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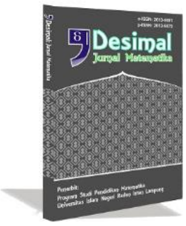

Mathematical modelling of covid-19 using health mask, vaccination, quarantine, and asymptomatic case

Muhammad Manaqib*, Madona Yunita Wijaya, Amelia Nur Yahya

UIN Syarif Hidayatullah Jakarta, Indonesia

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*Correspondence: E-mail:
muhammad.manaqib@uinjkt.ac.id

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ABSTRACT

This study develops a SEIR (Susceptible, Exposed, Infectious, and Recovered) model to model the spread of COVID-19 by adding the use of health masks, vaccinations, quarantines, and asymptomatic compartments. The model is analyzed using equilibrium point stability analysis and numerical simulation. Based on the system, two equilibrium points are obtained, namely the disease-free equilibrium point and the endemic equilibrium point, and the basic reproduction number (R_0). The stability analysis of the disease-free equilibrium point will be locally asymptotically stable if $R_0 < 1$. The numerical simulation results show that the disease will disappear from the population if $R_0 < 1$ and remain in the population if $R_0 > 1$. Based on the sensitivity analysis, parameters with significant impact are the level of awareness of individuals in using health masks, vaccination rates, contact rates with symptomatic or asymptomatic infected individuals, and quarantine rates for symptomatic infected individuals.

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INTRODUCTION

COVID-19 first appeared in Wuhan, China, in December 2019. Based on the information from WHO (World Health Organization) on June 12, 2022, the disease has become epidemic, with more than 533 million cases and more than 6.3 million deaths having been reported globally (World Health Organization, 2022). COVID-19 is a disease caused by the SARS-CoV-2 virus. The virus circulates in several animals, including cattle, camels, and bats. This virus that attacks the respiratory system has symptoms that appear 2-14 days after exposure, including fever, cough, shortness of breath, chills, muscle aches, and loss of taste or smell (Ali, Shah, Imran, & Khan, 2020). In addition to infected individuals who have symptoms (symptomatic), there are also infected individuals without symptoms (asymptomatic) who can also transmit the disease. However, the transmission rate from asymptomatic infected individuals is lower than from infected individuals with symptoms (Sayampanathan et al., 2021). Individuals aged 65 years and over and individuals with medical conditions such as having chronic lung disease, diabetes, chronic kidney disease, heart problems, and impaired immune systems are at a higher risk of serious illness (Yang et al., 2020).

The first case of COVID-19 in Indonesia was discovered on March 2, 2020, in the Depok area, West Java. After that the number of positive cases of COVID-19 in Indonesia continued to increase rapidly (Tosepu et al., 2020). Until June 26, 2022, more than two years after the discovery of the first case in Indonesia, it was recorded that this virus has infected 6,080,451 individuals, and 156,717 individuals died (Satuan Tugas Penanganan COVID-19, 2022). Transmission of COVID-19 through droplets containing the virus or airflow (aerosol) is the main route that causes the virus to spread and has a high transmission power (Atmojo, Akbar, Kuntari, Yulianti, & Darmayanti, 2020). The use of masks is one of the preventive measures that can limit the spread of respiratory diseases caused by viruses, including COVID-19. However, using a health mask alone is insufficient to provide an adequate level of protection; it must also be followed by other measures such as vaccination. Vaccines are given to healthy people to prevent certain diseases from infecting that person.

The COVID-19 vaccine is a form of prevention that functions to encourage the formation of specific immunity against COVID-19 to avoid contracting or possibly becoming seriously ill (Satuan Tugas Penanganan COVID-19, 2020). The Emergency Use Listing (EUL) includes several types of vaccines from WHO, namely Pfizer/BioNTech, AstraZeneca, Janssen, Moderna, Sinopharm, and Sinovac (World Health Organization, 2021). The government began implementing the COVID-19 vaccination program in Indonesia on January 13, 2021, at the State Palace (Ditjen P2P Kementrian Kesehatan, 2021). Until now, the government is still pursuing the target of 208 million Indonesians to get vaccinated. As of June 26, 2022, the number of vaccinations for the first dose has reached 201,366,276 people, and the second dose has reached 168,823,775 people from the vaccination target of 208,265,720 people (Satuan Tugas Penanganan COVID-19, 2022).

Since the onset of the COVID-19 pandemic, several researchers have developed mathematical models to analyze the behavior of the disease's spread. The efforts began with the simple SIR model (Susceptible, Infected, and Recovered), as studied by Imran et al. (2021), Ivanova & Dospatliev (2021), Liao, Lan, Liao, Zhang, & Liu (2020), Mitra (2020), and De León (2009). Subsequently, the models evolved by incorporating additional variables, including the work of Ali et al. (2020), who developed a mathematical model of the SEIR model by including compartments that were considered important in COVID-19 transmission, such as asymptomatic infected compartments, quarantine, and isolation. Another study by Ghostine, Gharamti, Hassrouny, & Hoteit (2021) developed the SEIR model by adding a vaccination compartment, which consisted of seven compartments, namely susceptible individuals (S), exposed but not infected individuals (E), infected individuals (I), quarantined individuals (Q), recovered individuals (R), death individuals (D), and vaccinated individuals (V). Furthermore, the study by Foy et al. (2021) developed the SEIR model by adding vaccination compartments (V), quarantine (Q), and death from disease (D). This study also assumed that recovered individuals could return to being susceptible individuals. Finally, a research study by Manaqib, Fauziah, & Mujiyanti (2019) discussed MERS-CoV disease, similar to COVID-19, which developed a SEIR model with the use of health masks and vaccinations.

This study combines studies of Ghostine et al. (2021), Foy et al. (2021), and Manaqib et al. (2019) with the assumption that there is no reinfection and death from the disease. So, we get a mathematical model for the spread of COVID-19 disease: the SEIR model, which adds the use of health masks, vaccinations, and quarantines. Based on this model, disease-free and endemic equilibrium points are sought for stability analysis and basic reproduction numbers. The stability analysis of equilibrium points is conducted to understand the behavior and properties of the system. Furthermore, numerical simulations are performed to visualize the model solutions, and sensitivity analysis of the basic reproduction number is carried out to identify the most influential parameters in the spread of COVID-19..

METHOD

The mathematical model in this study divides the individual population into ten subpopulations, i.e., susceptible individuals who are susceptible to disease and who do not use health masks (S), susceptible individuals who use health masks (S_M), vaccinated individuals who have been vaccinated COVID-19 in two stages (V), exposed individuals who are exposed to the virus but cannot transmit the disease (E), infected individuals who are infected and can transmit disease without using a health mask (I), infected individuals who use a health mask (I_M), asymptomatic or infected individuals without symptoms who do not use health masks (A), infected individuals without symptoms who use health masks (A_M), individuals who are quarantined/quarantine (Q), and individuals who have recovered, have immune from disease or died from disease/Removed (R).

The assumptions used in this study are as follows: (1) the population is assumed to be closed because the birth and death rates are the same and there is no migration; (2) the population is assumed to be homogeneous, meaning that each individual has the same opportunity to make contact with other individuals; (3) every individual born is susceptible to contracting the disease; (4) susceptible individuals who use a health mask (S_M) will return to the compartment of susceptible individuals who do not use a health mask (S) if they stop using a health mask, the same process also occurs in the compartment of symptomatic and asymptomatic infected individuals; (5) vaccination is carried out in two stages with the aim of reducing the risk of susceptible individuals being infected so that individuals who have been vaccinated can still be infected; (6) According to the efficacy of the COVID-19 vaccine, some individuals who have been fully vaccinated have immunity to the disease; (7) susceptible individuals can be infected when interacting with symptomatic or asymptomatic infected individuals; (8) infected individuals are divided into symptomatic infected, both mild and severe, and infected individuals without symptoms; (9) asymptomatic infected individuals can recover naturally and have immunity to disease; (10) infected individuals who have symptoms will be quarantined; (11) individuals who are quarantined can recover and have immunity to disease or die from disease. The parameters used in the model of the spread of COVID-19 are presented in Table 1.

