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Research Article

Effect of Vaccination and Culling on the Dynamics of Rabies Transmission from Stray Dogs to Domestic Dogs

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In this paper, the population dynamics of rabies-infected dogs are studied. The mathematical model is constructed by dividing the dog population into two categories: stray dogs and domestic dogs. On the other hand, the rabies virus is likely to spread in both populations. In the current model, disease-controlling strategies such as vaccination and culling are applied, and their impact is studied. Both subpopulations of susceptible individuals are vaccinated to control disease spread. The current study assumes that stray dogs can transmit rabies to domestic dogs but not the other way around. Because domestic dogs are under the control of their owners, they are well vaccinated. The model is medically and analytically correct because the findings are idealistic and limited. The next-generation matrix technique is used to compute the effective reproductive amount, and also, each parameter is subjected to sensitivity analysis. The equilibrium point free from disease is discovered, demonstrating that it was asymptotically steady locally and globally. A conditionally global asymptotically stable point of endemic equilibrium is also discovered using the Lyapunov function method. The numerical simulation, which makes use of approximations for parameter values, shows that the most efficient method for avoiding rabies transmission is a combination of vaccination and the culling of infected stray dogs. Using MATLAB's ode45, this numerical simulation investigation was carried out. Our early findings indicated that the annual dog birth rate is a critical factor in influencing the occurrence of rabies. In the body of the paper, the findings and discussion are organized logically.

1. Introduction

Infectious disease outbreaks have been ongoing in recent decades, and there are more and more instances when long-standing infections could be eradicated, but human conduct has prevented it. This conversation interaction between infectious illness processes and the dynamics of human nature partially explains the rise in interest in directly adding incorporating human nature into mathematical equations of the spread of infectious diseases [1]. Mathematical models that take into consideration human behavior may provide more clarity and more accurate predictions than models that neglect the significant influence that behavior can have on the dynamics of infectious diseases.

The acute infectious disease rabies, which is fatal, is carried on by lyssaviruses. The lyssavirus known as the "prototype species," or rabies lyssavirus, is the most widespread and the greatest hazard to public health. In mammals, it causes brain inflammation. Fever and tickling at the site of exposure are the first signs of infection, followed by one or more other signs such as frantic movement, inability to control certain body parts, loss of consciousness, confusion, fear of water, and unrestrained excitation. Before symptoms start to show up, it often takes one to three months from the day of introduction to the disease [2]. The duration of the symptoms can range from less than a week to over a year. Once the symptoms started to manifest, almost every instance resulted in death. When one animal or person bites or scratches another animal or person,

the infection spreads. Additionally, if the saliva of an infected animal touches the mouth, eyes, or nose of a susceptible animal, it might spread the rabies virus. The dog is typically the animal most frequently associated with the transmission of rabies [3].

The goal of vaccination, which is being implemented on a global scale to stop the spread of infectious diseases that have crippled many human societies in the recent past, is without a doubt to inhibit the spread of transmissible diseases. Significant advancements in public health, particularly in the prevention and treatment of infectious illnesses, were made during the 20th century. Vaccinations were critical to achieving that result [4]. Early research, however, merely assumed that mandatory and/or arbitrary vaccination should be practiced due to a lack of vaccination and information. As of today, we are aware that network vaccination programs are more successful when random vaccination is paired combining targeted vaccination and familiarity immunization [5]. Even though irregular immunization does not need topological knowledge of the network, it does require very broad coverage, which makes it quite expensive [6].

A deterministic model was created to examine the dynamics of dog-to-human and dog-to-dog rabies infection in China [7]. The model identified four groupings within both the dog and human populations: those who were susceptible, those exposed to infection, those infectious, and those who recovered. According to the findings, the most efficient ways to reduce human rabies in China are to decrease the dog fertility rate and increase the coverage amount of dog vaccinations. They suggested that mass vaccinations of susceptible dogs could take the place of large-scale culling. This is due to the possibility of community disruption and an increase in the immigration of diseased dogs during the dog culling operation.

In their paper, modeling the dynamic behavior stability analysis and the prevention of rabies spread with immunization [8], the researchers created an equation that is deterministic for rabies spread changing aspects popular among humans and animals in the region of Ethiopia's Addis Ababa. Their model integrates a dog immunization program. They computed the fundamental number of reproduction as well as the effective reproduction number. Their findings are completely reliant on the parameters of a population of dogs, indicating that the dog population is to blame for human and livestock infection. They calculated the specific both the total and an effective number of reproductions from data obtained from Addis Ababa's Ethiopian Public Health Institute and found them in the range of 2 and 1.6, respectively, representing the endemic nature of the illness. Domestic dogs and stray dogs are two subpopulations of dogs in our model. Domestic dogs are defined as dogs that live closest to humans [9], and stray dogs are defined as dogs that freely move in public [10]. Stray dogs have been related to negative effects on the environment as well as general health. The following sections form the paper: Introduction, Model Formulation, Stability Analysis, and Sensitivity Analysis, are the first four steps Section 5 is the simulations and Section 6 is the concluding remarks

2. Model Formulation

In this study, we develop the SEIR model of rabies for stray dogs and the domestic dog population based on the work obtainable in [11–14]. Each stray dog as well as the domestic dog population is divided into categories according to susceptibility, exposure, infection, and recovery. Susceptible collections are uninfected, but then again, if they make contact with rabid dogs, they are at risk of infection. Individuals who are exposed are those that have been infected with the virus but have not yet developed symptoms. Individuals who become infected develop clinical symptoms and, due to the nature of rabies, are unlikely to recover. The recovered classes are those who were vaccinated and recovered before becoming infectious, whereas the rest became infected and died.

The stray dog population has four compartments representing the susceptible stray dogs, S_s; exposed stray dogs E_s; infected stray dogs, $I_{s,}$ and recovered stray dogs, R_s. Thus, the total domestic dog population is N_s. Additionally, there are four divisions in the domestic dog population that represent susceptible domestic dogs S_d; exposed domestic dog, E_d; infected domestic dog, I_d; and recovered domestic dogs, R_d. Thus, the total population is N_d. It is expected that there is no domestic dogs' domestic dog spread of rabies infection in the domestic dog's submodel [15]. In the stray dog submodel, this is supposed that now, the rabies virus spreads directly through one stray dog to the other as well as from the division of infected stray dogs to the population of susceptible domestic dogs. It is further believed that such susceptible domestic dog group, S_d, is growing at a rate of A_d whereas the susceptible stray dog population, S_s, is growing at a rate of A_s through recruitment. The idea is that the infected stray dog meets and spreads at a rate of β_s into the stray dog division. Suppose that θ_s characterizes the switch plan outstanding to immunization in the susceptible stray dog's section; formerly the spread changing aspects develop, somewhere the no effectiveness (letdown) of the vaccine. Additionally, it is believed that domestic dog groups and infectious dogs come into interaction at a rate of β_s. Similar to how immunization is administered to a susceptible domestic dog, the dog's growth rate toward exposure changes, where the preexposure prevention indicates the domestic dog division's failing of preexposure prevention. The amount of down resistance in together divisions is characterized by $\boldsymbol{\alpha_s}, \boldsymbol{\alpha_d}$. Also, both an exposed stray and domestic dog move to infectious class directly. Strays and domestic dogs' natural mortality rates are denoted by μ_s and μ_d, respectively, and indicate the mortality rate of domestic and stray dogs, which is ε_s and ε_d, or the fatality rate related to rabies disease in stray and domestic dogs, respectively. Also, the culling rate of stray and domestic dogs are denoted as $\mathbf{c_s}, \mathbf{c_d}$, respectively. Rabies transmission among domestic dogs was neglect because of minor situations, since the ownership monitors domestic dogs. A person gets sick after being attacked by a rabid dog. The table below explains every one of the model's variables, of which all are positive.

2.1. Model Variables and Parameters with Their Descriptions. Tables 1 and 2 below, respectively, contain descriptions of the model's variables and parameters.

Table 1: Variables in the model and its explanation.

Symbol	Information about the variables
$S_s(t), S_d(t)$	Susceptible stray and domestic dog population at time t, respectively
$E_s(t), E_d(t)$	Exposed stray and domestic dog population at time t, respectively
$I_s(t), I_d(t)$	Infectious stray and domestic dog population at time t, respectively
$R_s(t), R_d(t)$	Recovered stray and domestic dog population at time t, respectively

Table 2: Details of the model parameters.

Parameter	Explanation
A_d	Number of domestic dog recruitment
A_s	Number of stray dog recruitment
β_d	Rate of stray dog transmission to domestic dogs
β_s	Rate of transmission from stray to a stray dog
δ_d	The proportion of exposed domestic dogs' clinical outcomes
δ_s	The proportion of exposed stray dogs' clinical outcomes
θ_d	Rate of domestic dog vaccination
θ_s	Rate of stray dog vaccination
μ_d	The natural death rate of domestic dogs
μ_s	The natural death rate of stray dogs
α_d	Rate of domestic dog vaccination immunity loss
α_s	Rate of stray dog vaccination immunity loss
ε_d	The ratio of rabies-related deaths in domestic dogs
ε_s	The ratio of rabies-related deaths in stray dogs
c_d	Rabid domestic dog culling rate
c_s	Rabid stray dog culling rate

2.2. Model Equations. The model is a system of eight ordinary differential equations, as shown by the transmission flowchart in Figure 1 and also the statements made on the connections between the variables and parameters.

$$\left.\begin{aligned}
\frac{dS_d}{dt} &= A_d + \alpha_d R_d - \beta_d S_d I_s - (\theta_d + \mu_d) S_d \\
\frac{dE_d}{dt} &= \beta_d S_d I_s - (\delta_d + \mu_d) E_d \\
\frac{dI_d}{dt} &= \delta_d E_d - (\varepsilon_d + \mathbf{c_d} + \mu_d) I_d \\
\frac{dR_d}{dt} &= \theta_d S_d - (\alpha_d + \mu_d) R_d \\
\frac{dS_s}{dt} &= A_s + \alpha_s R_s - \beta_s S_s I_s - (\theta_s + \mu_s) S_s \\
\frac{dE_s}{dt} &= \beta_s S_s I_s - (\delta_s + \mu_s) E_s \\
\frac{dI_s}{dt} &= \delta_s E_s - (\varepsilon_s + \mathbf{c_s} + \mu_s) I_s \\
\frac{dR_s}{dt} &= \theta_s S_s - (\alpha_s + \mu_s) R_s
\end{aligned}\right\}. \tag{1}$$

The total population for $N_d(t)$ and $N_s(t)$ is

$$\left.\begin{aligned}
N_d(t) &= S_d(t) + E_d(t) + I_d(t) + V_d(t) \\
N_s(t) &= S_s(t) + E_s(t) + I_s(t) + V_s(t)
\end{aligned}\right\}. \tag{2}$$

Due to this, combining the differential equations for the domestic dog and stray dog populations in system (1) will result in

$$\left.\begin{aligned}
\frac{dN_d}{dt} &= A_d - \mu_d N_d - (\mathbf{c_d} + \varepsilon_d) I_d \\
\frac{dN_s}{dt} &= A_s - \mu_s N_s - (\mathbf{c_s} + \varepsilon_s) I_S
\end{aligned}\right\}, \tag{3}$$

where N_d and N_s represent the entire populations of domestic dogs and stray dogs, correspondingly, during time t.

