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Mathematical and Stability Analysis of the Measles Dynamics Model with Vaccination

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Abstract

Measles, characterised by symptoms such as encephalitis, pneumonia, and blindness, is the leading cause of death among young children. To understand the mechanism behind the transmission dynamics of measles and propose control measures to curb its spread in the human population, a non-linear SEIR deterministic epidemiological model incorporating vaccination is developed and analysed in this study. The theory of positivity and boundedness of solutions is used to establish the well-posedness of the model, and the effective reproduction number is obtained using the next-generation matrix approach. The analysis revealed that the model possesses two equilibrium points: the measles-free and endemic equilibrium points. Additionally, a quadratic Lyapunov function is used to investigate the global asymptotic dynamics of the endemic equilibrium point. The analysis revealed that the measles-free equilibrium point is globally asymptotically stable when the effective reproduction number is less than unity (i.e., R0 = 0.59765 < 1). At the same time, the endemic equilibrium point is also globally asymptotically stable when R0 = 5.97652 > 1. Furthermore, key epidemiological parameters driving the menace of measles are investigated and identified using normalised forward sensitivity indices with a view to suggesting effective control measures that can be used to curb the dynamical spread of measles in the population.

Keywords: Measles, Mathematical Model, Vaccination, Stability, Lyapunov function.

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Introduction

Measles, also known as rubeola, is a highly contagious virus that primarily affects children but can affect anyone of any age if they have not received the vaccine or have already contracted it. It is brought on by the measles virus, which belongs to the Paramyxoviridae family [1]. When an infected individual coughs or sneezes, respiratory droplets are released into the air. Due to a decline in vaccination rates, measles remains a significant public health threat in certain parts of the world, despite the availability of a safe and effective vaccine [2], [3]. Ten to twelve days after exposure to the virus, measles typically manifests as fever, cough, runny nose, conjunctivitis (inflamed eyes), and

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sore throat [4]. A red, blotchy rash that typically begins on the face and moves down to the rest of the body is one of the classic symptoms of measles. Typically, this rash develops three to five days after the initial symptoms appear. The extremely contagious measles virus can survive for up to two hours in the air or on surfaces. When an infected individual coughs, sneezes, or even speaks, it can spread quickly through the air [5]. Direct contact with an infected person's throat or nasal secretions can also spread the virus [6], [7]. The contagious period lasts approximately four days after the rash develops, starting around four days before the rash appears. Serious complications can arise from measles, particularly in young children, pregnant women, and those with compromised immune systems [8]. Among the frequent issues are pneumonia which is a frequent and dangerous side effect that can lead to hospitalization and, in extreme situations, death, encephalitis, known as brain inflammation which can cause convulsions and brain damage, ear infections and diarrhea which are less serious but nonetheless can cause frequent side effects that might lead to dehydration and other health issues and pregnancy-related complications [9], [10], [11], [1].

The most efficient method of preventing measles is through vaccination. Typically, children receive two doses of the measles, mumps, and rubella (MMR) vaccine: one at 12 to 15 months of age and another at 4 to 6 years of age. After receiving two doses, approximately 97% of people develop protection, demonstrating the vaccine's tremendous effectiveness [12]. The World Health Organisation (WHO) and the Centres for Disease Control and Prevention (CDC) are among the many international health organisations that support the use of the vaccine, as it is safe and has undergone significant research. Some areas have seen a drop in vaccination rates recently, partly as a result of false information regarding the safety of vaccines, including the debunked theory that the MMR vaccine causes autism [12]. This has led to measles breakouts in nations that had previously achieved notable progress in eradicating the disease. Despite the vaccine's availability, measles continues to be a leading cause of death for young children worldwide. The World Health Organisation (WHO) reports that in 2018 alone, there were 147,000 measles-related deaths and 9.7 million illnesses. The disease is more prevalent in countries with inadequate healthcare systems and low vaccination rates. However, in many wealthy nations, where vaccination campaigns have largely eliminated measles, the situation has improved significantly [13]. On the other hand, outbreaks continue to occur often in areas with decreased vaccination rates or restricted access to vaccines. For example, measles outbreaks have occurred in the US and Europe as a result of decreased vaccination rates, which are frequently made worse by anti-vaccine campaigns. For many years, efforts have been made to eradicate measles worldwide. The Global Measles and Rubella Elimination Initiative, launched by the WHO in 2012, aims to eradicate measles in areas with low vaccination rates by 2020. Although there has been improvement, vaccination initiatives suffered major setbacks due to the COVID-19 pandemic, as medical resources were redirected to handle the emergency [14] (CDC, 2021).

