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*Research Article*

# A Mathematical Model of Treatment and Vaccination Interventions of Pneumococcal Pneumonia Infection Dynamics

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*Streptococcus pneumoniae* is one of the leading causes of serious morbidity and mortality worldwide, especially in young children and the elderly. In this study, a model of the spread and control of bacterial pneumonia under public health interventions that involve treatment and vaccination is formulated. It is found out that the model exhibits the disease-free and endemic equilibria. The disease-free equilibrium is stable if and only if the basic reproduction number $\mathcal{R}_0 < 1$ and the disease will be wiped out of the population. For $\mathcal{R}_0 \geq 1$, the endemic equilibrium is globally stable and the disease persists. We infer the effect of these interventions on the dynamics of the pneumonia through sensitivity analysis on the effective reproduction number $\mathcal{R}_e$, from which it is revealed that treatment and vaccination interventions combined can eradicate pneumonia infection. Numerical simulation to illustrate the analytical results and establish the long term behavior of the disease is done. The impact of pneumonia infection control strategies is investigated. It is revealed that, with treatment and vaccination interventions combined, pneumonia can be wiped out. However, with treatment intervention alone, pneumonia persists in the population.

## 1. Introduction

Pneumonia is the major cause of respiratory morbidity of more than 2 million children under 5 years of age mostly in low-income countries [1–6]. It is an infection of the lungs that is caused by bacteria, viruses, fungi, or other pathogens. Most common cause of bacterial pneumonia is the *Streptococcus pneumoniae*, also known as pneumococcus [6–8]. It is characterized primarily by inflammation in the air sacs (alveoli) in the lungs that are filled with fluid or pus making it difficult to breathe.

It is reported that about 30%–70% of young children carry *S. pneumoniae* in their nasopharynx, and up to 40% of the carriers are colonized with penicillin-nonsusceptible *S. pneumoniae*. Pneumococcus spreads through microaspiration of oropharyngeal organisms and inhalation of aerosols containing bacteria or viruses especially in children that carry the bacteria in their throats without being sick. It may also spread via airborne droplets from cough or sneeze of an infected person. Children become severely ill with high fever and rapid breathing. Infants usually suffer convulsions, unconsciousness, hypothermia, lethargy, and feeding problems [9]. The data on carriage among adults [10] is limited and most studies suggest that children are the source of transmission to adults in the family [11].

The risk factors associated with the spread of pneumonia include smoking history and passive smoking, malnutrition, crowded living conditions, lack of exclusive breastfeeding, indoor air pollution, heart disease, alcoholism and drug abuse, acidosis, diabetes, and antecedent viral infection [12, 13]. The overdiagnosis of pneumonia and underdiagnosis of asthma have led significantly to untreated respiratory morbidity and mortality among children less than five years in low-income countries. This has been due to some similarities of symptoms of pneumonia and asthma that often make it difficult to separate the two diseases without proper diagnostic tools [14].

Pneumonia classification depends on its origin and mode of transmission. Some of the pneumonia classifications include community-acquired, health care-associated, hospital-acquired, ventilator-associated, and walking pneumonia [15].

Pneumonia is preventable through vaccination, proper diagnosis, screening, environmental control measures, and appropriate treatment of other diseases [4, 5]. Vaccination is the most effective way to prevent certain bacterial and viral pneumonia in both children and adults. The two types of vaccines available against *S. pneumoniae* are the pneumococcal polysaccharide vaccine (PPV), based on purified capsular (PS) and pneumococcal conjugate vaccine (PCV), obtained by chemical conjugation of the capsular (PS) to a protein carrier [16]. PCVs were developed for use in children only and PPV for vaccination of the at-risk adults and the elderly [17, 18].

Newborn babies can be protected from pneumonia infection through early recognition and treatment at the level of the community or the primary-care health facility, testing pregnant mothers for Group B streptococcus and chlamydia trachomatis, and giving antibiotic treatment and vaccination with PPV that has a proven record of safety in pregnant and breastfeeding mothers for pneumococcal pneumonia prevention in infants. Suctioning the mouth and throat of babies with meconium-stained amniotic fluid decreases the rate of aspiration pneumonia [19]. Environmental measures for pneumonia prevention include reduction of indoor air pollution by encouraging good hygiene in crowded homes and smoking cessation that reduces risks of pneumonia infections among children and adults. Since the bacteria and viruses can also be spread to your hands and then to your mouth, it is important to wash hands with soap when around a person with pneumonia infection.

Appropriate antibiotics are used for treatment of bacterial pneumonia. Pneumonia treatment depends on the underlying cause of the pneumonia infection. Appropriate antibiotics are used for treatment of bacterial pneumonia. Effective and timely treatment together with better diagnostic tools and education prevents antibiotic resistance [20]. According to Wardlaw et al. [5], treatment alone could save at least 600,000 children's lives annually at a cost of US $600 million if antibiotic treatment is universally delivered to children with pneumonia. Amoxicillin is recommended as a suitable alternative because of its proven efficacy against *S. pneumoniae* and severe pneumonia cases should be hospitalized.

Vaccines are effective in reduction of the number of new cases and severity of the disease [21–23]. Childhood pneumonia is preventable through immunization with the effective two vaccines: Hib conjugate vaccine (HibCV) against the Haemophilus influenzae type b (Hib) and pneumococcal conjugate vaccine (PCV) against pneumococcus [24]. PCVs have additional protective qualities that enhance their use as they may reduce nasopharyngeal acquisition of vaccine-specific serotypes of *S. pneumoniae*, and this in turn reduces the incidence of pneumococcal pneumonia among nonvaccinated individuals [25, 26]. This is referred to as indirect or herd immunity. In this study, we focus on treatment and vaccination of *S. pneumoniae* among children with PCVs.

Mathematical models of infectious diseases have been recognized as powerful tools that can provide important insights into our understanding of epidemiological processes, the course of infection within a host, the transmission dynamics in a host population, and formulation or implementation of disease control programs [27, 28]. Compartmental mathematical models involving vaccination strategy for infectious disease control have been considered in [29, 30]. Greenhalgh et al. [31] and Lamb et al. [32] modeled the transmission of pneumonia among young children to explore the relationship between sequence types and serotypes. Other epidemic models to study pneumonia have been considered (see, e.g., [2, 33–35] and the references therein).

In this study, a deterministic compartmental model to investigate the effect of treatment and vaccination against *S. pneumoniae* transmission dynamics among children less than five years is formulated. The population studied is divided into a set of distinct compartments according to the disease status. The vaccination strategy consists of vaccination of a proportion of the newborn babies.

This paper is structured as follows. In Section 2, we formulate the model based on the assumptions and definitions of variables and parameters. In Section 3, the pneumonia model with treatment intervention is studied for its boundedness and positivity of solutions and equilibrium points and their stability. In Section 4, the model is extended to investigate the effect of treatment and vaccination interventions combined on the spread of pneumonia. In Section 5, sensitivity analysis of the effective reproduction number $\mathscr{R}_e$ is done. Numerical simulation of the model is carried out in Section 6. Finally, in Section 7, we discuss the results and make a conclusion.

## 2. Formulation of the Model

The model consists of four compartments categorizing individuals based on their status with respect to the disease. The assumptions and definitions of variables and parameters are given in Sections 2.1 and 2.2, respectively.

### 2.1. Assumptions

(1) The model assumes a homogeneous mixing of individuals in the population where all individuals have equal likelihood of catching the infection if they are exposed to the disease.

(2) All recovered individuals clear the bacteria from the body and thus do not participate in transmitting the disease.

(3) Newborns are given additional dose of vaccine to elicit booster optimal levels of response.

(4) All treated individuals get vaccinated after completing the dose.

(5) Vaccinated children do not evolve to the susceptible population because of booster vaccine doses.

*2.2. Variables and Parameters.* The model variables and parameter definitions represented are given as follows:

$S(t)$: susceptible individuals who are at risk of acquiring pneumonia infection at time $t$.

$C(t)$: carrier individuals who carry the pneumonia bacteria and can transmit the infection at time $t$.

$I(t)$: infective individuals capable of transmitting the infection to individuals at risk at time $t$.

$R(t)$: recovered individuals who have been treated of pneumonia at time $t$.

$V(t)$: vaccinated individuals at time $t$.

$\mu$: per capita natural mortality rate of individuals.

$\Lambda$: per capita recruitment rate into susceptible population.

$\theta$: proportion of susceptible individuals that joins the carriers.

$\sigma$: per capita disease induced mortality rate.

$\beta$: per capita recovery rate of carriers.

$\alpha$: force of infection of susceptible individuals.

$\tau$: per capita recovery rate of infected individuals.

$\pi$: rate at which carriers develop symptoms.

$\eta$: rate at which treated individuals become susceptible.

$\gamma$: rate at which susceptible individuals get vaccinated.

$\phi$: rate at which treated individuals are vaccinated.

$\omega$: transmission coefficient for the carrier subgroup.

$\delta$: rate of transmission.

$p$: probability that a contact is efficient enough to cause infection.

$\kappa$: rate of contact.

Based on assumptions and definitions of variables and parameters mentioned above, the following system of ordinary equations is obtained.

