - \mu x_6 = 0$ From Equation (3.36)	(3.37)
$x_{3} = \frac{(\mu_{1} + \mu + \beta_{2})x_{5}}{(\mu_{1} + \mu + \beta_{2})x_{5}}$	
α Substituting Equation (3.38) into Equation (3.34) gives	(3.38)
$\frac{\beta c x_5 x_1}{N} - \frac{(\mu + \alpha + \delta)(\mu_1 + \mu + \beta_2) x_5}{\alpha} = 0$	(3.39)
$x_{5}\left(\frac{\beta c x_{1}}{N}-\frac{(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})}{\alpha}\right)=0$	(3.40)
Either $x_5 = 0$ or $\frac{\beta c x_1}{N} = \frac{(\mu + \gamma + \lambda)(\mu_1 + \mu + \beta_2)}{\alpha}$	(3.41)
	(3.11)
If $x_5 = 0$ then from Equation (3.41) $\beta_{cx_1} = (\mu + \alpha + \delta)(\mu_1 + \mu + \beta_2)$	
$\frac{\beta c x_1}{N} = \frac{\left(\mu + \alpha + \delta\right) \left(\mu_1 + \mu + \beta_2\right)}{\alpha}$	(3.42)

$$x_{1} = \frac{N(\mu + \alpha + \delta)(\mu_{1} + \mu + \beta_{2})}{\alpha\beta c}$$
(3.43)

Substituting Equation (3.43) into Equation (3.33) gives

$$\frac{\gamma N(\mu + \alpha + \delta)(\mu_1 + \mu + \beta_2)}{\alpha \beta c} - \mu x_2 = 0$$

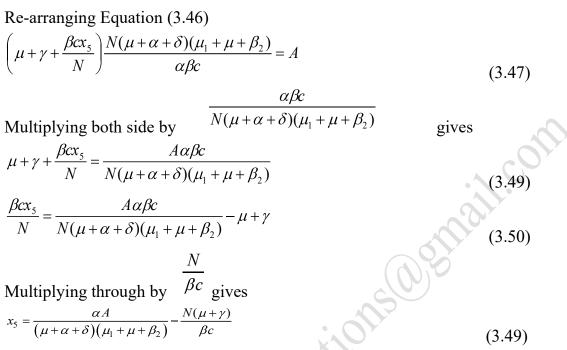
$$x_2 = \frac{\gamma N(\mu + \alpha + \delta)(\mu_1 + \mu + \beta_2)}{\alpha \beta c \mu}$$
(3.44)
(3.45)

Substituting Equation (3.43) into Equation (3.32) gives

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$$A - \left(\mu + \gamma + \frac{\beta c x_5}{N}\right) \frac{N(\mu + \alpha + \delta)(\mu_1 + \mu + \beta_2)}{\alpha \beta c} = 0$$
(3.46)

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Substituting Equation (3.49) into Equation (3.36) and then simplifying we have;

$$x_{3} = \frac{\left(\mu_{1} + \mu + \beta_{2}\right)}{\alpha} \left(\frac{\alpha A}{\left(\mu + \alpha + \delta\right)\left(\mu_{1} + \mu + \beta_{2}\right)} - \frac{N(\mu + \gamma)}{\beta c}\right)$$
(3.50)

Substituting Equation (3.50) into Equation (3.35) and then simplifying we have;

$$x_{4} = \frac{\delta(\mu + \mu_{1} + \beta_{2})}{\alpha(\mu + \omega)} \left(\frac{(\mu_{1} + \mu + \beta_{2})}{\alpha} \left(\frac{\alpha A}{(\mu + \alpha + \delta)(\mu_{1} + \mu + \beta_{2})} - \frac{N(\mu + \gamma)}{\beta c} \right) \right)$$
(3.51)

Substituting Equations (3.49) and (3.51) into Equation (3.37) and then simplifying we have;

$$x_{6} = \frac{1}{\mu} \begin{pmatrix} \beta_{2} \left(\frac{\alpha A}{(\mu + \alpha + \delta)(\mu_{1} + \mu + \beta_{2})} - \frac{N(\mu + \gamma)}{\beta c} \right) + \\ \frac{\omega \delta(\mu + \mu_{1} + \beta_{2})}{\alpha(\mu + \omega)} \left(\frac{(\mu_{1} + \mu + \beta_{2})}{\alpha} \left(\frac{\alpha A}{(\mu + \alpha + \delta)(\mu_{1} + \mu + \beta_{2})} - \frac{N(\mu + \gamma)}{\beta c} \right) \right) \end{pmatrix}$$
(3.52)

Disease free equilibrium (DFE)

The equilibrium state in the absence of infection is known as disease free equilibrium.

