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Mathematical Model and Simulation of the Spread of COVID-19 with Vaccination, Implementation of Health Protocols, and Treatment

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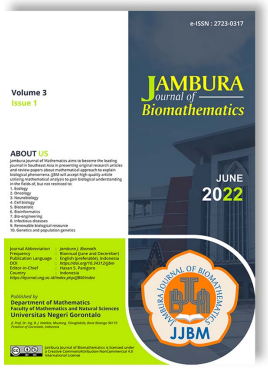

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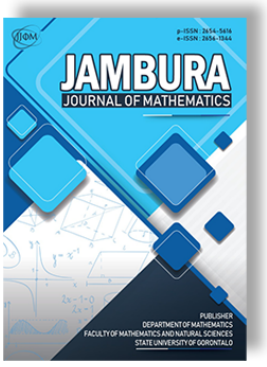

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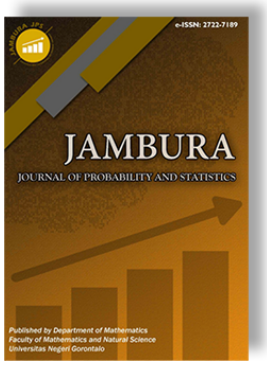

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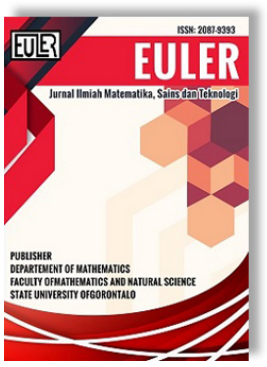

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Research Article

Mathematical Model and Simulation of the Spread of COVID-19 with Vaccination, Implementation of Health Protocols, and Treatment

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ABSTRACT. *This research develops the SVEIHQR model to simulate the spread of COVID-19 with vaccination, implementation of health protocols, and treatment. The population is divided into twelve subpopulations, resulting in a mathematical model of COVID-19 in the form of a system of twelve differential equations with twelve variables. From the model, we obtain the disease-free equilibrium point, the endemic equilibrium point, and the basic reproduction number* (R_0)*. The disease-free equilibrium point is locally asymptotically stable when* $R_0 < 1$ *and* $\Delta_5 > 0$*, where* Δ_5 *is the fifth-order Routh-Hurwitz matrix of the characteristic polynomial of the Jacobian matrix. Additionally, an endemic equilibrium point exists when* $R_0 > 1$*. The results of numerical simulations are consistent with the conducted analysis, and the sensitivity analysis reveals that the significant parameters influencing the spread of COVID-19 are the proportion of symptomatic infected individuals and the contact rate with asymptomatic infected individuals.*

1. Introduction

Coronavirus Disease 19 (COVID-19) is an infectious disease caused by a novel type of coronavirus [1]. It originated from the identification report of a new coronavirus (2019-nCoV) that caused an outbreak of acute respiratory illness in humans in Wuhan, China, on December 12, 2019. Subsequently, on January 26, 2020, a total of 2.794 laboratories reported infections, with 80 deaths [2]. Not limited to Wuhan, China, the first case of COVID19 outside China was reported on January 13, 2020. On January 30, 2020, the World Health Organization (WHO) declared it a global health threat. The President of Indonesia, Joko Widodo, reported the first two cases of COVID-19 in Depok, West Java, on March 2, 2020. Finally, on March 11, 2020, the WHO declared COVID-19 a pandemic worldwide [3].

The number of confirmed COVID-19 cases in Indonesia continues to increase, and as of January 24, 2023, there have been a total of 6,728,184 confirmed positive cases, with a death toll of 160,788 people [4]. To curb the spread of COVID-19, the government has implemented a gradual vaccination program starting in January 2021. Additionally, the government has implemented further preventive measures, including the implementation of health protocols such as the 3M (Wearing Masks, Keeping Distance, Washing Hands) movement and strengthening the 3T (Tracing, Testing, Treatment) approach [5]. After two years, specifically on January 17, 2023, the total number of vaccinations administered by the Indonesian government reached 444,303,130 vaccine doses. This includes 203,657,535 individuals who received the first dose, 172,693,321 individuals who received the second dose, and 67,952,274 individuals who received a booster dose [6].

The World Health Organization (WHO) has officially announced that COVID-19 transmission occurs through droplets. The transmission of COVID-19 through droplets is supported by several studies, including those conducted by [7–11]. Droplet transmission can occur when a person is nearby proximity (approximately 1 meter) to someone who is symptomatic, such as coughing or sneezing, resulting in droplets posing a risk of reaching the mucous membranes (mouth and nose) or conjunctiva (eyes). Additionally, transmission can also occur through objects/surfaces contaminated with droplets in the vicinity of an infected individual. Therefore, the transmission of the COVID-19 virus can occur through direct contact with an infected person and indirect contact with objects/surfaces used by the infected person, such as thermometers or stethoscopes [1]. The solution to prevent the spread of COVID-19 through droplets is by wearing masks, both for COVID-19 patients and non-patients. The Ministry of Health recommends medical masks for healthcare workers and three-layer cloth masks for the general public [1]. The use of masks is relatively effective in preventing the transmission of COVID-19 and can be easily adopted by the public.

Mathematical modeling is widely used in epidemiological studies to provide an understanding of the characteristics and spread of disease [12, 13]. Similarly, with COVID-19, mathematical models have been developed since the beginning of the pandemic in early 2020. The basic model for modeling the spread of COVID19 is the SIR model. The SIR model divides the population into three subpopulations: susceptible (S), infectious (I), and re-

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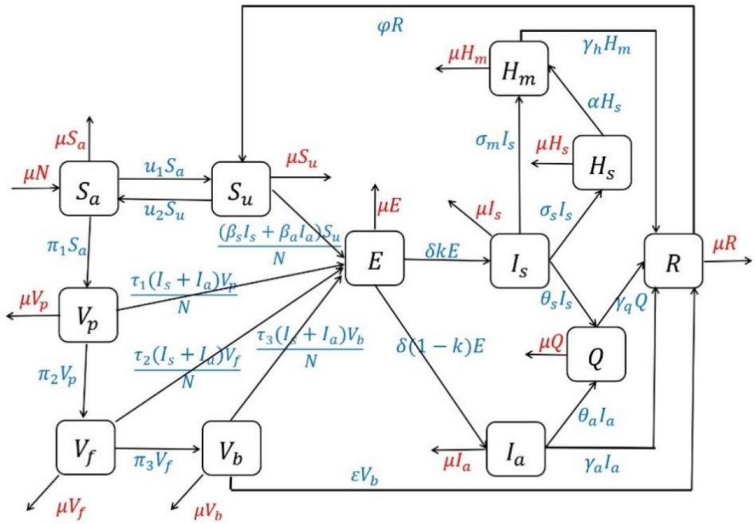

Figure 1. The transfer diagram of the mathematical model of COVID-19 transmission with vaccination, implementation of health protocols, and treatment

moved (R) This model was developed by Miroslava I. et al. (2020) [14], Zhifang L. et al. (2020) [15], and Asish M. (2020) [16]. Furthermore, Maher A. et al. (2021) [17], Matteo C. et al. (2020) [18], De Kai et al.(2020) [19], Adam J. K. et al. (2020) [20], Chaolong W. et al. (2020) [21], Joseph T. W. et al. (2020) [22], Zifeng Y. et al. (2020) [23], and Shi Zhao et al. (2020) [24] developed the SEIR/SLIR COVID-19 model by incorporating an exposed/latent (E/L) subpopulation into the SIR model.

The development of mathematical models for COVID-19 continues to progress over time. Idris Ahmed et al. (2021) [25] conducted research on the SEIQR model, which divides the infected compartments into two parts: symptomatic infections (I_s) and asymptomatic infections (I_a). Additionally, Enahoro A. Aboi et al. (2020) [26] made further advancements in the SEIR model by incorporating vaccinated individuals, dividing the E compartment into two parts, distinguishing between symptomatic (I_s) and asymptomatic (I_a) infected individuals, and adding a compartment for individuals receiving hospital care (I_h). Furthermore, Salihu S. M. et al. (2021) [27] developed the SEIRD mathematical model for COVID-19, dividing the susceptible subpopulation into those who adhere to health protocols and those who do not. Additionally, Salihu S. M. et al. (2021) [27] included a treatment class through both mild and severe hospital inpatient care.

This study develops the SVEIHQR model for the spread of COVID-19, considering vaccination, the implementation of health protocols, and treatment. The vaccination process consists of three stages: the first dose, the second dose, and the booster dose. Treatment is divided into two categories: hospital care, including mild and severe inpatient care. The model also considers COVID-19 cases with symptoms and without symptoms, including asymptomatic and symptomatic patients. Based on this model, an analysis of the equilibrium points is conducted, which is associated with the basic reproduction number. Subsequently, model simulations are performed to provide a geometric representation of the model's solutions and to verify the obtained theorems. Finally, a sensitivity analysis of the model's parameters is conducted to the basic reproduction number to identify the dominant parameters that influence the spread of COVID-19.