Table 1. List of Parameters of the Mathematical Model of Spread of COVID-19 with the Use of Health Masks, Vaccinations, Quarantine, and Asymptomatic Cases

Parameter	Definition	Unit
μ	Natural birth and death rates of individual populations	$\frac{1}{day}$
ρ	Vaccination rate of susceptible individual	$\frac{1}{day}$
ω	Vaccine inefficacy	$\frac{1}{day}$
β_A	Transmission rate in susceptible individual from asymptomatic infection	$\frac{1}{day}$
β_I	Transmission rate in susceptible individual from symptomatic infection	$\frac{1}{day}$
σ	Transmission rate from subpopulation E to I or A	$\frac{1}{day}$
p	Asymptomatic proportion	
α_1	Individual awareness rate in using health masks	$\frac{1}{day}$
α_2	Individual unawareness rate in using health masks	$\frac{1}{day}$
τ	Quarantine rate of infected with symptoms individual	$\frac{1}{day}$
θ	Removal rate for asymptomatic individual	$\frac{1}{day}$
γ	Removal rate for quarantined individual	$\frac{1}{day}$
ε	Removal rate for vaccinated individual	$\frac{1}{day}$

Based on the assumptions and the definition of variables and parameters, the transfer diagram for the spread of COVID-19 can be described as shown in Figure 1.

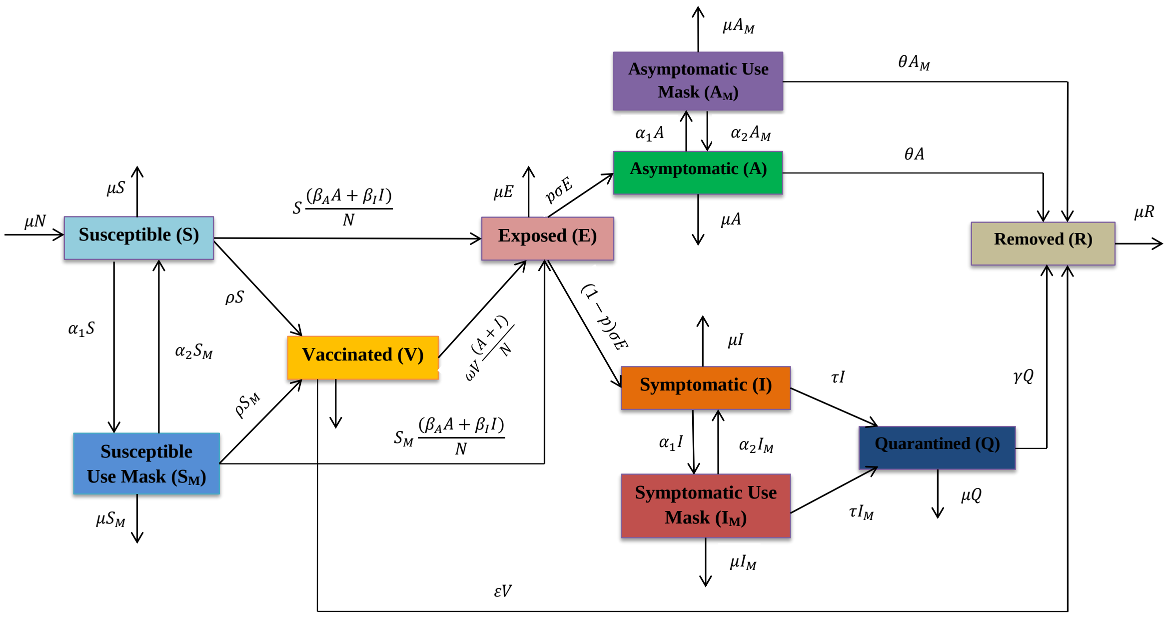


Figure 1. Transfer Diagram of a Mathematical Model for the Spread of COVID-19 with the Use of Health Masks, Vaccinations, Quarantine, and Asymptomatic Cases

Based on Figure 1, the spread of COVID-19 with the use of health masks, vaccinations, quarantines, and asymptomatic cases can be modeled into a system of nonlinear ordinary differential equations as follows:

$$\frac{dS}{dt} = \mu N + \alpha_2 S_M - (\mu + \alpha_1 + \rho)S - \frac{(\beta_A A + \beta_I I)}{N} S$$

$$\frac{dS_M}{dt} = \alpha_1 S - (\mu + \alpha_2 + \rho)S_M - \frac{(\beta_A A + \beta_I I)}{N} S_M$$

$$\frac{dV}{dt} = (S + S_M)\rho - \left(\mu + \varepsilon + \frac{\omega(A+I)}{N}\right) V$$

$$\frac{dE}{dt} = (S + S_M)\frac{(\beta_A A+\beta_I I)}{N} + \omega V \frac{(A+I)}{N} - \big(\mu + \big(p + (1-p)\big)\sigma\big)E$$

$$\frac{dI}{dt} = (1-p)\sigma E + \alpha_2 I_M - (\mu + \alpha_1 + \tau)I \qquad (1)$$

$$\frac{dI_M}{dt} = \alpha_1 I - (\mu + \alpha_2 + \tau)I_M$$

$$\frac{dA}{dt} = p\sigma E + \alpha_2 A_M - (\mu + \alpha_1 + \theta)A$$

$$\frac{dA_M}{dt} = \alpha_1 A - (\mu + \alpha_2 + \theta)A_M$$

$$\frac{dQ}{dt} = (I + I_M)\tau - (\mu + \gamma)Q$$

$$\frac{dR}{dt} = \big((A + A_M)\theta + \varepsilon V + \gamma Q\big) - \mu R$$

Suppose $N(t) = S(t) + S_M(t) + V(t) + E(t) + I(t) + I_M(t) + A(t) + A_M(t) + Q(t) + R(t)$. Thus, we obtained $\frac{dN(t)}{dt} = 0$. By solving the equation, we have that $N(t) = c$, where c is a positive integer. Thus, it can be defined that the domain of Equation (1) is

$$\Omega = \{(S, S_M, V, E, I, I_M, A, A_M, Q, R) \in \mathbb{R}_+^{10} \cup \bar{0} \mid S + S_M + V + E + I + I_M + A + A_M + Q + R = c\}$$

Since $N(t)$ is constant, the system (1) can be formed into a non-dimensional model, by assuming that

$$s = \frac{S}{N}, s_m = \frac{S_M}{N}, v = \frac{V}{N}, e = \frac{E}{N}, i = \frac{I}{N}, i_m = \frac{I_M}{N}, a = \frac{A}{N}, a_m = \frac{A_M}{N}, q = \frac{Q}{N}, r = \frac{R}{N}. \qquad (2)$$

Since the variable r does not affect the other compartments, it can be temporarily ignored by the system. So that Equation (1) can be formed into a non-dimensional of the following nine variables.

$$\frac{ds}{dt} = \mu + \alpha_2 s_m - (\mu + \alpha_1 + \rho)s - (\beta_a a + \beta_i i)$$

$$\frac{ds_m}{dt} = \alpha_1 s - (\mu + \alpha_2 + \rho)s_m - (\beta_a a + \beta_i i)s_m$$

$$\frac{dv}{dt} = (s + s_m)\rho - (\mu + \varepsilon + \omega(a + i))v$$

$$\frac{de}{dt} = (s + s_m)(\beta_a a + \beta_i i) + \omega v(a + i) - \big(\mu + \big(p + (1-p)\big)\sigma\big)e$$

$$\frac{di}{dt} = (1-p)\sigma e + \alpha_2 i_m - (\mu + \alpha_1 + \tau)i \qquad (3)$$

$$\frac{di_m}{dt} = \alpha_1 i - (\mu + \alpha_2 + \tau)i_m$$

$$\frac{da}{dt} = p\sigma e + \alpha_2 a_m - (\mu + \alpha_1 + \theta)a$$

$$\frac{da_m}{dt} = \alpha_1 a - (\mu + \alpha_2 + \theta)a_m$$

$$\frac{dq}{dt} = (i + i_m)\tau - (\mu + \gamma)q$$

RESULTS AND DISCUSSION

Equilibrium Point and Basic Reproductive Numbers

Analysis of the model is carried out by analyzing the stability of the equilibrium point of the model. The equilibrium point is obtained by making the right-hand side of the equation in Equation (3) equal to zero and solving it. The disease-free equilibrium point is the equilibrium point at which there is no disease in the population, so $i = i_m = a = a_m = 0$. The disease-free equilibrium point is obtained.