## 3. Pneumonia Model under Treatment

The population dynamics of the pneumonia model with treatment intervention is given by the following system of four ordinary nonlinear differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\alpha + \mu) S + \eta R, \\
\frac{dC}{dt} &= \alpha\theta S - (\mu + \beta + \pi) C, \\
\frac{dI}{dt} &= \alpha (1 - \theta) S + \pi C - (\tau + \mu + \sigma) I, \\
\frac{dR}{dt} &= \beta C + \tau I - (\mu + \eta) R,
\end{aligned} \tag{1}$$

together with

$$\frac{dN}{dt} = \Lambda - \mu N - \sigma I. \tag{2}$$

The initial conditions are $S(0) = S_0$, $C(0) = C_0$, $I(0) = I_0$, $R(0) = R_0$, $N(0) = N_0$, and the force of infection is

$$\alpha = \delta \left( \frac{I + \omega C}{N} \right), \quad \text{where } \delta = \kappa p, \tag{3}$$

where $\delta$ is the transmission rate, $\kappa$ is the contact rate, $p$ is the probability that a contact is efficient enough to cause infection, and $\omega$ is the transmission coefficient for the carrier subgroup.

*3.1. Positivity and Boundedness of the Solutions.* The positivity of solutions describes the nonnegativity of solutions of system (1).

**Lemma 1.** *Let the initial population be*

$$\{S_0, C_0, I_0, R_0 \geq 0\} \in \Omega. \tag{4}$$

*Then, the solution set* $\{S, C, I, R\}$ *of system (1) is positive for all* $t > 0$.

*Proof.* From the first equation of system (1),

$$\frac{dS}{dt} = \Lambda - (\alpha + \mu) S + \eta R \geq - (\alpha + \mu) S. \tag{5}$$

This implies

$$\frac{dS}{dt} \geq - (\alpha + \mu) S. \tag{6}$$

By separation of variables, (6) is integrated to obtain

$$\ln S \geq - (\alpha + \mu) t + K, \tag{7}$$

where $K$ is a constant of integration. Applying the initial conditions $S(0) = S_0$ to (7) gives

$$K = \ln S_0. \tag{8}$$

Hence,

$$S \geq S_0 e^{-(\alpha+\mu)t} \geq 0. \tag{9}$$

□

Similarly, it can be shown that the other equations of system (1) are also positive for all $t > 0$. Thus, the solutions of the model are positive for all values of $t > 0$.

It is important to establish whether system (1) is well-posed and biologically meaningful. Now, we study the invariant region which describes the region in which the solution to system (1) makes biological sense. It is assumed that all the state variables and parameters of the model are nonnegative for all $t \geq 0$.

In the absence of pneumonia,

$$N(t) \leq \frac{\Lambda}{\mu}. \tag{10}$$

Inequality (10) is referred to as the threshold population level. Therefore, the feasible solution set of system (1) enters and remains in the region;

$$\Omega = (S, C, I, R) \in \mathbb{R}_+^4: \quad 0 \le S + C + I + R = N \le \frac{\Lambda}{\mu}, \quad (11)$$

where $\mathbb{R}_+^4$ denotes the nonnegative cone of $\mathbb{R}^4$ including its lower dimensional faces. In this case, whenever $N > \Lambda/\mu$, then $dN/dt \le 0$, implying that the host population reduces asymptotically to the carrying capacity. However, whenever $N \le \Lambda/\mu$, every solution with initial conditions in $\mathbb{R}_+^4$ remains in that region for $t > 0$. Thus, the region $\Omega$ is positively invariant, that is, for all values of $t$, the solution remains positive and thus the model is well-posed and biologically meaningful.

*3.2. Equilibria of the Model.* We analyze the model for pneumonia transmission to determine the basic reproduction number $\mathscr{R}_0$ and other threshold parameters for pneumonia dynamics. The equilibria of system (1) are obtained by setting the right-hand side of system (1) equal to zero. The disease-free equilibrium is given by

$$E_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right). \quad (12)$$

**Theorem 2.** *There is a unique disease-free equilibrium $E_0$ for the model represented by system (1).*

*Proof.* This theorem is proved by substituting $E_0$ into system (1). The results show that all the derivatives are equal to zero, hence the disease-free equilibrium. □

*3.3. Basic Reproduction Number.* To establish the linear stability of $E_0$, we use the next generation operator approach on system (1) to compute the basic reproduction number $\mathscr{R}_0$. This is determined using the approach by van den Driessche and Watmough [38]. For the notation of the matrices $F$ and $V$, we have

$$F = \begin{bmatrix} \delta\omega\theta & \delta\theta \\ (1-\theta)\,\omega\delta & (1-\theta)\,\delta \end{bmatrix}, \qquad V = \begin{bmatrix} \mu+\beta+\pi & 0 \\ -\pi & \tau+\mu+\sigma \end{bmatrix}, \quad (13)$$

where $k_1 = \mu + \beta + \pi$ and $k_2 = \tau + \mu + \sigma$. This gives

$$V = \begin{bmatrix} k_1 & 0 \\ -\pi & k_2 \end{bmatrix}, \quad (14)$$

and, thus,

$$V^{-1} = \frac{1}{k_1 k_2}\begin{bmatrix} k_2 & 0 \\ \pi & k_1 \end{bmatrix},$$

$$FV^{-1} = \begin{bmatrix} \dfrac{\delta\theta\,(\omega k_2 + \pi)}{k_1 k_2} & \dfrac{\delta k_1 \theta}{k_1 k_2} \\ \dfrac{\delta\,(1-\theta)\,(\omega k_2 + \pi)}{k_1 k_2} & \dfrac{\delta k_1\,(1-\theta)}{k_1 k_2} \end{bmatrix}. \quad (15)$$

Thus, the eigenvalues for the matrix $FV^{-1}$ are

$$\xi = 0, \qquad \xi = \frac{\delta}{k_1 k_2}(1-\theta)\,k_1 + \theta\,(\omega k_2 + \pi). \quad (16)$$

The spectral radius is given by $\xi(FV^{-1}) = (\delta/k_1k_2)((1-\theta)k_1 + \theta(\omega k_2 + \pi))$, which gives the basic reproduction number

$$\mathscr{R}_0 = \frac{\delta}{k_1 k_2}\left(k_1\,(1-\theta) + \theta\,(\omega k_2 + \pi)\right). \quad (17)$$

The endemic equilibrium $E_e$ is defined as a steady state solution for system (1). This occurs when there is a persistence of the disease. Hence, the endemic equilibrium $E_e = (S, C, I, R)$ is determined by setting the right-hand side of system (1) equal to zero as follows:

$$\begin{aligned} \Lambda - (\alpha+\mu)\,S + \eta R &= 0, \\ \alpha\theta S - k_1 C &= 0, \\ \alpha\,(1-\theta)\,S + \pi C - k_2 I &= 0, \\ \beta C + \tau I - (\mu+\eta)\,R &= 0, \end{aligned} \quad (18)$$

together with

$$\Lambda - \mu N - \sigma I = 0, \quad (19)$$

$$\alpha = \delta\left(\frac{I + \omega C}{N}\right). \quad (20)$$

From the second equation of system (18)

$$\alpha = \frac{k_1 C}{\theta S}. \quad (21)$$

Plugging $\alpha$ in (21) into the first and third equations of system (18) gives

$$\Lambda - \frac{k_1 C}{\theta} - \mu S + \eta R = 0, \quad (22)$$

$$\frac{k_1\,(1-\theta)}{\theta} C + \pi C - k_2 I = 0. \quad (23)$$

Substituting for $\alpha$ in (20) into the second equation of system (18) gives

$$\delta\theta IS + \delta\theta\omega SC - k_1 CN = 0. \quad (24)$$

From the fourth equation of system (18), we have

$$R = \frac{\beta C}{\mu+\eta} + \frac{\tau I}{\mu+\eta}. \quad (25)$$

Substituting for $R$ in (22) gives

$$\Lambda + \left(\frac{\eta\beta}{\mu+\eta} - \frac{k_1}{\theta}\right) C + \frac{\eta\tau I}{\mu+\eta} - \mu S = 0. \quad (26)$$

From (23), we obtain

$$C = \frac{\theta k_2 I}{k_1 (1-\theta) + \pi\theta}. \tag{27}$$

Substituting for $C$ in (24) gives

$$\delta\theta IS + \delta\theta\omega S \frac{\theta k_2 I}{k_1 (1-\theta) + \pi\theta} - k_1 \frac{\theta k_2 I}{k_1 (1-\theta) + \pi\theta} N = 0. \tag{28}$$

Solving (28) yields

$$I = 0,$$

$$\text{or } S = \frac{k_1 k_2 N}{\delta \left(k_1 (1-\theta) + \theta (\omega k_2 + \pi)\right)}. \tag{29}$$

But

$$\mathscr{R}_0 = \frac{\delta}{k_1 k_2} \left(k_1 (1-\theta) + \theta (\omega k_2 + \pi)\right). \tag{30}$$