2. Model Formulation

The model used in this study is the SVEIHQR model, which divides the population into twelve sub-populations: susceptible individuals who adhere to health protocols (S_a), susceptible individuals who do not adhere to health protocols (S_u), individuals who have received the first dose of vaccination (V_p), individuals who have received the second dose of vaccination (V_f), individuals who have received the booster dose of vaccination (V_b), exposed/latent individuals (E), symptomatic infected individuals (I_s), asymptomatic infected individuals (I_a), mild inpatient individuals at the hospital (H_m), severe inpatient individuals at the hospital (H_s), quarantined individuals (Q), and recovered/immune individuals with temporary immunity to COVID-19 (R).

The assumptions for the development of the mathematical model of COVID-19 transmission with vaccination, implementation of health protocols, and treatment can be stated as follows: (1) Latent individuals cannot infect others; (2) The transmission rate for symptomatic and asymptomatic infected individuals in the vaccinated sub-population is equal; (3) The population is assumed to be closed, meaning no individuals enter or leave; (4) The population is assumed to be homogeneous, where each individual in the population has an equal chance of contacting others; (5) The natural birth rate and natural death rate are assumed to be equal, maintaining a constant total population; (6) Births enter the susceptible sub-population that adheres to health protocols; (7) Individuals in the susceptible sub-population that adheres to health protocols can become non-compliant, thus entering the susceptible sub-population that does not adhere to health protocols, and vice versa; (8) Individuals in the susceptible sub-population that adheres to health protocols receive the first dose of vaccination (partial vaccinated), second dose (full vaccinated), and booster dose (booster vaccinated) sequentially; (9) Individuals in the susceptible sub-population that does not adhere to health protocols can be exposed to COVID-19 and enter the exposed (latent) sub-population; (10) Individ-

Table 1. The list of parameters for the COVID-19 transmission model with vaccination, implementation of health protocols, and treatment

No.	Parameter	Definition	Requirement	Unit
1.	μ	The rates of natural birth and death	$0 < \mu \leq 1$	Per day
2.	β_s	The transmission rate by symptomatic infected individuals	$0 < \beta_s \leq 1$	Per day
3.	β_a	The transmission rate by asymptomatic infected individuals	$0 < \beta_a \leq 1$	Per day
4.	δ	The incubation rate	$0 < \delta \leq 1$	Per day
5.	k	The proportion of symptomatic infected individuals	$0 < k \leq 1$	Per day
6.	θ_s	The rate of quarantine for symptomatic infected individuals	$0 < \theta_s \leq 1$	Per day
7.	θ_a	The rate of quarantine for asymptomatic infected individuals	$0 < \theta_a \leq 1$	Per day
8.	γ_a	The rate of recovery for asymptomatic infected individuals who recover due to natural immunity	$0 < \gamma_a \leq 1$	Per day
9.	γ_q	The rate of recovery for individuals after undergoing quarantine	$0 < \gamma_q \leq 1$	Per day
10.	γ_h	The rate of recovery for individuals after receiving treatment in the hospital	$0 < \gamma_h \leq 1$	Per day
11.	π_1	The rate of vaccination for the first dose	$0 < \pi_1 \leq 1$	Per day
12.	π_2	The rate of vaccination for the second dose	$0 < \pi_2 \leq 1$	Per day
13.	π_3	The rate of vaccination for the booster dose	$0 < \pi_3 \leq 1$	Per day
14.	τ_1	The rate of infection among individuals who have received the first dose of the vaccine	$0 < \tau_1 \leq 1$	Per day
15.	τ_2	The rate of infection among individuals who have received the second dose of the vaccine	$0 < \tau_2 \leq 1$	Per day
16.	τ_3	The rate of infection among individuals who have received the booster dose of the vaccin e	$0 < \tau_3 \leq 1$	Per day
17.	ε	The rate of immune response among individuals who have received the booster dose of the vaccine	$0 < \varepsilon \leq 1$	Per day
18.	u_1	The rate of non-compliance with health protocols	$0 < u_1 \leq 1$	Per day
19.	u_2	The rate of compliance with health protocols	$0 < u_2 \leq 1$	Per day
20.	σ_s	The rate of treatment for symptomatic infected individuals in severe hospitalization	$0 < \sigma_s \leq 1$	Per day
21.	σ_m	The rate of treatment for symptomatic infected individuals in mild hospitalization	$0 < \sigma_m \leq 1$	Per day
22.	α	The rate of transition from severe hospitalization to mild hospitalization	$0 < \alpha \leq 1$	Per day
23.	φ	The rate of reinfection from individuals who have recovered and/or have temporary immunity to the disease	$0 < \varphi \leq 1$	Per day

uals who receive 1 dose of vaccine (partial vaccinated), 2 doses of vaccine (full vaccinated), and booster vaccine (booster vaccinated) can be exposed to COVID-19 and enter the exposed (latent) sub-population; (11) Individuals in the exposed (latent) sub-population can be infected with COVID-19 with two possibilities, either symptomatic or asymptomatic; (12) Asymptomatic individuals in the infected sub-population can undergo quarantine or recover/immune with temporary immunity; (13) Symptomatic individuals in the infected sub-population can undergo quarantine, mild hospitalization, or severe hospitalization; (14) Individuals in the severe hospitalization sub-population can transition to mild hospitalization; (15) Individuals in the mild hospitalization sub-population can recover/immune with temporary immunity; and (16) Individuals in the recovered/immune with temporary immunity sub-population can become susceptible again and enter the susceptible sub-population that does not adhere to health protocols. The parameters used in the model of COVID-19 transmission with vaccination, implementation of health protocols, and treatment are presented in Table 1.

Schematically, the mathematical model of COVID-19 transmission with vaccination, implementation of health protocols, and treatment can be represented in the transfer diagram shown in Figure 1. Based on the transfer diagram in Figure 1, the mathematical model can be formulated as the system of nonlinear ordinary differential equations eq. (1).

$$
\begin{aligned}
\frac{dS_a}{dt} &= \mu N + u_2 S_u - \mu S_a - u_1 S_a - \pi_1 S_a,\\
\frac{dS_u}{dt} &= u_1 S_a + \varphi R - \mu S_u - u_2 S_u - \frac{(\beta_s I_s + \beta_a I_a) S_u}{N},\\
\frac{dV_p}{dt} &= \pi_1 S_a - \mu V_p - \pi_2 V_p - \frac{\tau_1 (I_s + I_a) V_p}{N},\\
\frac{dV_f}{dt} &= \pi_2 V_p - \mu V_f - \pi_3 V_f - \frac{\tau_2 (I_s + I_a) V_f}{N},\\
\frac{dV_b}{dt} &= \pi_3 V_f - \mu V_b - \varepsilon V_b - \frac{\tau_3 (I_s + I_a) V_b}{N},\\
\frac{dE}{dt} &= \frac{(\beta_s I_s + \beta_a I_a) S_u}{N} + \frac{\tau_1 (I_s + I_a) V_p}{N}\\
&\quad + \frac{\tau_2 (I_s + I_a) V_f}{N} + \frac{\tau_3 (I_s + I_a) V_b}{N}\\
&\quad - \mu E - \delta k E - \delta(1-k)E,\\
\frac{dI_s}{dt} &= \delta k E - \mu I_s - \theta_s I_s - \sigma_s I_s - \sigma_m I_s,\\
\frac{dI_a}{dt} &= \delta(1-k)E - \mu I_a - \theta_a I_a - \gamma_a I_a,\\
\frac{dH_m}{dt} &= \sigma_m I_s + \alpha H_s - \mu H_m - \gamma_h H_m,\\
\frac{dH_s}{dt} &= \sigma_s I_s - \mu H_s - \alpha H_s,\\
\frac{dQ}{dt} &= \theta_a I_a + \theta_s I_s - \mu Q - \gamma_q Q,\\
\frac{dR}{dt} &= \varepsilon V_b + \gamma_a I_a + \gamma_h H_m + \gamma_q Q - \mu R - \varphi R,
\end{aligned}
\tag{1}
$$

with the value $N = S_a + S_u + V_p + V_f + V_b + E + I_s + I_a + H_m + H_s + Q + R$. It is obtained $\frac{dN}{dt} = 0$, thus $N(t) = c$ where c is a positive integer. Since $N(t)$ is constant, system eq. (1) can be transformed into a non-dimensional model to simplify the model. The proportions of individuals in each compartment can be expressed as eq. (2).

$$
\begin{aligned}
s_a &= \frac{1}{N} S_a, \quad & s_u &= \frac{1}{N} S_u, \quad & v_p &= \frac{1}{N} V_p, \quad & v_f &= \frac{1}{N} V_f,\\
v_b &= \frac{1}{N} V_b, \quad & e &= \frac{1}{N} E, \quad & i_s &= \frac{1}{N} I_s, \quad & i_a &= \frac{1}{N} I_a,\\
h_m &= \frac{1}{N} H_m, \quad & h_s &= \frac{1}{N} H_s, \quad & q &= \frac{1}{N} Q, \quad & r &= \frac{1}{N} R.
\end{aligned}
\tag{2}
$$

Therefore, from eq. (1) and eq. (2), the non-dimensional equation can be formed as system eq. (3).