$$E_0(s, s_m, v, e, i, i_m, a, a_m, q) = \left(\frac{\mu(\mu + \alpha_2 + \rho)}{(\mu + \rho)(\mu + \alpha_1 + \alpha_2 + \rho)}, \frac{\alpha_1 \mu}{(\mu + \rho)(\mu + \alpha_1 + \alpha_2 + \rho)}, \frac{\mu\rho}{(\mu + \varepsilon)(\mu + \rho)}, 0,0,0,0,0,0 \right)$$

For simplify, we now assume:

$$B = (\mu + \sigma), C = (\mu + \alpha_1 + \tau), D = (\mu + \alpha_2 + \tau), F = (\mu + \alpha_1 + \theta),$$

$$G = (\mu + \alpha_2 + \theta), H = (\mu + \gamma), K = (\mu + \varepsilon), L = (\mu + \rho), N = (\mu + \alpha_1 + \alpha_2 + \tau),$$

$$O = (\mu + \tau), Q(\mu + \alpha_1 + \alpha_2 + \theta), T = (\mu + \theta),$$

$$X = \frac{pG}{QT} + \frac{(1-p)D}{NO}, U = (\mu + \alpha_1 + \alpha_2 + \rho)$$

Next, the basic reproduction number is determined by using the next generation matrix. The determination of the basic reproduction number of Equation (3) is computed in the following way.

1. Linearize the infected subsystem at the disease-free equilibrium point

$$J_{(E)} = \begin{bmatrix} -(\mu+\sigma) & \frac{\mu\beta_i(\mu+\varepsilon)+\omega\mu\rho}{(\mu+\varepsilon)(\mu+\rho)} & 0 & \frac{\mu\beta_a(\mu+\varepsilon)+\omega\mu\rho}{(\mu+\varepsilon)(\mu+\rho)} & 0 & 0 \\ (1-p)\sigma & -(\mu+\alpha_1+\tau) & \alpha_2 & 0 & 0 & 0 \\ 0 & \alpha_1 & -(\mu+\alpha_2+\tau) & 0 & 0 & 0 \\ p\sigma & 0 & 0 & -(\mu+\alpha_1+\theta) & \alpha_2 & 0 \\ 0 & 0 & 0 & \alpha_1 & -(\mu+\alpha_2+\theta) & 0 \\ 0 & \tau & \tau & 0 & 0 & -(\mu+\gamma) \end{bmatrix}$$

2. Decompose Jacobian matrix ($\boldsymbol{J}$) into $\boldsymbol{J} = \boldsymbol{F} - \boldsymbol{V}$, with $\boldsymbol{F}$ is a transmission matrix and $\boldsymbol{V}$ is a transition matrix

$$\boldsymbol{F} = \begin{bmatrix} 0 & \frac{\mu\beta_i(\mu+\varepsilon)+\omega\mu\rho}{(\mu+\varepsilon)(\mu+\rho)} & 0 & \frac{\mu\beta_a(\mu+\varepsilon)+\omega\mu\rho}{(\mu+\varepsilon)(\mu+\rho)} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix},$$

$$\boldsymbol{V} = \begin{bmatrix} B & 0 & 0 & 0 & 0 & 0 \\ -(1-p)\sigma & C & -\alpha_2 & 0 & 0 & 0 \\ 0 & -\alpha_1 & D & 0 & 0 & 0 \\ -p\sigma & 0 & 0 & F & -\alpha_2 & 0 \\ 0 & 0 & 0 & -\alpha_1 & G & 0 \\ 0 & -\tau & -\tau & 0 & 0 & H \end{bmatrix}$$

3. Calculate R_0 with $R_0 = \rho(\boldsymbol{F}\boldsymbol{V}^{-\mathbf{1}})$

$$R_0 = \left(\frac{\mu\beta_i K + \omega\mu\rho}{KL}\right)\left(\frac{(1-p)\sigma D}{BNO}\right) + \left(\frac{\mu\beta_a K + \omega\mu\rho}{KL}\right)\left(\frac{p\sigma G}{BQT}\right) \qquad (4)$$

Next, we calculate the endemic equilibrium point, which is the equilibrium point when the infection is not zero or when the disease is spreading in the population. Endemic means that in a population there are always diseased individuals. The endemic equilibrium point is obtained $E_1 = (s^*, {s_m}^*, v^*, e^*, i^*, {i_m}^*, a^*, {a_m}^*, q^*)$ with

$$s^* = \frac{\mu(\mu+\alpha_2+\rho+\beta_a a^*+\beta_i i^*)}{(\mu+\alpha_1+\alpha_2+\rho+\beta_a a^*+\beta_i i^*)(\mu+\rho+\beta_a a^*+\beta_i i^*)}$$

$${s_m}^* = \frac{\mu\alpha_1}{(\mu+\alpha_1+\alpha_2+\rho+\beta_a a^*+\beta_i i^*)(\mu+\rho+\beta_a a^*+\beta_i i^*)}$$

$$v^* = \frac{\mu\rho}{(\mu+\rho+\beta_a a^*+\beta_i i^*)(K+\omega\sigma X e^*)}, i^* = \frac{(\mu+\alpha_2+\tau)(1-p)\sigma e^*}{(\mu+\alpha_1+\alpha_2+\tau)(\mu+\tau)}, \ {i_m}^* = \frac{\alpha_1(1-p)\sigma e^*}{(\mu+\alpha_1+\alpha_2+\tau)(\mu+\tau)}$$

$$a^* = \frac{(\mu+\alpha_2+\theta)p\sigma e^*}{(\mu+\alpha_1+\alpha_2+\theta)(\mu+\theta)}, \quad {a_m}^* = \frac{\alpha_1 p\sigma e^*}{(\mu+\alpha_1+\alpha_2+\theta)(\mu+\theta)}, q^* = \frac{(i^*+{i_m}^*)\tau}{(\mu+\gamma)}$$

where e^* is a solution of

$$f(e^*) = a_0 e^{*2} + a_1 e^* + a_2 = 0 \qquad (5)$$

with

$$a_0 = (\beta_a p\sigma BGNO + \beta_i(1-p)\sigma BDQT)(\omega\sigma X)$$

$$a_1 = (\beta_a p\sigma BGNO + \beta_i(1-p)\sigma BDQT)K + \left(\frac{\rho\mu\omega\sigma X}{K} + BL(1-R_0)\right)(NOQT\omega\sigma X)$$

$$a_2 = BKLNOQT(1-R_0)$$

Theorem 2. If $R_0 > 1$ then the endemic equilibrium point $E_1 = (s^*, {s_m}^*, v^*, e^*, i^*, {i_m}^*, a^*, {a_m}^*, q^*)$ exists.

Proof. The existence of an equilibrium point is seen from each positive element, according to the conditions for the formation of the model. It is clear that every element E_1 is positive if $e^* > 0$. According to the Descartes Rules of Sign, a polynomial has one positive root if there is a change in one sign of its coefficient (Levin, 2002). Considering the polynomial coefficient in Equation (5), it is clear that $a_0 > 0, a_1 < 0$ and $a_2 < 0$ if $R_0 > 1$. Hence, we obtained $e^* > 0$ if $R_0 > 1$.

■

Stability of the Equilibrium Point

Theorem 3. The disease-free equilibrium point of Equation (4) will be locally asymptotically stable if $R_0 < 1$ and $\Delta_4 > 0$.

