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LOCAL STABILITY ANALYSIS AND NUMERICAL SIMULATION OF A RABIES TRANSMISSION MODEL WITH VACCINATION AND CULLING

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ABSTRACT

Rabies remains a serious zoonotic disease requiring effective control strategies in both human and dog populations. This study analyzes the local stability of an SVEIR–SVEIR rabies transmission model incorporating vaccination and culling interventions. The model is analyzed analytically and numerically using parameter values obtained from relevant literature. The study involves identifying equilibrium states, deriving the basic reproduction number through the Next Generation Matrix approach, and analyzing the eigenvalues of the Jacobian matrix. The analysis indicates that the disease-free equilibrium remains locally asymptotically stable for $R_0 < 1$, whereas instability occurs when $R_0 > 1$. Numerical simulations confirm that increasing vaccination and culling rates reduces the infected populations, with dog vaccination having a stronger effect than culling in suppressing rabies transmission. This study is limited to local stability analysis and may be extended through global stability and optimal control analysis in future research.

Keywords: Rabies, Mathematical Model, Vaccination, Culling

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PRELIMINARY

Rabies refers to a zoonotic disease triggered by viruses classified under the Lyssavirus genus, with infection primarily targeting the host's central nervous system (Singh et al., 2017; Hampson et al., 2015). Approximately 99% of rabies infections in humans are linked to contact with infected dogs, particularly through bites or scratches that expose damaged skin or mucosal tissue to saliva carrying the virus (Fatima et al., 2023; WHO, 2024a). Once symptoms become clinically apparent, rabies almost always leads to death (WHO, 2024a). The spread of rabies has been documented in over 150 nations and territories worldwide, with Africa and Asia contributing to almost 95% of rabies-related mortality cases (WHO, 2024b). In Indonesia, 185,359 incidents involving attacks by rabies-carrying animals and 122 deaths were recorded in 2024, while 13,453 cases and 25 deaths had been reported by March 2025 (Kemenkes, 2025), highlighting the urgent need for effective prevention

strategies. The latent phase of rabies infection may last between two weeks and six years, although most cases commonly show an incubation duration of around two to three months (Singh et al., 2017).

To reduce the risk of rabies, various preventive measures have been implemented in both human and dog populations. In humans, rabies prevention includes pre-exposure prophylaxis (PrEP) vaccination to induce immunological memory before exposure and post-exposure prophylaxis (PEP), which involves wound cleaning, administration of rabies immunoglobulin (RIG), and subsequent vaccination after potential exposure (Ertl, 2019; Kaye et al., 2024; Tarantola et al., 2019). For dog populations, immunization programs are widely recognized as a key approach for controlling the spread of rabies along with the World Health Organization recommends maintaining vaccine coverage of at least 70% in urban settings, accompanied by population control measures such as sterilization or selective culling to limit transmission (Mengie et al., 2025; Morters et al., 2013). Although rabies is widely known as a disease with an almost 100% mortality rate after the onset of clinical symptoms, several rare studies have reported biologically possible recovery cases, including a presumptive recovery case in Ghana and laboratory-confirmed survival cases with severe neurological complications in India (Apanga et al., 2016; Manoj et al., 2016; Netravathi et al., 2015). Previous studies also described recovery in dogs infected with an Ethiopian strain of the rabies virus, where infected dogs showed typical rabies symptoms before recovering completely (Fekadu & Baer, 1980). Furthermore, studies have discussed the possibility of naturally acquired immunity in domestic dogs (Susannah et al., 2021). These findings support the inclusion of a recovered compartment in mathematical models of rabies transmission, although such recovery cases remain extremely rare.

Previous studies by Lv et al. (2023) and Thongtha & Modnak (2021) developed rabies transmission models involving vaccination and culling strategies to analyze epidemic trends, elimination targets, and optimal control interventions in human and dog populations. However, limited studies have focused on the local stability behavior of SVEIR-SVEIR rabies transmission models incorporating recovered compartments in both populations, particularly through comparative numerical investigations of vaccination and culling rates. Therefore, this study develops an SVEIR-SVEIR rabies transmission model with vaccination and culling interventions to analyze the basic reproduction number, equilibrium points, and local stability properties using the Jacobian matrix and Next Generation Matrix approaches. The novelty of this study lies in the incorporation of recovered compartments

and the numerical evaluation of different vaccination and culling rates to determine their effectiveness in reducing rabies transmission dynamics.