$$
\frac{ds_a}{dt} = \mu + u_2 s_u - \xi_1 s_a,
$$

$$
\begin{aligned}
\frac{ds_u}{dt} &= u_1 s_a + \varphi r - \xi_2 s_u - (\beta_s i_s + \beta_a i_a)\, s_u,\\
\frac{dv_p}{dt} &= \pi_1 s_a - \xi_3 v_p - \tau_1 (i_s + i_a)\, v_p,\\
\frac{dv_f}{dt} &= \pi_2 v_p - \xi_4 v_f - \tau_2 (i_s + i_a)\, v_f,\\
\frac{dv_b}{dt} &= \pi_3 v_f - \xi_5 v_b - \tau_3 (i_s + i_a)\, v_b,\\
\frac{de}{dt} &= (\beta_s i_s + \beta_a i_a)\, s_u + \tau_1 (i_s + i_a)\, v_p\\
&\quad + \tau_2 (i_s + i_a)\, v_f + \tau_3 (i_s + i_a)\, v_b - \xi_6 e, \qquad (3)\\
\frac{di_s}{dt} &= \delta k e - \xi_7 i_s,\\
\frac{di_a}{dt} &= \delta (1-k) e - \xi_8 i_a,\\
\frac{dh_m}{dt} &= \sigma_m i_s + \alpha h_s - \xi_9 h_m,\\
\frac{dh_s}{dt} &= \sigma_s i_s - \xi_{10} h_{s\prime},\\
\frac{dq}{dt} &= \theta_a i_a + \theta_s i_s - \xi_{11} q,\\
\frac{dr}{dt} &= \varepsilon v_b + \gamma_a i_a + \gamma_h h_m + \gamma_q q - \xi_{12} r,
\end{aligned}
$$

with $\xi_1 = \mu + u_1 + \pi_1, \xi_2 = \mu + u_2, \xi_3 = \mu + \pi_2, \xi_4 = \mu + \pi_3, \xi_5 = \mu + \varepsilon, \xi_6 = \mu + \delta k + \delta(1-k), \xi_7 = \mu + \theta_s + \sigma_s + \sigma_m, \xi_8 = \mu + \theta_a + \gamma_a, \xi_9 = \mu + \gamma_{h\prime} \xi_{10} = \mu + \alpha, \xi_{11} = \mu + \gamma_q$, and $\xi_{12} = \mu + \varphi$.

Since system eq. (3) describes the interaction of subpopulations, the solutions of the system must be non-negative and bounded [28, 29]. The following theorem ensures that the solutions of system eq. (3) are non-negative and bounded.

Theorem 1. *All solutions of system eq. (1) depend on non-negative initial values* $s_a(0) = s_{a0}, s_u(0) = s_{u0}, v_p(0) = v_{p0}, v_f(0) = v_{f0}, v_b(0) = v_{b0}, e = (0)e_0, i_s(0) = i_{s0}, i_a(0) = i_{a0}, h_m(0) = h_{m0}, h_s(0) = h_{s0}, q(0) = q_0, r(0) = r_0$ *is non-negative and bounded.*

Proof. First, prove that the solutions of system eq. (3) are non-negative by showing that s_a is non-negative, assuming the contrary for contradiction. Based on the Intermediate Value Theorem [30] the existence of $\tau > 0$ is guaranteed such that $s_a(\tau-) \geq 0, s_a(\tau) = 0$, and $s_a(\tau+) < 0$. From the first equation of system eq. (3), we have

$$\frac{ds_a}{dt}\Big|_{t=\tau} = \mu > 0.$$

This means that $s_a > 0$ in $(\tau, \tau+\varepsilon)$ for any small positive constant ε. This leads to a contradiction. Therefore, $s_a \geq 0$ for all t > 0. The non-negativity of $s_u, v_p, v_f, v_b, e, i_s, i_a, h_m, h_s, q$, and r can be proven analogously. Hence, all solutions of system eq. (3) are non-negative.

Next, prove that the solutions of system eq. (3) are bounded. It is known that $1 = s_a(t) + s_u(t) + v_p(t) + v_f(t) + v_b(t) + e(t) + i_s(t) + i_a(t) + h_m(t) + h_s(t) + q(t) + r(t)$. By summing all the equations in system eq. (3), we obtain $N(t) = c$, where c is a positive integer. Therefore, we can define a positive invariant set of system eq. (3) as follows:

$$
\begin{aligned}
\Gamma = \{&(s_a, s_u, v_p, v_f, v_b, e, i_s, i_a, h_m, h_s, q, r) \in R_+^{12}\\
&\mid s_a + s_u + v_p + v_f + v_b + e + i_s + i_a + h_m\\
&+ h_s + q + r = 1\}. \qquad (4)
\end{aligned}
$$

□

3. Model Analysis

3.1. Equilibrium Point and Basic Reproduction Number

The model of COVID-19 transmission with vaccination, implementation of health protocols, and treatment is represented by a system of nonlinear differential equations. This system has two equilibrium points, namely the disease-free equilibrium point and the endemic equilibrium point. According to [31], the equilibrium points for system eq. (3) are obtained if

$$
\begin{aligned}
\frac{ds_a}{dt} = \frac{ds_u}{dt} = \frac{dv_p}{dt} = \frac{dv_f}{dt} = \frac{dv_b}{dt} = \frac{de}{dt}\\
= \frac{di_s}{dt} = \frac{di_a}{dt} = \frac{dh_m}{dt} = \frac{dh_s}{dt} = \frac{dq}{dt} = \frac{dr}{dt} = 0. \qquad (5)
\end{aligned}
$$

Theorem 2. *The disease-free equilibrium point of system eq. (3) is*

$$
\begin{aligned}
E_0 = \Big(&s_a, \left(\tfrac{u_1\xi_3\xi_4\xi_5\xi_{12} + \varphi\varepsilon\pi_1\pi_2\pi_3}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right) s_a, \tfrac{\pi_1}{\xi_3} s_a,\\
&\tfrac{\pi_1\pi_2}{\xi_3\xi_4} s_a, \tfrac{\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5} s_a, 0, 0, 0, 0, 0, 0, \tfrac{\varepsilon\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5\xi_{12}} s_a\Big),
\end{aligned}
$$

with $s_a = \frac{\mu\xi_2\xi_3\xi_4\xi_5\xi_{12}}{\xi_1\xi_2\xi_3\xi_4\xi_5\xi_{12} - u_1u_2\xi_3\xi_4\xi_5\xi_{12} - \varphi\varepsilon u_2\pi_1\pi_2\pi_3}$.

Proof. The disease-free equilibrium point is the equilibrium point when there is no disease in the population. The condition for a disease-free equilibrium is that no individual is infected, meaning $i_s = i_a = 0$. By substituting $i_s = i_a = 0$ into system eq. (3), obtain the disease-free equilibrium point $E_0\,(s_a, s_u, v_p, v_f, v_b, e, i_s, i_a, h_m, h_s, q, r)$ which is given by

$$
\begin{aligned}
E_0 \Big(&s_a, \left(\tfrac{u_1\xi_3\xi_4\xi_5\xi_{12} + \varphi\varepsilon\pi_1\pi_2\pi_3}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right) s_a, \tfrac{\pi_1}{\xi_3} s_a, \tfrac{\pi_1\pi_2}{\xi_3\xi_4} s_a,\\
&\tfrac{\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5} s_a, 0, 0, 0, 0, 0, 0, \tfrac{\varepsilon\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5\xi_{12}} s_a\Big).
\end{aligned}
$$

Note that the condition for the existence of an equilibrium point is that each of its elements is positive, so need to show $s_a > 0$ by demonstrating that its denominator is positive. It is observed that the denominator of s_a is given by $\xi_1\xi_2\xi_3\xi_4\xi_5\xi_{12} - u_1u_2\xi_3\xi_4\xi_5\xi_{12} - \varphi\varepsilon u_2\pi_1\pi_2\pi_3 =$

$$
\begin{aligned}
&\left(\mu^2 + \mu u_1 + \mu\pi_1 + \mu u_2\right)\left(\mu^4 + \mu^3\varphi + \mu^3\varepsilon + \mu^3\pi_2 + \mu^3\pi_3\right.\\
&+ \mu^2\varphi\varepsilon + \mu^2\varphi\pi_2 + \mu^2\varphi\pi_3 + \mu^2\varepsilon\pi_2 + \mu^2\varepsilon\pi_3 + \mu^2\pi_2\pi_3\\
&\left.+\mu\varphi\varepsilon\pi_2 + \mu\varphi\varepsilon\pi_3 + \mu\varepsilon\pi_2\pi_3 + \mu\varphi\pi_2\pi_3 + \varphi\varepsilon\pi_2\pi_3\right)\\
&+ u_2\pi_1\left(\mu^4 + \mu^3\varphi + \mu^3\varepsilon + \mu^3\pi_2 + \mu^3\pi_3 + \mu^2\varphi\varepsilon + \mu^2\varphi\pi_2\right.\\
&\left.+ \mu^2\varphi\pi_3 + \mu^2\varepsilon\pi_2 + \mu^2\varepsilon\pi_3 + \mu^2\pi_2\pi_3 + \mu\varphi\varepsilon\pi_2 + \mu\varphi\varepsilon\pi_3\right.\\
&\left.+\mu\varepsilon\pi_2\pi_3 + \mu\varphi\pi_2\pi_3\right) > 0, \text{ thus } s_a > 0.
\end{aligned}
$$