2.3. The Model's Invariant Region. Here, the total population of domestic dogs and stray dog population needs to be

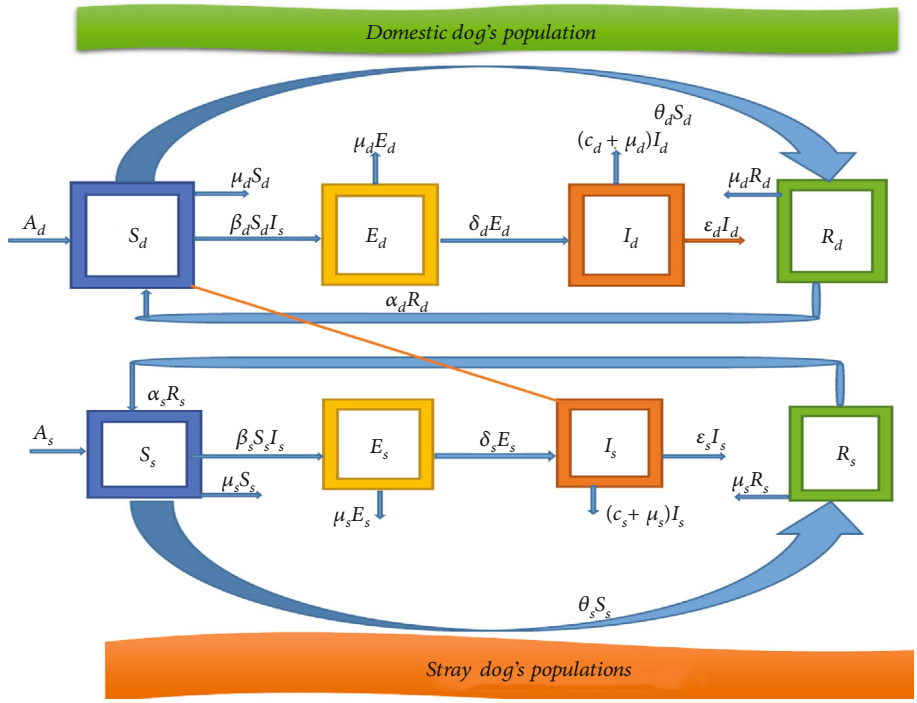


FIGURE 1: Flowchart illustrating the spread of rabies from stray dogs to domestic dogs.

bounded. To put it another way, all state variables and parameters are taken to be positive for all time $t \geq 0$, in order to study the model system in the feasible region. Two regions make up the model system (1); consequently, $\Omega = \Omega_d \times \Omega_s$. Consider the following lemma.

Lemma 1. *The solution set* $\{S_d, E_d, I_d, R_{\_d}, S_s, E_s, I_s, R_s\} \in R_+^8$ *is limited in the possible region of the model system (1)* Ω.

Proof. The total population of domestic dogs and stray dogs varies as time change. Due to changes in who is included in the susceptible class. The model yields the following rate of change for the entire domestic dog population:

$$\frac{dN_d}{dt} = \frac{dS_d}{dt} + \frac{dE_d}{dt} + \frac{dI_d}{dt} + \frac{dR_d}{dt} = A_d - \mu_d N_d - (c_d + \varepsilon_d) I_d. \tag{4}$$

□

If there is no disease-related mortality rate, then it follows that

$$\frac{dN_d}{dt} = A_d - \mu_d N_d. \tag{5}$$

Similarly,

$$\frac{dN_s}{dt} = A_s - \mu_s N_s. \tag{6}$$

Suppose $dN_d/dt \leq 0$ and $dN_s/dt \leq 0$; we will get $N_d \leq A_d/\mu_d$ and $N_s \leq A_s/\mu_s$, on differentiating inequality results in $0 \leq N_d \leq A_d/\mu_d$ and $0 \leq N_s \leq A_s/\mu_s$.

Therefore, equations (5) and (6) become

$$\frac{dN_d}{dt} \leq A_d - \mu_d N_d, \tag{7}$$

$$\frac{dN_s}{dt} \leq A_s - \mu_s N_s. \tag{8}$$

Integrating (7) and (8), use the integrating factor method and following some mathematical manipulation, the practical answer for the domestic dog and stray dog population in the area of the model system (1).

$$\left.\begin{aligned} \Omega_{.d} &= \left\{ (s_{.d}, E_{.d}, I_{.d}, R_{.d}) \in R_{.+}^4 N_{.d} \leq \frac{A_d}{\mu_d} \right\} \\ \Omega_s &= \left\{ (S_s, E_s, I_s, R_s) \in R_+^4, N_s \leq \frac{A_s}{\mu_s} \right\} \end{aligned}\right\}. \tag{9}$$

Consequently, a practical solution is given. Therefore, $\Omega = \Omega_{.d} \times \Omega_s$. It follows from the common comparison theorem applied to differential inequality in [1] that from equations (7) and (8), solutions of N_d and N_s become

$$N_d \leq N_{.d}(0) e^{-(\mu_{.d}).t} + \frac{A_d}{\mu_d}\left(1 - e^{-(\mu_{.d}).t}\right), \tag{10}$$

$$N_s \le N_s(0)e^{-(\mu_s)t} + \frac{A_s}{\mu_s}\left(1 - e^{-(\mu_s)t}\right). \tag{11}$$

Taking the limit as $t \longrightarrow \infty$ for equations (10) and (11) becomes

$$\begin{aligned} 0 \le N_d &\le \frac{A_d}{\mu_d}, \\ 0 \le N_s &\le \frac{A_s}{\mu_s}. \end{aligned} \tag{12}$$

The total population of domestic dog $N_d(t)$ and stray dog$N_s(t)$ approaches to A_d/μ_dandA_s/μ_s, respectively, where A_d/μ_d and A_s/μ_s are the upper bounds. This implies that at any time t, each and every solution with initial conditions in Ω is leftovers in Ω [7]. And if $N_d > A_d/\mu_d$ and $N_s > A_s/\mu_s$, then the solutions $\{S_d, E_d, I_d, R\_d, S_s, E_s, I_s, R_s\}$ enter the feasible region Ω at any time t. Therefore, every solution of system (1) is positively invariant, and hence, in region Ω, the model can continue to be mathematically sound and medically relevant. Thus, the investigation of solution $\{S_d, E_d, I_d, R\_d, S_s, E_s, I_s, R_s\}$ is restricted to the region.

2.4. Disease-Free Equilibrium Points (DFE). The disease-free equilibrium point of the model provided by the system is denoted $\mathscr{E}_0 = (S_d^*, E_d^*, I_d^*, R_d^*, S_s^*, E_s^*, S_s^*, I_s^*, R_s^*)$. Therefore, the next category will be 0 if there is no rabies. $E_d^* = I_d^* = E_s^* = I_s^* = 0$. Including this in system (1) results in

$$\left.\begin{aligned} A_{\cdot d} + \alpha_d R_d - (\theta_d + \mu_d)S_{\cdot d} &= 0 \\ \theta_d S_d - (\alpha_d + \mu_d)R_d &= 0 \\ A_s + \alpha_s R_s - (\theta_s + \mu_s)S_s &= 0 \\ \theta_s S_s - (\alpha_s + \mu_s)R_s &= 0 \end{aligned}\right\}. \tag{13}$$

The DFE $\mathscr{E}_0$ will be obtained by rearranging (13) mathematically.

$$\mathscr{E}_0 = \left(\frac{A_d(\mu_d + \alpha_d)}{\mu_d(\mu_d + \theta_d + \alpha_d)}, 0, 0, \frac{A_d\theta_d}{\mu_d(\mu_d + \theta_d + \alpha_d)}, \frac{A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)}, 0, 0, \frac{A_s\theta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)}\right). \tag{14}$$

If $R_e < 1$, the infection will not spread because, in general, throughout its contagious phase, an infected individual creates less than one new infectious disease.