Therefore,

$$S = \frac{N}{\mathscr{R}_0}. \tag{31}$$

Substituting for $C$ and $S$ in (26) gives

$$\begin{aligned} &\Lambda + \left(\frac{\eta\theta\beta - k_1 (\mu+\eta)}{\theta (\mu+\eta)}\right)\left(\frac{\theta k_2 I}{k_1 (1-\theta) + \pi\theta}\right) + \frac{\eta\tau I}{\mu+\eta} - \frac{(\Lambda - \sigma I)}{\mathscr{R}_0} = 0 \Longrightarrow \\ &I = \frac{\Lambda (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right) (\mathscr{R}_0 - 1)}{\mathscr{R}_0 \left[k_1 k_2 (\mu+\eta) - \eta\theta\beta - \eta\tau \left(k_1 (1-\theta) + \pi\theta\right)\right] - \sigma (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right)}. \end{aligned} \tag{32}$$

Finally, we have

$$\begin{aligned} C &= \frac{\theta k_2 \Lambda (\mu+\eta) (\mathscr{R}_0 - 1)}{\mathscr{R}_0 \left[k_1 k_2 (\mu+\eta) - \eta\theta\beta - \eta\tau \left(k_1 (1-\theta) + \pi\theta\right)\right] - \sigma (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right)}, \\ R &= \frac{\left(\beta\theta k_2 + \tau \left(k_1 (1-\theta) + \pi\theta\right)\right) \Lambda (\mathscr{R}_0 - 1)}{\mathscr{R}_0 \left[k_1 k_2 (\mu+\eta) - \eta\theta\beta - \eta\tau \left(k_1 (1-\theta) + \pi\theta\right)\right] - \sigma (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right)}. \end{aligned} \tag{33}$$

Therefore, we have the endemic equilibrium $E_e = (S, I, C, R)$, where

$$\begin{aligned} S &= \frac{N}{\mathscr{R}_0}, \\ C &= \frac{\theta k_2 \Lambda (\mu+\eta) (\mathscr{R}_0 - 1)}{\mathscr{R}_0 \left[k_1 k_2 (\mu+\eta) - \eta\theta\beta - \eta\tau \left(k_1 (1-\theta) + \pi\theta\right)\right] - \sigma (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right)}, \\ I &= \frac{\Lambda (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right) (\mathscr{R}_0 - 1)}{\mathscr{R}_0 \left[k_1 k_2 (\mu+\eta) - \eta\theta\beta - \eta\tau \left(k_1 (1-\theta) + \pi\theta\right)\right] - \sigma (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right)}, \\ R &= \frac{\left(\beta\theta k_2 + \tau \left(k_1 (1-\theta) + \pi\theta\right)\right) \Lambda (\mathscr{R}_0 - 1)}{\mathscr{R}_0 \left[k_1 k_2 (\mu+\eta) - \eta\theta\beta - \eta\tau \left(k_1 (1-\theta) + \pi\theta\right)\right] - \sigma (\mu+\eta) \left(k_1 (1-\theta) + \pi\theta\right)}. \end{aligned} \tag{34}$$

**Lemma 3.** *For $\mathscr{R}_0 > 1$, a unique endemic equilibrium $E_e$ exists and there is no endemic equilibrium otherwise.*

For the disease to be endemic, $dI/dt > 0$ and $dC/dt > 0$; that is,

$$\theta\delta (I + \omega C) \frac{S}{N} - k_1 C > 0, \tag{35}$$

$$(1-\theta)\delta (I + \omega C) \frac{S}{N} - k_2 I + \pi C > 0. \tag{36}$$

From inequality (35), we have

$$k_1 C < \theta\delta\left(I + \omega C\right)\frac{S}{N}. \tag{37}$$

Using the fact $S/N < 1$, we obtain

$$C < \frac{\theta\delta I}{k_1 - \delta\theta\omega}. \tag{38}$$

From inequality (36), we have

$$I < \frac{\left(1-\theta\right)\delta I + \left(1-\theta\right)\delta\omega C + \pi C}{k_2}, \tag{39}$$

and, substituting for $C$ in inequality (38), inequality (39) yields

$$\begin{aligned} I &< \frac{\left(1-\theta\right)\delta I + \left(1-\theta\right)\delta\omega\left(\delta\theta I/\left(k_1 - \delta\theta\omega\right)\right) + \pi\left(\delta\theta I/\left(k_1 - \delta\theta\omega\right)\right)}{k_2}, \\ I &< \frac{\left(1-\theta\right)\delta\left(k_1 - \delta\theta\omega\right)I + \left(1-\theta\right)\delta^2\theta\omega I + \pi\delta\theta I}{k_2\left(k_1 - \delta\theta\omega\right)}, \\ k_1 k_2 - k_2\delta\theta\omega &< \delta k_1\left(1-\theta\right) + \pi\delta\theta, \\ 1 &< \frac{\delta}{k_1 k_2}\left(\left(1-\theta\right)k_1 + \theta\left(\omega k_2 + \pi\right)\right) = \mathscr{R}_0. \end{aligned} \tag{40}$$

Thus, a unique endemic equilibrium exists when $\mathscr{R}_0 > 1$.

### 3.4. Local and Global Stability of the Disease-Free Equilibrium

**Lemma 4.** *The disease-free equilibrium $E_0$ of system (1) is locally asymptotically stable whenever $\mathscr{R}_0 < 1$ and unstable whenever $\mathscr{R}_0 > 1$.*

The threshold quantity $\mathscr{R}_0$ is a measure of the number of secondary infections caused by a single individual in his /her entire lifetime as an infective [39]. It is an important parameter that plays a big role in the control of the disease. The reduction of the disease from the population targets the parameters that will bring its value to less than unity.

When the reproduction number is less than unity, then the disease-free equilibrium is locally asymptotically stable, and thus there is a possibility that the disease will be wiped out of the population.

The Jacobian matrix for system (1) is given by

$$J = \begin{bmatrix} -\left(\alpha+\mu\right) & 0 & 0 & \eta \\ \alpha\theta & -\left(\mu+\beta+\pi\right) & 0 & 0 \\ \alpha\left(1-\theta\right) & \pi & -\left(\tau+\mu+\sigma\right) & 0 \\ 0 & \beta & \tau & -\left(\mu+\eta\right) \end{bmatrix}. \tag{41}$$

Evaluating the Jacobian matrix (41) at the disease-free equilibrium $E_0$ gives

$$J\left(E_0\right) = \begin{bmatrix} -\mu & 0 & 0 & \eta \\ 0 & -k_1 & 0 & 0 \\ 0 & \pi & -k_2 & 0 \\ 0 & \beta & \tau & -\left(\mu+\eta\right) \end{bmatrix}. \tag{42}$$

The disease-free equilibrium $E_0$ is asymptotically stable if and only if the trace$(J_{E_0}) < 0$ and the det$(J_{E_0}) > 0$.

Thus, from the Jacobian matrix (42),

$$\begin{aligned} \operatorname{trace}\left(J_{E_0}\right) &= -\mu - h_1 - h_2 - \mu - \eta \\ &= -\left(2\mu + h_1 + h_2 + \eta\right) < 0, \\ \det\left(J_{E_0}\right) &= -\mu\left(-k_1 k_2\left(\mu+\eta\right)\right) + \eta \times 0 \\ &= \mu k_1 k_2\left(\mu+\eta\right) > 0. \end{aligned} \tag{43}$$

Since the parameters $\mu$, $\eta$, $k_1$, and $k_2$ are all positive, then $-(2\mu + k_1 + k_2 + \eta) < 0$. Therefore trace$(J_{E_0}) < 0$.

On the other hand, $\mathscr{R}_0$ can never be negative and the numerator $((1-\theta)k_1 + \theta(\omega k_1 + \pi))$ is positive; that is, $k_1 k_2 > 0$. This implies that det$(J_{E_0}) > 0$ since $\mu(\mu+\eta) > 0$ and $k_1 k_2 > 0$. Thus,

$$\mathscr{R}_0 = \frac{\delta}{k_1 k_2}\left(\left(1-\theta\right)k_1 + \theta\left(\omega k_2 + \pi\right)\right) < 1. \tag{44}$$

The conditions trace$(J_{E_0}) < 0$ and det$(J_{E_0}) > 0$ above imply that $E_0$ is locally asymptotically stable whenever $\mathscr{R}_0 < 1$

**Theorem 5.** *The disease-free equilibrium is globally asymptotically stable in $\Omega$ if $\mathscr{R}_0 \leq 1$ and unstable if $\mathscr{R}_0 > 1$.*