□

Theorem 3. *For system eq. (3) under the assumptions of the fulfilled model, we obtain the basic reproduction number* (R_0),

$$R_0 = \left[\left(\frac{\left(\begin{array}{c} \beta_s u_1 \xi_3 \xi_4 \xi_5 \xi_{12} + \beta_5 \varphi \varepsilon \pi_1 \pi_2 \pi_3 \\ +\tau_1 \pi_1 \xi_2 \xi_4 \xi_5 \xi_{12} + \tau_2 \pi_1 \pi_2 \xi_2 \xi_5 \xi_{12} \\ +\tau_3 \pi_1 \pi_2 \pi_3 \xi_2 \xi_{12} \end{array} \right)}{\xi_1 \xi_2 \xi_3 \xi_4 \xi_5 \xi_{12} - u_1 u_2 \xi_3 \xi_4 \xi_5 \xi_{12} - \varphi \varepsilon u_2 \pi_1 \pi_2 \pi_3} \right) \frac{\delta k}{\xi_7} + \left(\frac{\left(\begin{array}{c} \beta_a u_1 \xi_3 \xi_4 \xi_5 \xi_{12} + \beta_a \varphi \varepsilon \pi_1 \pi_2 \pi_3 \\ +\tau_1 \pi_1 \xi_2 \xi_4 \xi_5 \xi_{12} + \tau_2 \pi_1 \pi_2 \xi_2 \xi_5 \xi_{12} \\ +\tau_3 \pi_1 \pi_2 \pi_3 \xi_2 \xi_{12} \end{array} \right)}{\xi_1 \xi_2 \xi_3 \xi_4 \xi_5 \xi_{12} - u_1 u_2 \xi_3 \xi_4 \xi_5 \xi_{12} - \varphi \varepsilon u_2 \pi_1 \pi_2 \pi_3} \right) \frac{\delta(1-k)}{\xi_8} \Bigg] \frac{\mu}{\xi_6}.$$

Proof. The calculation of the basic reproduction number is determined using the next generation matrices. To simplify the notation, express the derivative as $\frac{df}{dt} = \dot{f}$. The determination of the basic reproduction number is done as follows:

1. Linearization with respect to the infected subsystem at the disease-free equilibrium point yields the Jacobian matrix of the equations $\dot{e}, \dot{i}_s, \dot{i}_a, \dot{h}_m, \dot{h}_s, \dot{q}$, and $\dot{r}$,

$$\boldsymbol{J} = \begin{bmatrix} -\xi_6 & v_{12} & v_{13} & 0 & 0 & 0 & 0 \\ \delta k & -\xi_7 & 0 & 0 & 0 & 0 & 0 \\ \delta(1-k) & 0 & -\xi_8 & 0 & 0 & 0 & 0 \\ 0 & \sigma_m & 0 & -\xi_9 & \alpha & 0 & 0 \\ 0 & \sigma_s & 0 & 0 & -\xi_{10} & 0 & 0 \\ 0 & \theta_s & \theta_a & 0 & 0 & -\xi_{11} & 0 \\ 0 & 0 & \gamma_a & \gamma_h & 0 & \gamma_q & -\xi_{12} \end{bmatrix},$$

with

$$v_{12} = \left(\frac{\beta_s u_1 \xi_3 \xi_4 \xi_5 \xi_{12} + \beta_s \varphi \varepsilon \varphi \varepsilon \pi_1 \pi_2 \pi_3}{\xi_2 \xi_3 \xi_4 \xi_5 \xi_{12}} + \frac{\tau_1 \pi_1}{\xi_3} + \frac{\tau_2 \pi_1 \pi_2}{\xi_3 \xi_4} + \frac{\tau_3 \pi_1 \pi_2 \pi_3}{\xi_3 \xi_4 \xi_5} \right) s_a$$

$$v_{13} = \left(\frac{\beta_a u_1 \xi_3 \xi_4 \xi_5 \xi_{12} + \beta_a \varphi \varepsilon \varphi \varepsilon \pi_1 \pi_2 \pi_3}{\xi_2 \xi_3 \xi_4 \xi_5 \xi_{12}} + \frac{\tau_1 \pi_1}{\xi_3} + \frac{\tau_2 \pi_1 \pi_2}{\xi_3 \xi_4} + \frac{\tau_3 \pi_1 \pi_2 \pi_3}{\xi_3 \xi_4 \xi_5} \right) s_a$$

2. The decomposition of the Jacobian matrix $\boldsymbol{J} = \boldsymbol{F} - \boldsymbol{V}$ into the transmission matrix $\boldsymbol{F}$ and the transition matrix $\mathbf{V}$, obtained

$$\boldsymbol{F} = \begin{bmatrix} 0 & v_{12} & v_{13} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}, \text{and}$$

$$\boldsymbol{V} = \begin{bmatrix} \xi_6 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\delta k & \xi_7 & 0 & 0 & 0 & 0 & 0 \\ -\delta(1-k) & 0 & \xi_8 & 0 & 0 & 0 & 0 \\ 0 & -\sigma_m & 0 & \xi_9 & -\alpha & 0 & 0 \\ 0 & -\sigma_s & 0 & 0 & \xi_{10} & 0 & 0 \\ 0 & -\theta_s & -\theta_a & 0 & 0 & \xi_{11} & 0 \\ 0 & 0 & -\gamma_a & -\gamma_h & 0 & -\gamma_q & \xi_{12} \end{bmatrix}.$$

3. Calculating $R_0 = \rho\left(\boldsymbol{F}\boldsymbol{V}^{-1}\right)$ or R_0 obtained from the spectral radius of $\boldsymbol{F}\boldsymbol{V}^{-1}$,

$$R_0 = \left[\left(\frac{\left(\begin{array}{c} \beta_s u_1 \xi_3 \xi_4 \xi_5 \xi_{12} + \beta_s \varphi \varepsilon \pi_1 \pi_2 \pi_3 \\ +\tau_1 \pi_1 \xi_2 \xi_4 \xi_5 \xi_{12} + \tau_2 \pi_1 \pi_2 \xi_2 \xi_5 \xi_{12} \\ +\tau_3 \pi_1 \pi_2 \pi_3 \xi_2 \xi_{12} \end{array} \right)}{\xi_1 \xi_2 \xi_3 \xi_4 \xi_5 \xi_{12} - u_1 u_2 \xi_3 \xi_4 \xi_5 \xi_{12} - \varphi \varepsilon u_2 \pi_1 \pi_2 \pi_3} \right) \frac{\delta k}{\xi_7} + \left(\frac{\left(\begin{array}{c} \beta_a u_1 \xi_3 \xi_4 \xi_5 \xi_{12} + \beta_a \varphi \varepsilon \pi_1 \pi_2 \pi_3 \\ +\tau_1 \pi_1 \xi_2 \xi_4 \xi_5 \xi_{12} + \tau_2 \pi_1 \pi_2 \xi_2 \xi_5 \xi_{12} \\ +\tau_3 \pi_1 \pi_2 \pi_3 \xi_2 \xi_{12} \end{array} \right)}{\xi_1 \xi_2 \xi_3 \xi_4 \xi_5 \xi_{12} - u_1 u_2 \xi_3 \xi_4 \xi_5 \xi_{12} - \varphi \varepsilon u_2 \pi_1 \pi_2 \pi_3} \right) \frac{\delta(1-k)}{\xi_8} \Bigg] \frac{\mu}{\xi_6}.$$

□

Theorem 4. *If* $R_0 > 1$, *then there exists an endemic equilibrium point* $E_1 = E_1\left(s_a^*, s_u^*, v_p^*, v_f^*, v_b^*, e^*, i_s^*, i_a^*, h_m^*, h_s^*, q^*, r^*\right)$ *of system eq. (3), with*

$$\begin{aligned}
s_a^* &= JWYv_b^* + (AJXY + AJWZ + AKWY)v_b^* e^* \\
&\quad + \left(A^2JXZ + A^2KXY + A^2KWZ\right) v_b^* e^{*2} \\
&\quad + A^3KXZv_b^* e^{*3}, \\
s_u^* &= JLWYv_b^* + (AJLXY + AJLWZ + AKLWY)v_b^* e^* \\
&\quad + \left(A^2JLXZ + A^2KLXY + A^2KLWZ\right) v_b^* e^{*2} \\
&\quad + A^3KLXZv_b^* e^{*3} - \frac{\mu}{u_2}, \\
v_p^* &= WYv_b^* + (AXY + AWZ)v_b^* e^* + A^2XZv_b^* e^{*2}, \\
v_f^* &= Wv_b^* + AXv_b^* e^*, \\
v_b^* &= \frac{\xi_6 + \frac{B\mu}{u_2}}{A^3BLn_1 e^{*3} + \left(A^3XZ\tau_1 + A^2BLn_2\right) e^{*2} + \left(A^2m_1 + ABLn_3\right) e^* + \left(Am_2 + BLn_4\right)}, \\
i_s^* &= \frac{\delta k}{\xi_7} e^*, \\
i_a^* &= \frac{\delta(1-k)}{\xi_8} e^*, \\
h_m^* &= \left(\frac{\delta k \sigma_m \xi_{10} + \alpha \sigma_s \delta k}{\xi_7 \xi_9 \xi_{10}} \right) e^*, \\
h_s^* &= \frac{\sigma_s \delta k}{\xi_7 \xi_{10}} e^*, \\
q^* &= \left(\frac{\delta \theta_a (1-k) \xi_7 + \delta \theta_s k \xi_8}{\xi_7 \xi_8 \xi_{11}} \right) e^*, \\
r^* &= \frac{\varepsilon}{\xi_{12}} v_b^* + \left(\frac{\gamma_a \delta(1-k)}{\xi_8 \xi_{12}} + \frac{\gamma_h \delta k \sigma_m \xi_{10} + \gamma_h \alpha \sigma_s \delta k}{\xi_7 \xi_9 \xi_{10} \xi_{12}} \right. \\
&\quad \left. + \frac{\gamma_q \delta \theta_a (1-k) \xi_7 + \gamma_q \delta \theta_s k \xi_8}{\xi_7 \xi_8 \xi_{11} \xi_{12}} \right) e^*,
\end{aligned}$$