Mathematical modelling is a vital tool for examining the dynamic spread of infectious diseases in the human population, and numerous researchers have used it to examine the dynamics of measles transmission in the population [15] [16], [17], [18]. Edward et al [19] formulated a model for the control and elimination of measles dynamics. Their result indicated that the spread of the disease largely depends on the contact rate with infected individuals within the population and the importance of vaccination in preventing the spread of measles. Ochoche and Gweryina [20] investigated the impact of vaccination and two phases of infectiousness on the transmission of measles in the human population. Sowole et al. [21] investigated the existence, uniqueness, and stability of solutions to a mathematical model for measles. Verguet et al [22] studied how measles can be controlled using supplemental immunisation activities to inform optimal policy from a mathematical modelling approach. Their result suggested that regular supplemented immunisation activities will help prevent the outbreak of measles. Similarly, Arsal et al. [23] conducted a brief review of the mathematical model of measles, and Alemneh and Belay [24] focused on modelling, analysis, and simulation of measles disease transmission dynamics. The result of their findings stipulated that working on prevention and treatment strategies brings a significant reduction in the disease's effect on the human population. Furthermore, Peter et al. [25] designed a mathematical model of measles transmission using real data from Nigeria, and recently, Ahmed et al [26] conducted a robust analysis on the mathematical modelling of measles via a collocation approach.

Despite the availability of effective vaccines, measles remains a cause of high childhood mortality. Existing mathematical models do not account for the effect of vaccination on the susceptible population after birth and the potential for disease relapse after recovery. To eradicate measles worldwide, ongoing initiatives to inform communities and make vaccines accessible are essential. The decline in vaccination rates poses a significant threat to public health. The research focuses on developing and analysing a mathematical model that accounts for vaccination and relapse on the transmission dynamics of measles. The organisation of this work is structured as follows: Section 2 shows the formulation of the measles model. Vigorous analysis of the model is carried out in Section 3. Section 4 presents the numerical simulation, and Section 5 wraps up the concluding remarks of the study

Model Formulation

The human population denoted by $N(t)$ is subdivided into five mutually exclusive compartments of susceptible humans, exposed humans $E(t)$, infected humans $I(t)$ and recovered humans $R(t)$. Then the total human population

is given as

$$N(t) = S(t) + E(t) + I(t) + R(t) \quad (1)$$

Susceptible humans are recruited into the population at a rate π and the population is reduces by the force of infection $\frac{\beta(I+\theta E)}{N}$ where $\beta$is the effective transmission rate and $\theta$the modification parameter measuring the infectivity of the exposed human. The population is further reduced as a result of natural mortality and vaccination at the rates $\mu$and σ. Therefore, the rate of change of the susceptible human population is given as

$$\frac{dS}{dt} = \pi - \frac{\beta(I+\theta E)S}{N} - (\mu + \sigma)S \quad (2)$$

The exposed human population increases as a result of the force of infection from the susceptible human population at the rate $\frac{\beta(I+\theta E)}{N}$. The population is reduced as more people are likely to have active measles infection at a rate $\alpha$and natural mortality at a rate μ. Then the rate of change of the exposed human population is given by

$$\frac{dE}{dt} = \frac{\beta(I+\theta E)S}{N} - (\alpha + \mu)E \quad (3)$$

The infectious human population increases as a result of progression from the exposed compartment at a rate $\alpha$and immunity loss due to incomplete treatment or compromised immune system at the rate ω. The population diminishes as a result of disease induced death at a rate $\delta$and further shrinks due to natural death and treatment at the rates $\mu$and τ. Therefore, the rate of change of the infected human population is given by

$$\frac{dI}{dt} = \alpha E + \omega R - (\tau + \mu + \delta)I \quad (4)$$

Following proper treatment of the infected individuals at a rate τ, the recovered population develops. The population further increases as a result of susceptible population that got vaccinated at a rate σ. The population is further downsized as a result of relapse at a rate ω and further reduces due to natural death at a rate μ. Thus, the rate of change of recovered human population is given by

$$\frac{dI}{dt} = \tau I + \sigma S - (\mu + \omega)R \quad (5)$$

Consequently, following the assumptions and pairing the equations together, the system of ordinary differential equations governing the measles transmission dynamics is given by

$$\begin{aligned} \frac{dS}{dt} &= \pi - \frac{\beta(I+\theta E)S}{N} - (\mu + \sigma)S \\ \frac{dE}{dt} &= \frac{\beta(I+\theta E)S}{N} - (\alpha + \mu)E \\ \frac{dI}{dt} &= \alpha E + \omega R - (\tau + \mu + \delta)I \\ \frac{dR}{dt} &= \tau I + \sigma S - (\omega + \mu)R \end{aligned} \quad (6)$$

with non-negative initial conditions,

$$S(0) = S_0, E(0) = E_0, I(0) = I_0, R(0) = R_0 \quad (7)$$

The schematic diagram showing the transition from one compartment to another is given in Figure 1. The description of variables and parameters associated with the system (6) is given respectively in Table 1 and Table 2.