*Proof.* Consider the Lyapunov function defined by $L = (1/k_1)C + (1/k_2)I$. Its derivative along the solutions to system (1) is

$$\begin{aligned} \frac{dL}{dt} &= \frac{1}{k_1}\frac{dC}{dt} + \frac{1}{k_2}\frac{dI}{dt} = \frac{1}{k_1}\left(\alpha\theta S - k_1 C\right) \\ &\quad + \frac{1}{k_2}\left(\alpha\left(1-\theta\right)S + \pi C - k_2 I\right) = \frac{1}{k_1 k_2}\left(k_2\alpha\theta S\right. \end{aligned}$$

$$
\begin{aligned}
&- k_1k_2C) + \frac{1}{k_1k_2}\left(k_1\alpha(1-\theta)S + k_1\pi C - k_1k_2I\right)\\
&= \frac{1}{k_1k_2}\left(k_2\alpha\theta S - k_1k_2C + k_1\alpha(1-\theta)S + k_2\pi C\right.\\
&\left.- k_1k_2I\right),
\end{aligned}
\tag{45}
$$

but

$$
\begin{aligned}
&\alpha = \delta\left(\frac{I+\omega C}{N}\right) \Longrightarrow\\
&\frac{dL}{dt} \le \frac{\delta}{k_1k_2}\left((1-\theta)k_1 + \theta\left(\omega k_2 + \pi\right) - 1\right)\frac{S}{N}(C+I)\\
&\le \left(\mathscr{R}_0 - 1\right)(C+I)\frac{S}{N} \le 0 \quad \text{if } \mathscr{R}_0 \le 1.
\end{aligned}
\tag{46}
$$

□

Thus, $\mathscr{R}_0 < 1$ is necessary and sufficient for disease elimination. All the model parameters are positive, so that $dL/dt \le 0$ if $\mathscr{R}_0 \le 1$ with $dL/dt = 0$ if and only if $I = C = 0$. Hence, $L$ is a Lyapunov function on $\Omega$ and the largest compact invariant set in $\{(S, C, I, R) \in \Omega : dL/dt \le 0\}$ is the singleton $\{E_0\}$. Therefore, by LaSalle's invariance principle [40], every solution to system (1), with initial conditions in $\Omega$, approaches $E_0$ as $t \to \infty$ if $\mathscr{R}_0 < 1$. Hence the disease-free equilibrium $E_0$ of the pneumonia model with treatment intervention is globally asymptotically stable.

*3.5. Local and Global Stability Analysis of the Endemic Equilibrium.* We study the local stability of the endemic equilibrium by applying the Routh-Hurwitz criterion.

**Theorem 6.** *If $\mathscr{R}_0 > 1$, the endemic equilibrium $E_e$ of system (1) is locally asymptotically stable in $\Omega$.*

*Proof.* We evaluate the Jacobian matrix (41) at the endemic equilibrium to obtain

$$
J(E_e) = \begin{bmatrix}
-\overline{\alpha} - \mu & 0 & 0 & \eta\\
\overline{\alpha}\theta & -k_1 & 0 & 0\\
\overline{\alpha}(1-\theta) & \pi & -k_2 & 0\\
0 & \beta & \tau & -\mu - \eta
\end{bmatrix},
\tag{47}
$$

where $\overline{\alpha}$ is defined as the force infection at the endemic equilibrium. We obtain a characteristic equation $P(\xi) = |(\xi I - J(E_e)|$, where $I$ is a $4 \times 4$ unit matrix

$$
\begin{aligned}
&P(\xi)\\
&= \det\begin{bmatrix}
\xi + \overline{\alpha} + \mu & 0 & 0 & \eta\\
-\overline{\alpha}\theta & \xi + k_1 & 0 & 0\\
-\overline{\alpha}(1-\theta) & -\pi & \xi + k_2 & 0\\
0 & -\beta & -\tau & \xi + (\mu + \eta)
\end{bmatrix}.
\end{aligned}
\tag{48}
$$

Thus, the characteristic equation becomes

$$
P(\xi) = \xi^4 + a_1\xi^3 + a_2\xi^2 + a_3\xi + a_4,
\tag{49}
$$

where

$$
\begin{aligned}
a_1 &= 2\mu + \eta + k_1 + k_2 + \overline{\alpha},\\
a_2 &= (\eta + \mu)(k_1 + k_2 + \overline{\alpha} + \mu) + k_1k_2\\
&\quad + (\overline{\alpha} + \mu)(k_1 + k_2),\\
a_3 &= k_1k_2(\eta + \mu) + (k_1 + k_2)(\overline{\alpha} + \mu)(\eta + \mu)\\
&\quad + k_1k_2(\overline{\alpha} + \mu) + \eta\tau\overline{\alpha}(1-\theta) + \eta\beta\overline{\alpha}\theta,\\
a_4 &= k_1k_2(\overline{\alpha} + \mu)(\eta + \mu) + \eta\overline{\alpha}\theta\pi\tau + \eta k_1\overline{\alpha}\tau(1-\theta)\\
&\quad + \eta\beta\overline{\alpha}\theta k_1.
\end{aligned}
\tag{50}
$$

Thus, from Routh-Hurwitz criterion [41] we have the matrix

$$
\begin{bmatrix}
1 & a_2 & a_4 & \xi^4\\
a_1 & a_3 & 0 & \xi^3\\
a_2 - \dfrac{a_3}{a_1} & a_4 & 0 & \xi^2\\
a_3 - \dfrac{a_1a_4}{a_2 - a_3/a_1} & 0 & 0 & \xi\\
a_1 & 0 & 0 & 1
\end{bmatrix}.
\tag{51}
$$

According to the Routh-Hurwitz criterion, for $\mathscr{R}_0 > 1$, the endemic equilibrium $E_e$ is locally asymptotically stable if

$$
\begin{aligned}
a_1 &> 0,\\
\left(a_2 - \frac{a_3}{a_1}\right) &> 0,\\
\left(a_3 - \frac{a_1a_4}{a_2 - a_3/a_1}\right) &> 0,\\
a_4 &> 0.
\end{aligned}
\tag{52}
$$

□

The global stability of the endemic equilibrium $E_e$ is analyzed using the following constructed Lyapunov function.

**Theorem 7.** *If $\mathscr{R}_0 \ge 1$, the endemic equilibrium $E_e$ of system (1) is globally asymptotically stable.*

*Proof.* Let the Lyapunov function be

$$
\begin{aligned}
L(S_e, C_e, I_e, R_e) &= \left(S - S_e - S_e\log\left(\frac{S_e}{S}\right)\right)\\
&+ \left(C - C_e - C_e\log(C_eC)\right)\\
&+ \left(I - I_e - I_e\log\left(\frac{I_e}{I}\right)\right)\\
&+ \left(R - R_e - R_e\log\left(\frac{R_e}{R}\right)\right),
\end{aligned}
\tag{53}
$$

$$\begin{aligned}
\frac{dL}{dt} &= \left(\frac{S-S_e}{S}\right)\frac{dS}{dt} + \left(\frac{C-C_e}{C}\right)\frac{dC}{dt} + \left(\frac{I-I_e}{I}\right)\frac{dI}{dt} \\
&+ \left(\frac{R-R_e}{R}\right)\frac{dR}{dt} = \left(\frac{S-S_e}{S}\right)(\Lambda - \alpha S - \mu S + \eta R) \\
&+ \left(\frac{C-C_e}{C}\right)(\alpha\theta S - k_1 C) + \left(\frac{I-I_e}{I}\right) \\
&\cdot (\alpha(1-\theta)S + \pi C - k_2 I) + \left(\frac{R-R_e}{R}\right) \\
&\cdot (\beta C + \tau I - (\mu+\eta)R) = \left(\frac{S-S_e}{S}\right) \\
&\cdot (\Lambda - \alpha(S-S_e) - \mu(S-S_e) + \eta(R-R_e)) \\
&+ \left(\frac{C-C_e}{C}\right)(\alpha\theta(S-S_e) - k_1(C-C_e)) \\
&+ \left(\frac{I-I_e}{I}\right) \\
&\cdot (\alpha(1-\theta)(S-S_e) + \pi(C-C_e) - k_2(I-I_e)) \\
&+ \left(\frac{R-R_e}{R}\right) \\
&\cdot (\beta(C-C_e) + \tau(I-I_e) - (\mu+\eta)(R-R_e)) \\
&= \frac{(S-S_e)^2}{S}(-\alpha-\mu) - k_1\frac{(C-C_e)^2}{C} - k_2 \\
&\cdot \frac{(I-I_e)^2}{I} - (\mu+\eta)\frac{(R-R_e)^2}{R} + \Lambda - \frac{\Lambda S_e}{S} + \eta R \\
&- \frac{\eta R S_e}{S} - \eta R_e + \frac{R_e S_e}{S} + \alpha\theta S - \frac{\alpha\theta C_e S}{C} - \alpha\theta S_e \\
&+ \frac{\alpha\theta C_e S_e}{C} + \alpha(1-\theta)S - \alpha(1-\theta)S_e \\
&- \frac{\alpha(1-\theta)I_e S}{I} + \frac{\alpha(1-\theta)I_e S_e}{I} + \pi C - \pi C_e \\
&- \frac{\pi I_e C}{I} + \frac{\pi I_e C_e}{I} + \beta C - \beta C_e - \frac{\beta R_e C}{R} + \frac{\beta R_e C_e}{R} \\
&+ \tau I - \tau I_e - \frac{\tau R_e I}{R} + \frac{\tau R_e I_e}{R};
\end{aligned} \tag{54}$$

thus collecting positive terms together and negative terms together from the above

$$\frac{dL}{dt} = P - Q, \tag{55}$$

where

$$\begin{aligned}
P &= \Lambda + \eta R + \frac{\eta R_e S_e}{S} + \alpha\theta S + \frac{\alpha\theta C_e S_e}{C} + \alpha(1-\theta)S \\
&+ \frac{\alpha(1-\theta)I_e S_e}{I}\pi C + \frac{\pi I - eC_e}{I} + \beta C \\
&+ \frac{\beta R_e C_e}{R} + \tau I + \frac{\tau R_e I_e}{R},
\end{aligned}$$

$$\begin{aligned}
Q &= (\alpha+\mu)\frac{(S-S_e)^2}{S} - k_1\frac{(C-C_e)^2}{C} - k_2\frac{(I-I_e)^2}{I} \\
&- (\mu+\eta)\frac{(R-R_e)^2}{R} - \eta R_e - \frac{\Lambda S_e}{S} - \frac{\eta R S_e}{S} \\
&- \frac{\alpha\theta C_e S}{C} - \alpha\theta S_e - \alpha(1-\theta)S_e \\
&- \frac{\alpha(1-\theta)I_e S}{I} - \pi C_e - \frac{\pi I_e C}{I} - \beta C_e \\
&- \frac{\beta R_e C}{R} - \tau I_e - \frac{\tau R_e I}{R}.
\end{aligned} \tag{56}$$