where e^* *is the solution of*

$$a_0 e^{*4} + a_1 e^{*3} + a_2 e^{*^2} + a_3 e^* + a_4 = 0 \tag{6}$$

with

$$\begin{aligned}
a_0 &= A^3BCLn_1 - A^3BFLn_1, \\
a_1 &= A^3Cn_1m_3 + A^2BCLn_2 - A^3BDLn_1 \\
&\quad - A^3FXZ\tau_1 - A^2BFLn_2, \\
a_2 &= A^2Cn_2m_3 + ABCLn_3 - A^3DXZ\tau_1
\end{aligned}$$

$$
\begin{aligned}
&- A^2BDLn_2 - A^2Fm_1 - ABFLn_3,\\
a_3 &= BCLn_4 + ACn_3m_3 - A^2Dm_1 - ABDLn_3\\
&- AFm_2 - BFLn_4,\\
a_4 &= \tfrac{\xi_6(\xi_1\xi_2\xi_3\xi_4\xi_5\xi_{12} - u_1u_2\xi_3\xi_4\xi_5\xi_{12} - \varepsilon\varphi u_2\pi_1\pi_2\pi_3)}{u_2\pi_1\pi_2\pi_3\xi_{12}}\,(1-R_0),\\
n_1 &= KXZ,\ n_2 = JXZ + KXY + KWZ,\\
n_3 &= JXY + JWZ + KWY,\ n_4 = JWY,\\
m_1 &= X\tau_2 + XY\tau_1 + WZ\tau_1,\ m_2 = \tau_3 + W\tau_2 + WY\tau_1,\\
m_3 &= L\xi_2 - u_1,\ m_4 = \tfrac{\varepsilon\varphi}{\xi_{12}},\ J = \tfrac{\xi_3}{\pi_1},\ K = \tfrac{\tau_1}{\pi_1},\ L = \tfrac{\xi_1}{u_2},\\
W &= \tfrac{\xi_5}{\pi_3},\ X = \tfrac{\tau_3}{\pi_3},\ Y = \tfrac{\xi_4}{\pi_2},\ Z = \tfrac{\tau_2}{\pi_2},\ A = \tfrac{\delta k\xi_8 + \delta(1-k)\xi_7}{\xi_7\xi_8},\\
B &= \tfrac{\beta_s\xi_8\delta k + \beta_a\xi_7\delta(1-k)}{\xi_7\xi_8},\ C = \xi_6 + \tfrac{B\mu}{u_2},\ D = \tfrac{\mu\xi_2}{u_2},\ \textit{and}\\
F &= \tfrac{\mu B}{u_2} + \left(\tfrac{\varphi\gamma_a\delta(1-k)}{\xi_8\xi_{12}} + \tfrac{\varphi\gamma_h\delta k\sigma_m\xi_{10} + \varphi\gamma_h\alpha\sigma_s\delta k}{\xi_7\xi_9\xi_{10}\xi_{12}}\right.\\
&\left. + \tfrac{\varphi\gamma_q\delta\theta_a(1-k)\xi_7 + \varphi\gamma_q\delta\theta_s k\xi_8}{\xi_7\xi_8\xi_{11}\xi_{12}}\right).
\end{aligned}
$$

Proof. The endemic equilibrium point is a equilibrium point when there is a disease present and it causes an epidemic in a population, thus $i_s^* > 0$ and $i_a^* > 0$. It is clear that each element of E_1 is positive if $e^* > 0$. The polynomial eq. (6) has one positive root if there is a change in sign among its coefficients according to Descartes' Rule of Signs. Considering the coefficients in polynomial eq. (6), since $A, B, L, n_1 > 0$, so $a_0 > 0$. Obtained $a_4 < 0$ if $R_0 > 1$. Therefore, $e^* > 0$ if $R_0 > 1$. □

3.2. Stability of the Equilibrium Point

Theorem 5. *If $R_0 < 1$ and Δ_5 are positive, then the equilibrium point E_0 is locally asymptotically stable.*

Proof. The stability analysis of the equilibrium point can be determined by finding the eigenvalues of the Jacobian matrix obtained from linearizing the system around the equilibrium points of system eq. (3). The eigenvalues of the matrix $J_{(E_0)}$ are obtained by solving $det\left(J_{(E_0)} - \lambda I\right) = 0$, resulting in the characteristic eq. (7).

$$(\xi_9 + \lambda)(\xi_{10} + \lambda)(\xi_{11} + \lambda)PQ = 0. \tag{7}$$

with

$$
\begin{aligned}
P = &- \delta k\left(\left(\tfrac{\beta_s u_1\xi_3\xi_4\xi_5\xi_{12} + \beta_s\varphi\varepsilon\pi_1\pi_2\pi_3}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right)s_a + \tfrac{\tau_1\pi_1}{\xi_3}s_a\right.\\
&\left. + \tfrac{\tau_2\pi_1\pi_2}{\xi_3\xi_4}s_a + \tfrac{\tau_3\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5}s_a\right)(\xi_8 + \lambda) + (\xi_6 + \lambda)(\xi_7 + \lambda)\\
&(\xi_8 + \lambda) - \delta(1-k)\left(\left(\tfrac{\beta_a u_1\xi_3\xi_4\xi_5\xi_{12} + \beta_a\varphi\varepsilon\pi_1\pi_2\pi_3}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right)s_a\right.\\
&\left. + \tfrac{\tau_1\pi_1}{\xi_3}s_a + \tfrac{\tau_2\pi_1\pi_2}{\xi_3\xi_4}s_a + \tfrac{\tau_3\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5}s_a\right)(\xi_7 + \lambda),\\
Q = &- \varepsilon\varphi u_2\pi_1\pi_2\pi_3 + (\xi_4 + \lambda)(\xi_5 + \lambda)(\xi_{12} + \lambda)(\xi_3 + \lambda)\\
&((\xi_1 + \lambda)(\xi_2 + \lambda) - u_1u_2).
\end{aligned}
$$

Based on the characteristic eq. (7), obtain $\lambda_1 = -\xi_9, \lambda_2 = -\xi_{10}$, and $\lambda_3 = -\xi_{11}$. Since $\xi_9, \xi_{10}, \xi_{11} \geq 0$, all three eigenvalues are negative. From equation eq. (7), observe the characteristic equation for the remaining nine eigenvalues as follows.

First, considering P, which is a polynomial of degree three,

$$a_0\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0, \tag{8}$$

with

$$
\begin{aligned}
a_0 &= 1,\\
a_1 &= \xi_6 + \xi_7 + \xi_8,\\
a_2 &= \xi_6\xi_7 + \xi_6\xi_8 + \xi_7\xi_8\\
&- \delta k\left(\left(\tfrac{\beta_s u_1\xi_3\xi_4\xi_5\xi_{12} + \beta_s\varphi\varepsilon\pi_1\pi_2\pi_3}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right)s_a + \tfrac{\tau_1\pi_1}{\xi_3}s_a\right.\\
&\left. + \tfrac{\tau_2\pi_1\pi_2}{\xi_3\xi_4}s_a + \tfrac{\tau_3\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5}s_a\right) - \delta(1-k)\\
&\left(\left(\tfrac{\beta_a u_1\xi_3\xi_4\xi_5\xi_{12} + \beta_a\varphi\varepsilon\pi_1\pi_2\pi_3}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right)s_a + \tfrac{\tau_1\pi_1}{\xi_3}s_a + \tfrac{\tau_2\pi_1\pi_2}{\xi_3\xi_4}s_a\right.\\
&\left. + \tfrac{\tau_3\pi_1\pi_2\pi_3}{\xi_3\xi_4\xi_5}s_a\right),\\
a_3 &= \xi_6\xi_7\xi_8\,(1 - R_0).
\end{aligned}
$$