2.5. The Effective Reproduction Number (R_e). The average amount of reinfection brought on as a pathogen delivered into a group of susceptible domestic dogs and stray dogs is the effective reproduction ratio, the threshold value R_e, [16, 17]. A statistic known as the effective reproduction number (R_e) can help predict whether such an illness will spread across a community or go extinct. If $R_e < 1$, the infection will not spread because, in general, throughout its contagious phase, an infected individual creates less than one new infectious disease. On the other hand, if $R_e > 1$, so each infected person often creates more than one new infection, as well as the illness can spread all across the community. If $R_e = 1$, this illness gets endemic, which means it spreads from one susceptible dog to another at a constant speed from across the community [3]. Letting $f_{\cdot i}(x)$ stand the proportion of arrival of new contagions in the compartment $(i.)$, $V_{\cdot i}^{+}(x)$ remains the transmission of individuals addicted to the compartment $(i.)$ by completely other means; also, $V_{\cdot i}^{-}(x)$ remains the proportion of transmission of individuals out of the compartment $(i.)$. This one is expected that every function $(f_{\cdot i}, V_{\cdot i}^{+}, \text{and } V_{\cdot i}^{-})$ is continuously differentiable at a minimum double concerning each variable and $V_{\cdot i} = V_{\cdot i}^{-} - V_{\cdot i}^{+}$. To calculate the R_e, it is done by means of the next-generation method and taking the infectious compartments. $\rho(FV^{-})$ symbolizes the spectral radius of a matrix F.V^{-}, whereve $F = \partial f_{\cdot i}/\partial x_{\cdot j}$ and in addition, $V = \partial V_{\cdot i}(\mathscr{E}_0)/\partial x_{\cdot j}$ through $(i.) \ge 1$ aimed at the number of compartments, then $1 \le j \le n$ aimed at the diseased compartments only.

$$\left.\begin{aligned} \frac{dE_d}{dt} &= \beta_d S_d I_s - (\delta_d + \mu_d)E_d \\ \frac{dI_d}{dt} &= \delta_d E_d - (\varepsilon_d + c_d + \mu_d)I_d \\ \frac{dE_s}{dt} &= \beta_s S_s I_s - (\delta_s + \mu_s)E_s \\ \frac{dI_s}{dt} &= \delta_s E_s - (\varepsilon_s + c_s + \mu_s)I_s \end{aligned}\right\},$$

$$f_i = \begin{bmatrix} \beta_d S_d I_s \\ 0 \\ \beta_s S_s I_s \\ 0 \end{bmatrix},$$

$$F = \frac{\partial f_i}{\partial x_j} = \begin{bmatrix} 0 & 0 & 0 & \dfrac{\beta_d A_d(\mu_d + \alpha_d)}{\mu_d(\mu_d + \theta_d + \alpha_d)} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \dfrac{\beta_s A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)} \\ 0 & 0 & 0 & 0 \end{bmatrix},$$

$$V_i = \begin{bmatrix} (\delta_d + \mu_d)E_d \\ (\varepsilon_d + c_d + \mu_d)I_d - \delta_d E_d \\ (\delta_s + \mu_s)E_s \\ (\varepsilon_s + c_s + \mu_s)I_s - \delta_s E_s \end{bmatrix},$$

$$V = \frac{\partial V_i}{\partial x_j} = \begin{bmatrix} (\delta_d + \mu_d) & 0 & 0 & 0 \\ -\delta_d & (\varepsilon_d + c_d + \mu_d) & 0 & 0 \\ 0 & 0 & (\delta_s + \mu_s) & 0 \\ 0 & 0 & -\delta_s & (\varepsilon_s + c_s + \mu_s) \end{bmatrix},$$

$$V^{-1} = \begin{bmatrix} \frac{1}{(\delta_d + \mu_d)} & 0 & 0 & 0 \\ \frac{\delta_d}{(\delta_d + \mu_d)(\varepsilon_d + c_d + \mu_d)} & \frac{1}{(\varepsilon_d + c_d + \mu_d)} & 0 & 0 \\ 0 & 0 & \frac{1}{(\delta_s + \mu_s)} & 0 \\ 0 & 0 & \frac{\delta_s}{(\delta_s + \mu_s)(\varepsilon_s + c_s + \mu_s)} & \frac{1}{(\varepsilon_s + c_s + \mu_s)} \end{bmatrix} R_e = \rho(FV^{-1}). \tag{15}$$

In light of this, the effective reproduction number is provided by

$$R_e = \frac{\beta_s A_s (\alpha_s + \mu_s)\delta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}. \tag{16}$$

2.6. Endemic Equilibrium Points ($\mathscr{E}_1$). The steady-state conditions where the disease persists in the population are known as endemic equilibrium points. $\mathscr{E}_1 = (S_{.d}, E_{.d}, I_{.d}, R_{.d}, S_{.s}, E._s, I._s, R._s)$ is the formula for the model's endemic equilibrium point. We set $dS_d/dt = dE_d/dt = dI_d/dt = dR_d/dt = ds/dt = dE_s/dt = dI_s/dt = dR_s/dt = 0$. Within system (1) and solving for $S_d, E_d, I_d, R_d, S_s, E_s, I_s$, and R_s, we get

$$\begin{aligned}
S_s &= \frac{(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}{\beta_s \delta_s}, \\
R_s &= \frac{\theta_s(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}{\beta_s \delta_s (\alpha_s + \mu_s)}, \\
I_s &= \frac{\left(-\mu_s^4 + (-c_s - \alpha_s - \delta_s - \theta_s - \varepsilon_s)\mu_s^3 + ((-c_s - \alpha_s - \theta_s - \varepsilon_s)\delta_s - (\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_s^2 + \delta_s((-\varepsilon_s - c_s)\alpha_s + A_s\beta_s - \theta_s c_s - \theta_s\varepsilon_s)\mu_s + A_s\beta_s\delta_s\alpha_s\right)}{(\beta_s(\delta_s + \mu_s)(\alpha_s + \mu_s)(\varepsilon_s + c_s + \mu_s))}, \\
E_s &= \frac{1}{\delta_s(\delta_s + \mu_s)(\alpha_s + \mu_s)\beta_s}\left(-\mu_s^4 + (-c_s - \alpha_s - \delta_s - \theta_s - \varepsilon_s)\mu_s^3 + ((-c_s - \alpha_s - \theta_s - \varepsilon_s)\delta_s - (\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_s^2 + \delta_s((-c_s - \varepsilon_s)\alpha_s + A_s\beta_s - \theta_s c_s - \theta_s\varepsilon_s)\mu_s + A_s\beta_s\delta_s\alpha_s\right), \\
E_d &= -\frac{\left(A_d(\alpha_d + \mu_d)\beta_d\left(\mu_s^4 + (\delta_s + \theta_s + \varepsilon_s + c_s + \alpha_s)\mu_s^3 + ((\theta_s + \varepsilon_s + c_s + \alpha_s)\delta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_s^2 + \delta_s(-A_s\beta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_s - A_s\beta_s\delta_s\alpha_s\right)\right)}{\left((\delta_d + \mu_d)\left(-\beta_d(\alpha_d + \mu_d)\mu_s^4 + \left(\beta_s\mu_d^2 + (-\delta_d\beta_d + (\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\mu_d - \beta_d\alpha_d(\delta_s + \theta_s + \varepsilon_s + c_s + \alpha_s)\right) + \left(\beta_s(\delta_s + \varepsilon_s + c_s + \alpha_s)\mu_d^2 + (((\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\delta_s + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d)\beta_s - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_d - \beta_d((\theta_s + \varepsilon_s + c_s + \alpha_s)\delta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\alpha_d\right)\mu_s^2 + \left(\beta_s((\varepsilon_s + c_s + \alpha_s)\delta_s + \alpha_s(\varepsilon_s + c_s))\mu_d^2 + (((A_s\beta_d + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d))\beta_s - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\delta_s + \beta_s\alpha_s(\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d - \delta_s\beta_d(-A_s\beta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\alpha_d\right)\mu_s + \alpha_s\left((\varepsilon_s + c_s)\mu_d^2 + (A_s\beta_d + (\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d + A_s\beta_d\alpha_d\right)\beta_s\delta_s\right)\right)}, \\
S_d &= \frac{((\alpha_d + \mu_d)A_d\beta_s(\alpha_s + \mu_s)(\varepsilon_s + c_s + \mu_s)(\delta_s + \mu_s))}{\left(-\beta_d(\alpha_d + \mu_d)\mu_s^4 + \left(\beta_s\mu_d^2 + (-\delta_s\beta_d + (\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\mu_d - \beta_d\alpha_s(\delta_s + \varepsilon_s + c_s + \alpha_s)\right)\mu_s^3 + \left(\beta_s(\delta_s + \varepsilon_s + c_s + \alpha_s)\mu_d^2 + (((\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\delta_s + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d)\beta_d - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_d - \alpha_d((\theta_s + \varepsilon_s + c_s + \alpha_s)\delta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\beta_d\right)\mu_s^2 + \left(\beta_s((\varepsilon_s + c_s + \alpha_s)\delta_s + \alpha_s(\varepsilon_s + c_s))\mu_d^2 + (((A_s\beta_d + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d))\beta_s - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\delta_s + \beta_s\alpha_s(\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d - \delta_s\alpha_d(-A_s\beta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\beta_d\right)\mu_s + \delta_s\beta_s\alpha_s\left((\varepsilon_s + c_s)\mu_d^2 + (A_s\beta_d + (\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d + A_s\beta_d\alpha_d\right)\right)}, \\
I_d &= -\left(\frac{\beta_d\delta_d(\alpha_d + \mu_d)A_d\left(\mu_s^4 + (\delta_s + \theta_s + \varepsilon_s + c_s + \alpha_s)\mu_s^3 + ((\theta_s + \varepsilon_s + c_s + \alpha_s)\delta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_s^2 + \delta_s(-A_s\beta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_s - A_s\beta_s\delta_s\alpha_s\right)}{\left((\varepsilon_d + c_d + \mu_d)(\delta_d + \mu_d)\left(-\beta_d(\alpha_d + \mu_d)\mu_s^4 + \left(\beta_s\mu_d^2 + (-\delta_s\beta_d + (\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\mu_d - \beta_d\alpha_d(\delta_s + \theta_s + \varepsilon_s + c_s + \alpha_s)\right)\mu_s^3 + \left(\beta_s(\delta_s + \varepsilon_s + c_s + \alpha_s)\mu_d^2 + (((\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\delta_s + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d)\beta_s - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_d - \beta_d((\theta_s + \varepsilon_s + c_s + \alpha_s)\delta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\alpha_d\right)\mu_s^2 + \left(\beta_s((\varepsilon_s + c_s + \alpha_s)\delta_s + \alpha_s(\varepsilon_s + c_s))\mu_d^2 + (((A_s\beta_d + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d))\beta_s - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\delta_s + \beta_s\alpha_s(\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d - \delta_s\beta_d(-A_s\beta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\alpha_d\right)\mu_s + \alpha_s\left((\varepsilon_s + c_s)\mu_d^2 + (A_s\beta_d + (\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d + A_s\beta_d\alpha_d\right)\beta_s\delta_s\right)\right)}\right), \\
R_d &= \frac{(A_d\theta_d\beta_s(\alpha_s + \mu_s)(\varepsilon_s + c_s + \mu_s)(\delta_s + \mu_s))}{\left(-\beta_d(\alpha_d + \mu_d)\mu_s^4 + \left(\beta_s\mu_d^2 + (-\delta_s\beta_d + (\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\mu_d - \beta_d\alpha_d(\delta_s + \theta_s + \varepsilon_s + c_s + \alpha_s)\right)\mu_s^3 + \left(\beta_s(\delta_s + \varepsilon_s + c_s + \alpha_s)\mu_d^2 + (((\theta_d + \alpha_d)\beta_s - \beta_d(\theta_s + \varepsilon_s + c_s + \alpha_s))\delta_s + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d)\beta_s - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\mu_d - \alpha_d((\theta_s + \varepsilon_s + c_s + \alpha_s)\delta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\beta_d\right)\mu_s^2 + \left(\beta_s((\varepsilon_s + c_s + \alpha_s)\delta_s + \alpha_s(\varepsilon_s + c_s))\mu_d^2 + (((A_s\beta_d + (\varepsilon_s + c_s + \alpha_s)(\theta_d + \alpha_d))\beta_s - \beta_d(\varepsilon_s + c_s)(\theta_s + \alpha_s))\delta_s + \beta_s\alpha_s(\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d - \delta_s\alpha_d(-A_s\beta_s + (\varepsilon_s + c_s)(\theta_s + \alpha_s))\beta_d\right)\mu_s + \delta_s\beta_s\alpha_s\left((\varepsilon_s + c_s)\mu_d^2 + (A_s\beta_d + (\varepsilon_s + c_s)(\theta_d + \alpha_d))\mu_d + A_s\beta_d\alpha_d\right)\right)}.
\end{aligned} \tag{17}$$