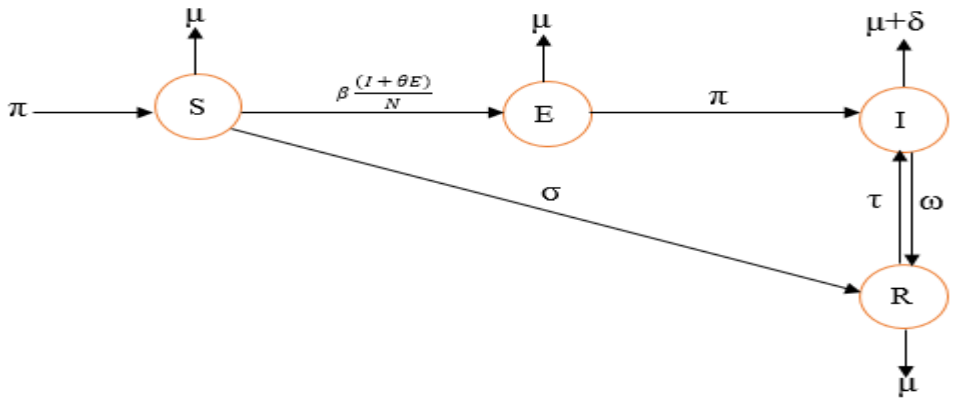

Figure 1. Schematic diagram of the measles model (6)

Table 1. Description of variables

Variable	Description
$S(t)$	Susceptible Humans

$E(t)$	Exposed Humans
$I(t)$	Infected Humans
$R(t)$	Recovered Humans
$N(t)$	Total Population

Table 2. Description parameters

Parameter	Description
π	Recruitment rate
β	Effective transmission rate
μ	Natural mortality rate
θ	Modification parameter
σ	Vaccination rate
α	Progression rate
τ	Recovery rate
ω	Relapse rate

Model Analysis

This section provides the qualitative analysis of the mathematical model describing the spread of measles in the human population.

Invariant region

***Theorem 1*:** Let the solution set of the system (6) be (S, E, I, R) with initial condition in a feasible region Ω, then $\Omega \subset R_+^4$ is positively invariant.

Proof: Sinc$N(t) = S(t) + E(t) + I(t) + R(t)$, then it is clear that adding the equations in system (6) gives

$$\frac{dN}{dt} = \pi - \mu N - \delta I \tag{8}$$

So that

$$\frac{dN}{dt} + \mu N \leq \pi \tag{9}$$

Then, it follows that

$$N(t) \leq N(0)e^{-\mu t} + \frac{\pi}{\mu}(1 - e^{-\mu t}) \tag{10}$$

Taking the limit as $t \to \infty$gives $N(t) \leq {}^{\pi}/_{\mu}$. Furthermore, if $N(0) \leq {}^{\pi}/_{\mu}$, then $N(t) \leq {}^{\pi}/_{\mu}$. Hence the region Ω is positively invariant.

Non-negativity of Solutions

***Theorem 2*:** Given the non-negative initial conditions (7), the solution sets $S(t)$, $E(t)$, $I(t)$ and $R(t)$ of the measles model are positive for all time

Proof: By employing the approach of ([27], [15]), it can be shown from the system (6) that

$$\left.\frac{dS}{dt}\right|_{S=0} = \pi > 0 \qquad \left.\frac{dE}{dt}\right|_{E=0} = \frac{\beta I}{S+I+R} \geq 0$$

$$\left.\frac{dI}{dt}\right|_{I=0} = \alpha E + \omega R \geq 0 \left.\frac{dR}{dt}\right|_{R=0} = \tau I + \sigma S \geq 0 \tag{11}$$

From (11), it is evident that all the rates of change on R_+^4 are non-negative. Since the vector field is directed inward on all bounding planes, then the non-negativity of the measles model (6) is established.

Existence and Uniqueness of Solutions

The measles model can be written as an initial value system in the form

$$\left.\begin{aligned} m^{!} &= F(m) \\ m(0) &= m_0 \end{aligned}\right\} \tag{12}$$

Where $m = (S,\ E,\ I,\ R)^T$ and $F = (f_1,\ f_2, \dots,\ f_4)^T$

$F(m)$ is Lipschitz continuous in m if there exists a constant $k > 0$ such that

$$\|F(m_1) - F(m_2)\| \leq k\|m_1 - m_2\| \quad (13)$$

Theorem 3:

There exists a unique solution $m(t)$ of the system (12) corresponding to the measles model (6)

Proof: The proof is based on satisfying the Lipschitz condition given in (13). Considering the first equation of the system (6) and keeping in mind that $N \leq \pi/\mu$ at the invariant region, one can show that

$$\|f_1(m_1) - f_2(m_2)\| \leq (2\beta + \sigma + \mu)\|m_1 - m_2\|$$

Similarly, putting other compartments of the system (6) into consideration, it can be shown that

$$\|f_2(m_1) - f_2(m_2)\| \leq (\alpha + \mu)\|m_1 - m_2\|$$
$$\|f_3(m_1) - f_3(m_2)\| \leq (\delta + \tau + \mu)\|m_1 - m_2\|$$
$$\|f_4(m_1) - f_4(m_2)\| \leq (\omega + \mu)\|m_1 - m_2\|$$

Consequently, $F(m)$ satisfies the Lipschitz condition

$$\|F(m_1) - F(m_2)\| \leq k\|m_1 - m_2\|$$

where $k = max\{(2\beta + \sigma + \mu),\ (\alpha + \mu),\ (\tau + \delta + \mu),\ (\omega + \mu)\}$.