Therefore from Equation (3.41) If $x_5 = 0$ (3.53) Then substituting Equation (3.53) into Equations (3.32), (3.34) and (3.37) and then simplifying we have;

$$x_{1} = \frac{A}{\mu + \gamma}$$
(3.54)

$$x_{3} = 0$$
(3.55)

$$\omega x_{4} - \mu x_{6} = 0$$
(3.56)
Substituting Equation (3.55) into Equation (3.35)

$$x_{4} = 0$$
(3.57)
Substitute Equation (3.57) into Equation (3.56) gives

$$x_{6} = 0$$
(3.58)
Substituting Equation (3.54) into Equation (3.33) and then simplifying we have;

$$x_{2} = \frac{\gamma}{2} \left(\frac{A}{2}\right)$$

$$(x_{1}, x_{2}, x_{3}, x_{4}, x_{5}, x_{6}) = \left(\frac{A}{\mu + \gamma}, \frac{\gamma}{\mu} \left(\frac{A}{\mu + \gamma}\right), 0, 0, 0, 0\right)$$

$$(3.59)$$

$$(3.60)$$

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The endemic equilibrium state

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Equations (3.43), (3.45), (3.49), (3.50), (3.51) and (3.52) give the endemic equilibrium state. That is;

$$\begin{pmatrix} \frac{N(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})}{\alpha\beta c}, \frac{\gamma N(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})}{\alpha\beta c\mu}, \\ \frac{(\mu_{1}+\mu+\beta_{2})}{\alpha} \begin{pmatrix} \frac{\alpha A}{(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})} - \frac{N(\mu+\gamma)}{\beta c} \end{pmatrix}, \\ \frac{\delta(\mu+\mu_{1}+\beta_{2})}{\alpha(\mu+\omega)} \begin{pmatrix} \frac{(\mu_{1}+\mu+\beta_{2})}{\alpha} \begin{pmatrix} \frac{\alpha A}{(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})} - \frac{N(\mu+\gamma)}{\beta c} \end{pmatrix}, \\ \frac{\alpha A}{(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})} - \frac{N(\mu+\gamma)}{\beta c}, \\ \frac{1}{\mu} \begin{pmatrix} \beta_{2} \begin{pmatrix} \frac{\alpha A}{(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})} - \frac{N(\mu+\gamma)}{\beta c} \end{pmatrix} + \\ \frac{\omega \delta(\mu+\mu_{1}+\beta_{2})}{\alpha(\mu+\omega)} \begin{pmatrix} \frac{(\mu_{1}+\mu+\beta_{2})}{\alpha} \begin{pmatrix} \frac{\alpha A}{(\mu+\alpha+\delta)(\mu_{1}+\mu+\beta_{2})} - \frac{N(\mu+\gamma)}{\beta c} \end{pmatrix} \end{pmatrix} \end{pmatrix} \end{pmatrix}$$

Stability Analysis of Disease Free Equilibrium State (DFES)

The Jacobean matrix of the system of Equations at disease-free equilibrium is:

$$J\left(\frac{A}{\mu+\gamma},\frac{\gamma}{\mu}\left(\frac{A}{\mu+\gamma}\right),0,0,0\right) = \begin{bmatrix} -(\mu+\gamma) & 0 & 0 & 0 & -\frac{\beta cA}{N(\mu+\gamma)} & 0\\ \gamma & -\mu & 0 & 0 & 0 & 0\\ 0 & 0 & -(\mu+\alpha+\delta) & 0 & \frac{\beta cA}{N(\mu+\gamma)} & 0\\ 0 & 0 & \delta & -(\mu+\omega) & 0 & 0\\ 0 & 0 & \alpha & 0 & -(\mu_1+\mu+\beta_2) & 0\\ 0 & 0 & 0 & \omega & \beta_2 & -\mu \end{bmatrix} (3.61)$$

The characteristic Equation is given by $(J-I\lambda)=0$

$$\begin{bmatrix} -(\mu+\gamma)-\lambda & 0 & 0 & 0 & -\frac{\beta cA}{N(\mu+\gamma)} & 0 \\ \gamma & -\mu-\lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu+\alpha+\delta)-\lambda & 0 & \frac{\beta cA}{N(\mu+\gamma)} & 0 \\ 0 & 0 & \delta & -(\mu+\omega)-\lambda & 0 & 0 \\ 0 & 0 & \alpha & 0 & -(\mu_1+\mu+\beta_2)-\lambda & 0 \\ 0 & 0 & 0 & \omega & \beta_2 & -\mu-\lambda \end{bmatrix} = 0$$
(3.62)

This gives: $(-(\mu+\gamma)-\lambda)(-(\mu-\lambda)(-(\mu+\alpha+\delta)-\lambda)(-(\mu+\omega)-\lambda)(-(\mu_1+\mu+\beta_2)-\lambda)(-(\mu-\lambda)=0 \quad (3.63)$