Thus if $P < Q$, then we obtain that $dL/dt \leq 0$, noting that $dL/dt = 0$ if and only if $S = S_e$, $C = C_e$, $I = I_e$, $R = R_e$. Therefore, the largest compact invariant set in $\{(S_e, C_e, I_e, R_e) \in \Omega : dL/dt = 0\}$ is the singleton $\{E_e\}$, where $E_e$ is the endemic equilibrium of system (1).

Thus, by LaSalle's invariance principle [40], it implies that $E_e$ is globally asymptotically stable in $\Omega$ if $P < Q$. □

## 4. Pneumonia Model under Treatment and Vaccination Interventions

In the this section, the model formulated in Section 3 is extended to investigate the impact of treatment and vaccination interventions on the transmission dynamics of pneumonia. The dynamics of the modified pneumonia model is described by the following system of five ordinary nonlinear differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\alpha+\mu+\gamma)S, \\
\frac{dC}{dt} &= \alpha\theta S - (\mu+\beta+\pi)C, \\
\frac{dI}{dt} &= \alpha(1-\theta)S + \pi C - (\tau+\mu+\sigma)I, \\
\frac{dR}{dt} &= \beta C + \tau I - (\mu+\phi)R, \\
\frac{dV}{dt} &= \gamma S - \mu V + \phi R,
\end{aligned} \tag{57}$$

with initial conditions $S(0) = S_0$, $C(0) = C_0$, $I(0) = I_0$, $R(0) = R_0$, $V(0) = V_0$, $N(0) = N_0$. The total population size is given by $N(t) = S(t) + C(t) + C(t) + R(t) + V(t)$ and is changing at the rate

$$\frac{dN}{dt} = \Lambda - \mu N - \sigma I. \tag{58}$$

The susceptible individuals become infected at rate $\alpha$ which is the force of infection; that is, the number of infected

individuals produced by adequate contact and is given by

$$\alpha = \delta\left(\frac{I + \omega C}{N}\right), \tag{59}$$

where $\delta = \kappa p$, $\delta$ is the transmission rate, $k$ is the rate of contact, and $p$ is the probability that a contact is efficient enough to cause infection.

*4.1. Analysis of the Model.* The equilibria of system (57) is obtained by setting the right-hand side of the equations to be equal to zero. The disease-free equilibrium $E_0$ is given by

$$\left(\frac{\Lambda}{(\mu+\gamma)}, 0, 0, 0, \frac{\Lambda\gamma}{\mu(\mu+\gamma)}\right). \tag{60}$$

*4.2. Effective Reproduction Number.* To establish the stability of $E_0$, we use the next-generation operator approach on system (57) to compute the effective reproduction number $\mathscr{R}_e$. Using the notation of the matrices $F$ and $V$, we have

$$F = \begin{bmatrix} \delta\omega\theta S & \delta\theta S \\ (1-\theta)\,\omega\delta S & (1-\theta)\,\delta S \end{bmatrix},$$
$$V = \begin{bmatrix} \mu+\beta+\pi & 0 \\ -\pi & \tau+\mu+\sigma \end{bmatrix}. \tag{61}$$

Evaluating $F$ at the disease-free equilibrium we to obtain

$$F = \begin{bmatrix} \delta\omega\theta\dfrac{\Lambda}{(\mu+\gamma)} & \delta\theta\dfrac{\Lambda}{(\mu+\gamma)} \\ (1-\theta)\,\omega\delta\dfrac{\Lambda}{(\mu+\gamma)} & (1-\theta)\,\delta\dfrac{\Lambda}{(\mu+\gamma)} \end{bmatrix}. \tag{62}$$

Let $k_1 = \mu + \beta + \pi$ and $k_2 = \tau + \mu + \sigma$; then

$$V = \begin{bmatrix} k_1 & 0 \\ -\pi & k_2 \end{bmatrix}, \tag{63}$$

and, thus,

$$V^{-1} = \frac{1}{k_1 k_2}\begin{bmatrix} k_2 & 0 \\ \pi & k_1 \end{bmatrix}. \tag{64}$$

Now we have

$$FV^{-1} = \frac{1}{k_1 k_2} \cdot \begin{bmatrix} \delta\omega\theta\dfrac{\Lambda}{(\mu+\gamma)} & \delta\theta\dfrac{\Lambda}{(\mu+\gamma)} \\ (1-\theta)\,\omega\delta\dfrac{\Lambda}{(\mu+\gamma)} & (1-\theta)\,\delta\dfrac{\Lambda}{(\mu+\gamma)} \end{bmatrix}\begin{bmatrix} k_2 & 0 \\ \pi & k_1 \end{bmatrix} \tag{65}$$
$$= \begin{bmatrix} \dfrac{\Lambda\delta\theta(\omega k_2 + \pi)}{k_1 k_2(\mu+\gamma)} & \dfrac{\lambda\psi k_1\theta}{k_1 k_2(\mu+\gamma)} \\ \dfrac{\Lambda\psi(1-\theta)(\omega k_2+\pi)}{k_1 k_2(\mu+\gamma)} & \dfrac{\Lambda\delta k_1(1-\theta)}{k_1 k_2(\mu+\gamma)} \end{bmatrix}.$$

The eigenvalues for the matrix $FV^{-1}$ are given by

$$\xi = 0,$$
$$\xi = \frac{\Lambda\delta}{k_1 k_2(\mu+\gamma)}\left((1-\theta)k_1 + \theta(\omega k_2 + \pi)\right). \tag{66}$$

The spectral radius is given by $\xi(FV^{-1}) = (\Lambda\delta/k_1k_2(\mu+\gamma))((1-\theta)k_1 + \theta(\omega k_2 + \pi))$, which gives the effective reproduction number as

$$\mathscr{R}_e = \frac{\Lambda\delta}{k_1 k_2(\mu+\gamma)}\left((1-\theta)k_1 + \theta(\omega k_2 + \pi)\right), \tag{67}$$

but

$$\mathscr{R}_0 = \frac{\delta}{k_1 k_2}\left((1-\theta)k_1 + \theta(\omega k_2 + \pi)\right). \tag{68}$$

Therefore,

$$\mathscr{R}_e = \frac{\Lambda\mathscr{R}_0}{(\mu+\gamma)}. \tag{69}$$

$\mathscr{R}_e$ is referred to as the effective reproduction number rather than the basic reproduction number because vaccination and treatment have been included in the model [32]. It is defined as the expected number of secondary cases caused by a typical infected individual entering an entirely susceptible population at equilibrium.