METHODS

This study employs a literature-based research method by examining previous mathematical models of rabies transmission. The developed model is modified from the studies of Lv et al. (2023) and Thongtha and Modnak (2021) through the addition of recovered compartments, vaccination interventions in both human and dog populations, and culling control, resulting in an SVEIR–SVEIR mathematical model represented by a system of differential equations. The analysis procedure includes model formulation, determination of equilibrium points, calculation of the basic reproduction number using the Next Generation Matrix (NGM), Jacobian matrix construction, eigenvalue analysis, local stability analysis, and numerical simulations under different vaccination and culling scenarios. Parameter values obtained from relevant literature are processed analytically and numerically using Python to visualize the dynamics of rabies transmission.

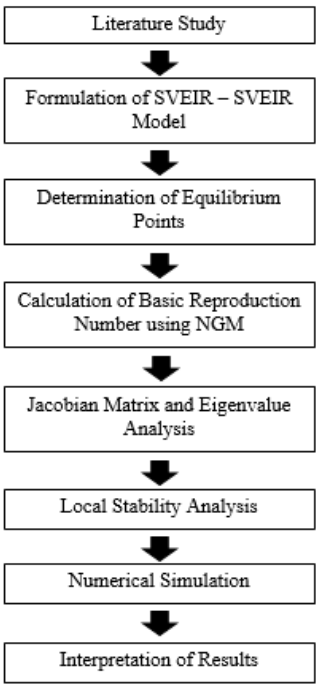


Figure 1. Research Flowchart

RESULT AND DISCUSSION

1. Constructing the Mathematical Model

This research proposes a deterministic compartment-based SVEIR–SVEIR framework to analyze the spread of rabies within interacting dog and human communities.

In the constructed model, each population is categorized into five epidemiological classes, namely susceptible (S), vaccinated (V), exposed (E), infected (I), and recovered (R). The model assumes a closed population without migration, transmission between infected and susceptible dogs as well as from infected dogs to susceptible humans, natural recruitment into the susceptible class, natural death in all compartments, disease-induced death only in infected compartments, and culling applied only to infected dogs. Humans are assumed to be dead-end hosts and do not contribute to secondary transmission. In addition, exposed individuals may receive vaccination before progressing to the infectious stage.

Based on these assumptions, the compartmental diagram of the model is shown in the following figure.

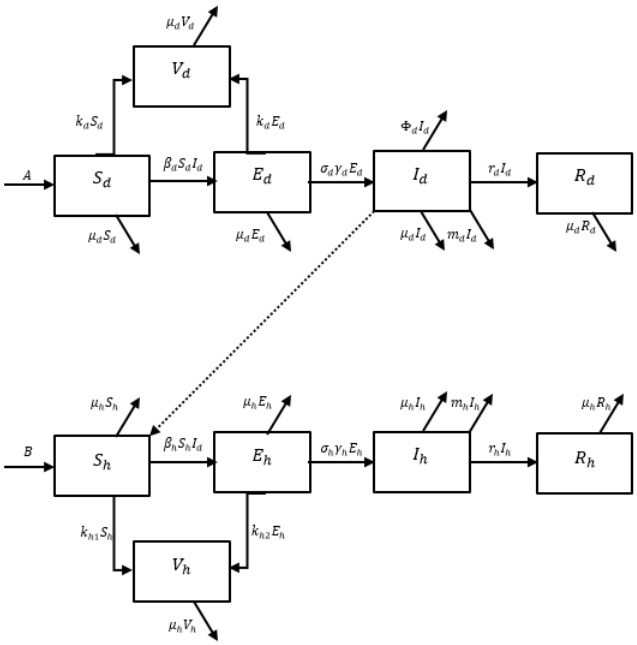


Figure 2. Compartment Diagram

Based on the compartments in Figure 2, a system of ordinary differential equations can be constructed as follows:

$$\frac{dS_d}{dt} = A - k_d S_d - \mu_d S_d - \beta_d S_d I_d \quad (1)$$

$$\frac{dV_d}{dt} = k_d S_d + k_d E_d - \mu_d V_d \quad (2)$$

$$\frac{dE_d}{dt} = \beta_d S_d I_d - k_d E_d - \mu_d E_d - \sigma_d \gamma_d E_d \quad (3)$$