According to the Lienard-Chipart Criteria [32], all eigenvalues for a cubic polynomial will be negative if and only if $a_1, a_3 > 0$ and $\Delta_2 > 0$. It is clear that $a_1 > 0$ and $a_3 > 0$ if $R_0 < 1$. The value of Δ_2 can be obtained based on the Routh-Hurwitz matrix, resulting in,

$$
\begin{aligned}
\Delta_2 &= \begin{vmatrix} a_1 & a_0\\ a_3 & a_2 \end{vmatrix}\\
&= 2\xi_6\xi_7\xi_8 + \xi_7^2\xi_8 + \xi_7\xi_8^2 + \xi_6\xi_7\,(\xi_6 + \xi_7)\,[1 - R_0\\
&\quad + \tfrac{\delta(1-k)}{\xi_6\xi_8}\left(\left(\tfrac{\beta_a u_1\xi_3\xi_4\xi_5\xi_{12} + \beta_a\varphi\varepsilon\pi_1\pi_2\pi_3 + \tau_1\pi_1\xi_2\xi_4\xi_5\xi_{12} + \tau_2\pi_1\pi_2\xi_2\xi_5\xi_{12} + \tau_3\pi_1\pi_2\pi_3\xi_2\xi_{12}}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right)s_a\right)\Big]\\
&\quad + \xi_6\xi_8\,(\xi_6 + \xi_8)\,[1 - R_0\\
&\quad + \tfrac{\delta k}{\xi_6\xi_7}\left(\left(\tfrac{\beta_s u_1\xi_3\xi_4\xi_5\xi_{12} + \beta_s\varphi\varepsilon\pi_1\pi_2\pi_3 + \tau_1\pi_1\xi_2\xi_4\xi_5\xi_{12} + \tau_2\pi_1\pi_2\xi_2\xi_5\xi_{12} + \tau_3\pi_1\pi_2\pi_3\xi_2\xi_{12}}{\xi_2\xi_3\xi_4\xi_5\xi_{12}}\right)s_a\right)\Big].
\end{aligned}
$$

Therefore, obtained $\Delta_2 > 0$ if $R_0 < 1$. Considering Q, which is a sixth-degree polynomial,

$$a_0\lambda^6 + a_1\lambda^5 + a_2\lambda^4 + a_3\lambda^3 + a_4\lambda^2 + a_5\lambda + a_6 = 0 \tag{9}$$

with

$$
\begin{aligned}
a_0 &= 1,\\
a_1 &= \xi_1 + \xi_2 + \xi_3 + \xi_4 + \xi_5 + \xi_{12},\\
a_2 &= \xi_1\xi_2 + \xi_1\xi_3 + \xi_1\xi_4 + \xi_1\xi_5 + \xi_1\xi_{12} + \xi_2\xi_3 + \xi_2\xi_4\\
&\quad + \xi_2\xi_5 + \xi_2\xi_{12} + \xi_3\xi_4 + \xi_3\xi_5 + \xi_3\xi_{12} + \xi_4\xi_5\\
&\quad + \xi_4\xi_{12} + \xi_5\xi_{12} - u_1u_2,\\
a_3 &= \left(\mu^2 + \mu u_1 + \mu\pi_1 + \mu u_2 + \pi_1u_2\right)(\xi_3 + \xi_4 + \xi_5 + \xi_{12})\\
&\quad + \xi_1\xi_3\xi_4 + \xi_1\xi_3\xi_5 + \xi_1\xi_3\xi_{12} + \xi_1\xi_4\xi_5 + \xi_1\xi_4\xi_{12}\\
&\quad + \xi_1\xi_5\xi_{12} + \xi_2\xi_3\xi_4 + \xi_2\xi_3\xi_5 + \xi_2\xi_3\xi_{12} + \xi_2\xi_4\xi_5\\
&\quad + \xi_2\xi_4\xi_{12} + \xi_2\xi_5\xi_{12} + \xi_3\xi_4\xi_5 + \xi_3\xi_4\xi_{12} + \xi_3\xi_5\xi_{12}\\
&\quad + \xi_4\xi_5\xi_{12},\\
a_4 &= \xi_1\xi_2\xi_3\xi_4 + \xi_1\xi_2\xi_3\xi_5 + \xi_1\xi_2\xi_3\xi_{12} + \xi_1\xi_2\xi_4\xi_5
\end{aligned}
$$

Table 2. The list of parameters values for the simulation of COVID-19 transmission model

Parameter	Value	Unit	Reference	Parameter	Value	Unit	Reference
μ	0.01250	Per day	[33]	π_3	0.01667	Per day	[34]
β_s	0.2	Per day	[35]	τ_1	0.01111	Per day	Assumption
β_a	0.5	Per day	[35]	τ_2	0.00833	Per day	[36][37]
δ	0.87959	Per day	[27]	τ_3	0.00556	Per day	Assumption
k	0.58		[35]	ε	0.14286	Per day	[36]
θ_s	0.084	Per day	[37]	u_1	0.1	Per day	[38]
θ_a	0.084	Per day	[37]	u_2	0.1	Per day	[38]
γ_a	0.03671	Per day	[27]	σ_s	0.13266	Per day	[27]
γ_q	0.155	Per day	[37]	σ_m	0.12590	Per day	[27]
γ_h	0.11624	Per day	[27]	α	0.16906	Per day	[27]
π_1	0.04	Per day	[38]	φ	0.00185	Per day	[39]
π_2	0.03571	Per day	[40]				

$$
\begin{aligned}
&+\xi_1\xi_2\xi_4\xi_{12}+\xi_1\xi_2\xi_5\xi_{12}+\xi_1\xi_3\xi_4\xi_5+\xi_1\xi_3\xi_4\xi_{12}\\
&+\xi_1\xi_3\xi_5\xi_{12}+\xi_1\xi_4\xi_5\xi_{12}+\xi_2\xi_3\xi_4\xi_5+\xi_2\xi_3\xi_4\xi_{12}\\
&+\xi_2\xi_3\xi_5\xi_{12}+\xi_2\xi_4\xi_5\xi_{12}+\xi_3\xi_4\xi_5\xi_{12}-u_1u_2\xi_3\xi_4\\
&-u_1u_2\xi_3\xi_5-u_1u_2\xi_3\xi_{12}-u_1u_2\xi_4\xi_5-u_1u_2\xi_4\xi_{12}\\
&-u_1u_2\xi_5\xi_{12},\\
a_5=&\left(\mu^2+\mu u_1+\mu\pi_1+\mu u_2+\pi_1u_2\right)\left(\xi_3\xi_4\xi_5+\xi_3\xi_4\xi_{12}\right.\\
&\left.+\xi_3\xi_5\xi_{12}+\xi_4\xi_5\xi_{12}\right)+\xi_1\xi_3\xi_4\xi_5\xi_{12}+\xi_2\xi_3\xi_4\xi_5\xi_{12},\\
a_6=&\left(\mu^2+\mu u_1+\mu\pi_1+\mu u_2\right)(\mu+\pi_2)(\mu+\pi_3)(\mu+\varepsilon)\\
&(\mu+\varphi)+\pi_1u_2\left(\mu^4+\mu^3\varepsilon+\mu^3\varphi+\mu^3\pi_2+\mu^3\pi_3\right.\\
&+\mu^2\varepsilon\varphi+\mu^2\varepsilon\pi_2+\mu^2\varepsilon\pi_3+\mu^2\varphi\pi_2+\mu^2\varphi\pi_3\\
&\left.+\mu^2\pi_2\pi_3+\mu\varepsilon\varphi\pi_2+\mu\varepsilon\varphi\pi_3+\mu\varepsilon\pi_2\pi_3+\mu\varphi\pi_2\pi_3\right).
\end{aligned}
$$

According to the Lienard-Chipart Criteria [32], all eigenvalues for a sixth-degree polynomial will be negative if and only if $a_1, a_3, a_5, a_6 > 0$ and $\Delta_3, \Delta_5 > 0$. It is clear that $a_1, a_3, a_5, a_6 > 0$ since each parameter has a positive value. The value of Δ_3 can be obtained using the Routh-Hurwitz matrix, resulting in,

$$
\Delta_3=\begin{vmatrix} a_1 & a_0 & 0\\ a_3 & a_2 & a_1\\ a_5 & a_4 & a_3\end{vmatrix}=a_1a_2a_3+a_1a_5-a_1^2a_4-a_3^2 \tag{10}
$$

Equation (10) can be expanded into the sum of the following positive terms

$$
\begin{aligned}
\Delta_3=&\,10\pi_3^3\varphi\mu u_2+128\mu^2\varphi^2u_2\varepsilon+7u_1\pi_2^2\pi_1u_2\varepsilon\\
&+7u_1\pi_2^2\pi_1u_2\pi_3+46u_1\pi_2^2\mu\varepsilon\varphi+44u_1\pi_2^2\mu u_2\varepsilon\\
&+44u_1\pi_2^2\mu u_2\pi_3+8u_1\pi_2^2u_2\varepsilon\varphi+8u_1\pi_2^2u_2\pi_3\varphi\\
&+8u_1\pi_2^2u_2\pi_3\varepsilon+8u_1\pi_2^2\pi_1\varepsilon\varphi+8u_1\pi_2^2\pi_1\pi_3\varphi\\
&+8u_1\pi_2^2\pi_1\pi_3\varepsilon+44u_1\pi_2^2\mu\pi_1\varepsilon+4\pi_1\pi_2^2\pi_3^2u_1\\
&+46\mu u_2^2\pi_2\pi_3\varphi+2u_1\pi_1^2\varepsilon^2u_2+30\pi_1^2\mu u_1\varepsilon\varphi\\
&+\cdots+128\pi_1^2\pi_3\mu^2\varphi+128\pi_1^2\pi_3\mu^2\varepsilon+3\pi_1^2\pi_3^2u_1\varepsilon\\
&+12\pi_1^2\pi_3^2\mu u_1+2\pi_1^3\pi_3\pi_2\varepsilon+22\pi_1^2\pi_3^2\mu\varphi+22\pi_1^2\pi_3^2\mu\varepsilon\\
&+22\pi_1^2\pi_3^2\mu\pi_2+10\pi_1^3\pi_3\mu\pi_2+22\pi_1^2\pi_3^2\mu u_2+10\pi_1^3\pi_3\mu\varphi\\
&+4\pi_1^2\pi_3^2\varepsilon\varphi+3\pi_1^2\pi_3^2u_1\pi_2+4\pi_1^2\pi_3^2\pi_2\varphi+4\pi_1^2\pi_3^2\pi_2\varepsilon\\
&+4\pi_1^2\pi_3^2u_2\varphi+4\pi_1^2\pi_3^2u_2\varepsilon
\end{aligned}
$$