3. Stability Analysis

3.1. Local Stability at the DFE Point. Toward analyzing local steadiness on the uninfected steadiness point, the Jacobian matrix of the model system (1) at $\mathscr{E}_0$ is evaluated. Then, stability is established based on the trace's indication and the determinant of the Jacobian matrix.

Theorem 2. *If $R_0 < 1$ then the disease-free equilibrium $\mathscr{E}_0$ of a system (1) is locally asymptotically stable or unstable otherwise.*

Proof. The Jacobian matrix of the system (1) at $\mathscr{E}_0$. From (14), the disease-free equilibrium point is given by

$$\mathscr{E}_0 = \left(S_d^0, E_d^0, I_d^0, R_d^*, S_s^0, E_s^0, S_s^0, I_s^0, R_s^0\right) = \left(\frac{A_d(\mu_d + \alpha_d)}{\mu_d(\mu_d + \theta_d + \alpha_d)}, 0, 0, \frac{A_d\theta_d}{\mu_d(\mu_d + \theta_d + \alpha_d)}, \frac{A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)}, 0, 0, \frac{A_s\theta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)}\right). \tag{18}$$

We determine the system's Jacobian matrix (1). To accomplish this, system (1)'s individual equations are differentiated by means of the state variable. $S._d, E._d, I_{.d}, R_{.d}, S_{.s}, E_{.s}, I_{.s}$, and $R_{.s}$. Let $J_{\mathscr{E}_0}$ be the jacobian matrix evaluated at the equilibrium without sickness $\mathscr{E}_0$.

$$J_{\mathscr{E}_0}=\begin{bmatrix} -(\mu_d+\theta_d) & 0 & 0 & \alpha_d & 0 & 0 & \frac{-\beta_d A_d(\alpha_d+\mu_d)}{\mu_d(\mu_d+\theta_d+\alpha_d)} & 0 \\ 0 & -(\mu_d+\delta_d) & 0 & 0 & 0 & 0 & \frac{\beta_d A_d(\alpha_d+\mu_d)}{\mu_d(\mu_d+\theta_d+\alpha_d)} & 0 \\ 0 & \delta_d & -(\mu_d+c_d+\varepsilon_d) & 0 & 0 & 0 & 0 & 0 \\ \theta_d & 0 & 0 & -(\mu_d+\alpha_d) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -(\mu_s+\theta_s) & 0 & \frac{-\beta_s A_s(\alpha_s+\mu_s)}{\mu_s(\mu_s+\theta_s+\alpha_s)} & \alpha_s \\ 0 & 0 & 0 & 0 & 0 & -(\mu_s+\delta_s) & \frac{\beta_s A_s(\alpha_s+\mu_s)}{\mu_s(\mu_s+\theta_s+\alpha_s)} & 0 \\ 0 & 0 & 0 & 0 & 0 & \delta_s & -(\mu_s+c_s+\varepsilon_s) & 0 \\ 0 & 0 & 0 & 0 & \theta_s & 0 & 0 & -(\mu_s+\alpha_s) \end{bmatrix}. \tag{19}$$

The trace of the above matrix will be

$$\begin{aligned} Tr\left(J_{\mathscr{E}_0}\right) = &-(\mu_d+\theta_d)-(\mu_d+\delta_d)-(\mu_d+c_d+\varepsilon_d) \\ &-(\mu_d+\alpha_d)-(\mu_s+\theta_s)-(\mu_s+\delta_s) \\ &-(\mu_s+c_s+\varepsilon_s)-(\mu_s+\alpha_s)<0. \end{aligned} \tag{20}$$

Since all parameters are positive, determine the determinant of the Jacobian matrix $J_{\mathscr{E}_0}$.

Let

$$\begin{aligned} a_1 &= -(\mu_d+\theta_d), \\ a_2 &= -(\mu_d+\delta_d), \\ a_3 &= -(\mu_d+c_d+\varepsilon_d), \\ a_4 &= -(\mu_d+\alpha_d), a_5-(\mu_s+\theta_s), \\ a_6 &= -(\mu_s+\delta_s), \\ a_7 &= \frac{-\beta_d A_d(\alpha_d+\mu_d)}{\mu_d(\mu_d+\theta_d+\alpha_d)}, \\ a_8 &= \frac{\beta_d A_d(\alpha_d+\mu_d)}{\mu_d(\mu_d+\theta_d+\alpha_d)} \\ a_9 &= \frac{-\beta_s A_s(\alpha_s+\mu_s)}{\mu_s(\mu_s+\theta_s+\alpha_s)} \\ a_{10} &= \frac{\beta_s A_s(\alpha_s+\mu_s)}{\mu_s(\mu_s+\theta_s+\alpha_s)} \\ a_{11} &= -(\mu_s+c_s+\varepsilon_s) a_{12} = -(\mu_s+\alpha_s). \end{aligned} \tag{21}$$

Then, the above Jacobian matrix will be

$$J_{\mathscr{E}_0}=\begin{bmatrix} a_1 & 0 & 0 & \alpha_d & 0 & 0 & a_7 & 0 \\ 0 & a_2 & 0 & 0 & 0 & 0 & a_8 & 0 \\ 0 & \delta_d & a_{\cdot 3} & 0 & 0 & 0 & 0 & 0 \\ \theta_d & 0 & 0 & a_{\cdot 4} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & a_{\cdot 5} & 0 & a_9 & \alpha_s \\ 0 & 0 & 0 & 0 & 0 & a_{\cdot 6} & a_{10} & 0 \\ 0 & 0 & 0 & 0 & 0 & \delta_s & a_{11} & 0 \\ 0 & 0 & 0 & 0 & \theta_s & 0 & 0 & a_{12} \end{bmatrix},$$

$$\det\left(J_{\mathscr{E}_0}\right)=\begin{bmatrix} a_1 & 0 & 0 & \alpha_d & 0 & 0 & a_7 & 0 \\ 0 & a_2 & 0 & 0 & 0 & 0 & a_8 & 0 \\ 0 & \delta_d & a_3 & 0 & 0 & 0 & 0 & 0 \\ \theta_d & 0 & 0 & a_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & a_5 & 0 & a_9 & \alpha_s \\ 0 & 0 & 0 & 0 & 0 & a_6 & a_{10} & 0 \\ 0 & 0 & 0 & 0 & 0 & \delta_s & a_{11} & 0 \\ 0 & 0 & 0 & 0 & \theta_s & 0 & 0 & a_{12} \end{bmatrix}$$

$$= a_3 \begin{bmatrix} a_1 & 0 & \alpha_d & 0 & 0 & a_7 & 0 \\ 0 & a_2 & 0 & 0 & 0 & a_8 & 0 \\ \theta_d & 0 & a_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & a_5 & 0 & a_9 & \alpha_s \\ 0 & 0 & 0 & 0 & a_6 & a_{10} & 0 \\ 0 & 0 & 0 & 0 & \delta_s & a_{11} & 0 \\ 0 & 0 & 0 & \theta_s & 0 & 0 & a_{12} \end{bmatrix}$$

$$= a_3 a_2 \begin{bmatrix} a_1 & \alpha_d & 0 & 0 & a_7 & 0 \\ \theta_d & a_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & a_5 & 0 & a_9 & \alpha_s \\ 0 & 0 & 0 & a_6 & a_{10} & 0 \\ 0 & 0 & 0 & \delta_s & a_{11} & 0 \\ 0 & 0 & \theta_s & 0 & 0 & a_{12} \end{bmatrix}$$

$$= a_3 a_2 \left[a_1 \begin{bmatrix} a_4 & 0 & 0 & 0 & 0 \\ 0 & a_5 & 0 & a_9 & \alpha_s \\ 0 & 0 & a_6 & a_{10} & 0 \\ 0 & 0 & \delta_s & a_{11} & 0 \\ 0 & \theta_s & 0 & 0 & a_{12} \end{bmatrix} - \theta_d \begin{bmatrix} a_d & 0 & 0 & a_7 & 0 \\ 0 & a_5 & 0 & a_9 & a_s \\ 0 & 0 & a_6 & a_{10} & 0 \\ 0 & 0 & \delta_s & a_{11} & 0 \\ 0 & \theta_s & 0 & 0 & a_{12} \end{bmatrix} \right]$$

