



A MATHEMATICAL MODEL OF COVID-19 WITH DOUBLE DOSES OF VACCINATION AND QUARANTINE

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Abstract

Covid-19 (coronavirus disease 2019) is a disease caused by a virus called SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) and began to appear at the end of 2019. One of the ways to prevent the spread of covid-19 from spreading is to provide double-dose vaccination and quarantine for individuals who can transmit covid-19 (infectious individuals). Through this research, a mathematical model was formed for the case of the spread of covid-19 by considering the existence of double-dose vaccination, and quarantine were given to infectious individuals. In the model formed, we get a basic reproduction number R_0 , and two equilibrium points, namely the disease-free equilibrium point (E_0) that will be locally asymptotically stable when $R_0 < 1$, and the endemic equilibrium point (E^) that will be locally asymptotically stable when $R_0 > 1$. Furthermore, in the numerical simulation carried out, it is known that double doses of vaccine and quarantine can decrease the value of R_0 , that means if $R_0 < 1$ is obtained (E_0 locally asymptotically stable), then the spread of covid-19 will gradually disappear from the population.*

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INTRODUCTION

Covid-19 (*coronavirus disease 2019*) is a disease caused by a virus named SARS-CoV-2 (Thevarajan et al., 2020) 2020), where this virus infects other individuals through droplets of saliva (droplets) of the patient that spreads through the air and attacks the target organs (Gennaro et al., 2020). This disease first appeared in the city of Wuhan, China at the end of 2019 (Li et al., 2020), and quickly spread to various countries. The massive spread of

covid-19 has caused a lot of losses in the health sector, the economy sector, and various other sectors. Several regulations have been implemented to break the spread of covid-19 and reduce the transmission, such as providing quarantine for individuals who can transmit the disease so that those who can transmit it could not contact with those who are susceptible, and the transmission of covid-19 can be stopped.

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Quarantine for infectious individuals is assumed to be effective because the risk of infection depends on the contact between susceptible and infectious individuals. Infectious individuals can be in the asymptomatic, symptomatic, or presymptomatic stage of infection (Moghadas *et al.*, 2021). Another regulation that has been implemented is the vaccine for susceptible individuals. This vaccine is given to increase the individual's immunity and reduce the chance of contracting covid-19. In a case study conducted by Yalçın *et al* (2022), among 148 medical personnel observed, 35.2% of them experienced an increase in anti-SARS-CoV-2 (IgGsp) antibodies after receiving the first dose of vaccination, and all medical personnel experienced increased antibodies after receiving the second dose of vaccination.

A mathematical model can be described as an idealization of a real-world situation even though it is never totally accurate, and it also can help us to plan, and make a strategy what to do in the future (Giordano *et al.*, 2014). One example of the application of mathematics in researching issues of covid-19 is to create a mathematical model that can represent the case of the disease as close as possible to the original case in the real world. Mathematical modeling for the case of the spread of covid-19 itself has been carried out by several researchers by involving factors that are considered to have an influence on the spread of covid-19 in the population. The research of Alsheri *et al* (2022) focuses on forming a mathematical model to see the effect of quarantine that given to infected individuals with covid-19 on the transmission that occurs in the population. Paul & Kuddus (2022) involved a mathematical model that carried out double doses of covid-19 vaccination. Musa *et al* (2021) formed a mathematical model by involving the program to raise awareness about the dangers of covid-19 and provide different hospitalization strategies for patients with severe and mild cases. Zeb *et al* (2020) formed a mathematical model by involving the isolation of infected individuals with covid-19 so as not to make contact with susceptible individuals. Diagne *et al* (2021) developed a

mathematical model that considers the existence of vaccination for susceptible individuals and treatment for infected individuals.