Existence of Equilibrium Points and Stability Analysis

Measles-free equilibrium

The measles-free equilibrium point is a steady state solution where the entire population is free from infection. This can be obtained by simultaneously solving the system (6) such that the infection-related compartments are absent (i.e E = I = 0). Therefore, the measles-free equilibrium point of the model (6) is obtained as

$$\varepsilon_0 = (S_0, 0, 0, R_0) = \left(\frac{\pi}{\sigma+\mu}, 0, 0, \frac{\pi\sigma}{(\sigma+\mu)(\omega+\mu)}\right) \quad (14)$$

Effective reproduction number

One can use the effective basic reproduction number to determine the requirement for local stability of the measles-free equilibrium state. By definition, the average number of new secondary infection cases in the population of susceptible individuals brought on by a single infectious person is known as the basic reproduction number [28]. The basic reproduction number R_0 can be obtained using the next generation matrix approach by considering only the infection related compartment of the system (6) at ε_0. Then, the matrices F (transmission matrix depicting the incidence terms) and V (transition matrix) obtained at ε_0, are given, respectively by

$$F = \begin{pmatrix} \frac{\beta\theta\mu}{k_1} & \frac{\beta\mu}{k_1} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad (15)$$

$$V = \begin{pmatrix} k_2 & 0 & 0 \\ -\alpha & k_3 & -\omega \\ 0 & -\tau & k_4 \end{pmatrix} \quad (16)$$

Where $k_1 = (\mu + \sigma),\ k_2 = (\alpha + \mu), k_3 = (\tau + \mu)$ and $k_4 = (\mu + \omega)$. Then the basic reproduction number which the dominant eigenvalue of the spectral radius of FV^{-1} denoted R_0 is obtained as

$$R_0 = \frac{\beta\mu\{\theta(k_3k_4 - \omega\tau) + \alpha k_4\}}{k_1k_2(k_3k_4 - \omega\tau)} \quad (17)$$

It is important to state that $k_3k_4 > \omega\tau$ by algebraic simplification, thereby making the effective reproduction number positive. Hence the following result for the local stability of the steady state is claimed.

Proposition 1: The measles-free equilibrium point of the system (6) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

The implication of Proposition 1 is that the transmission of measles can be effectively curbed if the threshold parameter $R_0 < 1$.

Global Asymptotic stability of measles-free equilibrium

The global stability of the measles model (6) around the measles-free equilibrium point is carried out using the approach of [29], [18]. The system (6) is then restructured in a compact form as follows:

$$\frac{dX_1}{dt} = F(X_1, X_2)$$
$$\frac{dX_2}{dt} = G(X_1, X_2), G(X_1, 0) = 0 \quad (18)$$

where $X_1 \epsilon R_2^+$ and $X_2 \epsilon R_2^+$. The uninfected class is represented by the component $X_1 = (S, R)$ and the diseased class

is represented by the component $X_2 = (E, I)$ while the measles-free equilibrium is given by $\varepsilon_0 = (X_1^*, 0)$. Then, the following properties must be satisfied in order to establish the global asymptotic dynamics of the measles-free equilibrium

M_1: For $\frac{dX_1}{dt} = F(X_1^*, 0)$, X_1^* is globally asymptotically stable

M_2: $G(X_1, X_2) = AX_2 - \hat{G}(X_1, X_2)$, $\hat{G}(X_1, X_2) \geq 0$ for $(X_1, X_2) \in D$

where $A = \frac{\partial G}{\partial X_2}$ is a Metzler matrix evaluated at $(X_1^*, 0)$.

Theorem 4: The measles-free equilibrium point of the system (6) is globally asymptotically stable whenever $R_0 < 1$ and, properties M_1 and M_2 are satisfied.

Proof: The functions $F(X_1, X_2)$ and $G(X_1, X_2)$ are obtained from (18) as follows

$$F(X_1, X_2) = \begin{pmatrix} \pi - \frac{\beta(\theta E + I)}{N} - (\sigma + \mu)S \\ \tau I + \sigma S - (\omega + \mu)R \end{pmatrix} \quad (19)$$

and

$$G(X_1, X_2) = \begin{pmatrix} \frac{\beta(\theta E + I)S}{N} - (\alpha + \mu)E \\ \alpha E + \omega R - (\tau + \delta + \mu)I \end{pmatrix} \quad (20)$$

Evaluating (19) at disease-free equilibrium gives

$$F(X_1, 0) = \begin{pmatrix} \pi - (\sigma + \mu)S \\ \sigma S - (\omega + \mu)R \end{pmatrix} \quad (21)$$