Proof. Analysis of the stability of the equilibrium point can be determined by finding the eigenvalues of the Jacobian matrix obtained through the linearization method of the system around the equilibrium points of Equation (3). The eigenvalue matrix $J_{(E_0)}$ is obtained by solving $\det\left(\lambda I - J_{(E_0)}\right) = 0$. So that the characteristic equation is obtained as follows:

$$(\lambda + K)(\lambda + H)(\lambda + L)(\lambda + U)P = 0 \quad (7)$$

with $P = a_0\lambda^5 + a_1\lambda^4 + a_2\lambda^3 + a_3\lambda^2 + a_4\lambda + a_5$

$$a_0 = 1, a_1 = B + N + O + Q + T, a_2 = BN + BQ + NQ + BT + NT + BO + OQ + OT + NO + QT - (1-p)\sigma\left(\frac{\beta_i\mu}{L} + \frac{\omega\mu\rho}{KL}\right) - p\sigma\left(\frac{\beta_a\mu}{L} + \frac{\omega\mu\rho}{KL}\right)$$

$$\begin{aligned} a_3 = \frac{1}{Y_1(1-p)DQT + Z_1pGNO}\Big(Y_1(1 &- p)[BN\alpha_2Q^2T + BN\alpha_2QT^2 \\ &+ BD(QT)^2 + ND(QT)^2 \\ &+ BODQ^2T + BODQT^2 \\ &+ OD(QT)^2] \\ &+ Z_1p[BQ\alpha_2N^2O + BTGN^2O \\ &+ BQ\alpha_2NO^2 + BTGNO^2 \\ &+ BG(NO)^2 + QG(NO)^2 \\ &+ TG(NO)^2] \\ &+ NOQT\big[Y_1(1-p)D(Q+T) \\ &+ Z_1pG(N+O) \\ &+ [B(Y_1(1-p)(D+Q+T) \\ &+ Z_1p(G+N+O))(1-R_0)]\big]\Big) \end{aligned}$$

$$\begin{aligned} a_4 = BNQT + BOQT + BNOQ + BNOT &\\ &+ NOQT \\ &- (1-p)\sigma\left(\frac{\beta_i\mu}{L} + \frac{\omega\mu\rho}{KL}\right)(DQ \\ &+ DT + QT) \\ &- p\sigma\left(\frac{\beta_a\mu}{L} + \frac{\omega\mu\rho}{KL}\right)(GN + GO \\ &+ NO) \end{aligned}$$

$$a_5 = BNOQT(1 - R_0)$$

Based on the characteristic in Equation (7), we obtained $\lambda_1 = -K, \lambda_2 = -H, \lambda_3 = -L, \lambda_4 = -U$. Since the values of $U, L, H,$ and K are positive, the sign of the real part of the four eigenvalues is negative. According to the Lienard-Chipart criteria (Daud, 2021), all eigenvalues for a fifth-degree polynomial will be negative if and only if $a_1, a_3, a_5 > 0$ and $\Delta_2, \Delta_4 > 0$. It is clear that $a_1 > 0$ and $a_3, a_5 > 0$ if $R_0 < 1$. Based on the Routh-Hurwitz matrix, the value of Δ_2 is

$$\Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} = a_1a_2 - a_3$$

$$\begin{aligned} = \frac{1}{Y_1(1-p)DQT + Z_1pGNO}\Big((B + N &\\ &+ O)Y_1(1-p)[BN\alpha_2QT \\ &+ BQ^2DT + NQ^2DT \\ &+ BT^2DQ \\ &+ NT^2DQ + BODQT \\ &+ OQ^2DT + OT^2DQ] \\ &+ (Q+T)Y_1(1-p)[BQ^2DT \\ &+ NQ^2DT + BT^2DQ \\ &+ NT^2DQ + OQ^2DT \\ &+ OT^2DQ + D(QT)^2] \\ &+ (B+Q+T)Z_1p[BGN^2O \\ &+ BQ\alpha_2NO + QGN^2O \\ &+ BTGNO + TGN^2O \\ &+ BGNO^2 + GNO^2Q \\ &+ GNO^2T] \\ &+ (N+O)Z_1p[BGN^2O \\ &+ QGN^2O + TGN^2O \\ &+ BGNO^2 + GNO^2Q \\ &+ GNO^2T + G(NO)^2] \\ &+ (N+O)NOQTY_1(1-p)D \\ &+ (Q+T)NOQTZ_1pG \\ &+ (N \\ &+ O)\big(BNOQTY_1(1-p)(1 \\ &- R_0)\big) \\ &+ (Q \\ &+ T)\big(BNOQTZ_1p(1-R_0)\big) \\ &+ BNOQT[B(Y_1(1-p) \\ &+ Z_1p)(1-R_0)] \\ &+ BNOQT(Y_1(1-p)D \\ &+ Z_1pG)R_0\Big) \end{aligned}$$

then $\Delta_2 > 0$ if $R_0 < 1$.

Based on the Routh-Hurwitz matrix, the value of Δ_4 is

$$\begin{aligned} \Delta_4 = \begin{vmatrix} a_1 & a_0 & 0 & 0 \\ a_3 & a_2 & a_1 & a_0 \\ a_5 & a_4 & a_3 & a_2 \\ 0 & 0 & a_5 & a_4 \end{vmatrix} &= (a_3a_4 - a_2a_5)\Delta_2 \\ &+ (a_5 - a_1a_4)(a_1a_4 - a_5) \end{aligned}$$

Thus, the disease-free equilibrium point E_0 is locally asymptotically stable if $R_0 < 1$ and $\Delta_4 > 0$.

■

Numerical Simulation

Simulation is carried out to see the stability of the disease-free equilibrium point and the endemic equilibrium point. Numerical simulation of the mathematical model of the spread of COVID-19 with the use of health masks, vaccinations, and quarantines by taking parameter values from several studies as shown in Table 2.

Table 2. Parameter Value of Disease-Free Equilibrium Point

Parameter	Value	Unit	Reference
μ	0.0125	$\frac{1}{day}$	(Badan Pusat Statistik, 2020)
β_i	0.2	$\frac{1}{day}$	(Aldila, Khoshnaw, et al., 2020)
β_a	0.5	$\frac{1}{day}$	(Aldila, Khoshnaw, et al., 2020)
ρ	0.0074	$\frac{1}{day}$	(Nuha, Achmad, & Supu, 2021)
ω	0.0083	$\frac{1}{day}$	(Kertes et al., 2022)
σ	0.1960784314	$\frac{1}{day}$	(Aldila, Ndii, & Samiadji, 2020)
ε	0.0714285714	$\frac{1}{day}$	(Pani et al., 2021)
p	0.42		(Aldila, Khoshnaw, et al., 2020)
τ	0.084	$\frac{1}{day}$	(Manaqib, Fauziah, & Hartati, 2021)
α_1	0.6	$\frac{1}{day}$	(Manaqib et al., 2021)
α_2	0.4	$\frac{1}{day}$	(Manaqib et al., 2021)
θ	0,1428571429	$\frac{1}{day}$	(Iboi, Ngonghala, & Gumel, 2020)
γ	0,0714285714	$\frac{1}{day}$	(Angeli, Neofotistos, Mattheakis, & Kaxiras, 2022)

The simulation study is carried out using the Maple 2020 program by using the parameters in Table 2 and the initial values $s(0) = 0.3$, $s_m(0) = 0.2$, $v(0) = 0.06$, $e(0) = 0.17$, $i(0) = 0.08$, $i_m(0) = 0.07$, $a(0) = 0.06$, $a_m(0) = 0.04$, $q(0) = 0.01$, and $r(0) = 0.01$. From these, we obtain that $R_0 = 0.7068273190$. The simulation results are presented in Figure 2.