$$= \mathrm{a}_3 a_2 \left[a_1 a_4 \begin{bmatrix} a_5 & 0 & a_9 & \alpha_s \\ 0 & a_6 & a_{.10} & 0 \\ 0 & \delta_s & a_{.11} & 0 \\ \theta_s & 0 & 0 & a_{.12} \end{bmatrix} - \theta_d \alpha_d \begin{vmatrix} a_5 & 0 & a_9 & \alpha_s \\ 0 & a_{.6} & a_{.10} & 0 \\ 0 & \delta_s & a_{11} & 0 \\ \theta_s & 0 & 0 & a_{.12} \end{vmatrix} \right],$$

$$a_3 a_2 [a_1 a_4 - \theta_d \alpha_d] \begin{vmatrix} a_{.5} & 0 & a_9 & \alpha_s \\ 0 & a_{.6} & a_{10} & 0 \\ 0 & \delta_s & a_{11} & 0 \\ \theta_s & 0 & 0 & a_{12} \end{vmatrix}$$

$$= a_3 a_2 [a_1 a_4 - \theta_d \alpha_d] \left[a_5 \begin{vmatrix} a_6 & a_{10} & 0 \\ \delta_s & a_{11} & 0 \\ 0 & 0 & a_{12} \end{vmatrix} - \theta_s \begin{vmatrix} 0 & a_{.9} & \alpha_s \\ a_6 & a_{10} & 0 \\ \delta_s & a_{11} & 0 \end{vmatrix} \right]$$

$$= a_3 a_2 [a_1 a_4 - \theta_d \alpha_d][a_5 a_{12}(a_6 a_{11} - a_{10}\delta_s) - \theta_s \alpha_s (a_6 a_{11} - a_{10}\delta_s)]$$

$$= a_3 a_2 [a_1 a_4 - \theta_d \alpha_d][a_6 a_{11} - a_{10}\delta_s][a_5 a_{12} - \theta_s \alpha_s]. \tag{22}$$

Insert the value of $a_{.1}, a_{.2}, a_{.3}, a_{.4}, a_{.5}, a_{.6}, a_{.10}, a_{.11}, a_{.12}$; we will get

$$\begin{aligned} \det\left(J_{\mathscr{E}_0}\right) &= (\mu_d + c_d + \varepsilon_d)(\mu_d + \delta_d)[(\mu_d + \theta_d)(\mu_d + \alpha_d) \\ &\quad - \theta_d \alpha_d]\left[(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s) - \frac{\beta_s A_s (\alpha_s + \mu_s)\delta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)}\right] \\ &\quad \cdot [(\mu_s + \theta_s)(\mu_s + \alpha_s) - \theta_s \alpha_s], \det\left(J_{\mathscr{E}_0}\right) \\ &= (\mu_d + c_d + \varepsilon_d)(\mu_d + \delta_d)\mu_d(\mu_d + \theta_d + \alpha_d) \\ &\quad \cdot \left[(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s) - \frac{\beta_s A_s (\alpha_s + \mu_s)\delta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)}\right] \mu_s(\mu_s + \theta_s + \alpha_s). \end{aligned} \tag{23}$$

Since $(\mu_d + \theta_d)(\mu_d + \alpha_d) - \theta_d \alpha_d = \mu_d(\mu_d + \theta_d + \alpha_d)$ and $(\mu_s + \theta_s)(\mu_s + \alpha_s) - \theta_s \alpha_s = \mu_s(\mu_s + \theta_s + \alpha_s)$,

$$\begin{aligned} \det\left(J_{\mathscr{E}_0}\right) &= (\mu_d + c_d + \varepsilon_d)(\mu_d + \delta_d)\mu_d(\mu_d + \theta_d + \alpha_d) \\ &\quad \cdot \frac{(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}{(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)} \\ &\quad \cdot \left[(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s) - \frac{\beta_s A_s (\alpha_s + \mu_s)\delta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)}\right] \mu_s \\ &\quad \cdot (\mu_s + \theta_s + \alpha_s), \end{aligned}$$

$$\begin{aligned} \det\left(J_{\mathscr{E}_0}\right) &= (\mu_d + c_d + \varepsilon_d)(\mu_d + \delta_d)\mu_d(\mu_d + \theta_d + \alpha_d) \\ &\quad \cdot (\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s) \\ &\quad \cdot \left[1 - \frac{\beta_s A_s (\alpha_s + \mu_s)\delta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}\right] \mu_s \\ &\quad \cdot (\mu_s + \theta_s + \alpha_s), \end{aligned}$$

$$\begin{aligned} \det\left(J_{\mathscr{E}_0}\right) &= (\mu_d + c_d + \varepsilon_d)(\mu_d + \delta_d)\mu_d(\mu_d + \theta_d + \alpha_d) \\ &\quad \cdot (\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)[1 - R_e]\mu_s(\mu_s + \theta_s + \alpha_s). \end{aligned} \tag{24}$$

From equation (16), $R_e = (\beta_s A_s(\alpha_s + \mu_s)\delta_s)/(\mu_s(\mu_s + \theta_s + \alpha_s)(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s))$.

Thus, for $R_e < 1$, there are the disease-free equilibrium points $(\mathscr{E}_0)$ which are locally asymptotically stable if $\mathrm{Tr}(J_{\mathscr{E}_0}) < 0$ and $\mathrm{Det.}(J_{\mathscr{E}_0}) > 0$, otherwise it is unstable if $R_e > 1$. The theorem is proved.

3.2. Global Stability of DFE $(\mathscr{E}_0)$. We used the technique suggested by [18] to examine the global stability of the DFE of the system (1).

Theorem 3. *Under the condition that $R_e < 1$, the DEF $\mathscr{E}_0$ for model system (1) is globally stable.*

Proof. Letting $\mathscr{M}_1$, $\mathscr{M}_2$, $\mathscr{M}_3$, and $\mathscr{M}_4$ be positive constants, let $\mathscr{L}$ be a Lyapunov function.

$$\begin{aligned}\mathscr{L} = &\left(S_s - S_s^0 - S_s^0 \ln \frac{S_s}{S_s^0}\right) + \mathscr{M}_1 E_s + \mathscr{M}_2 I_s \\ &+ \left(R_s - R_s^0 - R_s^0 \ln \frac{R_s}{R_s^0}\right) + \left(S_d - S_d^0 - S_d^0 \ln \frac{S_d}{S_d^0}\right) \\ &+ \mathscr{M}_3 E_d + \mathscr{M}_4 I_d + \left(R_d - R_d^0 - R_d^0 \ln \frac{R_d}{R_d^0}\right)\Bigg\}.\end{aligned} \tag{25}$$

□

The derivative of $\mathscr{L}$ with respect to time is

$$\begin{aligned}\frac{d\mathscr{L}}{dt} = &\left(1 - \frac{S_s^0}{S_s}\right)\frac{dS_s}{dt} + \mathscr{M}_1 \frac{dE_s}{dt} + \mathscr{M}_2 \frac{dI_s}{dt} \\ &+ \left(1 - \frac{R_s^0}{R_s}\right)\frac{dR_s}{dt} + \left(1 - \frac{S_d^0}{S_d}\right)\frac{dS_d}{dt} \\ &+ \mathscr{M}_3 \frac{dE_d}{dt} + \mathscr{M}_4 \frac{dI_d}{dt} + \left(1 - \frac{R_d^0}{R_d}\right)\frac{dR_d}{dt}\Bigg\}.\end{aligned} \tag{26}$$

From system (1), substitute dS_s/dt, $dE_s/.dt$, $dI_s/.dt$, $dR_s/.dt$, $dS_d/.dt$, dE_d/dt, dI_d/dt, and $dR_d/.dt$ into equation (26) to obtain

$$\begin{aligned}\frac{d\mathscr{L}}{dt} = &\left(1 - \frac{S_s^0}{S_s}\right)[A_s + \alpha_s R_s - \beta_s S_s I_s - (\theta_s + \mu_s)S_s] \\ &+ \mathscr{M}_1[\beta_s S_s I_s - (\delta_s + \mu_s)E_s] + \mathscr{M}_2[\delta_s E_s - (\varepsilon_s + c_s + \mu_s)I_s] \\ &+ \left(1 - \frac{R_s^0}{R_s}\right)[\theta_s S_s - (\alpha_s + \mu_s)R_s] + \left(1 - \frac{S_d^0}{S_d}\right)[A_d + \alpha_d R_d \\ &- \beta_d S_d I_s - (\theta_d + \mu_d)S_d] + \mathscr{M}_3[\beta_d S_d I_s - (\delta_d + \mu_d)E_d] \\ &+ \mathscr{M}_4[\delta_d E_d - (\varepsilon_d + c_d + \mu_d)I_d] \\ &+ \left(1 - \frac{R_d^0}{R_d}\right)[\theta_d S_d - (\alpha_d + \mu_d)R_d]\Bigg\}.\end{aligned} \tag{27}$$

With the Lyapunov function $\mathscr{L}$ formed just on space of the state variables S_s, E_s, I_s, R_s, S_d, E_d, I_d, and R_d, it is evident that if $E_s(t)$, $I_s(t)$, $E_d(t)$, and $I_d(t)$ at the DFE are globally stable (therefore, $E_s = I_s = E_d = 0$ and $I_d = 0$), then $S_s(t) \longrightarrow S_s^0$, $R_s(t) \longrightarrow R_s^0$, $S_d(t) \longrightarrow S_d^0$, and $R_d(t) \longrightarrow R_d^0$ as $t \longrightarrow \infty$.