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Which further simplifies to;

$$(-(\mu + \gamma) - \lambda_1) = 0 \text{ or } (-\mu - \lambda_2) = 0 \text{ or } (-(\mu + \alpha + \delta) - \lambda_3) = 0 \text{ or } (-(\mu + \omega) - \lambda_4) = 0$$

or $(-(\mu_1 + \mu + \beta_2) - \lambda_5) = 0 \text{ or } (-\mu - \lambda_5) = 0$ (3.64)

Therefore,

$$\lambda_{1} = -(\mu + \gamma), \lambda_{2} = -\mu, \lambda_{3} = -(\mu + \alpha + \delta), \lambda_{4} = -(\mu + \omega), \lambda_{5} = -(\mu_{1} + \mu + \beta_{2}) \text{ and } \lambda_{6} = -\mu (3.65)$$

Hence, DFE is stable since all the Eigen-values are less than zero.

Stability Analysis of Endemic Equilibrium State (EES)

An important criterion by Routh-Hurwitz gives the necessary and sufficient conditions for all roots of the characteristics (with real coefficients) to lie in the left half of the complex plane. In other words, all the roots of the polynomial are negative or have negative real roots if and only if the determinant of all Routh-Hurwitz matrices is positive.

Theorem 3.2 (Routh-Hurwitz Conditions)

 $J = \begin{pmatrix} f_x(x_*, y_*) & f_y(x_*, y_*) \\ g_x(x_*, y_*) & g_y(x_*, y_*) \end{pmatrix}$ be the Jacobian matrix of the non-linear system $\frac{dx}{dt} = f(x, y)$ (3.66) $\frac{dy}{dt} = g(x, y)$ (3.67)

Evaluated at the critical point (x_*, y_*) , then the critical point (x_*, y_*) ;

- 1. Is locally asymptotically stable if trace (J)<0 and determinant (j)>0
- Is stable but not asymptotically stable if trace (J)=0 and determinant (J)>0
- 3. Is unstable if either, trace (J)>0 or determinant (J)<0

Jacobean matrix of the system of Equations at endemic equilibrium state is:

$$J(x_{1}^{*}, x_{2}^{*}, x_{3}^{*}, x_{4}^{*}, x_{5}^{*}, x_{6}^{*}) = \begin{bmatrix} -(\mu + \gamma + \frac{\beta c x^{*} 5}{N}) & 0 & 0 & 0 & -\frac{\beta c x^{*} 1}{N} & 0\\ \gamma & -\mu & 0 & 0 & 0 & 0\\ \frac{\beta c x^{*} 5}{N} & 0 & -(\mu + \alpha + \delta) & 0 & \frac{\beta c x^{*} 1}{N} & 0\\ 0 & 0 & \delta & -(\mu + \omega) & 0 & 0\\ 0 & 0 & \alpha & 0 & -(\mu_{1} + \mu + \beta_{2}) & 0\\ 0 & 0 & 0 & \omega & \beta_{2} & -\mu \end{bmatrix}$$

$$(3.68)$$

The determinant gives:

$$\frac{1}{N}(((\mu + \mu_{1} + \beta_{2})(\mu + \lambda)(\mu + \alpha + \delta)N + \beta cx^{*}_{5} + (2\beta cx^{*}_{5}\mu + (\beta cx^{*}_{5} - \beta cx^{*}_{1})\alpha + \beta cx^{*}_{5}(\beta_{2} + \delta + \mu_{1})) + \beta cx^{*}_{5}\mu^{2} + ((\beta cx^{*}_{5} - \beta cx^{*}_{1})\alpha + \beta cx^{*}_{5}(\beta_{2} + \delta + \mu_{1})) + (-\gamma\beta cx^{*}_{1} + \beta cx^{*}_{5}(\beta_{2} + \mu_{1}))\alpha + \beta cx^{*}_{5}\delta(\beta_{2} + \mu_{1}))\alpha + \beta cx^{*}_{5}\delta(\beta_{2} + \mu_{1})(\mu + \omega + \lambda)(\mu)^{2})$$
(3.69)

$$= -\left((\mu + \gamma + \frac{\beta c x_1^*}{N})(\mu) (\mu + \alpha + \delta) (\mu + \omega) (\mu_1 + \mu + \beta_2)(\mu) \right)$$
trace

(3.70)

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Since the trace (J) < 0 and the determinant > 0, the Endemic Equilibrium State is locally asymptotically stable.

Conclusion:

In this study we developed and analysed a deterministic compartmental model for transmission and control of measles incorporating vaccination and treatment. The model has feasible solutions in the region $D = (S, V, E, E_T, I, R) \in$ R_{+}^{6} The solution set $\{S, V, E, E_T, I, R\}(t)$ of the system of Equations (3.1) to (3.6) is positive for all t > 0. The model has stable Disease Free and Endemic Equilibrium States signifying the possibility of complete eradication of the disease if necessary measures are put in place.

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