Journal of Basics and Applied Sciences Research (JOBASR)
ISSN (print): 3026-9091, ISSN (online): 1597-9962
Volume 3(3) May 2025
DOI: https://dx.doi.org/10.4314/jobasr.v3i3.22

Mathematical Modelling of Measles Disease with Double Dose Vaccination

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ABSTRACT

This article presents a mathematical model for measles disease incorporating double dose vaccination strategies as control measures. The model, developed using a system of differential equations, aims to understand the dynamics of measles transmission and the impact of vaccination interventions. The basic reproduction number, (R_0), is obtained using the next-generation operator, providing insights into the disease's transmission potential. Analysis of the model revealed that the disease-free equilibrium is locally and asymptotically stable when $R_0 < 1$ and unstable otherwise. Numerical simulations revealed a progressive reduction of susceptible individuals to zero over time, indicative of successful disease control. Sensitivity analysis identified the contact rate of infection (β) as positively influential on disease transmission, emphasizing the importance of reducing this parameter. Conversely, the vaccination rate (α_1) exhibited a negative sensitivity index, emphasizing the critical role of enhancing vaccination efforts in disease prevention. These findings highlight the effectiveness of vaccination campaigns and targeted interventions in controlling measles outbreaks. Recommendations include intensifying vaccination programs, promoting awareness, and adapting control measures to local contexts to sustain disease control efforts and prepare for future challenges. This study contributes to the evidence base for informed public health policies aimed at reducing measles transmission and improving population health outcomes.

Keywords:
Measles,
Mathematical modelling,
Infectious Disease,
Basic reproduction number,
Sensitivity Analysis,
Double Vaccinations,
Numerical Simulation.

INTRODUCTION

Measles, caused by the measles virus (MeV), is a highly contagious viral infection characterized by symptoms such as fever, cough, runny nose, red eyes, and a distinctive red rash. This disease can lead to severe complications, particularly in young children, including pneumonia, encephalitis, and even death (WHO 2023). Historical records dating back to at least the 9th century highlight measles as a longstanding human ailment, with large epidemics causing significant global morbidity and mortality before the advent of measles vaccination (NCDC 2023). The measles virus, classified within the Morbillivirus genus of the *Paramyxoviridae* family, spreads easily through respiratory droplets, surviving on surfaces and in the air for several hours, thereby facilitating transmission in crowded or poorly ventilated environments. Measles transmission occurs primarily through airborne particles expelled when infected individuals cough or sneeze. Additionally, direct contact with infected respiratory secretions or contaminated surfaces can contribute to the spread of the virus. Diagnosis of measles often relies on clinical manifestations, notably the characteristic rash and fever, especially in regions where measles is prevalent. Laboratory confirmation through blood tests or throat swabs may also be performed to confirm diagnosis

(WHO 2023). Vaccination stands as the most effective means of preventing measles, typically administered as part of the measles-mumps-rubella (MMR) or measles-mumps-rubella-varicella (MMRV) vaccine series. Beyond individual protection, vaccination fosters herd immunity, reducing disease transmission within communities (APP 2019). While supportive care is recommended to alleviate symptoms such as fever and hydration, no specific antiviral treatment exists for measles. Severe cases or complications may necessitate hospitalization and supportive therapies. Despite global declines in measles incidence following vaccination program implementation, outbreaks persist, often exacerbated by inadequate immunization coverage (NCDC 2021). Measles poses significant health risks, particularly to vulnerable populations such as young children and individuals with compromised immune systems. Complications may include pneumonia, encephalitis, blindness, and mortality. Even in non-fatal cases, measles can weaken the immune system, rendering individuals susceptible to secondary infections for weeks to months post-recovery. The measles vaccine, administered in two doses typically at 12-15 months and 4-6 years of age, provides durable immunity, offering over 95% protection against measles (Agbata *et al*, 2019). The aim of the study is to mathematically model the transmission dynamics of measles disease in a population with a focus on the effect of double dose vaccination on disease control and elimination the objectives include.

1. Model Development: To develop a mathematical model that describes the transmission dynamics of measles disease, incorporating parameters such as population demographics, contact rates, transmission probabilities, and vaccination coverage.
2. Validation: To validate the mathematical model using historical measles outbreak data, ensuring that the model accurately captures the observed patterns of disease spread.
3. Parameter Estimation: To estimate model parameters such as the basic reproduction number (R_0), vaccine efficacy, and duration of vaccine-induced immunity from available epidemiological data and literature.
4. Vaccination Scenarios: To investigate the impact of different vaccination strategies, including single dose and double dose vaccination schedules, on the transmission dynamics of measles disease. Compare the effectiveness of these strategies in reducing measles incidence and achieving disease elimination goals.
5. Sensitivity Analysis: Perform sensitivity analysis to identify key parameters and factors influencing the effectiveness of vaccination strategies. Determine the robustness of model predictions to variations in parameter values and assumptions.

Smith and Shim (2020), provided a detailed examination of mathematical modeling's role in understanding measles outbreaks and control strategies. They stressed the need to integrate data-driven methods with mathematical models to enhance decision-making in measles control. Their review highlights the challenges posed by factors like population mixing and vaccine hesitancy, underscoring ongoing research's importance in refining models for effective public health intervention.

Yiman *et al.* (2020), employ mathematical modeling to assess the impact of double-dose measles vaccination on disease transmission. Their study, utilizing an SEIR model, compares single and double dose vaccination strategies, finding that the latter significantly boosts population immunity and reduces measles outbreak risks. Their findings underscore the necessity of high vaccination coverage and sustained immunity to maintain measles elimination efforts. Some of the relevant mathematical models include. (Achneje *et al*, 2024; Odeh *et al*, 2024; Stephen *et al*, 20214; Vanden-Driessche and Watmough, 2002; Oko *et al*, 2023).

MATERIALS AND METHODS

Model Formulation

The total population $N(t)$, is divided into six epidemiological groups: susceptible individuals (S),, individuals who have received the first dose of vaccination but can still be infected due to vaccine failure (V_1),, individuals who have completed the second dose of vaccine (V_2), exposed individuals (E), infected individuals (I), and recovered individuals (R). Let λ be the constant recruitment rate. Suppose ρ denotes the fraction of individuals who refused vaccination before entering the population, and $(1-\rho)$ represents individuals who have taken the first dose of vaccine before entering the population, where α_1 is the rate at which susceptible individuals take the first dose of vaccine, and β denotes the probability of transmission by an infected individual with measles. ω is the rate at which those who took the first dose of vaccine become exposed due to vaccine failure, and ψ denotes the rate at which initially vaccinated individuals become infected due to vaccine failure. α_2 is the rate of vaccination of initially vaccinated individuals, α_3 represents the recovery rate of vaccinated individuals, σ is the rate at

which exposed individuals become infected, and f is the recovery rate of infected individuals. μ represents the natural death rate, and ε is the disease-induced death rate.