Then $\frac{dX_1}{dt} = F(X_1, 0)$ means that

$$\begin{aligned} \frac{dS}{dt} &= \pi - (\sigma + \mu)S \\ \frac{dR}{dt} &= \sigma S - (\omega + \mu)R \end{aligned} \quad (22)$$

Solving (22) simultaneously yields

$$\begin{aligned} S(t) &= \frac{\pi}{\mu + \sigma} + \left(S(0) - \frac{\pi}{\mu + \sigma}\right) e^{-(\sigma + \mu)t} \\ R(t) &= \frac{\sigma\pi}{(\mu + \omega)(\sigma + \mu)} + \left(R(0) - \frac{\sigma\pi}{(\mu + \omega)(\sigma + \mu)}\right) e^{-(\mu + \omega)t} \end{aligned} \quad (23)$$

One can see that $(S, R) \longrightarrow \left(\frac{\pi}{\mu + \sigma}, \frac{\sigma\pi}{(\mu + \sigma)(\mu + \omega)}\right)$ as $t \longrightarrow \infty$, satisfying property M_1 and that X_1^* is globally asymptotically stable. Establishing Property M_2, the M-matrix with non-negative off diagonal entries is obtained as

$$A = \frac{\partial G}{\partial X_2}\Big|_{(X_1^*, 0)} = \begin{pmatrix} \frac{\beta\theta S^0}{N} - (\alpha + \mu) & \frac{\beta S^0}{N} \\ \alpha & -(\tau + \delta + \mu) \end{pmatrix} \begin{pmatrix} E \\ I \end{pmatrix} \quad (24)$$

Then, $G(X_1, X_2) = AX_2 - \hat{G}(X_1, X_2)$ gives

$$\begin{pmatrix} \frac{\beta\theta S^0 E}{N} - (\alpha + \mu)E + \frac{\beta I S^0}{N} \\ \alpha E - (\tau + \delta + \mu)I \end{pmatrix} - \begin{pmatrix} \frac{\beta\theta SE}{N} - (\alpha + \mu)E + \frac{\beta IS}{N} \\ \alpha E - (\tau + \delta + \mu)I \end{pmatrix}$$

$$\begin{pmatrix} \frac{\beta\theta E}{N}(S^0 - S) + \frac{\beta I}{N}(S^0 - S) \\ 0 \end{pmatrix} \quad (25)$$

Since $0 \leq S \leq S^0$ and $0 \leq R \leq R^0$, it is evident that $\hat{G}(X_1, X_2) \geq 0$ satisfying Property M_2.Therefore, the measles-free equilibrium point of the system (6) is globally asymptotically stable.

Measles-present Equilibrium

The measles-present equilibrium point is a steady state solution where there is presence of measles in the population. It is used to provide more insights into the long-term effects of the dynamical spread of measles in the population. Let the measles-present equilibrium point be denoted by $\mathcal{E}^{**} = (S^{**}, E^{**}, I^{**}, R^{**})$ and the measles force of infection be $\lambda^{**} = \frac{\beta(\theta E^{**} + I^{**})}{N^{**}}$ where $N^{**} = \pi/\mu$ at steady state. Then, solving (6) simultaneously as a function of λ^{**} yields

$$\begin{aligned} S^{**} &= \frac{\pi}{k_1 + \lambda^{**}} \\ E^{**} &= \frac{\pi\lambda^{**}}{k_2(k_1 + \lambda^{**})} \\ I^{**} &= \frac{\pi\{k_4\alpha\lambda^{**} + k_2\sigma\omega\}}{k_2(k_1 + \lambda^{**})\{k_3k_4 - \tau\omega\}} \\ R^{**} &= \frac{\pi\{\alpha\tau\lambda^{**} + k_2k_3\sigma\}}{k_2(k_1 + \lambda^{**})\{k_3k_4 - \tau\omega\}} \end{aligned} \quad (26)$$

Substituting E^{**} and I^{**} in (26) into the force of infection λ^{**} yields the following quadratic polynomial

$$A_1\lambda^{**2} + A_2\lambda^{**} - A_3 = 0 \quad (27)$$

where

$$A_1 = k_2(k_3k_4 - \omega\tau)$$
$$A_2 = k_1k_2(k_3k_4 - \omega\tau)\{1 - R_0\}$$
$$A_3 = k_2\beta\mu\sigma\omega$$

Consequently, it can be seen that $A_1 > 0$, $A_2 > 0$ if $R_0 < 1$ and $A_3 < 0$. Similarly, if $R_0 > 1$ in A_2, then by Descarte's rule there exists only one sign change. Hence, the system (6) exhibits a unique endemic equilibrium point. This means that the control of measles transmission in the population will not be difficult.

Global stability of endemic equilibrium point

Here, the investigation of the global asymptotic dynamics of the measles model (6) around the endemic equilibrium point is carried out. This is done using the approach of ([28], [15], [30]).

Theorem 5: The endemic equilibrium point of the measles model (6) is globally asymptotically stable whenever the effective reproduction number is greater than unity, $R_0 > 1$.