$$\frac{dI_d}{dt} = \sigma_d \gamma_d E_d - \mu_d I_d - m_d I_d - \phi_d I_d \quad (4)$$

$$\frac{dR_d}{dt} = r_d I_d - \mu_d R_d \quad (5)$$

$$\frac{dS_h}{dt} = B - k_{h1} S_h - \mu_h S_h - \beta_h S_h I_d \quad (6)$$

$$\frac{dV_h}{dt} = k_{h1}S_h + k_{h2}E_h - \mu_h V_h \quad (7)$$

$$\frac{dE_h}{dt} = \beta_h S_h I_d - k_{h2}E_h - \mu_h E_h - \sigma_h \gamma_h E_h \quad (8)$$

$$\frac{dI_h}{dt} = \sigma_h \gamma_h E_h - \mu_h I_h - m_h I_h \quad (9)$$

$$\frac{dR_h}{dt} = r_h I_h - \mu_h R_h \quad (10)$$

All model parameters are considered to be positive for $t > 0$, with non-negative initial conditions. The definitions of the parameters and their biological interpretations are presented in the following table.

Table 1. Parameter Description

Parameter	Description
A	Natural birth rate of the dog population
B	Natural birth rate of the human population
k_d	Vaccination rate in the dog population
k_{h1}	Vaccination rate in humans before exposure (Pre-Exposure Prophylaxis / PrEP)
k_{h2}	Vaccination rate in humans after exposure (Post-Exposure Prophylaxis / PEP)
β_d	Rabies transmission rate among dogs
β_h	Rabies transmission rate from dogs to humans
σ_d	Progression rate from the incubation phase to the infectious phase in dogs
σ_h	Progression rate from the incubation phase to the infectious phase in humans
γ_d	Progression rate from the infectious phase to the clinical phase in dogs
γ_h	Progression rate from the infectious phase to the clinical phase in humans
μ_d	Natural death rate of the dog population
μ_h	Natural death rate of the human population
m_d	Death rate of dogs due to rabies
m_h	Death rate of humans due to rabies
r_d	Recovery (survival) rate of dogs from the clinical phase
r_h	Recovery (survival) rate of humans from the clinical phase
ϕ_d	Reduction rate of the dog population through culling

2. Equilibrium Points

The equilibrium points are determined by equating all differential equations to zero. From this, the following equations are obtained:

$$\frac{dS_d}{dt} = \frac{dV_d}{dt} = \frac{dE_d}{dt} = \frac{dI_d}{dt} = \frac{dR_d}{dt} = \frac{dS_h}{dt} = \frac{dV_h}{dt} = \frac{dE_h}{dt} = \frac{dI_h}{dt} = \frac{dR_h}{dt} = 0 \quad (11)$$

Then, the system is solved to determine the value of each variable at equilibrium conditions. Through this analytical process, two possible steady-state conditions are obtained, namely the disease-free state (DFE) and the endemic state (EE).

By substituting the disease-free conditions $E_d = I_d = R_d = E_h = I_h = R_h = 0$, into equation (11), the disease-free equilibrium point is obtained as follows: $E_0 = (S_d^*, V_d^*, E_d^*, I_d^*, R_d^*, S_h^*, V_h^*, E_h^*, I_h^*, R_h^*) = (\frac{A}{k_d+\mu_d}, \frac{Ak_d}{\mu_d(k_d+\mu_d)}, 0,0,0, \frac{B}{k_{h1}+\mu_h}, \frac{Bk_{h1}}{\mu_h(k_{h1}+\mu_h)}, 0,0,0)$.