Model Assumptions

The model is developed under the following mathematical assumptions

1. Uniform Interaction: The model assumes that individuals within the population mix uniformly, meaning everyone has an equal likelihood of encountering others.
2. Stable Population Size: Throughout the model, the total population remains constant, with negligible birth and death rates over the modeled period.
3. First Vaccination Dose Group (V1): These individuals have had one dose of the measles vaccine but can still be susceptible to infection due to vaccine ineffectiveness.
4. Vaccine Effectiveness and Failures: We assumed that individuals receiving the first vaccine dose might still become exposed or infected due to vaccine failure, indicating that the vaccine isn't entirely effective after the initial dose.
5. Duration of Immunity: The model assumes that individuals who recover from measles or complete the vaccination series (two doses) gain immunity for a certain period, with the possibility of immunity waning over time.

Transmission Dynamics: The model follows a susceptible-infected-recovered (SIR) framework, with individuals transitioning between susceptible, infected, and recovered states based on transmission rates and probabilities.

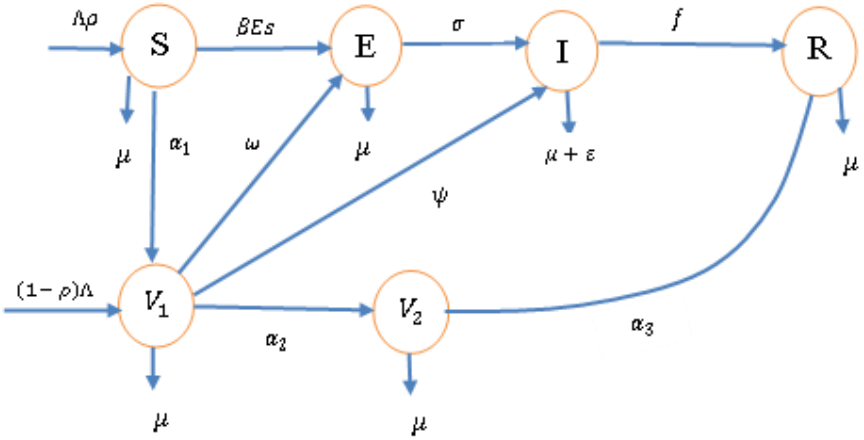

Figure: 1 Schematic diagram for the Model

Figure 1 (Agbata *et al*, 2024) serves a pivotal role by visually representing the structure, interactions, and dependencies within a model. This diagram provides a clear framework for organizing variables, parameters, and equations, helping modelers conceptualize and communicate the complexities of the system under study. It facilitates the formulation of mathematical relationships and the establishment of initial conditions or constraints, guiding the development and validation of the model against empirical data or theoretical principles (Odeh *et al*, 2024). Additionally, schematic diagram enhances transparency and enable effective collaboration among researchers by serving as a common visual language to discuss and refine model designs across diverse scientific disciplines.

Model Equation

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda\rho - (\beta E + \alpha_1 + \mu)\mathrm{S} \\
\frac{d\,\mathrm{V}_1}{dt} &= (1-\rho)\Lambda + \alpha_1 \mathrm{S} - (\omega + \psi + \alpha_2 + \mu)\,\mathrm{V}_1 \\
\frac{d\,\mathrm{V}_2}{dt} &= \alpha_2\,\mathrm{V}_1 - (\alpha_3 + \mu)\,\mathrm{V}_2 \\
\frac{dE}{dt} &= \beta SE + \omega\,\mathrm{V}_1 - (\sigma + \mu)\,\mathrm{E} \\
\frac{dI}{dt} &= \sigma E + V_1\psi - (f + \varepsilon + \mu)\,\mathrm{I} \\
\frac{dR}{dt} &= fI + \alpha_3\,\mathrm{V}_2 - \mu R
\end{aligned}\right\} \quad (1)$$

Variables and Parameters Interpretation

Table 1. Parameters and variables used.

Variables	**Interpretation**
$S(t)$	Susceptible population
$V_1(t)$	First dose of vaccinated humans
$V_2(t)$	Second dose of vaccinated individuals due to vaccine failure
$E(t)$	Exposed individuals
$I(t)$	Infected individuals
$R(t)$	Recovered humans at time t
Parameter	**Description**
Λ	Constant recruitment rate of susceptible individuals
ρ	Rate of unvaccinated individuals
$1-\rho$	Rate of initial vaccination
β	Contact rate of infection
α_1	Vaccination rate of susceptible individuals
α_2	Rate of second dose vaccination of V_1
α_3	Recovery rate of vaccinated individuals
ω	Progression rate from V_1 to E
ψ	Progression rate from V_1 to I
μ	Natural death rate
ε	Disease induced death
f	Recovery rate of infected individuals

Invariant Region of the Model

In dynamical system, invariant region (D) refers to a subset of the state space of a system where all solutions of the system remain within (D) for all t > 0 (Bhatia and Szego, 2023). Thus D is invariant if for every initial condition $x(0) \in D$, the solution $x(t)$ satisfies $x(t) \in D$ for all t > 0. Invariant region is fundamental for analyzing the long-term behavior and stability properties of dynamical systems as it provides insights into whether trajectories converge, remain bounded, or exhibit specific qualitative behavior within the defined region D

Theorem 1

The model solutions are feasible for all t > 0, if they are contained in the invariant region D, which is given by:

$$D=\left\{\begin{array}{l}\left(S,V_1,V_2,E,I,R\right)\in R_+^6:\\ S>0,V_1>0,V_2>0,E>0,\\ I>0,R>0,N<\dfrac{\Lambda}{\mu}\end{array}\right\}$$

Proof:

The total population of the model is given as

$$N(t)=S+V_1+V_2+E+I+R$$

Adding thethe differential equations is

$$N'(t)=S'+V_1'+V_2'+E'+I'+R'$$

On evaluating the algebraic terms, we obtain

$$N'(t)=\Lambda-\left(S+V_1+V_2+E+I+R\right)\mu-\varepsilon I$$

$$N'(t)=\Lambda-\mu N-\varepsilon_1 I$$

$$\frac{dN}{dt}\le\Lambda-\mu N$$

Solving the differential equation using the integrating factor method, we obtained

$$N(t) \le \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu} \right) e^{-\mu t}$$

Applying Birkhoff and Rota's theorem on the inequality, we obtain

$$0 \le N \le \frac{\Lambda}{\mu} \text{ as } t \to \infty$$

Therefore, D remains a positively invariant set within the trajectory outlined by model (1), ensuring that no solution trajectory exits through the boundary of region *D*. Consequently, within this domain, the model can be deemed both epidemiologically and mathematically well-defined .

Epidemiological Meaning of the fraction $\frac{\Lambda}{\mu}$

In the model, the ratio $\frac{\Lambda}{\mu}$ holds significance in understanding the demographic dynamics of the population in relation to the spread of measles. The constant recruitment rate (Λ) signifies the rate at which new individuals are added to the population, either through birth or migration. In the case of measles, this influx of susceptible individuals into the population could contribute to the pool of individuals who are at risk of contracting the disease. On the other hand, the natural death rate (μ) represents the rate at which individuals in the population die due to causes unrelated to measles infection. This includes deaths from old age, diseases other than measles, accidents, and other non-measles-related factors (Diekmann & Heesterbeek, 2000).

Therefore, the ratio $\frac{\Lambda}{\mu}$ indicates the balance between the addition of new susceptible individuals to the population and the removal of individuals through natural mortality. In the context of measles, a higher $\frac{\Lambda}{\mu}$ ratio suggests a population with a greater influx of susceptible individuals, potentially leading to a higher likelihood of measles transmission and outbreaks. Conversely, a lower ratio indicates a population where natural deaths are more prevalent, which may reduce the pool of susceptible individuals and thus the potential for measles transmission (Gao *et al*, 2016)

Understanding the $\frac{\Lambda}{\mu}$ ratio within the measles disease model helps assess the population's vulnerability to measles outbreaks and aids in designing effective vaccination strategies and public health interventions.