Hence, it can be considered that

$$\left.\begin{aligned}S_s \le S_s^0 = \frac{A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)}, R_s \le R_s^0 = \frac{A_s\theta_s}{\mu_s(\mu_s + \theta_s + \alpha_s)} \\ S_d \le S_d^0 = \frac{A_d(\mu_d + \alpha_d)}{\mu_d(\mu_d + \theta_d + \alpha_d)}, R_d \le R_s^0 = \frac{A_d\theta_d}{\mu_d(\mu_d + \theta_d + \alpha_d)}\end{aligned}\right\}. \tag{28}$$

Inserting equation (28) into (27), we get

$$\begin{aligned}\frac{d\mathscr{L}}{dt} \le &\left(1 - \frac{S_s^0}{S_s^0}\right)[A_s + \alpha_s R_s - \beta_s S_s^0 I_s - (\theta_s + \mu_s)S_s^0] \\ &+ \mathscr{M}_1[\beta_s S_s^0 I_s - (\delta_s + \mu_s)E_s] + \mathscr{M}_2[\delta_s E_s - (\varepsilon_s + c_s + \mu_s)I_s] \\ &+ \left(1 - \frac{R_s^0}{R_s^0}\right)[\theta_s S_s^0 - (\alpha_s + \mu_s)R_s^0] + \left(1 - \frac{S_d^0}{S_d^0}\right) \\ &\cdot [A_d + \alpha_d R_d^0 - \beta_d S_d^0 I_s - (\theta_d + \mu_d)S_d^0] + \mathscr{M}_3[\beta_d S_d^0 I_s - (\delta_d + \mu_d)E_d] \\ &+ \mathscr{M}_4[\delta_d E_d - (\varepsilon_d + c_d + \mu_d)I_d] + \left(1 - \frac{R_d^0}{R_d^0}\right)[\theta_d S_d^0 - (\alpha_d + \mu_d)R_d^0]\Bigg\}.\end{aligned} \tag{29}$$

At the disease-free equilibrium point, $S_s(t) \longrightarrow S_s^0$, $R_s(t) \longrightarrow R_s^0$, $S_d(t) \longrightarrow S_d^0$, $R_d(t) \longrightarrow R_d^0$ as $t \longrightarrow \infty$.

$$\begin{aligned}\frac{d\mathscr{L}}{dt} \le &\mathscr{M}_1[\beta_s S_s^0 I_s - (\delta_s + \mu_s)E_s] + \mathscr{M}_2[\delta_s E_s - (\varepsilon_s + c_s + \mu_s)I_s] \\ &+ \mathscr{M}_3[\beta_d S_d^0 I_s - (\delta_d + \mu_d)E_d] + \mathscr{M}_4[\delta_d E_d - (\varepsilon_d + c_d + \mu_d)I_d]\},\end{aligned} \tag{30}$$

$$\begin{aligned}\frac{d\mathscr{L}}{dt} \le &[\mathscr{M}_2\delta_s - \mathscr{M}_1(\delta_s + \mu_s)]E_s[\mathscr{M}_1\beta_s S_s^0 + \mathscr{M}_3\beta_d S_d^0 - \mathscr{M}_2(\varepsilon_s + c_s + \mu_s)]I_s \\ &\cdot [\mathscr{M}_4\delta_d - \mathscr{M}_3(\delta_d + \mu_d)]E_d - [\mathscr{M}_4(\varepsilon_d + c_d + \mu_d)]I_d\}.\end{aligned} \tag{31}$$

When the coefficients of E_s, I_s, E_d, and I_d in (31) tend to zero, the following results appear:

$$\begin{aligned}\mathscr{M}_4 &= 0, \\ \mathscr{M}_3 &= 0, \\ \mathscr{M}_1 &= \delta_s, \\ \mathscr{M}_2 &= (\mu_s + \delta_s).\end{aligned} \tag{32}$$

Inserting equation (32) into equation (31) yields

$$\begin{aligned}\frac{d\mathscr{L}}{dt} \le &[(\mu_s + \delta_s)\delta_s - \delta_s(\delta_s + \mu_s)]E_s \\ &+ \left[\delta_s\beta_s S_s^0 - (\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)\right]I_s.\end{aligned} \tag{33}$$

From equation (14), $S_s^0 = (A_s(\mu_s + \alpha_s))/(\mu_s(\mu_s + \theta_s + \alpha_s))$; then, insert this in equation (33); we get

$$\frac{d\mathscr{L}}{dt} \le \left[\delta_s\beta_s \frac{A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)} - (\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)\right]I_s,$$

$$\frac{d\mathscr{L}}{dt} \le \left[\delta_s\beta_s \frac{A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)} - (\mu_s + \delta_s)(\varepsilon_s + c_s + \mu_s)\right]I_s,$$

$$\begin{aligned}\frac{d\mathscr{L}}{dt} \le &\frac{(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}{(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)} \\ &\cdot \left[\delta_s\beta_s \frac{A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)} - (\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)\right]I_s,\end{aligned}$$

Table 3: Modeling parameters and their values (unit: month^{-1}).

Parameter	Rate	Explanation	Basis
A_d	120	Number of domestic dog recruitment	[16]
A_s	32	Number of stray dog recruitment	[16]
β_d	0.000004	Rate of stray dog transmission to domestic dogs	Estimation
β_s	0.000008	Rate of transmission from stray to a stray dog	Estimation
δ_d	0.37	The proportion of exposed domestic dogs' clinical outcomes	[8]
δ_s	0.35	The proportion of exposed stray dogs' clinical outcomes	[8]
θ_d	0.54	Rate of domestic dog vaccination	[16]
θ_s	0.54	Rate of stray dog vaccination	[16]
μ_d	0.11	The natural death rate of domestic dogs	[19]
μ_s	0.24	The natural death rate of stray dogs	[19]
α_d	0.5	Rate of domestic dog vaccination immunity loss	[19]
α_s	0.5	Rate of stray dog vaccination immunity loss	[19]
ε_d	1	The ratio of rabies-related deaths in domestic dogs	[19]
ε_s	1	The ratio of rabies-related deaths in stray dogs	[19]
c_d	0.5	Rabid domestic dog culling rate	[16]
c_s	0.5	Rabid stray dog culling rate	Estimation

$$\frac{d\mathscr{L}}{dt} \le (\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s) \ddot{A}\ddot{n}\left[\delta_s\beta_s \frac{A_s(\mu_s + \alpha_s)}{\mu_s(\mu_s + \theta_s + \alpha_s)(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)} - \frac{(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}{(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)}\right] I_s. \quad (34)$$

Therefore,

$$\frac{d\mathscr{L}}{dt} \le (\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s)[R_e - 1]I_s \le 0, \quad \text{if } R_0 \le 1. \quad (35)$$

Additionally, $d\mathscr{L}/dt = 0$ if and only if $I_s = 0$.Therefore, for $E_s = I_s = E_d = I_d = 0$, it shows that $S_d(t) \longrightarrow S_s^0 = (A_s(\mu_s + \alpha_s))/(\mu_s(\mu_s + \theta_s + \alpha_s))$, $R_s(t) \longrightarrow R_s^0 = A_s\theta_s/(\mu_s(\mu_s + \theta_s + \alpha_s))$, $S_d \longrightarrow S_d^0 = (A_d(\mu_d + \alpha_d))/(\mu_d(\mu_d + \theta_d + \alpha_d))$, $R_d \longrightarrow R_s^0 = A_d\theta_d/(\mu_d(\mu_d + \theta_d + \alpha_d))$ as $t \longrightarrow \infty$.

As a result, the singleton set $\{\mathscr{E}_0\}$ is the biggest compact invariant set in the set $\{(S_s, E_s, I_s, R_s, S_d, E_d, I_d, R_d) \in \Omega : (dL/dt) \le 0\}$. We thus draw the conclusion that $\mathscr{E}_0$ is globally asymptotically stable in the case where $R_0 \le 1$ is based on La Salle's invariance principle [9, 10, 18].

4. Sensitivity Analysis for R_E

The effect of model parameter values on output estimation of R_e is shown in this section. The value of a particular input parameter determines the output value of R_e. Since the model's parameter values are unknown, changes in the input parameter values can influence the effective reproduction number's output values. Sensitivity analysis is used to measure this uncertainty to assess whether or not rabies is spreading in the population. The proportion of the relative changes in a variable, and a parameter is known as the normalized forward sensitivity index. Its research is also focused here on parameter values displayed in Table 3 below.

Table 4: Sensitivities of R_e.

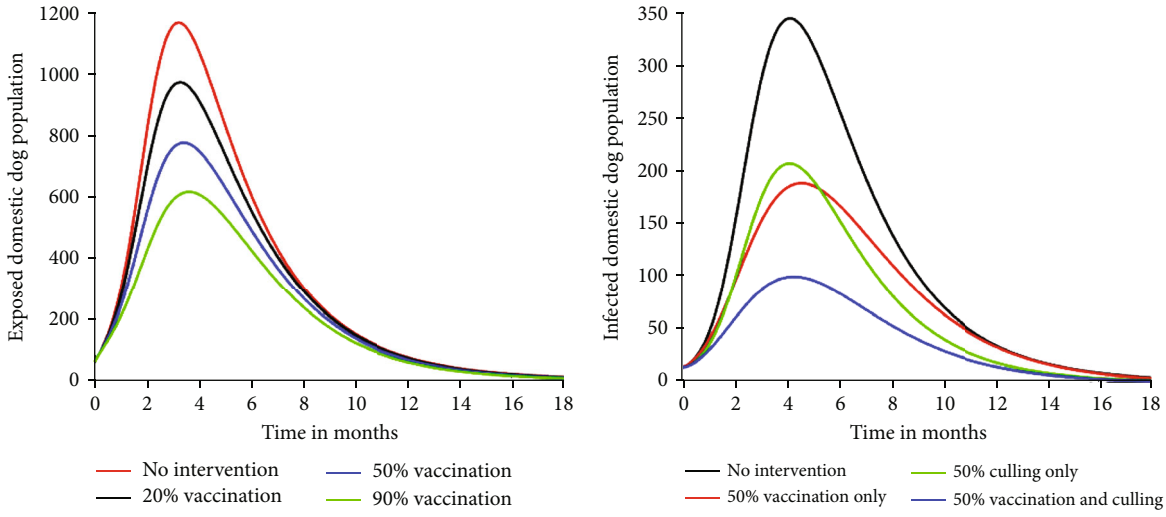
The symbol for the parameter	Value for the sensitivity index
β_s	+1
δ_s	+0.4067796610
A_s	+1
α_s	+0.2850506757
μ_s	−1.413934758
θ_s	−0.4218750000
ε_s	−0.5747126437
c_s	−0.2873563218

Table 5: Initial conditions used in the rabies model.