Furthermore, from equation (11), the endemic equilibrium point is obtained. From the equilibrium equations of the dog population, the following relations are first derived $E_d^* = \frac{(\mu_d+m_d+\phi_d+r_d)I_d^*}{\sigma_d\gamma_d}, R_d^* = \frac{r_dI_d^*}{\mu_d}, V_d^* = \frac{k_d}{\mu_d}(S_d^* + E_d^*)$, and $S_d^* = \frac{A}{k_d+\mu_d+\beta_dI_d^*}$. Substituting the expressions for S_d^*, V_d^*, E_d^*, and R_d^* into the infected dog equilibrium equation and simplifying algebraically yields $I_d^* = \frac{M_1}{\beta_dM_2}$, where $M_1 = A\beta_d\sigma_d\gamma_d - (\mu_d + k_d)^2(\mu_d + m_d + \phi_d + r_d) - \sigma_d\gamma_d(\mu_d + k_d)(\mu_d + m_d + \phi_d + r_d)$ and $M_2 = (\mu_d + m_d + \phi_d + r_d)(\sigma_d\gamma_d + \mu_d + k_d)$. Thus, the endemic equilibrium point is expressed as $E^* = (S_d^*, V_d^*, E_d^*, I_d^*, R_d^*, S_h^*, V_h^*, E_h^*, I_h^*, R_h^*) = (\frac{A}{k_d+\mu_d+\beta_dI_d^*}, \frac{k_d}{\mu_d}(S_d^* + E_d^*), \frac{(\mu_d+m_d+\phi_d+r_d)I_d^*}{\sigma_d\gamma_d}, \frac{M_1}{\beta_dM_2}, \frac{r_dI_d^*}{\mu_d}, \frac{B}{k_{h1}+\mu_h+\beta_hI_d^*}, \frac{k_{h1}S_h^*+k_{h2}E_h^*}{\mu_h}, \frac{\beta_hS_h^*I_d^*}{\mu_h+k_{h2}+r_h+\sigma_h\gamma_h}, \frac{\sigma_h\gamma_hE_h^*}{\mu_h+m_h}, \frac{r_hI_h^*}{\mu_h})$ with $S_d^* > 0, V_d^* > 0, E_d^* > 0, I_d^* > 0, R_d^* > 0, S_h^* > 0, V_h^* > 0, E_h^* > 0, I_h^* > 0, R_h^* > 0$.

3. Basic Reproduction Number (R_0)

The basic reproduction number (R_0) is a parameter that serves as a determinant of whether a disease will spread or disappear or persist. It describes how many new infections can arise from one infected individual in a population where all individuals are susceptible (Winarni et al., 2025). Since humans are assumed to be dead-end hosts and do not contribute to further transmission, the Next Generation Matrix (NGM) method is applied only to the infected dog compartments E_d and I_d. The matrices of new infection and transition terms are given by

$$F = \begin{bmatrix} 0 & \beta_dS_d \\ 0 & 0 \end{bmatrix}, \qquad V = \begin{bmatrix} \mu_d + k_d + \sigma_d\gamma_d & 0 \\ -\sigma_d\gamma_d & \mu_d + m_d + \phi_d + r_d \end{bmatrix}$$

In this model, the basic reproduction number (R_0) corresponds to the largest eigenvalue associated with the matrix FV^{-1}. From the above calculations, the value of R_0 is obtained, namely:

$$R_0 = \frac{A\beta_d\sigma_d\gamma_d}{(\mu_d+k_d)(\mu_d+k_d+\sigma_d\gamma_d)(\mu_d+m_d+\phi_d+r_d)} \quad (12)$$

4. Local Stability of the Equilibrium Point

The eigenvalues obtained from the Jacobian matrix evaluated at E_0 are used to examine the local stability behavior of the disease-free equilibrium. Since humans act as dead-end hosts and do not contribute to further transmission, the stability analysis can be reduced to the infected dog compartments E_d^* and I_d^*. Thus, the reduced Jacobian matrix is obtained as

$$J(E_d, I_d) = \begin{bmatrix} -(\mu_d + k_d + \sigma_d\gamma_d) & \frac{A\beta_d}{\mu_d + k_d} \\ \sigma_d\gamma_d & -(\mu_d + m_d + \phi_d + r_d) \end{bmatrix}$$

From this Jacobian matrix, the eigenvalues can be determined as:

$$\lambda^2 + (a+b)\lambda + ab - \frac{A\beta_d\sigma_d\gamma_d}{\mu_d+k_d} \quad (13)$$

With

$$a = \mu_d + k_d + \sigma_d\gamma_d \qquad b = \mu_d + m_d + \phi_d + r_d.$$

From equations (12) and (13), it can be stated that:

$$\frac{A\beta_d\sigma_d\gamma_d}{\mu_d + k_d} = abR_0$$

Thus, the characteristic equation becomes:

$$\lambda^2 + (a+b)\lambda + ab(1 - R_0) = 0 \quad (14)$$

For $R_0 < 1$, equation (14) has positive coefficients, which leads to eigenvalues whose real components are entirely negative. As a result, the disease-free condition is stable in the local asymptotic sense. However, once $R_0 > 1$, a positive eigenvalue emerges, making the disease-free condition unstable while the system evolves toward an endemic condition.