*4.3. Local Stability of the Disease-Free Equilibrium.* The Jacobian matrix for the system is given by

$$J = \begin{bmatrix} -(\alpha+\mu+\gamma) & 0 & 0 & 0 & 0 \\ \alpha\theta & -(\mu+\beta+\pi) & 0 & 0 & 0 \\ \alpha(1-\theta) & \pi & -(\tau+\mu+\sigma) & 0 & 0 \\ 0 & \beta & \tau & -(\mu+\phi) & 0 \\ \gamma & 0 & 0 & \phi & -\mu \end{bmatrix}. \tag{70}$$

The disease-free equilibrium point $E_0$ is discussed by examining the Jacobian matrix (70) at the steady point $E_0$. Now, at the disease-free equilibrium

$$\left(\frac{\Lambda}{(\mu+\gamma)}, 0, 0, 0, \frac{\Lambda\gamma}{\mu(\mu+\gamma)}\right), \tag{71}$$

the Jacobian matrix is given by

$$J = \begin{bmatrix} -(\mu+\gamma) & 0 & 0 & 0 & 0 \\ 0 & -k_1 & 0 & 0 & 0 \\ 0 & \pi & -k_2 & 0 & 0 \\ 0 & \beta & \tau & -(\mu+\phi) & 0 \\ \gamma & 0 & 0 & \phi & -\mu \end{bmatrix}. \tag{72}$$

For stability of the disease-free equilibrium, it is required that the trace$(J_{E_0}) < 0$ and the det$(J_{E_0}) > 0$. Thus, from the Jacobian matrix (72), it is clearly seen that

$$\begin{aligned} \operatorname{trace}\left(J_{E_0}\right) &= -\left[(\mu+\gamma) + k_1 + k_2 + (\mu+\phi) + \mu\right] \\ &= -(\gamma+\beta+\pi+\tau+\delta+\phi+5\mu) < 0. \end{aligned} \tag{73}$$

The determinant of the Jacobian matrix is also given by

$$\begin{aligned} &\det\left(J_{E_0}\right) \\ &= \det\begin{bmatrix} -(\mu+\gamma) & 0 & 0 & 0 & 0 \\ 0 & -k_1 & 0 & 0 & 0 \\ 0 & \pi & -k_2 & 0 & 0 \\ 0 & \beta & \tau & -(\mu+\phi) & 0 \\ \gamma & 0 & 0 & \phi & -\mu \end{bmatrix} \\ &= -(\mu+\gamma)\det\begin{bmatrix} -k_1 & 0 & 0 & 0 \\ \pi & -k_2 & 0 & 0 \\ \beta & \tau & (\mu+\phi) & 0 \\ 0 & 0 & \phi & -\mu \end{bmatrix} \\ &= k_1 k_2 \mu(\mu+\phi)(\mu+\gamma) > 0. \end{aligned} \tag{74}$$

Therefore, the disease-free equilibrium of the pneumonia model under treatment and vaccination interventions is locally asymptotically stable. This is established by the fact that the trace$(J_{E_0}) < 0$ and the det$(J_{E_0}) > 0$.

**Proposition 8.** *$\mathcal{R}_e < \mathcal{R}_0$ for any given parameters.*

*Proof.*

$$\mathcal{R}_e = \frac{\Lambda\mathcal{R}_0}{(\mu+\gamma)} \tag{75}$$

implies that

$$\mathcal{R}_e = \frac{\Lambda\mathcal{R}_0}{(\mu+\gamma)} < \mathcal{R}_0. \tag{76}$$

Thus $\mathcal{R}_e < \mathcal{R}_0$. □

The above result leads us to the following theorem.

**Theorem 9.** *The disease-free equilibrium $E_0$ of the pneumonia model under treatment and vaccination interventions is locally asymptotically stable if $\mathcal{R}_e < 1$ and unstable if $\mathcal{R}_e \geq 1$.*

The proof of the theorem follows from the Jacobian matrix (72).

The endemic equilibrium $E_e$ is defined as a steady state solution for system (57). This occurs when there is a persistence of the disease. Hence, $E_e = (S, C, I, R, V)$ can be determined as below. Consider system (57) with right-hand side equal to zero to obtain

$$\begin{aligned} \Lambda - (\alpha+\mu+\gamma)S &= 0, \\ \alpha\theta S - (\mu+\beta+\pi)C &= 0, \\ \alpha(1-\theta)S + \pi C - (\tau+\mu+\sigma)I &= 0, \\ \beta C + \tau I - (\mu+\phi)R &= 0, \\ \gamma S - \mu V + \phi R &= 0, \end{aligned} \tag{77}$$

together with

$$\begin{aligned} \Lambda - \mu N - \sigma I &= 0, \\ \alpha &= \delta\left(\frac{I+\omega C}{N}\right). \end{aligned} \tag{78}$$

Solving system (77) together with (78) gives the endemic equilibrium $E_e = (S, I, C, R)$, where

$$\begin{aligned} S &= \frac{\Lambda\sigma k_1 N}{\left[(k_1 - \sigma\theta\omega)(\Lambda - (\mu+\sigma)N) + \omega\theta(\Lambda - (\mu+\sigma)N)\right] + (\mu+\sigma)N\sigma k_1}, \\ C &= \frac{\theta(\Lambda - (\mu+\gamma)N)}{k_1}, \\ I &= \frac{(k_1 - \sigma\theta\omega)(\Lambda - (\mu+\gamma)N)}{\sigma k_1}, \\ R &= \frac{\beta\theta\sigma(\Lambda - (\mu+\gamma)N) + \tau(k_1 - \sigma\theta\omega)(\Lambda - (\mu+\gamma)N)}{\sigma k_1(\mu+\phi)}, \end{aligned}$$

$$V = \frac{\gamma\Lambda\sigma k_1 N}{p} + \frac{\phi\beta\theta\sigma\left(\Lambda - (\mu+\gamma)N\right) + \tau\left(k_1 - \sigma\theta\omega\right)\left(\Lambda - (\mu+\gamma)N\right)}{(\mu+\phi)\sigma k_1}, \tag{79}$$

where

$$\begin{aligned} k_1 &= \mu + \beta + \pi, \\ k_2 &= \tau + \mu + \sigma, \\ p &= \left[\left(k_1 - \sigma\rho\omega\right)\left(\Lambda - (\mu+\sigma)N\right)\right. \\ &\quad \left. + \omega\rho\left(\Lambda - (\mu+\sigma)N\right)\right] + (\mu+\sigma)N\sigma k_1. \end{aligned} \tag{80}$$

*4.4. Local Stability of the Endemic Equilibrium.* The Jacobian matrix for system (57) is given by

$$J = \begin{bmatrix} -(\alpha+\mu+\gamma) & 0 & 0 & 0 & 0 \\ \alpha\theta & -(\mu+\beta+\pi) & 0 & 0 & 0 \\ \alpha(1-\theta) & \pi & -(\tau+\mu+\sigma) & 0 & 0 \\ 0 & \beta & \tau & -(\mu+\phi) & 0 \\ \gamma & 0 & 0 & \phi & -\mu \end{bmatrix}. \tag{81}$$

Evaluating the Jacobian matrix (81) at the endemic equilibrium gives

$$J_{E_e} = \begin{bmatrix} -(\alpha^*+\mu+\gamma) & 0 & 0 & 0 & 0 \\ \alpha^*\theta & -(\mu+\beta+\pi) & 0 & 0 & 0 \\ \alpha^*(1-\theta) & \pi & -(\tau+\mu+\sigma) & 0 & 0 \\ 0 & \beta & \tau & -(\mu+\phi) & 0 \\ \gamma & 0 & 0 & \phi & -\mu \end{bmatrix}, \tag{82}$$

where

$$\alpha^* = \delta\left(\frac{I+\omega C}{N}\right). \tag{83}$$

We now obtain the characteristic equation $P = |(\xi)I - J(E_e))|$, where $I$ is a $5 \times 5$ unit matrix.

$$P(\xi) = \det\begin{bmatrix} \xi + k_1 & 0 & 0 & 0 & 0 \\ -\alpha^*\theta & \xi + k_2 & 0 & 0 & 0 \\ -\alpha^*(1-\theta) & -\pi & \xi + k_3 & 0 & 0 \\ 0 & -\beta & -\tau & \xi + k_4 & 0 \\ -\gamma & 0 & 0 & -\phi & \xi + \mu \end{bmatrix}, \tag{84}$$

where

$$\begin{aligned} k_1 &= \alpha^* + \mu + \gamma, \\ k_2 &= \mu + \beta + \pi, \\ k_3 &= \tau + \mu + \sigma, \\ k_4 &= \mu + \theta. \end{aligned} \tag{85}$$

Thus the characteristic equation becomes

$$P(\xi) = \xi^5 + a_1\xi^4 + a_2\xi^3 + a_3\xi^2 + a_4\xi + a_5, \tag{86}$$

where

$$\begin{aligned} a_1 &= k_1 + k_2 + k_3 + k_4 + \mu, \\ a_2 &= k_1k_2 + k_2k_3 + k_1k_4 + k_1\mu + k_2k_3 + k_2\mu + k_2k_4 \\ &\quad + k_3\mu + k_3k_4 + \theta, \\ a_3 &= k_1k_2k_3 + k_1k_2\mu + k_1k_2k_4 + k_1k_3\mu + k_1k_3k_4 \\ &\quad + k_2k_3\mu + k_4k_3\mu + k_1\theta + \theta\mu + k_3\phi, \\ a_4 &= k_1k_2k_3k_4\mu + k_1k_3k_4\mu + k_1\theta\mu + k_1k_3\phi + k_2k_3\phi, \\ a_5 &= k_1k_2k_3\phi. \end{aligned} \tag{87}$$

The necessary and sufficient conditions for the local asymptotic stability of endemic equilibrium are that the Hurwitz determinants $H_i$ are all positive for the Routh-Hurwitz criteria. For a fifth-degree polynomial [42], these criteria are given by

$$\begin{aligned} H_1 &= a_1 > 0, \\ H_2 &= a_1a_2 - a_3 > 0, \\ H_3 &= a_1a_2a_3 + a_1a_3 + a_1a_5 - a_1a_4 - a_3 > 0, \\ H_4 &= (a_3a_4 - a_2a_5)(a_1a_2 - a_3) - (a_1a_4 - a_5) > 0, \\ H_5 &= a_5H_4 > 0, \end{aligned} \tag{88}$$

from which we can conclude that the endemic equilibrium is locally asymptotically stable.