Positivity of Solution of the Model

Demonstrating the non-negativity of all state variables of the model throughout time is essential to establish the epidemiological and mathematical validity of the model within a feasible region D as defined by:

$$D = \left\{ \begin{matrix} \left(S, \mathrm{V}_1, V_2, E, I, \mathrm{R} \right) \in R_+^6 : \\ \left(S + V_1 + V_2 + E + I + R \right) \le N \end{matrix} \right\}$$

This is done by considering,

$$\left\{ \left(S, \mathrm{V}_1, V_2, E, I, R \right) \ge 0 \in R_+^6 \right\}$$

Lemma 1:

Let the initial data for the model (1) be $\left(S, \mathrm{V}_1, V_2, E, I, R \right) > 0$. Then the solutions $\left(S, \mathrm{V}_1, V_2, E, I, R \right)$ of the model (2) are positive for all time $t > 0$

Proof

Let $t_1 = \sup \left\{ \begin{matrix} t > 0 : S > 0, \mathrm{V}_1 > 0, V_2 > 0, E > 0, \\ I > 0, R > 0 \in [0, t] \end{matrix} \right\}$

. Thus $t > 0.$

We have from the first equation that

$$\frac{dS}{dt} = \Lambda - (\beta E + \mu) S$$

$$\frac{dS}{dt} \ge -(\beta E + \mu) S$$

This can also be written as

$$\int \frac{dS}{S} \ge -\int (\beta E + \mu) dt$$

We obtained:

$$\ln S \ge -(\beta E + \mu) t + C$$

$$S(t) \ge C e^{-(\beta E + \mu) t}$$

Applying the given initial condition; when $t = 0,\ S(0) = C$

Therefore, $S(t) \ge S(0) e^{-(\beta E + \mu) t} \ge 0$ since $(\beta E + \mu) > 0$

Similarly, it can be demonstrated that $\mathrm{V}_1, V_2, E, I, R$ are positive for all $t > 0$

Asymptotic Stability of the Disease Free Equilibrium of the Model

The concept of "disease-free equilibrium" in epidemiological modeling refers to a scenario where there are no infected individuals in a population, signifying that the disease is not spreading (Bhatia and Szego 2023). Disease-free equilibrium occurs when interventions like vaccination or isolation have effectively halted the transmission of the disease. Understanding this equilibrium is essential for

assessing the feasibility of disease eradication efforts and the impact of public health measures. At this state where there is no infection (or absence of disease), $E = I = R = 0$. The disease-free equilibrium model (1) denoted η_0 is given by

$$\eta_0 = \left\{ S^*, V_1^*, V_2^*, E^*, I^* R^* > 0 \right\}$$

$$= \left\{ \frac{\Lambda\rho}{\mu}, \frac{(1-\rho)\Lambda + \alpha_1\Lambda}{(\omega+\psi+\alpha_2+\mu)}, \frac{(1-\rho)\alpha_2\Lambda + \alpha_1\alpha_2\Lambda}{(\omega+\psi+\alpha_2+\mu)(\alpha_3+\mu)}, 0, 0, 0 \right\}$$

Basic Reproduction Number (R_0) of the Model

The basic reproduction number R_0 for infected individuals represents the average number of secondary infections generated by a single infectious individual within an entirely susceptible population throughout their entire infectious period (Diekmann & Heesterbeek, 2000). This metric is determined through the application of the next-generation operator to the dynamic system outlined in model (1).

Hence, it follows that

$R_0 = \rho\left(FV^{-1}\right)$ ρ is given by dominant eigen value of FV^{-1}

$$F = \begin{bmatrix} \frac{\beta\rho\Lambda}{\mu} & 0 \\ 0 & 0 \end{bmatrix} \quad V = \begin{bmatrix} P_4 & 0 \\ -\sigma & P_5 \end{bmatrix}$$

$$F.V^{-1} = \begin{bmatrix} \frac{\beta\rho\Lambda}{\mu P_4} & 0 \\ 0 & 0 \end{bmatrix}$$

Therefore the basic reproduction number of the model is

$$R_0 = \frac{\beta\rho\Lambda}{\mu P_4} \text{ where } \mu P_4 \neq 0$$

The basic reproduction number (R_0) of an infectious disease is a critical epidemiological measure indicating the average number of secondary infections generated by a single infected individual in a fully susceptible population, without any interventions. It depends on factors such as the mode of transmission, duration of infectiousness, contact rates, and the likelihood of transmission per contact. This metric guides public health strategies by highlighting the need for interventions like vaccination, quarantine, and behavior modification to reduce R_0 and mitigate the spread of measles diseases.

Local Asymptotic Stability of the DFE of the Model

Local stability in mathematical modeling, such as in epidemiology, refers to how a system behaves near an equilibrium point. An equilibrium is a balanced state, like when the number of infected people in a disease model stops changing (Agbata *et al*, 2024). Local stability means that if this balance is slightly disturbed, the system will eventually return to that point. Mathematicians study this by simplifying the equations around the equilibrium and observing their reactions to small changes. This analysis helps predict whether a disease outbreak will fade away (if the equilibrium is stable) or potentially grow (if it is unstable). Understanding local stability is crucial for comprehending how diseases spread and how interventions can effectively control them.

Theorem 2

The disease-free equilibrium point of the is locally asymptotically stable (LAS) if $R_0 < 1$, *and unstable if* $R_0 > 1$.

Proof

Using Jacobian matrix to prove the local stability of the disease free equilibrium point

$$J(\varepsilon_0) = \begin{bmatrix} -P_1 & 0 & 0 & \frac{-\beta\rho\Lambda}{\mu} & 0 & 0 \\ \alpha_1 & -P_2 & 0 & 0 & 0 & 0 \\ 0 & \alpha_2 & -P_3 & 0 & 0 & 0 \\ \frac{\beta\rho\Lambda}{\mu} & \omega & 0 & \frac{\beta\rho\Lambda}{\mu} - P_4 & 0 & 0 \\ 0 & \psi & 0 & \sigma & -P_5 & 0 \\ 0 & 0 & \alpha_3 & 0 & f & -P_6 \end{bmatrix}$$

Since the diagonal of the first and last column consist of only the diagonal element, we can reduce $J(\varepsilon_0)$ to

$$J_1(\varepsilon_0) = \begin{bmatrix} -P_1 & 0 & 0 & \frac{-\beta\rho\Lambda}{\mu} \\ \alpha_1 & -P_2 & 0 & 0 \\ 0 & \alpha_2 & -P_3 & 0 \\ \frac{\beta\rho\Lambda}{\mu} & \omega & 0 & \frac{\beta\rho\Lambda}{\mu} - P_4 \end{bmatrix}$$