5. Numeric Simulation

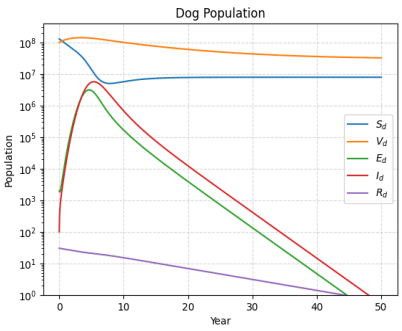
To reinforce the theoretical analysis, numerical simulations were carried out focusing on the behavior of equilibrium conditions and the basic reproduction number. Several parameter values were adopted from previous studies, while some were assumed to reflect realistic conditions. The human pre-exposure vaccination rate was assumed as $k_{h1} = 0.05$ per year because rabies vaccination is generally limited to high-risk groups (Kessels et al., 2017; Rao et al., 2022). The dog culling rate was assumed as $\phi_d = 0.03$ per year since culling is mainly used as an emergency response strategy (Taylor et al., 2017). In addition,

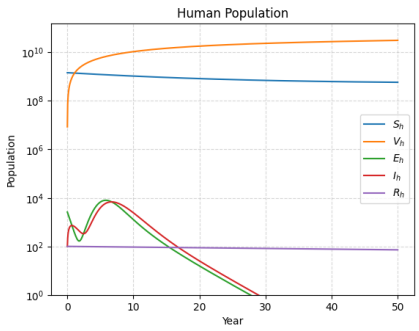
because rabies mortality approaches 100% after the onset of clinical symptoms (Yang et al., 2025), the recovery rates were assumed to be very small, namely $r_d = 0.0000001$ and $r_h = 0.00001$. The parameter values used in the simulations are presented in Table 2.

Table 2. Parameter Value

Parameter	Value	Unit	Reference
A	3000000	/ year	(Thongtha & Modnak, 2021)
B	30000000	/ year	(Thongtha & Modnak, 2021)
k_d	0.3	/ year	(Lv et al., 2023)
k_{h1}	0.05	/ year	Assumption
k_{h2}	0.85	/ year	(Lv et al., 2023)
β_d	0.0000001	/ year	(Thongtha & Modnak, 2021)
β_h	0.00000000000229	/ year	(Thongtha & Modnak, 2021)
σ_d	6	/ year	(Thongtha & Modnak, 2021)
σ_h	6	/ year	(Thongtha & Modnak, 2021)
γ_d	0.4	/ year	(Thongtha & Modnak, 2021)
γ_h	1/6	/ year	(Thongtha & Modnak, 2021)
μ_d	0.08	/ year	(Thongtha & Modnak, 2021)
μ_h	0.0066	/ year	(Thongtha & Modnak, 2021)
m_d	1	/ year	(Thongtha & Modnak, 2021)
m_h	1	/ year	(Thongtha & Modnak, 2021)
r_d	0.0000001	/ year	Assumption
r_h	0.00001	/ year	Assumption
ϕ_d	0.03	/ year	Assumption

The numerical simulation is conducted based on the parameter values in Table 2, with the initial conditions $S_d(0) = 129220000$, $V_d(0) = 99276000$, $E_d(0) = 1960$, $I_d(0) = 100$, $R_d(0) = 30$, $S_h(0) = 1451700000$, $V_h(0) = 8505800$, $E_h(0) = 2600$, $I_h(0) = 100$, $R_h(0) = 100$. The results of the numerical simulation are presented in graphical form to illustrate the dynamic behavior of each compartment over time.