Proof: Consider the following positive definite quadratic Lyapunov function $\mathcal{L}: \Omega \in R_+^4 \to R_+$ defined by

$$\mathcal{L} = \frac{1}{2}\{(S - S^{**}) + (E - E^{**}) + (I - I^{**}) + (R - R^{**})\}^2 \qquad (28)$$

Differentiating (28) with respect to time gives

$$\dot{\mathcal{L}} = \{(S - S^{**}) + (E - E^{**}) + (I - I^{**}) + (R - R^{**})\}\frac{d}{dt}(S + E + I + R)$$
$$= \{(S - S^{**}) + (E - E^{**}) + (I - I^{**}) + (R - R^{**})\}\{\pi - \mu(S + E + I + R) - \delta I\}$$
$$\dot{\mathcal{L}} \leq \{(S - S^{**}) + (E - E^{**}) + (I - I^{**}) + (R - R^{**})\}\{\pi - \mu(S + E + I + R)\}$$
$$= \mu\{(S - S^{**}) + (E - E^{**}) + (I - I^{**}) + (R - R^{**})\}\left\{(S + E + I + R) - \frac{\pi}{\mu}\right\} \qquad (29)$$

Since $N^{**} = \frac{\pi}{\mu}$, then (29) becomes

$$\dot{\mathcal{L}} \leq \{(S - S^{**}) + (E - E^{**}) + (I - I^{**}) + (R - R^{**})\}$$
$$\times \{(S + E + I + R) - (S^{**} + E^{**} + I^{**} + R^{**})\}$$
$$\leq -\mu\{(S - S^{**}) + (E - E^{**}) + (I - I^{**}) + (R - R^{**})\}^2 \qquad (30)$$

Sufficiently, $\dot{\mathcal{L}} \leq 0$, indicating that the derivative of the Lyapunov function is negative semidefinite. Furthermore, $\dot{\mathcal{L}} = 0$ provided $S = S^{**}$, $E = E^{**}$, $I = I^{**}$ and $R = R^{**}$. Then, by LaSalle's invariance principle [31], the largest invariance set for which $\dot{\mathcal{L}} = 0$ is the singleton set $\{\mathcal{E}^{**}\}$, which implies that the endemic equilibrium point of the measles model (6) is globally asymptotically stable.

Sensitivity analysis

By calculating the sensitivity indices of the effective reproduction number, changes in the dynamics of measles are observed. According to the model's parameter values, sensitivity analysis is crucial for determining the most effective way to reduce the spread of measles by examining the relative critical aspects that contribute to its prevalence and transmission. Nonetheless, the ratio of the relative change in the variable to the relative change in the parameter is the normalized forward sensitivity index of a variable to a parameter [32], [33]. Therefore, the normalised forward sensitivity index of the effective reproduction number, R_0 relative to its parameter, h given by

$$\varkappa_h^{R_0} = \frac{\partial R_0}{\partial h} \times \frac{h}{R_0} \qquad (31)$$

When (31) is used, the sensitivity of the parameters associated with the effective reproduction number is calculated, the values of the parameters are presented in Table 3, and the result of the sensitivity index is presented in Table 4.

Table 3. Values of the parameters for the measles model

Parameter	Value	Source
β	0.40000	Assumed
α	0.50000	Asssumed
τ	0.06237	[34]
μ	0.00875	[19]
ω	0.09091	[19]
δ	0.03372	[34]

σ	0.00329	[34]

Table 4. Sensitivity indices of the parameters of the measles model

Parameter	Value	SI
β	0.40000	+1.0000
α	0.50000	+0.01456
τ	0.06237	−0.11390
μ	0.00875	−0.03011
ω	0.09091	+0.10390
δ	0.03372	−0.70144
σ	0.00329	−0.27301

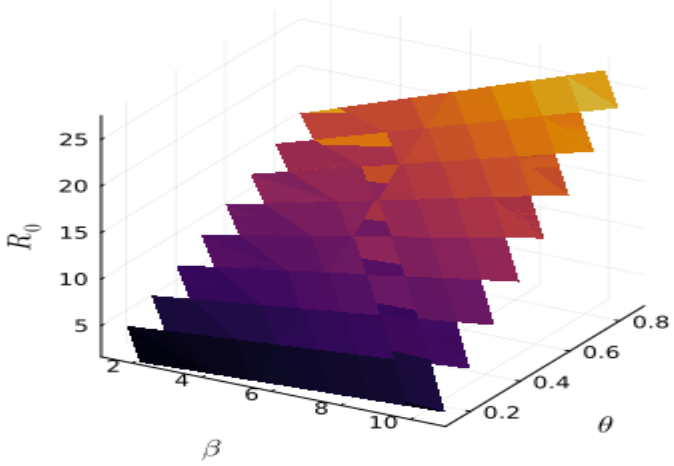

Figure 2. Impact of effective transmission rate β and modification parameter θ on R_0