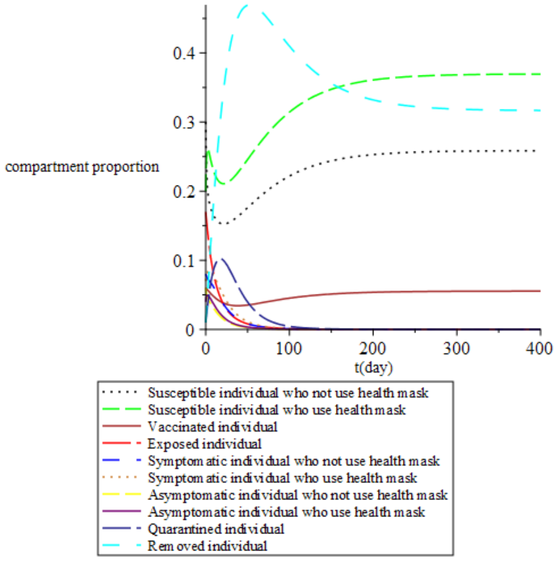


Figure 2. System Simulation (4) Towards Disease-Free Equilibrium Point

Based on Figure 2 on the 400th day, each compartment will be stable towards a disease-free equilibrium point (0.2586099435, 0.3695307600, 0.05538329947, 0, 0, 0, 0, 0, 0, 0.3164759971). The conclusion from the first simulation is that the disease will disappear from the population after 400 days if $R_0 < 1$.

Next, a numerical simulation of the endemic equilibrium points for $R_0 > 1$. The parameter values used are the same as the simulation of E_0, except that the parameter of transmission rate in susceptible individuals from symptomatic infection (β_i) is increased to 0.4, the individual unawareness rate in using health masks (α_2) is increased to 0.85, and the parameter value of the individual unawareness rate in using health masks (α_1) is reduced to 0.15 so that the basic reproduction number is obtained $R_0 =$

1.923265537 and the initial value is equal to E_0. The simulation results are shown in Figure 3.

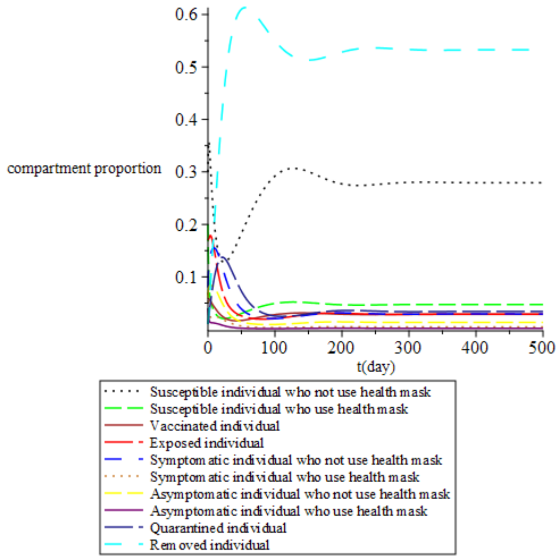


Figure 3. System Simulation (4) Towards the Endemic Equilibrium Point

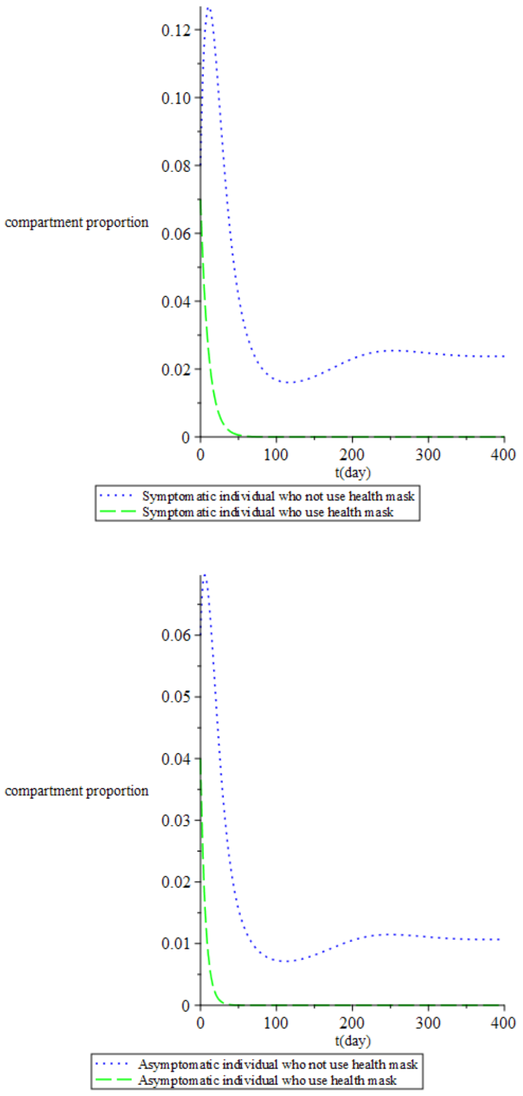
Based on Figure 3 on the 400th day, each compartment will be stable towards the endemic equilibrium point (0.2794188389, 0.04718463754, 0.02867538272, 0.02881780516, 0.02931591051, 0.004645944613, 0.01329269082, 0.001983278914, 0.03399075882, 0.5326747522). The conclusion obtained from this second simulation is that the disease will persist in the population if $R_0 > 1$.

Next, a numerical simulation will be carried out to see the level of effectiveness of the use of health masks by changing the parameter values for the individual awareness rate in using health masks (α_1) and the individual unawareness rate in using health masks (α_2) which are presented in Table 4.

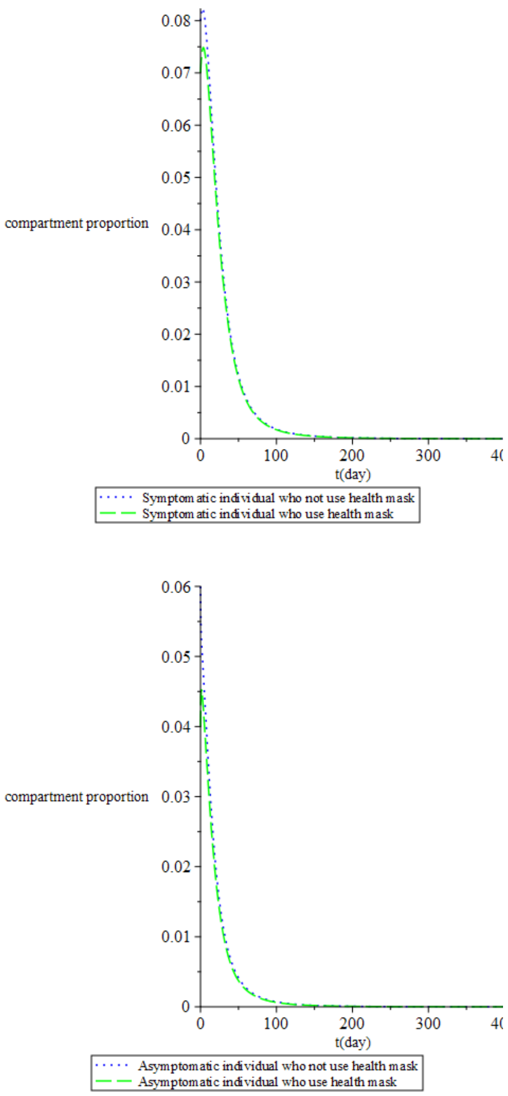
Table 4. Comparison of the Effectiveness of the Use of Health Masks

α_1	α_2	R_0
0	0	1.511788771
1	1	0.8010993784
1	0	0.1701863507
0.15	0.85	1.310548408
0.9	0.1	0.3043465927

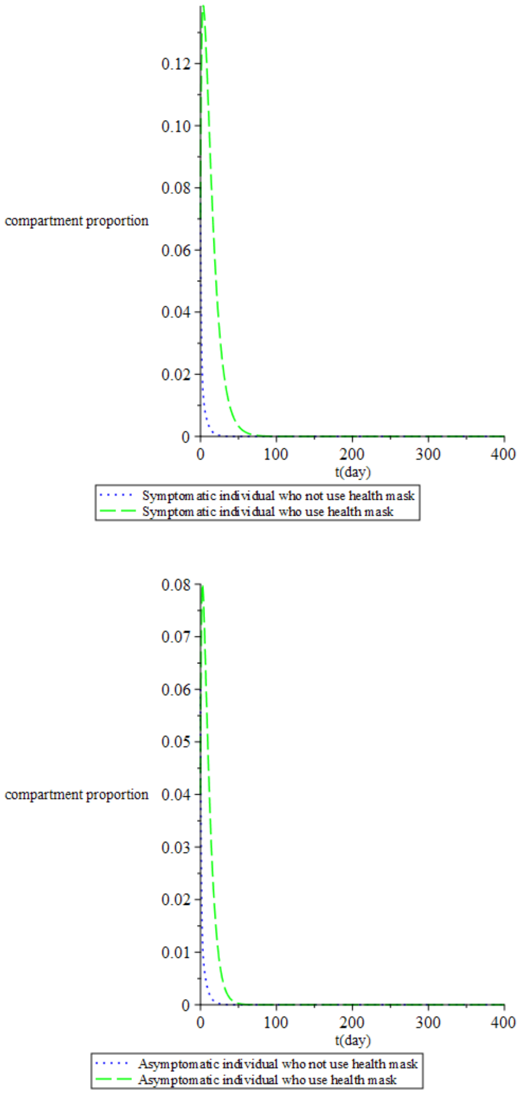
The graphical form is presented in Figure 4.