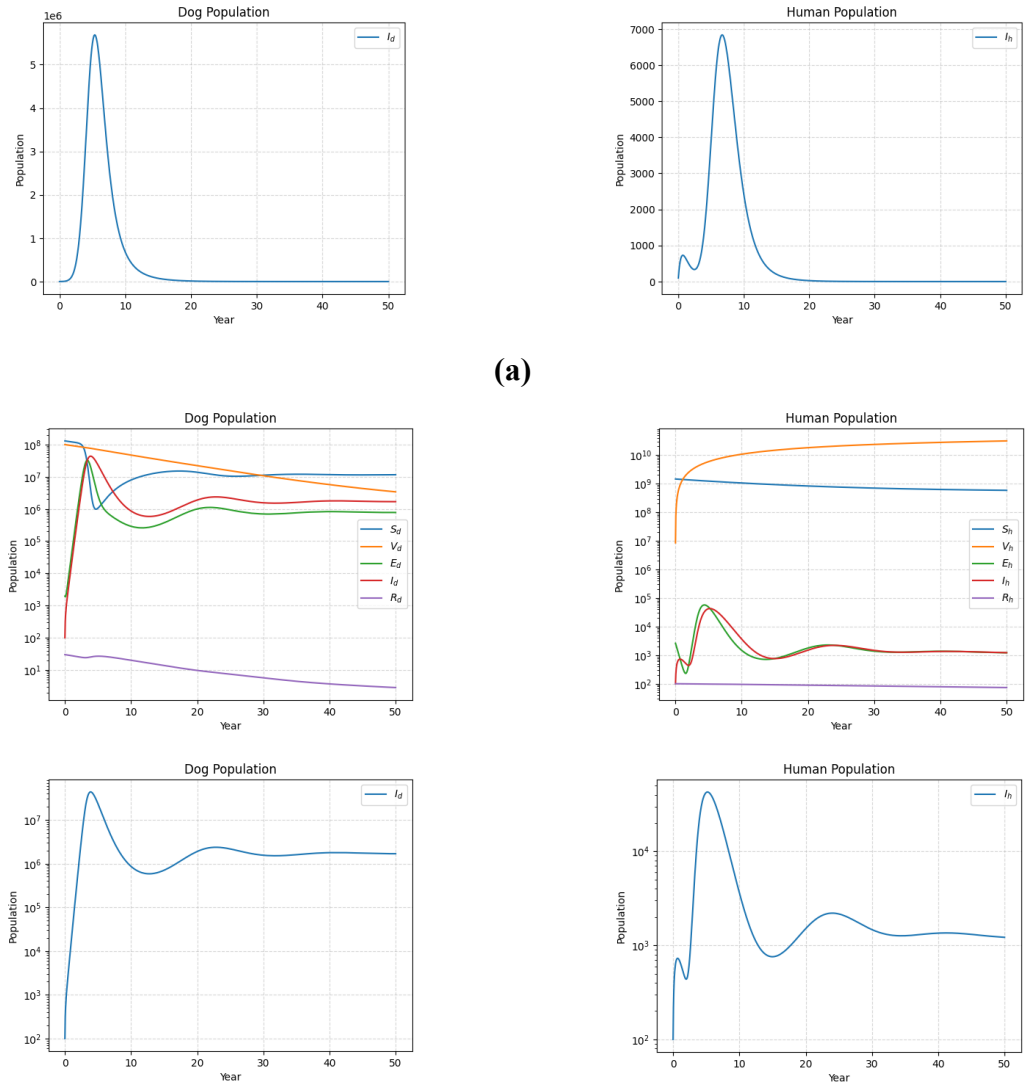


Figure 3. Numerical simulations of rabies transmission dynamics under (a) disease-free conditions $R_0 < 1$ and (b) endemic conditions $R_0 > 1$ in dog and human populations.

Figure 3 illustrates the rabies transmission dynamics under disease-free and endemic conditions. Using the parameter values in Table 2, the model produces $R_0 = 0.614018 < 1$ with all eigenvalues negative, showing that the disease-free state remains asymptotically stable. As shown in Figure 3(a), the exposed and infected populations in both dogs and humans gradually decrease toward zero over time, indicating that rabies transmission cannot persist in the population.

To obtain the condition $R_0 > 1$, the dog vaccination rate was reduced to $k_d = 0.01$, resulting in produces $R_0 = 2.89446 > 1$with one positive eigenvalue, indicating that the disease-free equilibrium point becomes unstable. Figure 3(b) shows that the exposed and

infected populations initially increase significantly and then persist before stabilizing, indicating an endemic state in both populations.

Subsequently, numerical simulations were performed on the infected dog subpopulation (I_d), which acts as the primary source of rabies transmission. The dog vaccination rate (k_d) and culling rate (ϕ_d) were varied at 0.1, 0.5, and 0.9 to evaluate their effects on the dynamics of rabies transmission and the basic reproduction number (R_0). In addition, simulations were also conducted by varying the transmission rate among dogs (β_d) using values around the baseline parameter reported by Thongtha & Modnak (2021), namely 0.00000005, 0.0000001, and 0.0000002, in order to analyze its influence on the infected dog population and disease persistence.