State variable	S_d	E_d	I_d	R_d	S_s	E_s	I_s	R_s
Initial value	3200	60	15	25	2800	80	20	0

The formulation of the sensitivity index is as such when the variable is a differentiable function of the parameter: the following is the definition of the normalized forward sensitivity index of variable X that depends on parameter ω : $S_\omega^X = (\partial X/\partial\omega) \times (\omega/X)$.

In this instance, we have the number of effective reproductions $R_e = (\beta_s A_s(\alpha_s + \mu_s)\delta_s)/(\mu_s(\mu_s + \theta_s + \alpha_s)(\mu_s + \delta_s)(\mu_s + c_s + \varepsilon_s))$ computed.



(a) Exposed domestic dog

(b) Infected domestic dog

FIGURE 2: The effect of vaccination (parameter θ_d and θ_s) and culling (parameter c_d and c_s) on the exposed and infected domestic dog populations.

From the model, the sensitivity index of R_e concerning β_s is given by

$$S_{\beta_s}^{R_e} = \frac{\partial R_e}{\partial \beta_s} \times \frac{\beta_s}{R_e} = +1. \tag{36}$$

Again, the sensitivity index of R_e concerning δ_s is given by

$$S_{\beta_s}^{R_e} = \frac{\partial R_e}{\partial \delta_s} \times \frac{\delta_s}{R_e} = +0.4067796610. \tag{37}$$

Similarly, the sensitivity index concerning θ_s, c_s, and ε_s is given by

$$\begin{aligned}
S_{A_s}^{R_e} &= \frac{\partial R_e}{\partial A_s} \times \frac{A_s}{R_e} = +1,\\
S_{\alpha_s}^{R_e} &= \frac{\partial R_e}{\partial \alpha_s} \times \frac{\alpha_s}{R_e} = 0.2850506757,\\
S_{\mu_s}^{R_e} &= \frac{\partial R_e}{\partial \mu_s} \times \frac{\mu_s}{R_e} = -1.413934758,\\
S_{\theta_s}^{R_e} &= \frac{\partial R_e}{\partial \theta_s} \times \frac{\theta_s}{R_e} = -0.4218750000,\\
S_{\varepsilon_s}^{R_e} &= \frac{\partial R_e}{\partial \varepsilon_s} \times \frac{\varepsilon_s}{R_e} = -0.5747126437,\\
S_{c_s}^{R_e} &= \frac{\partial R_e}{\partial c_s} \times \frac{c_s}{R_e} = -0.2873563218.
\end{aligned} \tag{38}$$

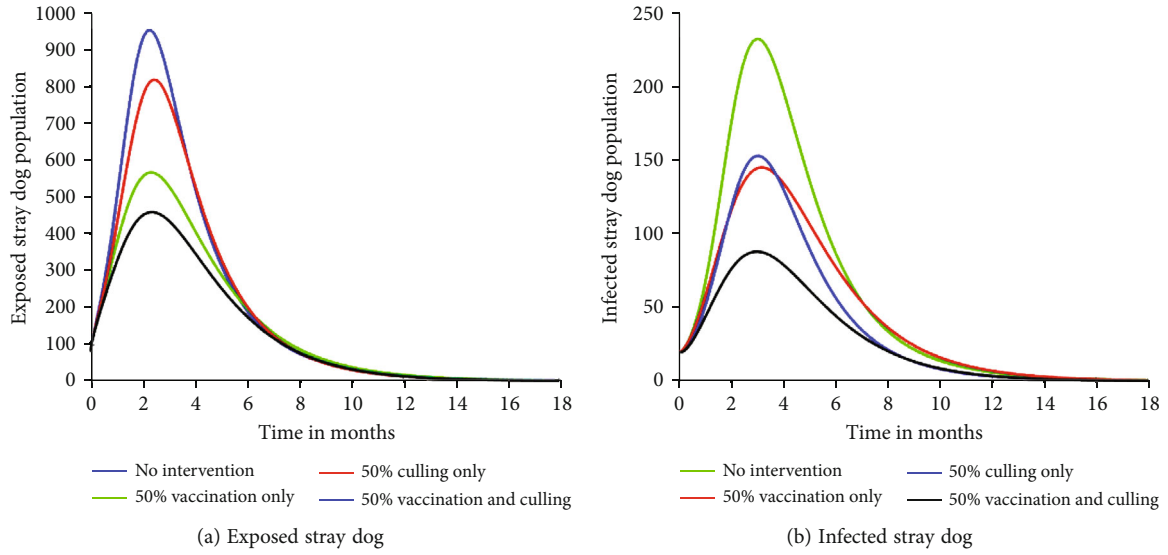
The sensitivity indices of R_e concerning parameters ω are obtained and summarized in Table 4.

The infection rates of stray dogs β_s and annual stray dog births A_s are the most sensitive and positive parameters, followed by the proportion of exposed stray dogs' clinical outcome parameter δ_s and the loss rate of vaccination immunity of stray dogs α_s, on the basis of the sensitivity indicators. As a result of increasing these parameters, the effective reproduction number R_e will increase. Furthermore, the most negatively sensitive indicator is the stray dog mortality rate μ_s, which is followed by the rabies mortality rate ε_s, the stray dog vaccination rate θ_i, and stray dog culling rate c_s. As a result, as these parameters are increased, the effective reproduction number R_e decreases.

5. Numerical Simulations

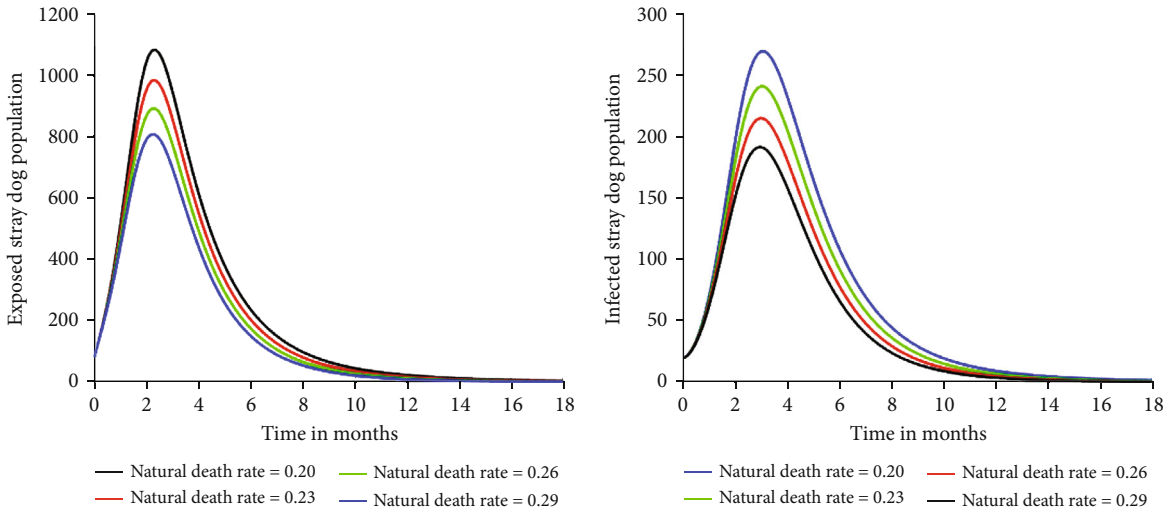
Several findings and their interpretations have been discussed in this section. ODE45 is the default solver in MATLAB for solving ordinary differential equations (ODEs). This function implements the Runge-Kutta process with a configurable time step for effective calculation. The simulation's main goal is to see how model parameters respond during a rabies epidemic. Its research is also focused on the parameter values in Table 3 and initial condition values shown in Table 5 below.

Figure 2 curves demonstrate that if no intervention was used ($\theta_d = \theta_s = c_d = c_s = 0$), the number of exposed domestic dogs increases at first, then starts to decrease. After being bitten by rabid dogs, the susceptible domestic moves to the exposed domestic compartment, causing this. When rabies symptoms appear in the exposed domestic dog's compartment, the exposed domestic dogs are transferred to the infected compartment, reducing the number of exposed domestic dogs. Figure 2(b) indicates that when no intervention is used ($\theta_d = \theta_s = \theta_d = \theta_i = 0$), the quantity of domestic dogs with the disease increases before declining, due to the large number of rabies-positive domestic dogs that moved into the infected compartment. Since all infected domestic dogs die and there is no rabies treatment, the number of infected domestic dogs continues to decrease. We can see



(a) Exposed stray dog (b) Infected stray dog

FIGURE 3: The effect of vaccination (parameter θ_d and θ_s) and culling (parameter c_d and c_s) on the exposed and infected stray dog populations.

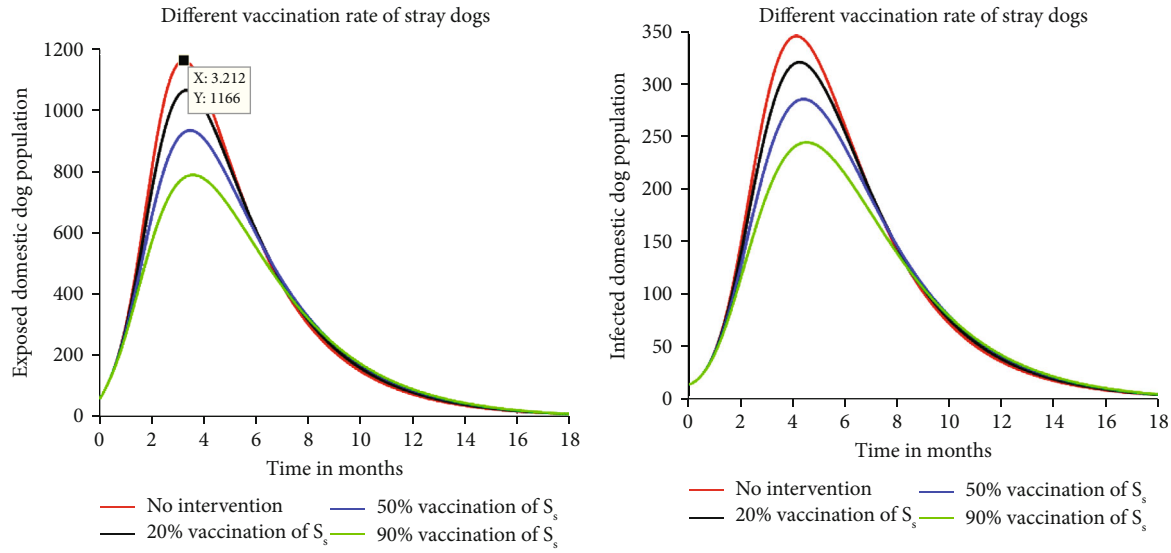


(a) Exposed stray dog (b) Infected stray dog

FIGURE 4: The impact of natural mortality rate (parameter μ) on the exposed and infected stray dog populations.