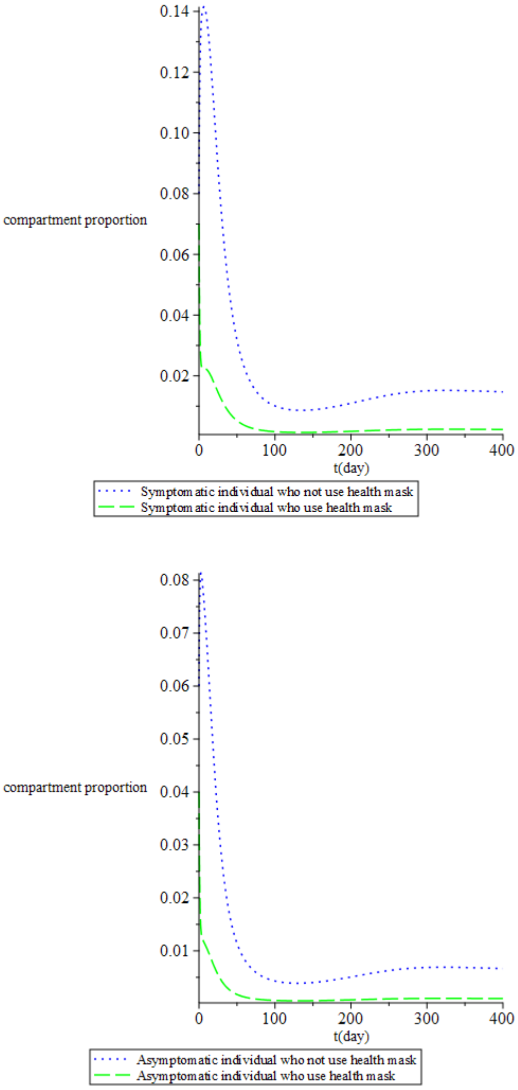
(a) Simulation of point i and i_m and a and a_m when $\alpha_1 = 0$ and $\alpha_2 = 0$



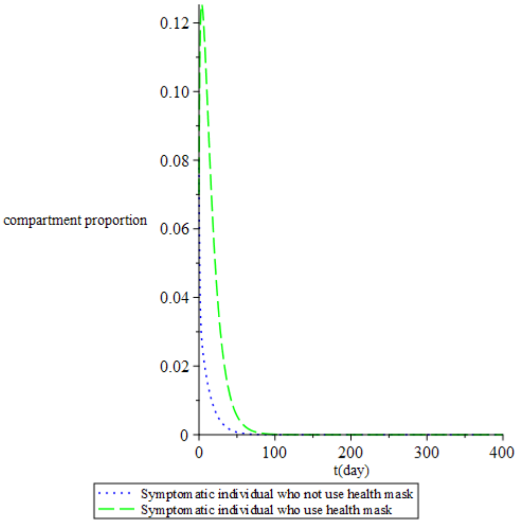
(b) Simulation of point i and i_m and a and a_m when $\alpha_1 = 1$ dan $\alpha_2 = 1$

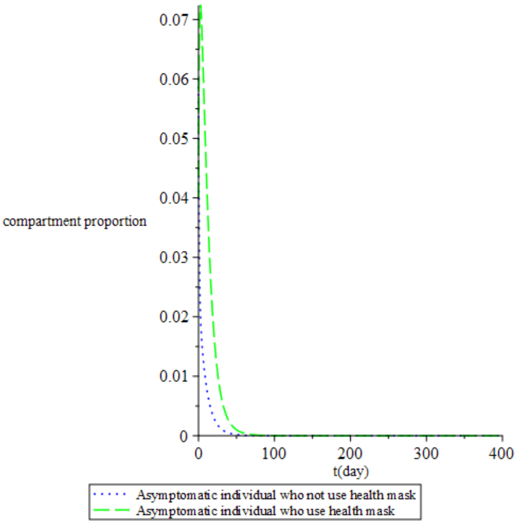


(c) Simulation of point i and i_m and a and a_m when $\alpha_1 = 1$ and $\alpha_2 = 0$



(d) Simulation of point i and i_m and a and a_m when $\alpha_1 = 0.15$ and $\alpha_2 = 0.85$





(e) Simulation of point i and i_m and a and a_m when $\alpha_1 = 0.9$ and $\alpha_2 = 0.1$

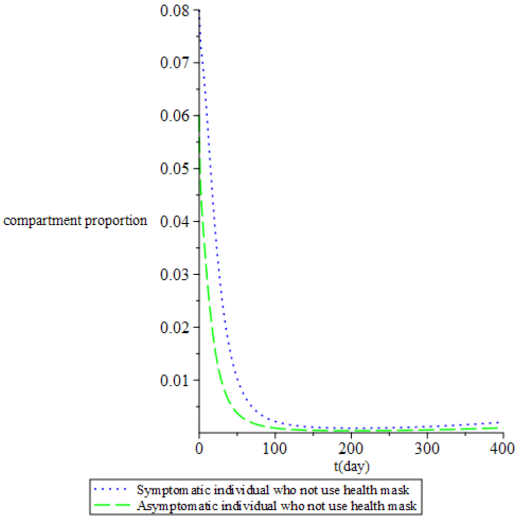
Figure 4. (a) Simulation of point i and i_m and a and a_m when $\alpha_1 = 0$ and $\alpha_2 = 0$, **(b)** Simulation of point i and i_m and a and a_m when $\alpha_1 = 1$ and $\alpha_2 = 1$, **(c)** Simulation of point i and i_m and a and a_m when $\alpha_1 = 1$ and $\alpha_2 = 0$, **(d)** Simulation of point i and i_m and a and a_m when $\alpha_1 = 0.15$ and $\alpha_2 = 0.85$, **(e)** Simulation of point i and i_m and a and a_m when $\alpha_1 = 0.9$ and $\alpha_2 = 0.1$

The conclusion obtained from the third simulation is that the disease will disappear from the population when the individual awareness rate in using health masks (α_1) is greater than or equal to the individual unawareness rate in using health masks (α_2). The larger α_1, the smaller R_0 will be, thus the disease will disappear more quickly from the population.

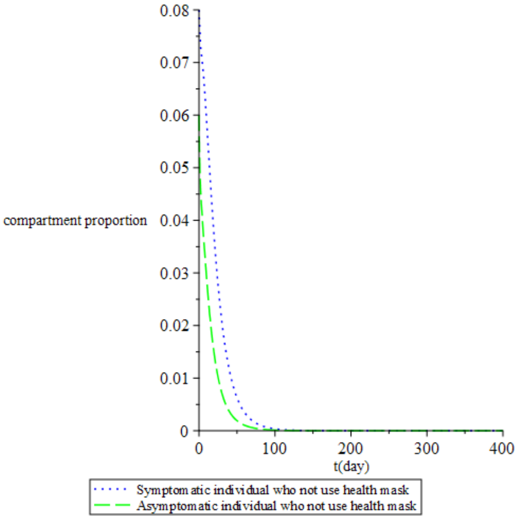
Furthermore, numerical simulations are carried out by changing the parameter value of the vaccination rate of susceptible individuals (ρ) to determine how much the effect of ρ as presented in Table 5 and visualized in graphical form in Figure 5.