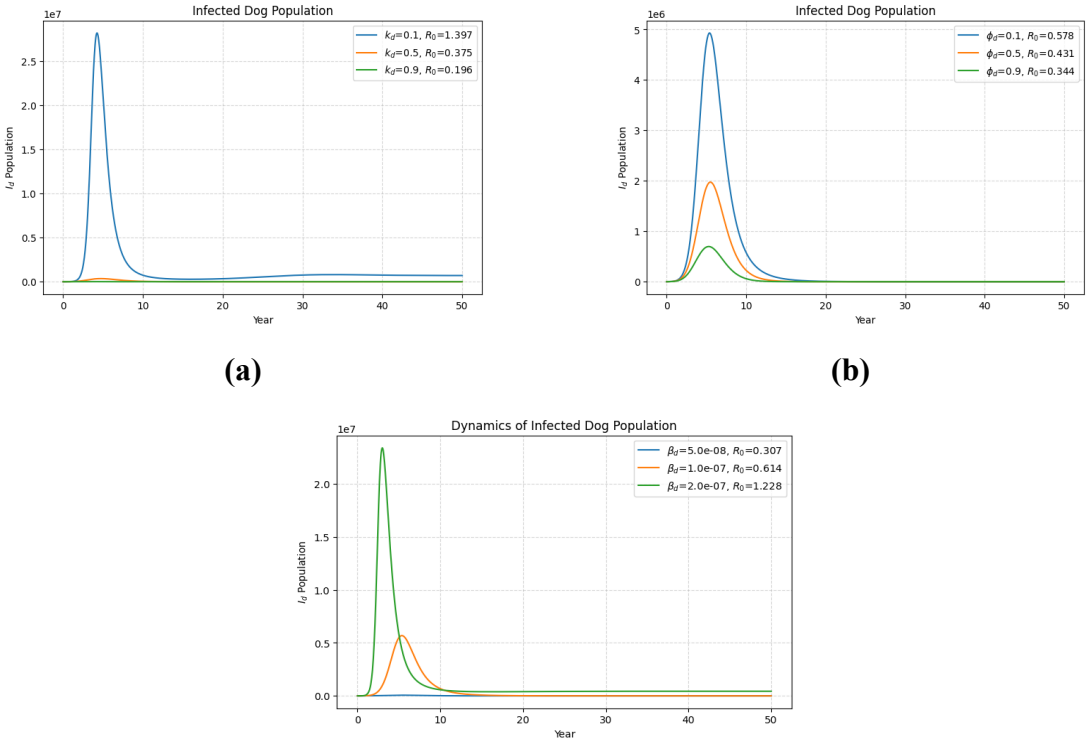


Figure 4. Simulation of the infected dog subpopulation dynamics under variations of (a) dog vaccination rate (k_d), (b) dog culling rate (ϕ_d), and (c) dog-to-dog transmission rate (β_d).

Based on Figure 4, variations in k_d, ϕ_d, and β_d produce different values of the basic reproduction number and affect the infected dog subpopulation (I_d). An increase in the dog vaccination rate (k_d) significantly reduces both R_0 and the infected dog population, indicating that vaccination is the most effective strategy for controlling rabies transmission. Likewise, increasing the culling rate (ϕ_d) also decreases R_0 and the number of infected dogs, although its effect is relatively smaller than that of vaccination. On the other hand, higher

values of the dog-to-dog transmission rate (β_d) increase disease transmission and raise R_0, indicating that contact intensity among dogs strongly influences the persistence of rabies. Since β_d is influenced by population density, contact patterns, and environmental conditions, its value may vary across different regions and populations.

CONCLUSION

The results show that the rabies transmission model has two equilibrium points, namely the disease-free and endemic equilibria, determined by the basic reproduction number. The disease-free equilibrium is locally stable when $R_0 < 1$, indicating that rabies transmission will gradually disappear, whereas $R_0 > 1$ leads to endemic persistence. Numerical simulations confirm that increasing dog vaccination and culling rates reduces R_0 and suppresses the infected dog population, with vaccination showing a stronger effect than culling. Future research may extend this study through global stability, stochastic analysis, spatial mobility, or optimal control approaches.

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