The characteristics polynomial of $J_1(\varepsilon_0)$ is

$$\lambda^4+\frac{\left(P_1\mu+P_2\mu+P_3\mu+P_4\mu-\beta\rho\Lambda\right)\lambda^3}{\mu}+\frac{\left(\beta\rho\Lambda\beta\rho\Lambda+P_2P_1\mu^2+P_3P_1\mu^2+P_1P_4\mu^2-P_1\beta\mu\rho\Lambda+P_3P_2\mu^2+P_2P_4\mu^2-P_2\beta\mu\rho\Lambda+P_3P_4\mu^2-P_3\beta\mu\rho\Lambda\right)\lambda^2}{\mu^2}+$$

$$\frac{\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\beta\rho\Lambda\beta\rho\Lambda P_3+P_3P_2P_1\mu^2+P_1P_2P_4\mu^2-P_1P_2\beta\mu\rho\Lambda+P_1P_3P_4\mu^2-P_1P_3\beta\mu\rho\Lambda+P_2P_3P_4\mu^2-P_2P_3\beta\mu\rho\Lambda+\omega\alpha_1\beta\rho\Lambda\mu\right)\lambda}{\mu^2}+$$

$$\frac{P_3\left(\beta\rho\Lambda\beta\rho\Lambda P_2+P_1P_2P_4\mu^2-P_1P_2\beta\mu\rho\Lambda+\omega\alpha_1\beta\rho\Lambda\mu\right)}{\mu^2}$$

$$\lambda^4+\frac{\left(P_1\mu+P_2\mu+P_3\mu+P_4\mu-\beta\rho\Lambda\right)\lambda^3}{\mu}+\frac{\left(\beta\rho\Lambda\beta\rho\Lambda+P_2P_1\mu^2+P_3P_1\mu^2+P_1P_4\mu^2-P_1\beta\mu\rho\Lambda+P_3P_2\mu^2+P_2P_4\mu^2-P_2\beta\mu\rho\Lambda+P_3P_4\mu^2-P_3\beta\mu\rho\Lambda\right)\lambda^2}{\mu^2}+$$

$$\frac{\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\beta\rho\Lambda\beta\rho\Lambda P_3+P_3P_2P_1\mu^2+P_1P_2P_4\mu^2-P_1P_2\beta\mu\rho\Lambda+P_1P_3P_4\mu^2-P_1P_3\beta\mu\rho\Lambda+P_2P_3P_4\mu^2-P_2P_3\beta\mu\rho\Lambda+\omega\alpha_1\beta\rho\Lambda\mu\right)\lambda}{\mu^2}+$$

$$\frac{P_3\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\omega\alpha_1\beta\rho\Lambda\mu\right)}{\mu^2}+\frac{P_3\left(P_1P_2P_4\mu^2-P_1P_2\beta\mu\rho\Lambda\right)}{\mu^2}$$

$$\lambda^4+\frac{\left(P_1\mu+P_2\mu+P_3\mu+P_4\mu-\beta\rho\Lambda\right)\lambda^3}{\mu}+\frac{\left(\beta\rho\Lambda\beta\rho\Lambda+P_2P_1\mu^2+P_3P_1\mu^2+P_1P_4\mu^2-P_1\beta\mu\rho\Lambda+P_3P_2\mu^2+P_2P_4\mu^2-P_2\beta\mu\rho\Lambda+P_3P_4\mu^2-P_3\beta\mu\rho\Lambda\right)\lambda^2}{\mu^2}+$$

$$\frac{\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\beta\rho\Lambda\beta\rho\Lambda P_3+P_3P_2P_1\mu^2+P_1P_2P_4\mu^2-P_1P_2\beta\mu\rho\Lambda+P_1P_3P_4\mu^2-P_1P_3\beta\mu\rho\Lambda+P_2P_3P_4\mu^2-P_2P_3\beta\mu\rho\Lambda+\omega\alpha_1\beta\rho\Lambda\mu\right)\lambda}{\mu^2}+$$

$$\frac{P_3\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\omega\alpha_1\beta\rho\Lambda\mu\right)}{\mu^2}+\frac{P_1P_2P_3\mu\left(P_4\mu-\beta\rho\Lambda\right)}{\mu^2}$$

$$\lambda^4+\frac{\left(P_1\mu+P_2\mu+P_3\mu+P_4\mu-\beta\rho\Lambda\right)\lambda^3}{\mu}+\frac{\left(\beta\rho\Lambda\beta\rho\Lambda+P_2P_1\mu^2+P_3P_1\mu^2+P_1P_4\mu^2-P_1\beta\mu\rho\Lambda+P_3P_2\mu^2+P_2P_4\mu^2-P_2\beta\mu\rho\Lambda+P_3P_4\mu^2-P_3\beta\mu\rho\Lambda\right)\lambda^2}{\mu^2}+$$

$$\frac{\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\beta\rho\Lambda\beta\rho\Lambda P_3+P_3P_2P_1\mu^2+P_1P_2P_4\mu^2-P_1P_2\beta\mu\rho\Lambda+P_1P_3P_4\mu^2-P_1P_3\beta\mu\rho\Lambda+P_2P_3P_4\mu^2-P_2P_3\beta\mu\rho\Lambda+\omega\alpha_1\beta\rho\Lambda\mu\right)\lambda}{\mu^2}+$$

$$\frac{P_3\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\omega\alpha_1\beta\rho\Lambda\mu\right)}{\mu^2}+\frac{P_1P_2P_3P_4\mu^2\left(1-\frac{\beta\rho\Lambda}{P_4\mu}\right)}{\mu^2}$$

$$\lambda^4+\frac{\left(P_1\mu+P_2\mu+P_3\mu+P_4\mu-\beta\rho\Lambda\right)\lambda^3}{\mu}+\frac{\left(\beta\rho\Lambda\beta\rho\Lambda+P_2P_1\mu^2+P_3P_1\mu^2+P_1P_4\mu^2-P_1\beta\mu\rho\Lambda+P_3P_2\mu^2+P_2P_4\mu^2-P_2\beta\mu\rho\Lambda+P_3P_4\mu^2-P_3\beta\mu\rho\Lambda\right)\lambda^2}{\mu^2}+$$

$$\frac{\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\beta\rho\Lambda\beta\rho\Lambda P_3+P_3P_2P_1\mu^2+P_1P_2P_4\mu^2-P_1P_2\beta\mu\rho\Lambda+P_1P_3P_4\mu^2-P_1P_3\beta\mu\rho\Lambda+P_2P_3P_4\mu^2-P_2P_3\beta\mu\rho\Lambda+\omega\alpha_1\beta\rho\Lambda\mu\right)\lambda}{\mu^2}+$$

$$\frac{P_3\left(\beta\rho\Lambda\beta\rho\Lambda P_2+\omega\alpha_1\beta\rho\Lambda\mu\right)}{\mu^2}+P_1P_2P_3P_4\left(1-R_0\right)$$

Applying Routh-Hurwitz criterion to the Characteristics polynomial, we have that

$$\left(1-R_0\right)>0$$

$$\Rightarrow R_0<1$$

Thus the DFE point of the model is locally asymptotically stable.