Table 5. Effect of Vaccination Rate

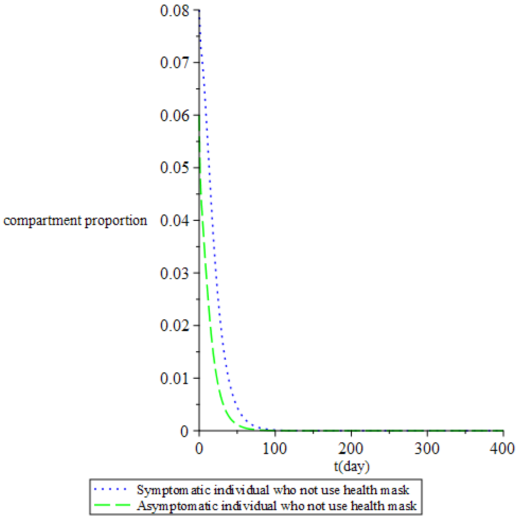
ρ	R_0
0	1.122491704
0.02	0.4346146753
0.04	0.2708344306
0.06	0.1974157000
0.08	0.1557456099
0.1	0.1288915518



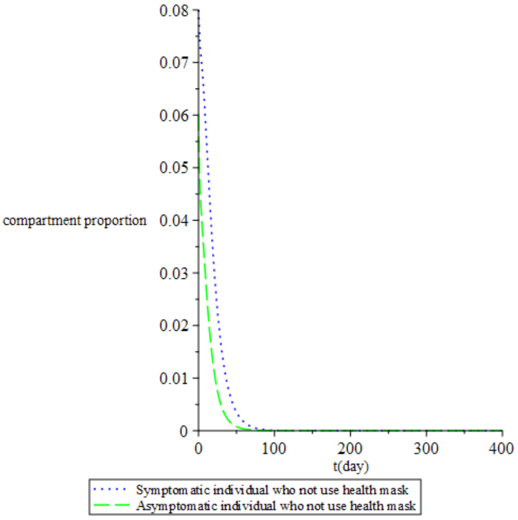
(a) Simulation of point i dan a when $\rho = 0$



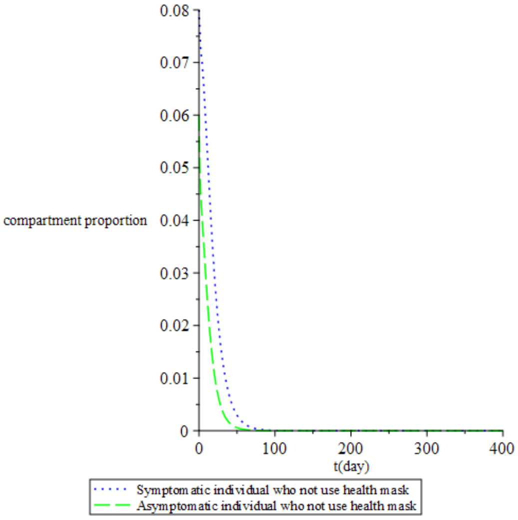
(b) Simulation of point i dan a when $\rho = 0.02$



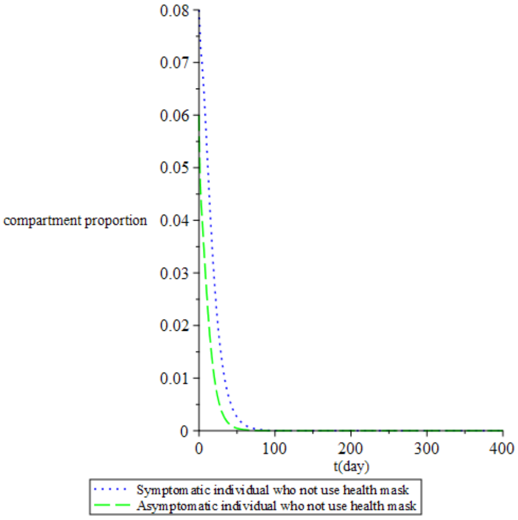
(c) Simulation of point i dan a when $\rho = 0.04$



(d) Simulation of point i dan a when $\rho = 0.06$



(e) Simulation of point i dan a when $\rho = 0.08$



(f) Simulation of point i dan a when $\rho = 0.1$

Figure 5. (a) Simulation of point i dan a when $\rho = 0$, **(b)** Simulation of point i dan a when $\rho = 0.02$, **(c)** Simulation of point i dan a when $\rho = 0.04$, **(d)** Simulation of point i dan a when $\rho = 0.06$, **(e)** Simulation of point i dan a when $\rho = 0.08$, **(f)** Simulation of point i dan a when $\rho = 0.1$

The conclusion obtained from the fourth simulation is that the higher the vaccination rate (ρ), the smaller R_0 will be; hence the disease will disappear from the population more quickly.

Sensitivity Analysis

The sensitivity index measures the association of a parameter model with the basic reproduction number (R_0). This index provides information on whether a parameter has a significant effect on the R_0 value. A parameter with a high effect on the R_0 value indicates that the parameter has the most important effect on the spread of COVID-19. Sensitivity analysis is calculated by taking the first derivative of the R_0 equation to the parameter p (Resmawan & Yahya, 2020). In the following example, the sensitivity index of the parameter β_i can be calculated as follows:

$$C_{\beta_i}^{R_0} = \frac{\partial R_0}{\partial \beta_i} \times \frac{\beta_i}{R_0}$$
$$= \frac{\mu(1-p)\sigma(\mu+\alpha_2+\tau)}{(\mu+\rho)(\mu+\sigma)(\mu+\alpha_1+\alpha_2+\tau)(\mu+\tau)}$$
$$\times \frac{\beta_i}{R_0} = 0.4547213333$$

Table 6. Sensitivity Index for the Model Parameters

Parameter	Sensitivity Index
β_a	+0.5428104680
α_1	-0.5320421745
β_i	+0.4547213333
θ	-0.4272504996
α_2	+0.4045302123
ρ	-0.3693910976
τ	-0.3550224068
μ	+0.2213470644
p	+0.2131174651
σ	+0.05992949450
ω	+0.002468198436
ε	-0.002100594393

Based on Table 6, it shows the sensitivity index of each parameter used in this model. The sensitivity index is ordered based on how much effect the parameter has on the value of R_0.Seven parameters are found with positive sensitivity indices, i.e., $\beta_a, \beta_i, \alpha_2, \mu, p, \sigma,$

and ω. This means that if the value of these parameters increases, the spread of COVID-19 will also increase, and vice versa. In contrast, five parameters are found with negative sensitivity indices, i.e., $\alpha_1, \theta, \rho, \tau,$ and ε. This means that increasing the value of these parameters will decrease the spread of COVID-19, and vice versa.

The sensitivity index of $\beta_a = +0.5428104680$ is interpreted as if the parameter value of β_a is increased (or decreased) by 10%, the value of R_0 will increase (or decrease) by 5.428104680%. On the other hand, the parameter sensitivity index of $\alpha_1 = -0.5320421745$ means that by increasing (or decreasing) the parameter value of α_1 by 10%, the value of R_0 will decrease (or increase) by 5.320421745%.

CONCLUSIONS AND SUGGESTIONS

Based on the assumptions that have been set in this study, it can be concluded that a mathematical model of the spread of COVID-19 is obtained by using health masks, vaccinations, and quarantines. The model obtained is a system of nonlinear differential equations. From the model, two equilibrium points are obtained, namely the disease-free equilibrium point and the endemic equilibrium point. The disease-free equilibrium point will be locally asymptotically stable when $R_0 < 1$, and the endemic equilibrium point exists if $R_0 > 1$. When $R_0 < 1$, the model has two endemic equilibrium points. The numerical simulation of the model supports the analysis results obtained. Based on the results of sensitivity analysis, the parameter that has the most effect on the value of R_0 can be identified. Some things that can be done so that the disease disappears from the population are increasing individual awareness of the use of masks (α_1) on susceptible and symptomatic infected individuals or infected without symptoms when going out of the house and in crowded places, reducing contact with symptomatic infected individuals (β_i) or asymptomatic infected (β_a), increasing the rate of individuals being vaccinated (ρ), and increasing the quarantine rate (τ) for symptomatic infected individuals.