METHODS

A literature study is used to analyze the problems so a mathematical model is formed and can represent the case of the spread of COVID-19 by considering the existence of double-dose vaccination and quarantine for infectious individuals. The stages that carried out in this research are determining the problem to be studied, formulating problems that arise, literature study, analysis and solving problems that arise, and make a conclusion from the obtained result. At the stage of analysis and problem solving, the main steps taken are taking facts and assumptions about the problem that will be used as a reference for mathematical models, forming mathematical models, looking for equilibrium points and basic reproduction numbers, then analyzing the existence and stability of the equilibrium point, followed by numerical simulation to see the illustration of the existence and stability of the obtained equilibrium points..

RESULTS AND DISCUSSION

1. Model Formulation

It is known that the risk of covid-19 depends on the contact of a susceptible individual with an infectious individual (Moghadas *et al.*, 2021), so quarantine is given to infectious individuals to stop contact with vulnerable individuals, so that the transmission of covid-19 can be stopped (Kemenkes, 2021b). Vaccines can increase anti-SARS-CoV-2 (IgGsp) antibodies in the body with different increments between doses (Yalçın *et al.*, 2022). The vaccination is given twice or in two doses with a distance between doses of 28-60 days (Kemenkes, 2020, 2021a). It is known that there are cases where individuals do not experience an increase in antibodies after receiving the vaccine, so there is a possibility of vaccination failure both at the first dose and at the second dose so that individuals are still susceptible to contracting

covid-19 (WHO, 2020; Yalçın *et al.*, 2022). Infected individuals can recover and have immunity that lasts for approximately 180 to 240 days (Dan *et al.*, 2021), and it is known that covid-19 can cause death (Huang *et al.*, 2020).

In forming the mathematical model, several assumptions are set as the boundaries. The population is assumed to be homogeneous, or each individual has the same opportunity to make contact with other individuals. It is assumed that the population is closed or there is no migration or emigration in the population. This research focuses on the spread of covid-19 in the population, so it is assumed that there is only one disease that is spreading in the population, it is covid-19 (coronavirus disease 2019) that caused by the dominant variant of SARS-CoV-2. It is assumed that only individuals from the group of individuals with the first vaccine will receive the second dose of vaccination, and it is assumed that individuals who have received both the first and second doses of vaccine have a chance to become susceptible again. Transmission of covid-19 is assumed to occur when susceptible individuals come into contact with infectious. Quarantine is given to infectious individuals with the aim of reducing the contact of infectious individuals with susceptible individuals because quarantined individuals cannot meet other individuals, and quarantined infected individuals are assumed to only be able to get out from the quarantine if they have recovered and move to a group of recovered individuals. Infected individuals are assumed to be able to recover, and are assumed not to return to being susceptible, and do not get vaccinated because they have post-immunity after infection. The mathematical model formed divides the population into 6 classes: susceptible individual class (S), individual with the first dose of vaccine class (V_1), individual with the second dose of vaccine class (V_2), infectious individual class (I), quarantined infectious individual class (Q), recovered individual class (R). The mathematical model formed is illustrated in the covid-19 transmission diagram, which is presented in

Figure 1:

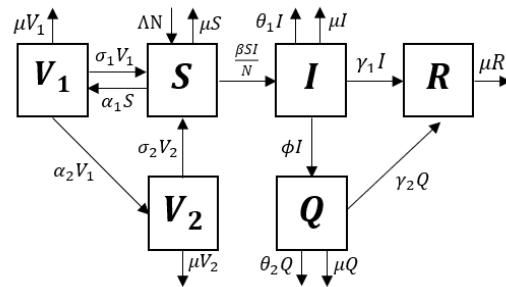


Figure 1. Transmission diagram

Individuals who are born are assumed to be susceptible to contracting covid-19, so they enter the sub-population at a recruitment rate (Λ). Furthermore, susceptible individuals who receive the first dose of vaccine will move into the sub population by proportion α_1 , and are likely to become susceptible again by proportion σ_1 . Individuals who receive the next second dose of vaccine move into the sub-population by a proportion α_2 , and are likely to become susceptible again by a proportion σ_2 . Transmission of covid-19 depends on the contact of a susceptible individual with an infectious with a probability of β . Quarantine is given to infectious in a ϕ proportion to reduce contact between susceptible individuals and infectious individuals. In the population there are death rate due to covid-19 which are represented by θ_1 for infectious, and θ_2 for individuals who are quarantined, and natural deaths that are not caused by covid-19 are represented by μ . Formulated a mathematical model of the spread of covid-19 through a system of equations (1).