Where

$$P_1=(\alpha_1+\mu),P_2=(\omega+\psi+\alpha_2+\mu),P_3=(\alpha_3+\mu),P_4=(\sigma+\mu),$$

Remark: Epidemiologically,

(i) *if* $R_0<1$

When R_0 is less than 1, each infected person, on average, infects fewer than one other person. This suggests that the disease is unlikely to spread

extensively and will eventually die out in the population without intervention. Actions in this scenario typically include:

- Monitoring and Surveillance: Despite the low R_0, continued monitoring and surveillance are essential to detect and respond to any potential outbreaks.
- Prompt Case Management: Early detection, isolation of cases, and treatment remain important to prevent sporadic cases from leading to larger outbreaks.
- Maintaining Population Immunity: Ensuring high vaccination coverage and immunity in the population can prevent the disease from gaining a foothold and spreading (Anderson and May 1992).

$(ii)\ if\ \ R_0 = 1$

When R_0 equals 1, each infected person, on average, infects exactly one other person. In this scenario, the disease persists at a stable endemic level within the population. Actions typically include:

- Maintaining Endemic Control: Further research is needed to sustain effective control measures that keep R_0 stable at 1. Understanding factors that maintain endemic stability, such as population immunity levels and seasonal variations, can guide ongoing public health strategies.
- Sustaining Control Measures: Continual vaccination programs and public health interventions are necessary to keep R_0 at 1 or below and prevent sporadic outbreaks.
- Enhancing Surveillance: Monitoring disease trends and maintaining robust surveillance systems to detect any changes in transmission dynamics.
- Adapting Response Strategies: Flexibility in response strategies to address changes in disease patterns or population immunity over time (Diekmann *et al*, 1990; Diekmann & Heesterbeek, 2012).
- $(iii)\ if\ \ R_0 > 1$

When the basic reproduction number (R_0) is greater than 1, each infected individual, on average, spreads the disease to more than one other person. This indicates that the disease has the potential to spread rapidly within a susceptible population and may lead to outbreaks or epidemics. In such cases, proactive measures are crucial:

- Understanding Transmission Dynamics: Further research is essential to investigate deeper into the specific factors influencing transmission, such as modes of transmission (e.g., respiratory, fecal-oral), contact patterns, and environmental factors that facilitate spread. This knowledge can inform more targeted interventions to reduce R_0 and prevent large outbreaks.
- Vaccine Development: Research into developing effective vaccines is crucial, especially for diseases with high R_0 values like measles or influenza. Vaccination plays a critical role in reducing susceptibility and lowering R_0, thereby preventing widespread transmission.
- Behavioral Studies: Investigating human behavior related to disease transmission, such as compliance with preventive measures (e.g., hand hygiene, mask-wearing), can provide insights into strategies for promoting behavioral change and reducing R_0 (Heesterbeek and Dretz, 1996)

Epidemiological Implication of Basic Reproduction Less than 1 ($R_0 < 1$)

When the basic reproduction number (R_0) is less than 1, it indicates that, on average, each infected individual will transmit the measles virus to fewer than one other individual during their infectious period. This finding holds significant epidemiological implications for the dynamics of measles transmission and control efforts. A basic reproduction number below 1 suggests that the disease is not self-sustaining within the population. In other words, the chain of transmission is not perpetuated, and the number of new infections generated by each existing case is insufficient to maintain the disease at endemic levels. Instead, the infection tends to die out over time as the number of susceptible individuals decreases due to immunity acquired through vaccination or recovery from previous infection (Fine, 2019).

From an epidemiological perspective, a basic reproduction number below 1 is a promising sign for disease control and elimination efforts. It signifies that the spread of measles is inherently limited within the population, making it more sfeasible to implement interventions aimed at reducing transmission and preventing outbreaks. With an (R_0) less than 1, there's a reduced risk of widespread measles transmission within the community. Control measures such as vaccination campaigns, contact tracing, isolation of cases, and public health education can be more effective in containing the disease and preventing its resurgence. Vaccination strategies, in particular, play a crucial role in boosting population immunity and reducing the pool of susceptible individuals, further

lowering the likelihood of measles transmission. (Brauer *et al*, 2019).

Furthermore, a basic reproduction number below 1 indicates the potential for achieving measles elimination in a given population. Elimination occurs when the disease is no longer continuously transmitted within a defined geographic area or population group. By maintaining high vaccination coverage and implementing robust surveillance systems to detect and respond to sporadic cases, it becomes possible to interrupt the chain of transmission and achieve sustained measles control (Britton, 2020).

A basic reproduction number (R_0) less than 1 provides valuable information to epidemiologists, health workers, and policymakers, assisting them in several key ways:

Guiding Control Strategies: Epidemiologists rely on the (R_0) value to assess disease transmission potential and devise appropriate control measures. A (R_0) below 1 indicates that the disease is not self-sustaining, guiding decisions on the intensity and duration of interventions such as vaccination campaigns and case isolation (Britton, 2020).

1. Optimizing Resource Allocation: Health workers and policymakers can allocate resources more effectively based on the (R_0) value. With (R_0) below 1, resources can be prioritized for interventions in areas with the highest risk of transmission, ensuring maximum impact.
2. Informing Vaccination Strategies: For vaccine-preventable diseases like measles, knowledge of (R_0) below 1 underscores the importance of achieving high vaccination coverage. This information guides vaccination strategies and coverage targets to interrupt transmission (Fine, 2019).
3. Supporting Policy Decisions: Policymakers use epidemiological data, including (R_0), to make informed decisions about public health policies. A (R_0) below 1 provides evidence of effective control measures, supporting continued investment in disease prevention programs.
4. Monitoring Progress towards Goals: Epidemiologists monitor progress towards disease control and elimination goals using (R_0) as a metric. Regular surveillance of disease dynamics helps detect changes in (R_0) and ensures ongoing progress towards elimination targets.

Global Asymptotic Stability of the Disease free equilibrium Point of the Model.

In mathematical epidemiology, global stability is a crucial concept that pertains to the long-term behavior of infectious disease models. It centers on the equilibrium points of these models, specifically the disease-free equilibrium (DFE) and the endemic equilibrium (EE) (Braver and Castillo-Chavez 2012). The DFE represents a state where there are no infected individuals in the population, indicating the disease has been eradicated under prevailing conditions. Conversely, the EE signifies a stable state where infections persist at a steady level over time (Agbata *et al*, 2024). The stability of these equilibria is assessed through rigorous mathematical analyses rooted in dynamical systems theory. Stability analysis examines how small deviations from equilibrium conditions influence the system's trajectory over time. A disease-free equilibrium is deemed globally stable if any disruptions from this state lead the system back towards the absence of infections asymptotically. Similarly, an endemic equilibrium is considered globally stable if the system tends to persistently maintain a stable level of infections despite perturbations .

The implications of global stability analysis are profound for public health strategies. If a disease-free equilibrium is globally stable, it suggests that disease eradication is achievable through interventions such as widespread vaccination or effective containment measures (Bolaji *et al.* 2024). Conversely, if an endemic equilibrium is globally stable, it implies that the disease will persist unless sustained efforts are made to control transmission. This understanding guides policymakers and health authorities in formulating effective measures to combat outbreaks, manage endemic diseases, and potentially eliminate infectious diseases from populations (Braver and Castillo-Chavez 2012). To investigate the global stability of the disease free equilibrium, we apply the method implemented by.