thus $\Delta_3 > 0$. The value of Δ_5 can be obtained using the Routh-Hurwitz matrix, resulting in,

$$
\begin{aligned}
\Delta_5=&\begin{vmatrix} a_1 & a_0 & 0 & 0 & 0\\ a_3 & a_2 & a_1 & a_0 & 0\\ a_5 & a_4 & a_3 & a_2 & a_1\\ 0 & a_6 & a_5 & a_4 & a_3\\ 0 & 0 & 0 & a_6 & a_5\end{vmatrix}\\
=&\left(a_4a_5-a_3a_6\right)\Delta_3-a_1a_2^2a_5^2-a_1^3a_6^2+2a_1^2a_2a_5a_6\\
&-a_6^3+a_2a_3a_6^2+a_1a_4a_5^2-2a_1a_3a_5a_6.
\end{aligned}
$$

Therefore, the disease-free equilibrium point E_0 is locally asymptotically stable if $R_0 < 1$ and Δ_5 in the equation Q is positive. □

3.3. Numerical Simulation

Numerical simulations aim to visualize the geometric behavior of the model solutions and support the analysis results. The simulations are performed using the 4th-order Runge-Kutta method with parameters obtained from previous research on the mathematical model of COVID-19 and relevant assumptions about COVID-19. Systematically, the parameter values can be presented in Table 2.

The simulation results with initial values of $s_a(0) = 0.095, s_u(0) = 0.08, v_p(0) = 0.07, v_f(0) = 0.05, v_b(0) = 0.03, e(0) = 0.24, i_s(0) = 0.105, i_a(0) = 0.085, h_m(0) = 0.06, h_s(0) = 0.05, q(0) = 0.065$, and $r(0) = 0.07$ yield $R_0 = 0.1217644522$ and $\Delta_5 = 9.322298383 \times 10^{-14}$ as shown in Figure 2.

Based on Figure 2, after 300 days, the model solution converges towards the disease-free equilibrium point

$$
\begin{aligned}
&(0.2021774, 0.1833206, 0.1677473, 0.2053568,\\
&\qquad 0.0220346, 0, 0, 0, 0, 0, 0, 0.2193634).
\end{aligned}
$$

Therefore, from this first simulation, it can be concluded that the disease will disappear from the population if $R_0 < 1$. This result is in line with Theorem 5.

Next, a numerical simulation of the endemic equilibrium point E_1 is performed for $R_0 > 1$. The parameter values used are the same as in the E_0 simulation, except for some parameters, the transmission rate by symptomatic infected individuals (β_s) is increased to 0.7, the transmission rate by asymptomatic infected individuals (β_a) is increased to 1, the non-compliance

Table 3. Parameter sensitivity index

Parameter	Sensitivity Index	Parameter	Sensitivity Index
k	-0.9527342987	σ_m	-0.06377320949
β_a	$+0.7883528697$	θ_s	-0.04254924221
u_1	$+0.7532901376$	φ	$+0.04145143835$
u_2	-0.6830316557	τ_1	$+0.02433377353$
π_1	-0.5511127089	τ_2	$+0.02233540471$
θ_a	-0.5171718800	δ	$+0.01401203835$
μ	$+0.3309083152$	π_3	$+0.008313074252$
γ_a	-0.2260164252	ε	$+0.002357780373$
β_s	$+0.1633783203$	τ_3	$+0.001599631703$
σ_s	-0.06719741039	π_2	$+0.0005197482695$

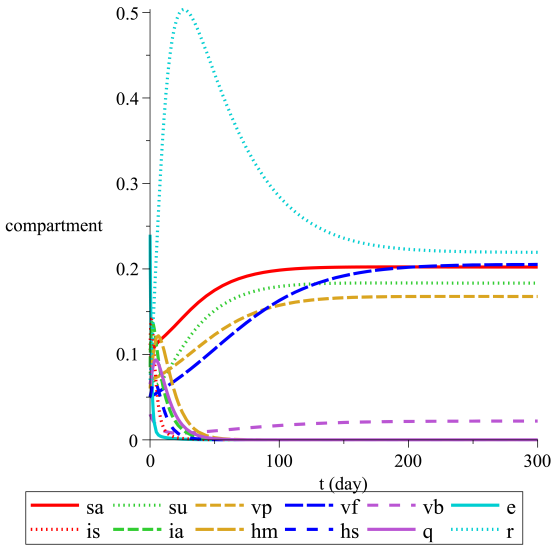

Figure 2. Simulation of system eq. (3) towards the disease-free equilibrium

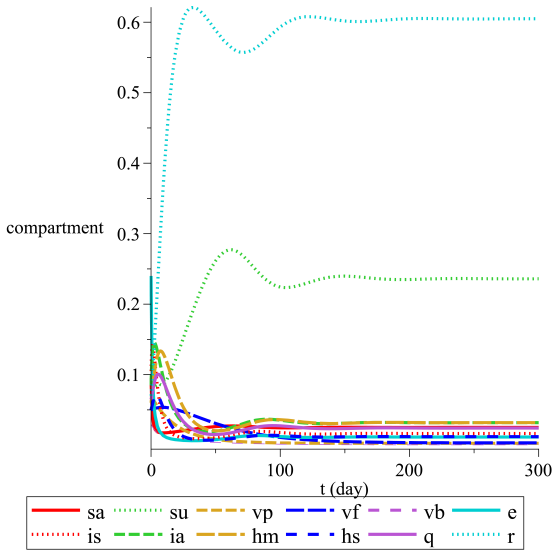

Figure 3. Simulation of system eq. (3) towards the endemic equilibrium

rate with health protocols (u_1) is increased to 0.95, the compliance rate with health protocols (u_2) is decreased to 0.05, and the vaccination rate for the first dose (π_1) is decreased to 0.005. This yields a basic reproduction number of $R_0 = 3.884347307$. The same initial values as E_0 are used in the simulation, and the results are shown in Figure 3.

Based on Figure 3, after 300 days, the solution converges to the endemic equilibrium point of the disease

$$(0.02511621137, 0.2359986899, 0.002576206498, 0.003110900074, 0.0003332211430, 0.01147003065, 0.01648052744, 0.03180953523, 0.03193011371, 0.01204178657, 0.02421710606, 0.5846590408)$$

From this second simulation, it can be observed that when the parameters related to the virus transmission are increased and those related to virus control are decreased, resulting in $R_0 > 1$, an endemic occurrence arises, and the disease persists in the population.

Next, determine the sensitivity indices with the aim of identifying parameters that significantly influence the value of R_0. Parameters with a high influence on R_0 indicate that they have the most dominant effect on the spread of COVID-19. According to [41], the sensitivity index of parameter p with respect to the value of R_0 is defined as eq. (11)

$$C_p^{R_0} = \frac{\partial R_0}{\partial p} \times \frac{p}{R_0}. \tag{11}$$

Furthermore, a numerical simulation was carried out to see the influence of several parameters that describe the spread of the COVID-19 disease using different values.

1. Effect of Vaccination
   By changing the value of parameter π_1 (dose 1 vaccination rate), the effectiveness of dose 1 vaccination can be seen as shown in the Table 4, Figure 4, and Figure 5. It show that the influence of the parameter "rate of vaccination dose 1" on the spread of COVID-19. The larger the rate of vaccination dose 1, the faster the disease disappears. This is consistent with the sensitivity index of the parameter "rate of vaccination dose 1 " which is -0.5511127089.
2. Effect of Implementing the Health Protocols
   By changing the value of parameter u_2 (awareness rate of complying with health protocols), the effectiveness of implementing health protocols can be seen as shown in Table 5, Figure 6, and Figure 7. It show that the influence of the parameter "rate of compliance with health protocols" on the spread of COVID-19. The larger the rate of compliance with health protocols, the faster the disease disappears. This is consistent with the sensitivity index of the pa-

Table 4. The effect of vaccination rates

π_1	R_0	Condition of i_s	Condition of i_a
0.00005	0.8813532337	Disappeared on day 50	Disappeared on day 70
0.005	0.7410541885	Disappeared on day 48	Disappeared on day 69
0.05	0.3183129039	Disappeared on day 40	Disappeared on day 59
0.5	0.07892297717	Disappeared on day 27	Disappeared on day 50

Table 5. The effect of implementing health protocols

u_2	R_0	Condition of i_s	Condition of i_a
0.00001	1.261933158	Be endemic and stable on day 555	Be endemic and stable on day 563
0.001	1.230241002	Be endemic and stable on day 440	Be endemic and stable on day 633
0.1	0.3614470162	Disappeared on day 44	Disappeared on day 62
1	0.06650617276	Disappeared on day 26	Disappeared on day 50