For further researchers, it is recommended to add the assumption of death due to disease because in the case of Covid-19. This research only discusses local stability; further research can investigate global stability.

REFERENCES

Aldila, D., Khoshnaw, S. H. A., Safitri, E., Anwar, Y. R., Bakry, A. R. Q., Samiadji, B. M., … Salim, S. N. (2020). A mathematical study on the spread of covid-19 considering social distancing and rapid assessment: The case of jakarta, indonesia. *Chaos, Solitons & Fractals*, *139*, 110042. https://doi.org/10.1016/j.chaos.2020.110042

Aldila, D., Ndii, M. Z., & Samiadji, B. M. (2020). Optimal control on covid-19 eradication program in Indonesia under the effect of community awareness. *Mathematical Biosciences and Engineering*, *17*(6), 6355–6389. https://doi.org/10.3934/mbe.2020335

Ali, M., Shah, S. T. H., Imran, M., & Khan, A. (2020). The role of asymptomatic class, quarantine and isolation in the transmission of covid-19. *Journal of Biological Dynamics*, *14*(1), 389–408. https://doi.org/10.1080/17513758.2020.1773000

Angeli, M., Neofotistos, G., Mattheakis, M., & Kaxiras, E. (2022). Modeling the effect of the vaccination campaign on the covid-19 pandemic. *Chaos, Solitons & Fractals*, *154*, 111621. https://doi.org/10.1016/j.chaos.2021.111621

Atmojo, J. T., Akbar, P. S., Kuntari, S., Yulianti, I., & Darmayanti, A. T. (2020). Definisi dan jalur penularan severe acute respiratory syndrome coronavirus 2 (sars-cov-2) atau covid-19. *Jurnal Pendidikan Kesehatan*, *9*(1), 57. https://doi.org/10.31290/jpk.v9i1.1513

Badan Pusat Statistik. (2020). *Hasil sensus penduduk 2020*.

Daud, A. A. M. (2021). A note on lienard-chipart criteria and its application to epidemic models. *Mathematics and Statistics*, *9*(1). https://doi.org/10.13189/ms.2021.090107

De León, C. V. (2009). Constructions of lyapunov functions for classic sis, sir and sirs epidemic models with variable population size. *Foro-Red-Mat: Revista Electrónica de Contenido Matemático*, *26*(5).

Ditjen P2P Kementrian Kesehatan. (2021). *Program vaksinasi covid-19 mulai dilakukan, presiden orang pertama penerima suntikan vaksin covid-19*.

Foy, B. H., Wahl, B., Mehta, K., Shet, A., Menon, G. I., & Britto, C. (2021). Comparing covid-19 vaccine allocation strategies in india: A mathematical modelling study. *International Journal of Infectious Diseases*, *103*. https://doi.org/10.1016/j.ijid.2020.12.075

Ghostine, R., Gharamti, M., Hassrouny, S., & Hoteit, I. (2021). An extended seir model with vaccination for forecasting the covid-19 pandemic in saudi arabia using an ensemble kalman filter. *Mathematics*, *9*(6), 636. https://doi.org/10.3390/math9060636

Iboi, E. A., Ngonghala, C. N., & Gumel, A. B. (2020). Will an imperfect vaccine curtail the covid-19 pandemic in the U.S.? *Infectious Disease Modelling*, *5*. https://doi.org/10.1016/j.idm.2020.07.006

Imran, M., Wu, M., Zhao, Y., Be?ed, E., Alonazi, W., & Khan, M. J. (2021). Mathematical modelling of sir for covid-19 forecasting. *Revista Argentina de Clinica Psicologica*, *30*(1), 218.

Ivanova, M., & Dospatliev, L. (2021). Data analytics and sir modeling of covid-19 in bulgaria. *International Journal of Apllied Mathematics*, *33*(6). https://doi.org/10.12732/ijam.v33i6.10

Kertes, J., Gez, S. B., Saciuk, Y., Supino-Rosin, L., Stein, N. S., Mizrahi-Reuveni, M., & Zohar, A. E. (2022). Effectiveness of mrna bnt162b2 vaccine 6 months after vaccination among patients in large health maintenance organization, israel. *Emerging Infectious Diseases*, *28*(2), 338–346. https://doi.org/10.3201/eid2802.211834

Levin, S. A. (2002). *Descartes' rule of signs - How hard can it be?* .

Liao, Z., Lan, P., Liao, Z., Zhang, Y., & Liu, S. (2020). Tw-sir: time-window based sir for covid-19 forecasts. *Scientific Reports*, *10*(1), 22454. https://doi.org/10.1038/s41598-020-80007-8

Manaqib, M., Fauziah, I., & Hartati, E. (2021). Model matematika penyebaran covid-19 dengan penggunaan masker kesehatan dan karantina. *Jambura Journal of Biomathematics (JJBM)*, *2*(2), 68–79. https://doi.org/10.34312/jjbm.v2i2.10483

Manaqib, M., Fauziah, I., & Mujiyanti, M. (2019). Mathematical model for mers-cov disease transmission with medical mask usage and vaccination. *InPrime: Indonesian Journal of Pure and Applied Mathematics*, *1*(2). https://doi.org/10.15408/inprime.v1i2.13553

Mitra, A. (2020). Covid-19 in india and sir model. *JOURNAL OF MECHANICS OF CONTINUA AND MATHEMATICAL SCIENCES*, *15*(7).

https://doi.org/10.26782/jmcms.2020.07.00001

Nuha, A. R., Achmad, N., & Supu, N. ’ain. (2021). Analisis model matematika penyebaran covid-19 dengan intervensi vaksinasi dan pengobatan. *Jurnal Matematika UNAND*, *10*(3), 406. https://doi.org/10.25077/jmu.10.3.406-422.2021

Pani, A., Cento, V., Vismara, C., Campisi, D., Di Ruscio, F., Romandini, A., … Scaglione, F. (2021). Results of the renaissance study: Response to bnt162b2 covid-19 vaccine—short- and long-term immune response evaluation in health care workers. *Mayo Clinic Proceedings*, *96*(12), 2966–2979. https://doi.org/10.1016/j.mayocp.2021.08.013

Resmawan, R., & Yahya, L. (2020). Sensitivity analysis of mathematical model of coronavirus disease (covid-19) transmission. *CAUCHY: Jurnal Matematika Murni Dan Aplikasi*, *6*(2), 91–99. https://doi.org/10.18860/ca.v6i2.9165

Satuan Tugas Penanganan COVID-19. (2020). *Apakah vaksin covid-19 adalah obat?*

Satuan Tugas Penanganan COVID-19. (2022). *Situasi covid-19 di indonesia* .

Sayampanathan, A. A., Heng, C. S., Pin, P. H., Pang, J., Leong, T. Y., & Lee, V. J. (2021). Infectivity of asymptomatic versus symptomatic COVID-19. *The Lancet*, Vol. 397. https://doi.org/10.1016/S0140-6736(20)32651-9

Tosepu, R., Gunawan, J., Effendy, D. S., Ahmad, L. O. A. I., Lestari, H., Bahar, H., & Asfian, P. (2020). Correlation between weather and covid-19 pandemic in jakarta, indonesia. *Science of The Total Environment*, *725*, 138436. https://doi.org/10.1016/j.scitotenv.2020.138436

World Health Organization. (2021). WHO validates sinovac covid-19 vaccine for emergency use and issues interim policy recommendations. *World Health Organization*.

World Health Organization. (2022). *Weekly epidemiological update on covid-19*.

Yang, J., Zheng, Y., Gou, X., Pu, K., Chen, Z., Guo, Q., … Zhou, Y. (2020). Prevalence of comorbidities and its effects in patients infected with sars-cov-2: A systematic review and meta-analysis. *International Journal of Infectious Diseases*, *94*, 91–95. https://doi.org/10.1016/j.ijid.2020.03.017