We write the equation in the uninfected class as

$$\frac{dX}{dt} = F(X, Z)$$

And we re-write the equation in the infected class as

$$\frac{dz}{dt} = G(X, Z)$$

Where $X = S \in R^1_+$ represents the uninfected compartment and

$Z = (E, I, R) \in R^3_+$ represents the infected compartment

$\varepsilon_0 = (X^*, 0)$ denotes the disease free equilibrium of the system, and it globally

asymptotically stable if it satisfies the following conditions:

$$H_1: \frac{dX}{dt} = F\left(X^*, 0\right), X^* \text{ is globally}$$

asymptotically stable

$$H_2: \frac{dZ}{dt} = D_Z G\left(X^*, 0\right) Z - \hat{G}\left(X, Z\right)$$

$\hat{G}\left(X, Z\right) \geq 0$ for all $\left(X, Z\right) \in D$ and where $D_Z G\left(X^*, 0\right)$ is an M- matrix (i.e the diagonal elements are no-negative and it is also the Jacobian of $\hat{G}\left(X, Z\right) \geq 0$ evaluated at $(X^*, 0).$

If the system satisfies the above condition, then the theorem below holds (Agbata *et al*, 2024)

Theorem 3

The equilibrium point $\varepsilon_0 = (X^*, 0).$ *is globally asymptotically stable if* $R_0 \leq 1$

$$F(X, Z) = \begin{bmatrix} \Lambda\rho - (\beta E + \mu)\mathrm{S} \\ (1-\rho)\Lambda + \alpha_1 S - (\omega + \psi + \alpha_2 + \mu)\mathrm{V}_1 \\ \alpha_2 \mathrm{V}_1 - (\alpha_3 + \mu)\mathrm{V}_2 \\ fI + \alpha_3 \mathrm{V}_2 - \mu R \end{bmatrix}$$

$$G(X, Z) = \begin{bmatrix} \beta SE + \omega \mathrm{V}_1 - (\sigma + \mu)\mathrm{E} \\ \sigma E + V_1\psi - (f + \varepsilon + \mu)\mathrm{I} \end{bmatrix}$$

At disease free equilibrium,

$H_1:$

$$\frac{dS}{dt} = \Lambda\rho - \mu S$$

$$\frac{dR}{dt} = 0$$

$$S^{**} = \frac{\Lambda\rho}{E^{**}\beta + \mu + \alpha_1}$$

$$V_1^{**} = -\frac{\Lambda\left(E^{**}\beta\rho - E^{**}\beta + \mu\rho - \mu - \alpha_1\right)}{\left(E^{**}\beta + \mu + \alpha_1\right)\left(\omega + \psi + \alpha_2 + \mu\right)}$$

$$V_2^{**} = -\frac{\Lambda\left(\left(\rho - 1\right)\mu + E\left(\rho - 1\right)\beta - \alpha_1\right)\alpha_2}{\left(E^{**}\beta + \mu + \alpha_1\right)\left(\omega + \psi + \alpha_2 + \mu\right)\left(\alpha_3 + \mu\right)}$$

$$I^{**} = \frac{\beta\sigma\left(\omega + \psi + \alpha_2 + \mu\right)E^{**2} + \left(\left(\omega + \psi + \alpha_2 + \mu\right)\left(\alpha_1 + \mu\right)\sigma - \psi\beta\Lambda\left(\rho - 1\right)\right)E + \psi\left(\left(1-\rho\right)\mu + \alpha_1\right)\Lambda}{\left(E^{**}\beta + \mu + \alpha_1\right)\left(\omega + \psi + \alpha_2 + \mu\right)\left(f + \grave{o} + \mu\right)}$$

$H_2:$

$$D_Z G\left(X^*, 0\right) Z = \begin{bmatrix} BE + \omega V_1 - (\alpha + \mu) \\ \sigma E + V_1\psi - (f + \varepsilon + \mu)I \end{bmatrix}$$

$$\hat{G}\left(X, Z\right) = D_Z G\left(X^*, 0\right) Z - G\left(X, Z\right)$$

$$\hat{G}\left(X, Z\right) = \begin{bmatrix} \beta E\left(1 - \frac{S}{N}\right) \\ 0 \end{bmatrix}$$

Clearly, $1 \geq S$ this means that $\hat{G}\left(X, Z\right) \geq 0$.

Hence, the disease free equilibrium of the given model is globally asymptotically stable.

Endemic Equilibrium Point of the Model

The endemic equilibrium point in mathematical epidemiology refers to a stable state where the disease persists within a population at a constant level over time. Mathematically, it represents a situation where the rates of infection and recovery (or other relevant processes) balance each other, leading to a steady state in disease dynamics. To obtain the endemic equilibrium we set the RHS of the differential equations in (1) to zero and solve for the state variables.

Thus, at the endemic equilibrium point,

$$\frac{dS}{dt} = \frac{dV_1}{dt} = \frac{dV_2}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0.$$

Let $\varepsilon^{**} = \left(S^{**}, V_1^{**}, V_2^{**}, E, ^{**} I^{**}, R^{**}\right)$ be the endemic equilibrium point of the at $E = E^{**}$ is given below

$$\left(\begin{array}{l} E^{**}\sigma\mu^3+\left(E^{**2}\beta\sigma+\sigma\left(\alpha_1+\alpha_2+\alpha_3+\psi+\omega\right)E^{**}-\psi\Lambda\left(\rho-1\right)\right)\mu^2+ \\ \left(\begin{array}{l}\beta\sigma\left(\alpha_2+\alpha_3+\psi+\omega\right)E^{**2}+\left(\sigma\left(\alpha_1+\alpha_2+\psi+\omega\right)\alpha_3-\psi\beta\Lambda\left(\rho-1\right)+\alpha_1\sigma\left(\omega+\psi+\alpha_2\right)\right)E^{**} \\ +\left(-\left(\rho-1\right)\left(\alpha_2+\psi\right)\alpha_3+\alpha_1\psi\right)\Lambda\end{array}\right)\mu \\ +\left(\begin{array}{l}\beta\sigma\left(\omega+\psi+\alpha_2\right)E^{**2}+\left(\begin{array}{l}-\beta\left(\rho-1\right)\left(\alpha_2+\psi\right)\Lambda \\ +\alpha_1\sigma\left(\omega+\psi+\alpha_2\right)\end{array}\right)E^{**}+\alpha_1\Lambda\left(\alpha_2+\psi\right)\end{array}\right)\alpha_3 \end{array}\right)$$

$$R^{**}=\frac{f-\alpha_2\left(\left(\rho-1\right)\mu+E\left(\rho-1\right)\beta-\alpha_1\right)\left(\grave{o}+\mu\right)\alpha_3\Lambda}{\left(E^{**}\beta+\mu+\alpha_1\right)\left(\omega+\psi+\alpha_2+\mu\right)\left(f+\grave{o}+\mu\right)\left(\alpha_3+\mu\right)\mu}$$

Sensitivity Analysis of the Model

Sensitivity analysis is carried out to determine the parameters that enhance the spread of measles as well as control of the infection in a population.