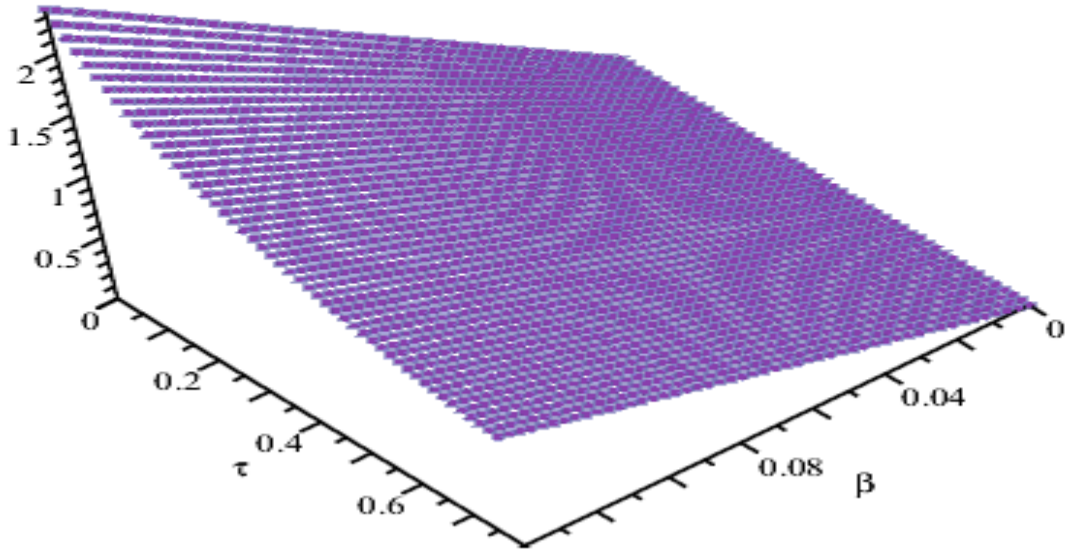

Figure 3. Effects of the treatment and effective contact rate on R_0

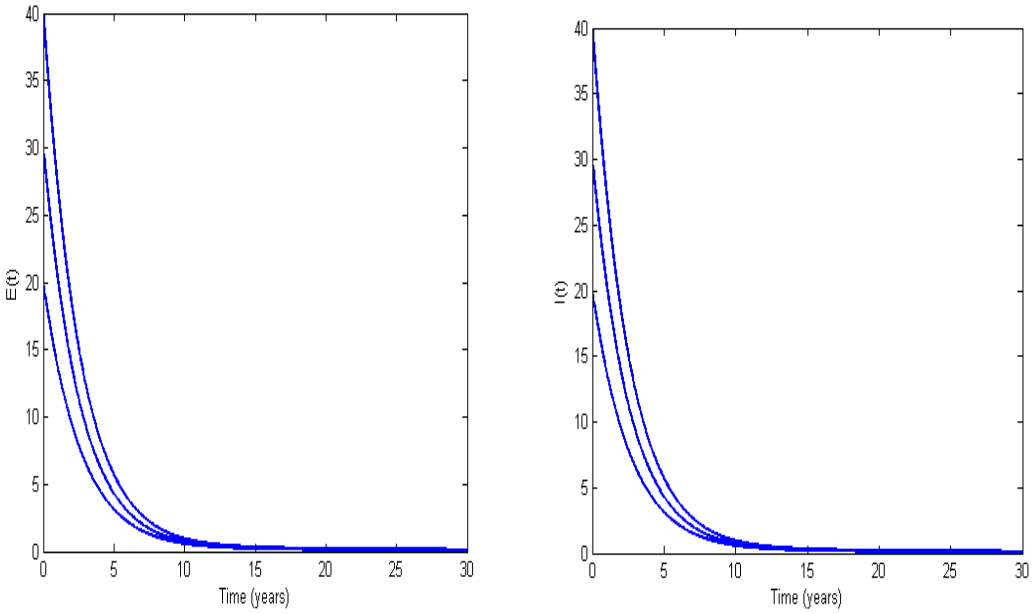

Figure 4. **Global asymptotic stability of infectious individuals around the measles-free equilibrium, indicating absence of infection regardless of the initial size of the population**

Result and Discussion

In this section, numerical simulations are performed using Julia and Maple computing software to support the analytical solutions of the measles model (6) established in Section 3, and the outcomes are presented graphically. It is pertinent to state that $R_0 = 0.59765$ when $\beta = 0.04$ at the measles-free equilibrium point and $R_0 = 5.97652$ when $\beta = 0.4$ at the measles-present equilibrium point. The practical implication of having $R_0 = 0.59765$ which is less than one is suggesting the elimination of measles completely in the population while $R_0 = 5.97652$ implies the persistence of measles in the population. The impact of the effective transmission rate and the modification parameter on the effective reproduction number are depicted in Figure 2. As observed, there is a consistent increase in R_0 as both parameters increased. This indicates that measles will persist in the population. The influence of treatment rate and the transmission rate is shown in Figure 3. It is evident that as the treatment rate increases, there is a corresponding decrease in the effective reproduction number. By implication, it means that treatment will go a long way in curbing or mitigating the spread of measles in the population. Figure 4 shows the convergence of the exposed and diseased population to the measles-free equilibrium point. This implies that measles can be controlled in the population, regardless of the system's population size. It should be noted that this result aligns with existing studies on global asymptotic models of infectious diseases [35], [15], [34]. The conduct of both the exposed and infected individuals at the endemic equilibrium is depicted in Figure 5. It is agreed that at any preceding rate of the infectious population, it will converge to a unique measles-present equilibrium