## 5. Sensitivity Analysis

Intervention strategies to reduce the mortality and morbidity due to pneumonia should target the parameters that have a high impact on the effective reproduction number, $\mathscr{R}_e$. Sensitivity analysis is used to obtain the sensitivity index that is a measure of the relative change in a state variable when a parameter changes. We compute the sensitivity indices of $\mathscr{R}_e$ to the model parameters with the approach used by Chitnis et al. [43]. These indices show the importance of each individual parameter in the disease transmission dynamics and prevalence.

*Definition 10.* The normalized forward sensitivity index of a variable, $v$, that depends differentiability on index on a parameter, $p$, is defined as

$$\gamma_p^v = \frac{\partial v}{\partial p} * \frac{p}{v}. \tag{89}$$

We use the formula for $\mathscr{R}_e$ to derive an expression for the sensitivity of $\mathscr{R}_e$ given by

$$\gamma_p^{\mathscr{R}_e} = \frac{\partial \mathscr{R}_e}{\partial p} * \frac{p}{\mathscr{R}_e}, \tag{90}$$

to each of the ten parameters given in Table 1. In the following example, we obtain the sensitivity index of $\mathscr{R}_e$ with respect to $\delta$:

$$\gamma_\delta^{\mathscr{R}_e} = \frac{\partial \mathscr{R}_e}{\partial \delta} * \frac{\delta}{\mathscr{R}_e} = 1. \tag{91}$$

The same method is used to obtain the indices of $\gamma_\Lambda^{\mathscr{R}_e}$, $\gamma_\mu^{\mathscr{R}_e}, \gamma_\gamma^{\mathscr{R}_e}, \gamma_\theta^{\mathscr{R}_e}, \gamma_\beta^{\mathscr{R}_e}, \gamma_\omega^{\mathscr{R}_e}, \gamma_\tau^{\mathscr{R}_e}, \gamma_\pi^{\mathscr{R}_e}$, and $\gamma_\sigma^{\mathscr{R}_e}$.

The parameters given in Table 1 are ordered from most sensitive to the least sensitive. The parameter values $\delta = 7.6$, $\mu = 0.0002$, $\Lambda = 10.09$, $\sigma = 0.33$, $\omega = 0.001124$, $\tau = 0.0714$, $\pi = 0.01096$, $\beta = 0.0115$, $\theta = 0.336$, and $\eta = 0.0241$ are used to determine the sensitivity indices.

*5.1. Interpretation of Sensitivity Indices.* It is noted from the sensitivity indices given in Table 1 that the value of $\mathscr{R}_e$ increases when the parameter values $\delta$, $\theta$, $\omega$, and $\Lambda$ increase while other parameter values are kept fixed. This implies an increase in the endemicity of the disease since the indices have positive signs. On the other hand, when the parameter values $\mu$, $\sigma$, $\beta$, $\tau$, $\pi$, and $\eta$ are decreased while the rest of the parameter values are kept fixed, the value of $\mathscr{R}_e$ decreases. This shows a decrease in the disease endemicity because the indices have negative signs. The transmission rate $\delta$ and recruitment rate $\Lambda$ are the most sensitive parameters. The transmission coefficient of the carrier subgroup $\omega$ and proportion of susceptible population that become carriers $\theta$ are the other key parameters that are sensitive.

## 6. Numerical Simulation

We illustrate the analytical results of the model by carrying out numerical simulation of the models using a set of estimated parameter values obtained from literature. The system is simulated using ODE solvers coded in MATLAB programming language. Simulation of the pneumonia model under treatment intervention alone and the model with treatment and vaccination interventions combined is carried out to investigate the impact of the key parameters on the spread of pneumonia and how their influence can be controlled. The parameter values are presented in Table 2.

Table 1: Numerical values of sensitivity indices of $\mathscr{R}_e$.

| Parameter symbols | Sensitivity Index |
|---|---|
| $\Lambda$ | +1 |
| $\delta$ | +1 |
| $\omega$ | +0.874 |
| $\theta$ | +0.643 |
| $\tau$ | −0.743 |
| $\eta$ | −0.432 |
| $\beta$ | −0.0574 |
| $\mu$ | −0.0086 |
| $\pi$ | −0.0045 |
| $\sigma$ | −0.0014 |

## 7. Discussion and Conclusion

In the study, a deterministic model is formulated and analyzed to investigate the role of treatment and vaccination in the transmission dynamics of pneumonia. The model is well-posed and exists in a feasible region where disease-free and endemic equilibrium are obtained and their stability is investigated.

When the equilibrium is locally stable, all the points near it tend to move towards it over time and when the equilibrium point is globally stable, all the initial starting conditions lead to it over time.

The basic model of pneumonia under treatment intervention alone has a locally and globally asymptotically stable disease-free equilibrium if its associated reproduction number $\mathscr{R}_0 < 1$ and has a unique and globally asymptotically stable endemic equilibrium when the reproduction number exceeds unity.

The disease-free equilibrium is locally stable implying that if initial conditions were to start near it, they would move towards it over time but the initial conditions do not always start at neighborhood of disease-free equilibrium. When the disease-free equilibrium of model is globally stable, it means that all initial starting conditions would lead to it over time; hence treatment would decrease the disease prevalence. The endemic equilibrium of model is globally stable if and only if $\mathscr{R}_0 > 1$, implying that all the points near it tend to move towards it over time.

In order to make the endemic equilibrium unstable so that it switches to disease-free equilibrium, intervention measures like treatment with high efficacy drugs and vaccination programs are necessary.

Table 2: Parameter estimates for pneumonia model under interventions.

| Symbol | Description | Value | Source |
|---|---|---|---|
| $\mu$ | Per capita natural mortality rate | 0.0002/day | [2] |
| $\Lambda$ | Per capita recruitment rate | 10.09/day | Estimated |
| $\theta$ | Fraction of susceptible individuals that join the carriers | 0.338/day | Estimated |
| $\sigma$ | Per capita disease induced mortality rate | 0.33/day | [2] |
| $\beta$ | Per capita recovery rate of carriers | 0.0115/day | Estimated |
| $\alpha$ | Force of infection of susceptible individuals | 0.0287/day | Estimated |
| $\tau$ | Per capita recovery rate of infective individuals | 0.0714/day | [36] |
| $\pi$ | Rate at which carriers develop symptoms | 0.01096/day | [7] |
| $\eta$ | Rate at which treated individuals become susceptible | 0.0241/day | Estimated |
| $\gamma$ | Rate at which susceptible individuals get vaccinated | 0.0621/day | Estimated |
| $\phi$ | Rate at which treated individuals are vaccinated | 9.4/day | Estimated |
| $\omega$ | Transmission coefficient for the carrier subgroup | 0.001124 | [37] |
| $\delta$ | Transmission rate | 7.6/day | Estimated |
| $p$ | Probability for a contact to cause infection | 0.89–0.99 | [37] |
| $\kappa$ | Contact rate | 1–10/day | [37] |

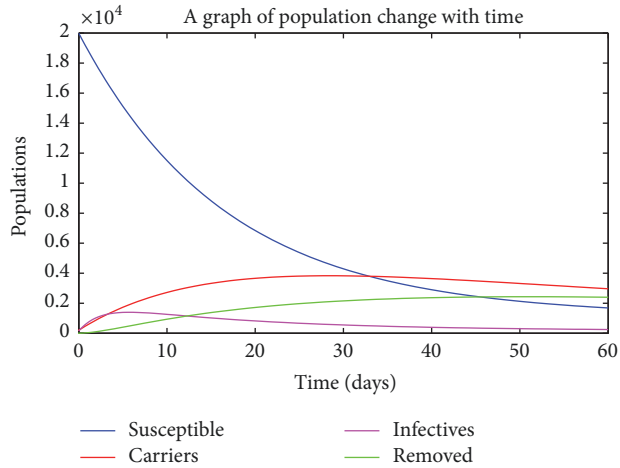


Figure 1: Variation of the population under treatment intervention alone.

The pneumonia model under treatment and vaccination interventions have a disease-free equilibrium which is locally asymptotically stable whenever its associated effective reproduction number $\mathcal{R}_e < 1$. This implies that the initial conditions would tend to the disease-free equilibrium point and hence pneumonia will be wiped out of the population.

Sensitivity analysis identifies the transmission rate $\delta$ as the key factor in fueling the spread of pneumonia, whereas vaccination rate $\gamma$ and recovery rate $\tau$ are the parameters that inhibit the spread of the disease. From the results obtained, we conclude that a combination of vaccination and treatment interventions programs targeting children can effectively eliminate pneumonia infection from the population.