that intervention is very effective at decreasing the amount of exposed and infected domestic dogs once we compare curves with no intervention with those with intervention for both exposed and infected domestic dogs. The amount of domestic dogs exposed to the infection going to the infected compartment is also decreased. When comparing the two interventions, it appears that a combination of culling and vaccination ($\theta_d = \theta_s = 50\%$ and $c_d = c_s = 50\%$) has the greatest effect on reducing the number of exposed and infected domestic dogs, followed by vaccination only ($\theta_d = \theta_s = 50\%$ and $c_d = c_s = 0$) and then culling only ($\theta_d = \theta_s = 0$ and $c_d = c_s = 50\%$). Vaccination alone ($\theta_d = \theta_s = 50\%$ and $c_d = c_s = 0$) is more effective than culling alone ($\theta_d = \theta_s = 0$ and $c_d = c_s = 50\%$) in exposed group populations. However, culling the population of an infected group is more effective than vaccination alone.

According to the existence of the graphs in Figure 3, when no intervention ($\theta_d = \theta_s = c_d = c_s = 0$), is made, the number of exposed and infected stray dogs increases at first and then begins to decrease. When infected stray dogs bite other stray dogs, the bitten dogs become rabies-infected and shift from the safe compartment to the exposed compartment. When symptoms appear, exposed stray dogs become infectious and reach the diseased compartment, increasing the amount of infected stray dogs while declining the exposed compartment. In addition, the curves of infected stray dogs are declining because all infected stray dogs are dead. After all, rabies treatment is not available. In comparison to when no intervention ($\theta_d = \theta_s = c_d = c_s = 0$) is used, the number of exposed and infected stray dogs decreases faster when one ($\theta_d = \theta_s = 0$ and $c_d = c_s = 50\%$) or ($\theta_d = \theta_s = 50\%$ and $c_d = c_s = 0$) is used. That when susceptible stray dogs



(a) Exposed domestic dog

(b) Infected domestic dog

FIGURE 5: The effect of stray dog's vaccination (parameter θ_s) on the exposed and infected domestic dog populations.

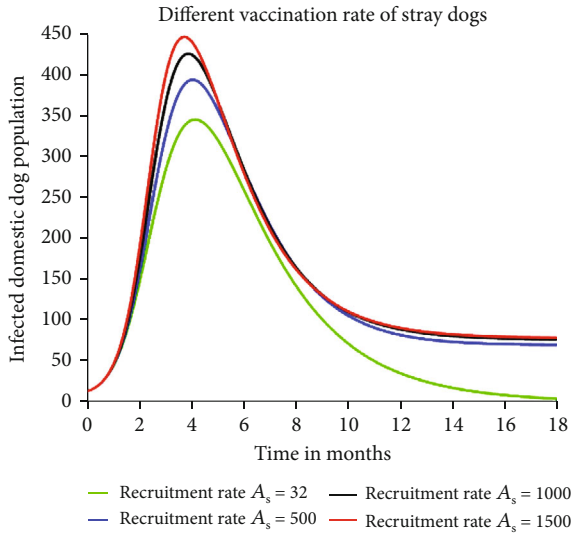


FIGURE 6: Effect of stray dog recruitment rate (parameter A_s) on the infected domestic dog population.

are vaccinated, the vaccinated stray dogs are moved to the recover compartment, reducing the number of susceptible stray dogs. It has been discovered that combining vaccination and culling ($\theta_d = \theta_s = c_d = c_s = 50\%$) has a greater impact than either vaccination or culling only.

One of most sensitive factors formulating the characteristics of dog rabies spread seems to be the natural death rate (μ), according to the sensitivity report. Figure 4 illustrates how a small rise in the number of stray dogs dying naturally leads toward reduction in the quantity of exposed and stray dogs which can be contagious and conversely. You should keep in mind that preventing rabies deaths by vaccination would cause stray dogs to die naturally.

Variables in the vaccination rate (θ_s) for stray dogs were used in the simulation (see Figure 5). Increased stray dog vaccination rates (θ_s) have been shown to have an important effect in regards to the rate of rabies spread in exposed and infected domestic dogs. Furthermore, increasing the vaccination rate (θ_s) of stray dogs within the model decreased the number of exposed and infected domestic dog populations.

Figure 6 shows how greatly the overall number of infected dogs can be decreased by reducing the number of puppies born to stray dogs each year. This explains the reason that minimizing the annual production of stray dog pups is essential for preventing the spread of rabies.

6. Conclusion

We have settled a mathematical compartmental deterministic analysis of the behavior of rabies spread in this study. It was a model intended to depict the spreading disease rabies from strays to domestic dogs because traditional rabies is widespread in the dog population. In the model, vaccinations were only administered to susceptible households and stray dogs. It is not practicable to vaccine exposed dogs since it is very challenging to identify the exposed dogs who need to be vaccinated. We study the fundamental characteristics of epidemic models in terms of the boundedness and positivity of solutions for our model and find that the model is positive for all positive initial condition values. We carry out stability and equilibrium analyses as well as reproduction number calculations. We demonstrate that both locally and globally, the DFE is asymptotically stable. Our simulation shows that the effective technique for preventing the spread of rabies is vaccination together with the culling of infected dogs and that the yearly dog birth amount has a major influence on the incidence of rabies disease. The model utilized in this study can be properly examined if statistics on the dog population are available. The government

might develop rabies-eradication plans using the study's findings, such as managing the dog population. We also suggest that dog population monitoring be done to estimate the annual dog birth rate.

Data Availability

The data used to support the findings of this manuscript are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

References

[1] Z. Wanga, C. T. Bauchc, S. Bhattacharyya et al., "Statistical physics of vaccination," *Physics Reports*, vol. 664, pp. 1–113, 2016.

[2] O. C. Eze, G. E. Mbah, D. U. Nnaji, and N. E. Onyiaji, "Mathematical modelling of transmission dynamics of rabies virus," *International Journal of Mathematics Trends and Technology (IJMTT)*, vol. 66, no. 7, pp. 40–64, 2020.

[3] K. M. Addo, *An SEIR mathematical model for dog rabies*, Case study: Bongo District, Ghana. Kwame Nkrumah University of Science and Technology, 2012.

[4] A. Maccari, "Chaos, solitons and fractals in the nonlinear Dirac equation," *Physics Letters A*, vol. 336, no. 2-3, pp. 117–125, 2005.

[5] R. Pastor-Satorras, C. Castellano, P. V. Mieghem, and A. Vespignani, "Epidemic processes in complex networks," *Reviews of Modern Physics*, vol. 87, no. 3, pp. 925–979, 2015.

[6] R. Pastor-Satorras and A. Vespignani, "Immunization of complex networks," *Physical Review E*, vol. 65, no. 3, article 036104, 2002.

[7] J. Zhang, Z. Jin, G.-Q. Sun, T. Zhou, and S. Ruan, "Analysis of rabies in China: transmission dynamics and control," *PLoS One*, vol. 6, no. 7, article e20891, 2011.

[8] T. T. Ega, "Modeling the dynamics of rabies transmission with vaccination and stability analysis," *Applied and Computational Mathematics*, vol. 4, no. 6, pp. 409–419, 2015.

[9] R. M. Anderson, H. C. Jackson, R. M. May, and A. M. Smith, "Population dynamics of fox rabies in Europe," *Nature*, vol. 289, no. 5800, pp. 765–771, 1981.

[10] S. C. Totton, A. I. Wandeler, J. Zinsstag et al., "Stray dog population demographics in Jodhpur, India following a population control/rabies vaccination program," *Preventive Veterinary Medicine*, vol. 97, no. 1, pp. 51–57, 2010.

[11] M. Sambo, S. Cleaveland, H. Ferguson et al., "The burden of rabies in Tanzania and its impact on local communities," *PLoS Neglected Tropical Diseases*, vol. 7, no. 11, article e2510, 2013.

[12] M. Sambo, *Epidemiological dynamics of rabies in Tanzania and its impacts on local communities [M.S. thesis]*, University of Glasgow, 2012.

[13] E. R. Gordon, A. T. Curns, J. W. Krebs, C. E. Rupprecht, L. A. Real, and J. E. Childs, "Temporal dynamics of rabies in a wildlife host and the risk of cross-species transmission," *Epidemiology and Infection*, vol. 132, pp. 515–524, 1999.

[14] S. Dürr, N. K. Dhand, C. Bombara, S. Molloy, and M. P. Ward, "What influences the home range size of free-roaming domestic dogs?," *Epidemiology and Infection*, vol. 145, no. 7, pp. 1339–1350, 2017.

[15] World Health Organization, *WHO Expert Consultation on Rabies. Second Report*, World Health Organization, Geneva, 2013.

[16] E. D. Salahot, *Mathematical modelling of rabies transmission and the impact of prevention strategies: a case study of Tanzania [Ph.D. thesis]*, Salaam University College of Education (DUCE), Tanzania, 2016.

[17] D. Dejene and P. R. Koya, "Population dynamics of dogs subjected to rabies disease," *InterOSR Journal of Mathematics (IOSR-JM)*, vol. 12, no. 3, pp. 2319–2765, 2016.

[18] D. Dejene, T. Worku, and P. Rao Koya, "Modeling the transmission and dynamics of COVID-19 using self-protection and isolation as control measures," *Mathematical Modelling and Applications*, vol. 5, no. 3, pp. 191–201, 2020.

[19] S. Ruan, "Modeling the transmission dynamics and control of rabies in China," *Mathematical biosciences*, vol. 286, pp. 65–93, 2017.