The sensitivity index of the reproduction number of the model with respect to any parameter say x is given by:

$$\Im_x^{R_0}=\frac{\partial R_0}{\partial x}\times\frac{x}{R_0}$$

Given that

$$R_0=\frac{\beta\rho\Lambda}{\mu P_4}$$

$$\Im_\beta^{R_0}=1.0000$$

$$\Im_\Lambda^{R_0}=1.0000$$

$$\Im_\mu^{R_0}=-\frac{\mu}{\alpha+\mu}=-0.9868$$

$$\Im_\alpha^{R_0}=-\frac{\theta}{\mu+\theta}=-0.0131$$

$$\Im_\omega^{R_0}=-\frac{\theta}{\mu+\theta}=-1$$

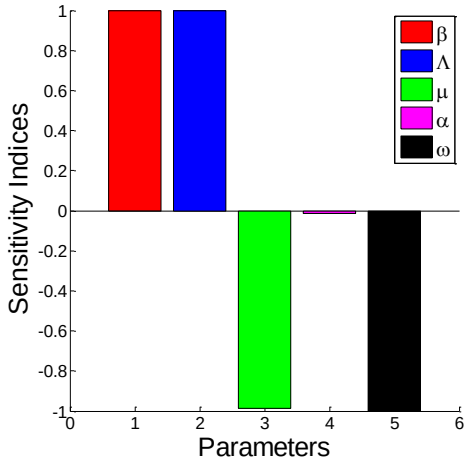

Figure 2 Sensitivity bar chat

The sensitivity bar chart presented in the figure highlights the impact of various parameters on the dynamics of disease transmission. Parameters exhibiting positive sensitivity indices are identified as factors that promote or enhance the spread of the disease. For example, the contact rate shows a positive sensitivity index, indicating that it plays a significant role in facilitating transmission. Therefore, any intervention or control strategy aimed at reducing the contact rate—such as social distancing, use of protective equipment, or limiting gatherings—would have a substantial effect in lowering the overall disease transmission within the population (Bolaji *et al*, 2024). In contrast, parameters with negative sensitivity indices are those that contribute to suppressing the spread of the disease. Specifically, the first-dose vaccination rate displays a negative sensitivity index, which implies that increasing vaccination coverage directly supports efforts toward disease control and eventual eradication. By enhancing vaccination efforts, the susceptible population is reduced, thus interrupting transmission chains and decreasing the basic reproduction number (R0). This underscores the critical importance of vaccination campaigns and public health initiatives in controlling infectious diseases.

RESULTS AND DISCUSSION

Results

Numerical Simulations of the Model

Numerical simulations allow modelers to validate their mathematical models against real-world data and calibrate model parameters to improve accuracy. This iterative process ensures that the model reflects observed patterns of measles transmission and vaccination outcomes. Double-dose vaccination introduces additional variables like the timing between doses and the effectiveness of boosting immunity. Numerical simulations enable the exploration of different vaccination scenarios, including varying levels of vaccine coverage and efficacy, to asses assess their impact on disease control. Numerical simulations helps in understanding the disease dynamics over time, identifying critical parameters, and optimizing control measures. By running simulations, modelers can

observe the progression of the disease under different conditions, helping to predict outbreaks, assess the effectiveness of public health measures, and inform policy decisions.

Table 2: Parameter values used for simulation.

Parameter	Value	Source
Λ	0.02755	Stephen *et al*, 2014
μ	0.0087	Agbata *et al*, 2024
α_1	0.167	Stephen *et al*, 2014
β	0.08	Agbata *et al*, 2024
ρ	0.40	Assumed
α_2	0.7	Stephen *et al*, 2014
α_3	0.167	Stephen *et al*, 2014
σ	0.002	Assumed
ω	0.09091	Stephen *et al*, 2014
ψ	0.001	Assumed
f	0.004	Stephen *et al*, 2014
ε	0.002	Assumed