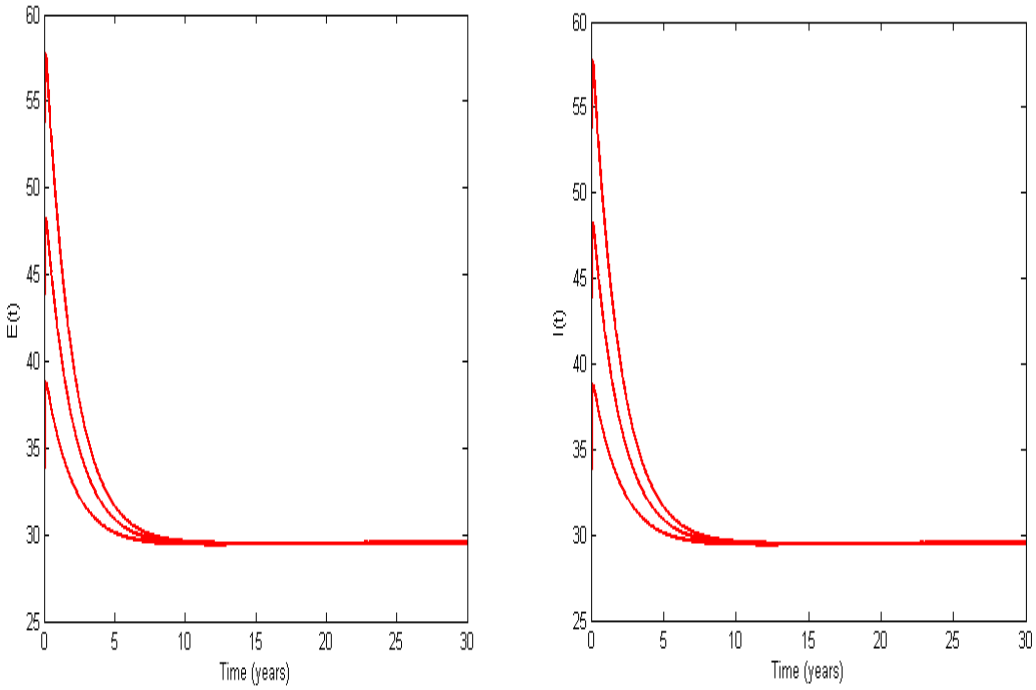

Figure 5. Global stability of infectious individuals at endemic equilibrium depicting the existence of measles in the population

Conclusion

A mathematical model incorporating vaccination to study the dynamics of measles transmission was formulated and rigorously analysed in this study. The model was stratified into four mutually exclusive compartments: susceptible individuals, exposed individuals, infected individuals, and recovered individuals, respectively, using a system of ordinary differential equations (ODEs). An analytical investigation of the system showed that it possesses two equilibrium points, the measles-free and measles-present equilibrium points. The principle of positivity and boundedness of solutions was used to investigate the well-posedness, while the existence and uniqueness of the solution were established using the Lipschitz condition.

Employing the next-generation matrix, the effective reproduction number was calculated, and the Castillo-Chavez method was used to ascertain the global asymptotic stability of the measles-free equilibrium. A quadratic Lyapunov function was used to determine the global asymptotic dynamics of the measles-present equilibrium. Furthermore, using the normalised forward sensitivity index, the influence of the parameters of the effective reproduction number was investigated, and the analysis revealed the critical parameters driving the dynamics of measles transmission, including the effective contact rate, vaccination rate, progression rate, and relapse rate. Numerical simulations further corroborated the qualitative findings. Additionally, policymakers and healthcare practitioners are advised to make a determined attempt to increase the values of parameters with negative sensitivity indices and reduce the values of parameters with positive sensitivity indices in order to curb the transmission of measles in the human population. It is worth noting that the values of the parameters used in this study were selected from the existing literature on the dynamics of measles transmission. The study recommends mass vaccination with an effective vaccine and social distancing to effectively control the dynamics of measles in the population. Real data can be used to validate the study's findings by fitting the model to actual measles case data in the population. This is one limitation of our study.

Author Contributions

O. A. conceptualized the problem; O. A., H. O. and S. O. did the formal analysis; H. O., S. O., W. O and J. I. wrote the original draft. All authors reviewed and edited the manuscript.

Data Availability

The data that support the findings of this study are available within the article

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Conflicts of Interest

The authors declare no conflict of interest

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