Numerical simulation of the pneumonia model under treatment strategy $\tau$ for the set of parameter estimates presented in Table 2 and initial values of population sizes are carried out. The results show that when there is a pneumonia outbreak, the population sizes of the infected and carriers increase with time while the susceptible population size decreases with time until an endemic equilibrium is attained as shown in Figure 1. In Figure 2, it is shown that with treatment intervention in place for the different subgroups, the infected population decreases until it equals the treated population. When both treatment and vaccination strategies are applied, numerical simulation reveals a sharp decline in the susceptible population and a rise in both the infected and carrier populations during the initial stages of the epidemic until a disease-free equilibrium is attained as shown in Figure 3. The effect of treatment and vaccination interventions on the population leads to a decrease in the susceptible, infected, carriers, and treated populations and an increase in the vaccinated populations as presented in Figure 4. This confirms that a combination of treatment and

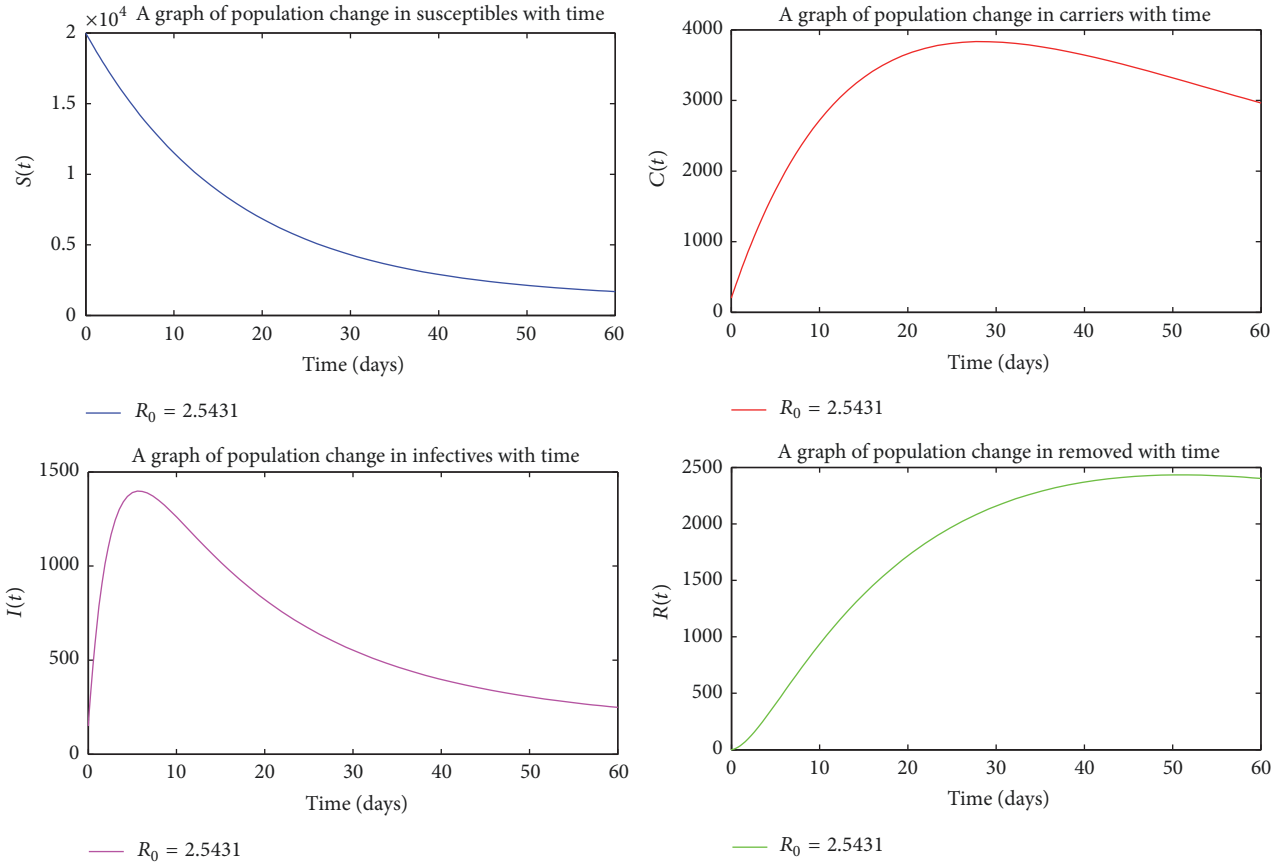


Figure 2: Variation of the population under treatment intervention alone.

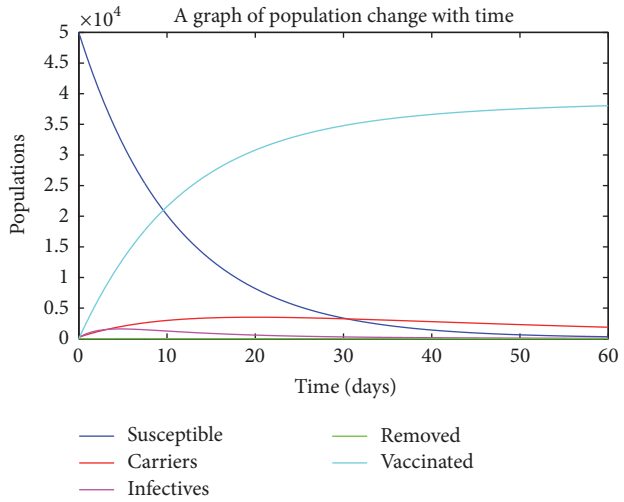


Figure 3: Variation of the population under treatment and vaccination interventions.

vaccination interventions can eradicate the disease from the community.

The results have important public health implications since they determine the severity and outcome of the epidemic (i.e., clearance or persistence of infection) and provide a framework for the design of control strategies. The study further shows that a combination of treatment and vaccination has much more impact than treatment alone. Furthermore, analysis of the effective reproduction number $\mathcal{R}_e$ demonstrates that vaccination and treatment reduce the average number of secondary infections when implemented. Thus, in order to control the pneumonia spread, infected

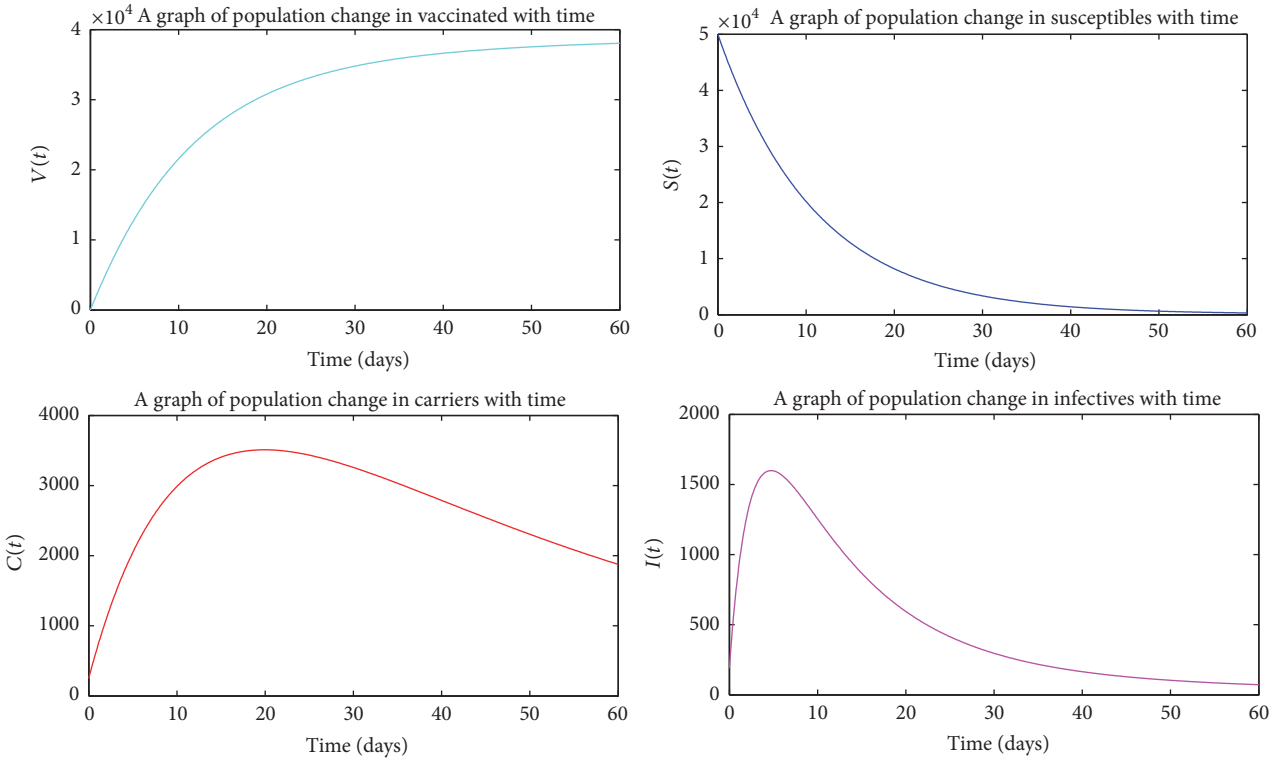


Figure 4: Variation of the population under treatment and vaccination interventions.

individuals should be treated immediately; all individuals with compromised immunity including newborn babies and the elderly should be vaccinated.

## Conflicts of Interest

The authors declare that no conflicts of interest took place during the preparation of the manuscript.

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