Table 6. The effect of treatment

σ_m	σ_s	R_0	Condition of i_s	Condition of i_a
0.0005	0.00005	0.5353772778	Disappeared on day 95	Disappeared on day 83
0.005	0.005	0.5131662250	Disappeared on day 85	Disappeared on day 76
0.05	0.05	0.4139023940	Disappeared on day 53	Disappeared on day 62
0,5	0.5	0.3174901915	Disappeared on day 29	Disappeared on day 57

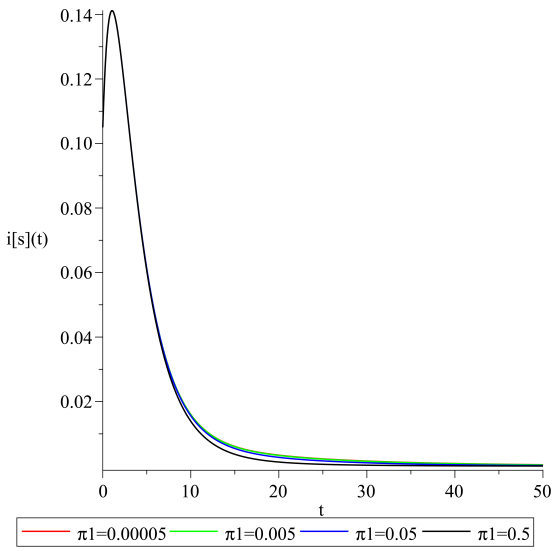

Figure 4. Simulation i_s of the effect of vaccination

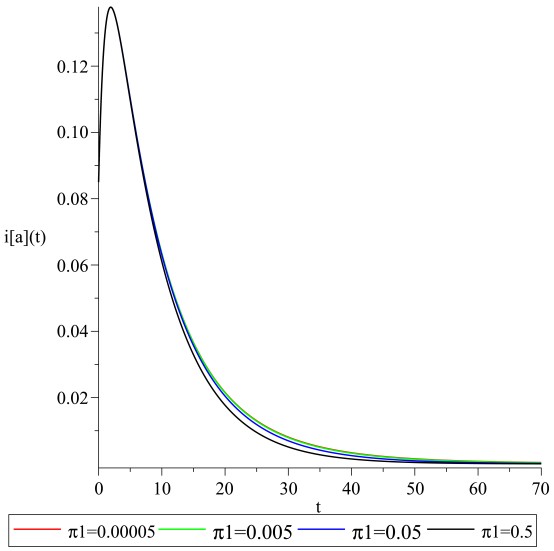

Figure 5. Simulation i_a of the effect of vaccination

rameter "rate of compliance with health protocols" which is -0.6830316557.

3. Effect of Treatment
   By simultaneously changing the values of the parameters σ_m (the rate of treatment for symptomatic infected individuals in mild hospitalization) and σ_s (the rate of treatment for symptomatic infected individuals in severe hospitalization), the effectiveness of the treatment can be determined, as shown in Table 6, Figure 8, and Figure 9. It show that the impact of treatment represented by the parameters σ_m (the rate of treatment for symptomatic infected individuals in mild hospitalization) and σ_s (the rate of treatment for symptomatic infected individuals in severe hospitalization) on the spread of COVID-19. The higher the treatment rate, the faster the disease disappears. This is consistent with the sensitivity indices of the parameters σ_m and σ_s which are -0.06377320949 and -0.06719741039, respectively.

4. Conclusion

The mathematical model for the spread of COVID-19, SVEI-HQR, incorporates the following compartments: Susceptible, Vaccination, Exposed, Infected, Hospitalized, Quarantined, and Removed. It includes the implementation of health protocols, divides the vaccination compartment into three (first dose, second dose, and booster dose), divides the infected compartment into symptomatic and asymptomatic, and introduces the treatment compartment, which consists of mild and severe hospitalization.

The mathematical model formulated has two equilibrium points: the disease-free equilibrium point $E_0\left(s_a, s_u, v_p, v_f, v_b, e, i_s, i_a, h_m, h_s, q, r\right)$ which is locally asymptotically stable when $R_0 < 1$ and $\Delta_5 > 0$, and the endemic equilibrium point $E_1\left(s_a^*, s_u^*, v_p^*, v_f^*, v_b^*, e^*, i_s^*, i_a^*, h_m^*, h_s^*, q^*, r^*\right)$ which exists when $R_0 > 1$.

Based on the stability analysis of the equilibrium points and

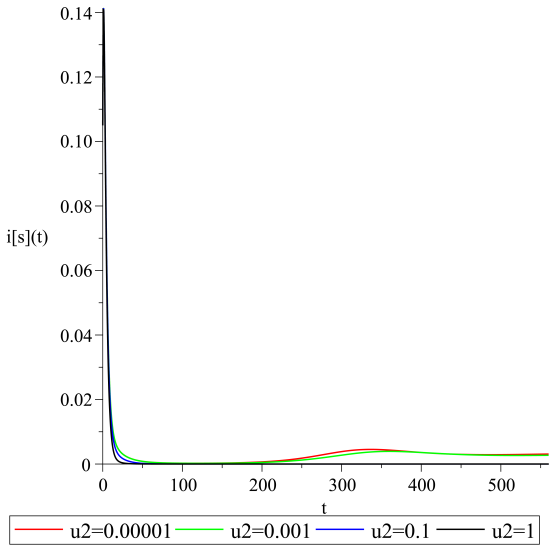

Figure 6. Simulation i_s of the effect of implementing health protocols

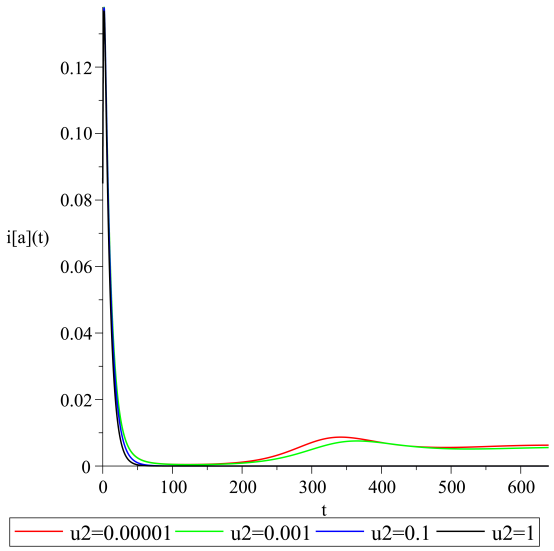

Figure 7. Simulation i_a of the effect of implementing health protocols

numerical simulations, it can be concluded that the disease will disappear from the population if $R_0 < 1$ and the endemic equilibrium point exists if $R_0 > 1$. The sensitivity analysis reveals that the proportion of symptomatic individuals has the most significant impact on R_0. Furthermore, based on numerical simulations and sensitivity analysis, the implementation of vaccination, health protocols, and treatment have a positive impact on controlling the COVID-19 outbreak, resulting in a faster disappearance of the disease.

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Data availability. Several parameter values are cited from some references. See Table 2.

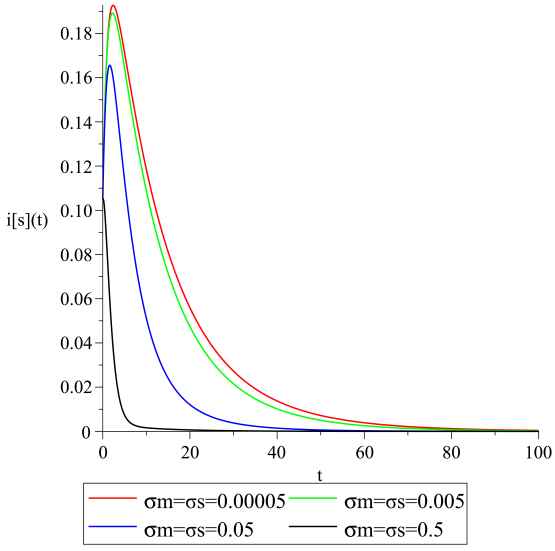

Figure 8. Simulation i_s of the effect of treatment

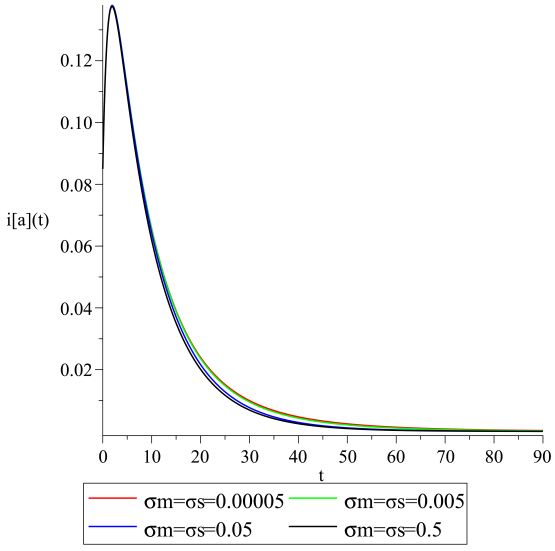

Figure 9. Simulation i_a of the effect of treatment

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