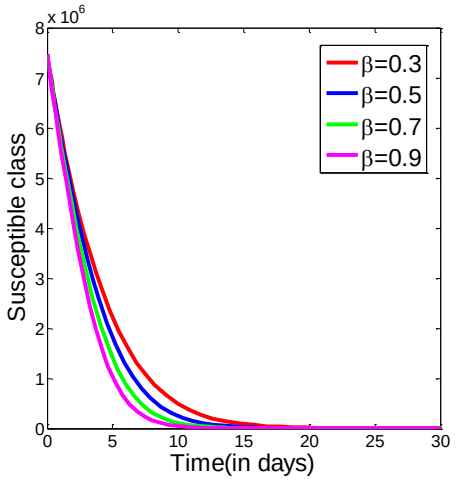

Figure 3a. Graph of Susceptible human against time

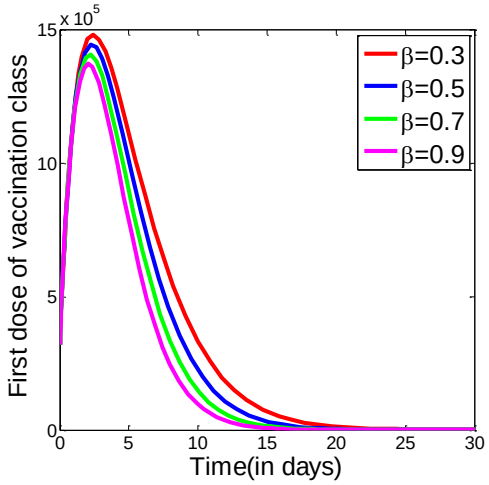

Figure 3b. Graph of first dose of vaccination

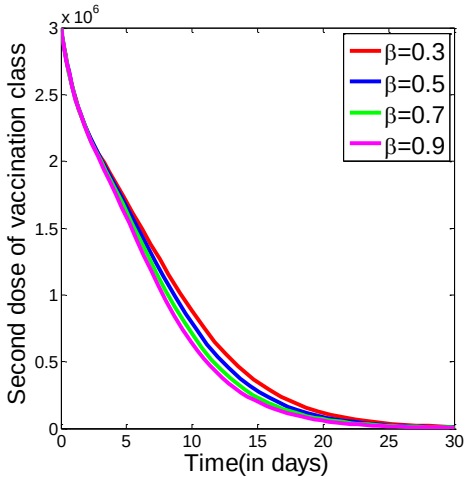

Figure 3c. Graph of second dose of vaccination

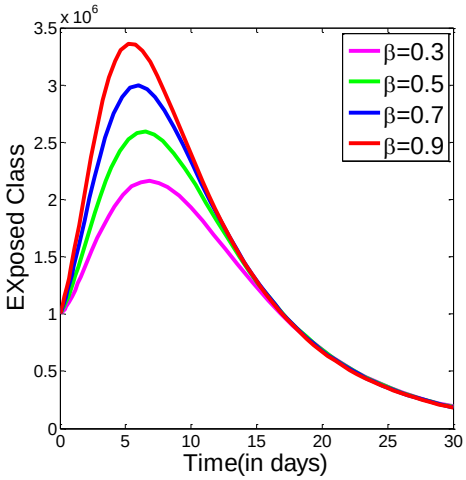

Figure 3d. Graph of exposed human against time

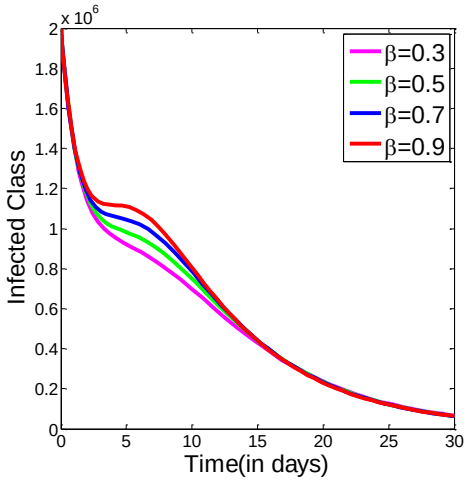

Figure 3e. Graph of infected human against time

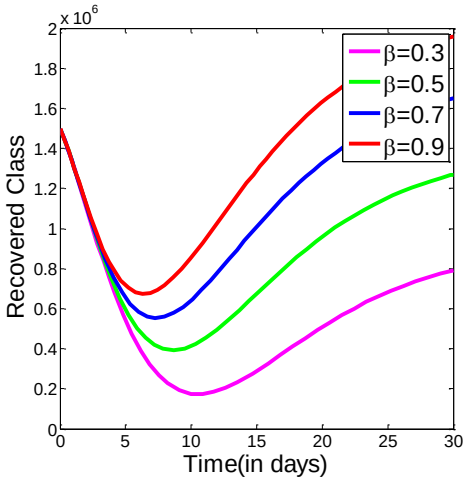

Figure 3f. Graph of recovered human against time

Discussion

From the sensitivity analysis and the resultant bar chat in Figure 2, it is observed that the parameters with positive sensitivity indices enhance the transmission of the disease within the human population. Thus, parameters like β and Λ enhance the endemicity of the disease within the population. Also, parameters such as α_1, μ, ω with negative sensitivity indices will ultimately curb the prevalence of the disease within the human population. Specifically, the contact rate of infection, (β),was identified with a positive sensitivity index, indicating that reducing this contact rate would effectively mitigate the spread of measles among the population.Conversely, the vaccination rate (α_1) of susceptible humans exhibited a negative sensitivity index. This finding suggests that enhancing efforts to improve or encourage higher vaccination rates would significantly aid in controlling measles within the population. These insights emphasized the critical role of vaccination campaigns and strategies in disease prevention and highlight the potential impact of targeted interventions aimed at reducing disease transmission rates. In Figure 3a, the decline of susceptible humans to zero indicates effective disease control, as no individuals remain susceptible to the disease over time. Figure 3d shows an initial increase followed by a rapid decrease in the number of exposed individuals, nearing zero due to successful implementation of control measures. Figure 3b illustrates a sharp rise and subsequent decline in first dose vaccination rates, attributed to the decrease in infected individuals (as seen in Figure 3e) and consequently fewer individuals completing their second vaccination dose (as observed in Figure 3c). This trend correlates with a notable increase in recovery rates depicted in Figure 3f. Overall, the double dose vaccination strategy emerges as an effective measure in containing the spread of measles, as evidenced by these interconnected figures showcasing the dynamics of disease transmission and vaccination impacts over time.

The study provides valuable insights into the dynamics of measles transmission and the efficacy of control measures, particularly double vaccination strategies. The analysis demonstrates that achieving (R_0) values below 1 through vaccination efforts can lead to the elimination of measles transmission. Furthermore, the numerical simulations and sensitivity analysis validate the model's robustness and applicability to real-life scenarios. The findings emphasized the importance of implementing comprehensive vaccination programs and ensuring access to effective treatment to mitigate the spread of measles and prevent outbreaks. The study also emphasizes the critical role of mathematical modeling in informing public health policies and interventions aimed at controlling infectious diseases like measles.

CONCLUSION

This study presents a thorough mathematical analysis of measles transmission dynamics incorporating double-dose vaccination as a critical control measure. The sensitivity analysis reveals that parameters with positive sensitivity indices, such as the contact rate, significantly enhance the spread and endemicity of the disease within the population. This finding emphasizes that reducing the contact rate through behavioral interventions and public health measures can effectively diminish disease transmission. Conversely, parameters exhibiting negative sensitivity indices, particularly the vaccination rate of susceptible individuals, are shown to play a pivotal role in decreasing disease prevalence. Increasing vaccination coverage emerges as a vital strategy to promote disease eradication, underscoring the importance of robust

vaccination campaigns and public awareness efforts in controlling measles outbreaks. Numerical simulations further validate the effectiveness of the double-dose vaccination strategy, demonstrating a progressive decline in the susceptible population alongside a reduction in infection rates and an increase in recovery. The analysis confirms that maintaining the basic reproduction number, (R_0) values below one through enhanced vaccination efforts is essential for halting disease transmission and achieving long-term control. The study highlights the significance of comprehensive vaccination programs combined with targeted interventions to reduce transmission parameters. The mathematical model's robustness and applicability provide valuable insights for public health policymakers, guiding the design and implementation of effective disease control strategies. Sustained vaccination efforts, coupled with continuous monitoring and adaptive control measures, are essential for preventing future outbreaks and improving population health outcomes.

Findings from the Study:

- Effectiveness of Double Dose Vaccination: The model demonstrates that double dose vaccination effectively reduces the number of susceptible individuals to zero over time due to high recovery rates facilitated by effective control measures.
- Positive Sensitivity of Contact Rate (β): The contact rate of infection (β) was found to have a positive sensitivity index, indicating that reducing this rate would significantly mitigate measles transmission in the population.
- Negative Sensitivity of Vaccination Rate (α_1): The vaccination rate (α_1) of susceptible individuals exhibited a negative sensitivity index, highlighting that increasing vaccination rates would substantially aid in controlling measles outbreaks.
- Impact of Control Measures: Effective control measures, including vaccination campaigns, play a crucial role in disease prevention and transmission reduction, as evidenced by the model's outcomes.
- Role of Recovery Rate: The high recovery rate under effective control measures contributes significantly to the elimination of susceptible individuals over time, further reducing the disease burden in the population.
- Validation through Sensitivity Analysis: The sensitivity analysis validates the importance of vaccination strategies and interventions aimed at reducing disease transmission rates, providing actionable insights for public health policies.
- Future Preparedness:The study emphasizes the importance of continuous monitoring, preparedness, and enhancement of vaccination programs to sustain disease control efforts and prevent resurgence.

Recommendations Based on the Study

These recommendations aim to leverage the study's findings to strengthen measles control measures, mitigate transmission risks, and enhance public health preparedness against future outbreaks.

- Enhance Vaccination Campaigns: Effort should be taken to promote and facilitate higher vaccination rates, especially among susceptible populations, to bolster herd immunity and prevent measles outbreaks.
- Target Reduction in Contact Rates: Implement measures to reduce the contact rate of infection (β), such as promoting social distancing, improving hygiene practices, and timely isolation of infected individuals.
- Invest in Education and Awareness: Launch educational campaigns to address vaccine hesitancy, misinformation, and promote the benefits and safety of vaccinations to enhance community acceptance and uptake.
- Implement Routine Surveillance: Establish robust surveillance systems to monitor disease trends, vaccination coverage, and potential outbreaks, allowing for timely intervention and response.
- Adapt Control Measures to Local Contexts: Tailor vaccination strategies and control measures to local epidemiological contexts and demographic characteristics to maximize effectiveness.
- Support Research and Development: Invest in research to improve vaccine efficacy, develop new vaccine formulations, and enhance understanding of measles transmission dynamics for better control strategies.
- Collaborate Across Sectors: Foster collaboration between public health authorities, healthcare providers, policymakers, and community stakeholders to ensure coordinated efforts in measles control and prevention.

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