$$\begin{aligned}
 \frac{dS}{dt} &= \Lambda N + \sigma_1 V_1 + \sigma_2 V_2 - \frac{\beta SI}{N} - (\alpha_1 + \mu)S \\
 \frac{dV_1}{dt} &= \alpha_1 S - (\alpha_1 + \sigma_1 + \mu)V_1 \\
 \frac{dV_2}{dt} &= \alpha_2 V_1 - (\sigma_2 + \mu)V_2 \\
 \frac{dI}{dt} &= \frac{\beta SI}{N} - (\phi + \theta_1 + \gamma_1 + \mu)I \\
 \frac{dQ}{dt} &= \phi I - (\theta_2 + \gamma_2 + \mu)Q \\
 \frac{dR}{dt} &= \gamma_1 I + \gamma_2 Q - \mu R
 \end{aligned} \tag{1}$$

With initial conditions $S \geq 0, V_1 \geq 0, V_2 \geq 0, I \geq 0, Q \geq 0$, and $R \geq 0$.

It is known that the total population value is

$$N = S + V_1 + V_2 + I + Q + R$$

and

$$\frac{dN}{dt} = (\Lambda - \mu)N - \theta_1 I - \theta_2 Q$$

To simplify the model, it is assumed that the recruitment rate (Λ) is equal to the natural death rate (μ). The death rate of infectious individuals due to covid-19 (θ_1) and the death rate of individuals quarantined due to covid-19 (θ_2) is assumed to be very small or close to 0, so these parameters will be ignored ($\theta_1 = \theta_2 = 0$). We can write it as

$$\frac{dN}{dt} = 0,$$

and it is known that $N(t) = a$, which a is a constant positive interger. Furthermore, the system of mathematics model can be simplified by expressing each class into the proportion for each class to the total population as follows:

$$s = \frac{S}{N}, v_1 = \frac{V_1}{N}, v_2 = \frac{V_2}{N}, i = \frac{I}{N}, q = \frac{Q}{N}, r = \frac{R}{N}$$

so

$$\begin{aligned} s + v_1 + v_2 + i + q + r \\ = \frac{S}{N} + \frac{V_1}{N} + \frac{V_2}{N} + \frac{I}{N} + \frac{Q}{N} + \frac{R}{N} = \frac{N}{N} = 1 \end{aligned}$$

So that the system of equations (1) becomes a dimensionless system of equations, as follows:

$$\frac{ds}{dt} = \Lambda + \sigma_1 v_1 + \sigma_2 v_2 - \beta si - (\alpha_1 + \mu)s$$

$$\frac{dv_1}{dt} = \alpha_1 s - (\alpha_2 + \sigma_1 + \mu)v_1$$

$$\frac{dv_2}{dt} = \alpha_2 v_1 - (\sigma_2 + \mu)v_2$$

$$\frac{di}{dt} = \beta si - (\phi + \theta_1 + \gamma_1 + \mu)i$$

(2)

$$\frac{dq}{dt} = \phi i - (\theta_2 + \gamma_2 + \mu)q$$

$$\frac{dr}{dt} = \gamma_1 i + \gamma_2 q - \mu r$$

2. Model Analysis

Further analysis of the mathematical model is carried out by finding the equilibrium point, basic reproduction number, and stability analysis

of the obtained equilibrium point. From the system of the mathematical model obtained, the equilibrium point is determined by setting all equations equal to zero, or it can be written as follows:

$$\frac{ds}{dt} = \frac{dv_1}{dt} = \frac{dv_2}{dt} = \frac{di}{dt} = \frac{dq}{dt} = \frac{dr}{dt} = 0$$

and we get:

- 1.) Disease free equilibrium point, $E_0 = (s_0, v_{10}, v_{20}, 0, 0, 0)$, where

$$s_0 = \frac{\Lambda(\alpha_2 + \sigma_1 + \mu)(\sigma_2 + \mu)}{\sigma_2 \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu) + \mu(\alpha_1 \alpha_2 + \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu))}$$

$$v_{10} = \frac{\Lambda \alpha_1 (\sigma_2 + \mu)}{\sigma_2 \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu) + \mu(\alpha_1 \alpha_2 + \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu))}$$

$$v_{20} = \frac{\Lambda \alpha_1 \alpha_2}{\sigma_2 \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu) + \mu(\alpha_1 \alpha_2 + \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu))}$$

- 2.) Endemic equilibrium point $E^* = (s^*, v_1^*, v_2^*, i^*, q^*, r^*)$, where

$$s^* = \frac{\phi + \theta_1 + \gamma_1 + \mu}{\beta}$$

$$v_1^* = \frac{\alpha_1 s^*}{(\alpha_2 + \sigma_1 + \mu)}$$

$$v_2^* = \frac{\alpha_2 v_1^*}{(\sigma_2 + \mu)}$$

$$i^* = \frac{\Lambda}{(\phi + \theta_1 + \gamma_1 + \mu)} - \frac{\frac{1}{\beta} (\sigma_2 \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu) + \mu(\alpha_1 \alpha_2 + \mu(\alpha_1 + \alpha_2 + \sigma_1 + \mu)))}{(\alpha_2 + \sigma_1 + \mu)(\sigma_2 + \mu)}$$

$$q^* = \frac{\phi i^*}{(\theta_2 + \gamma_2 + \mu)}$$

$$r^* = \frac{\gamma_1 i^* + \gamma_2 q^*}{\mu}$$

3. Basic Reproduction Number (R_0)

Furthermore, the calculation of the basic reproduction number is carried out, where the calculation is carried out by finding the largest positive eigen value from the next generation matrix involving the infected compartment, where in this mathematical model are the infectious individual compartment, and

quarantined individual compartment, which are presented in equation (3) and (4).

$$\frac{di}{dt} = \beta si - (\phi + \theta_1 + \gamma_1 + \mu)i \quad (3)$$

$$\frac{dq}{dt} = \phi i - (\theta_2 + \gamma_2 + \mu)q \quad (4)$$

To find next generation matrix, it is necessary to linearize equations (3) and (4) with the jacobian matrix.

$$J = \begin{pmatrix} \frac{\partial(\frac{di}{dt})}{\partial i} & \frac{\partial(\frac{di}{dt})}{\partial q} \\ \frac{\partial(\frac{dq}{dt})}{\partial i} & \frac{\partial(\frac{dq}{dt})}{\partial q} \end{pmatrix}$$

$$\Leftrightarrow J = \begin{pmatrix} \beta s - (\phi + \theta_1 + \gamma_1 + \mu) & 0 \\ \phi & -(\theta_2 + \gamma_2 + \mu) \end{pmatrix} \quad (5)$$

Substitution of the disease-free equilibrium point is carried out in equation (5), and decomposition is conducted.

$$J(E_0) = \begin{pmatrix} \beta s_0 & 0 \\ 0 & 0 \end{pmatrix} - \begin{pmatrix} (\phi + \theta_1 + \gamma_1 + \mu) & 0 \\ \phi & -(\theta_2 + \gamma_2 + \mu) \end{pmatrix} \quad (6)$$

$$R_0 = \frac{\Lambda \beta (\alpha_2 + \sigma_1 + \mu) (\sigma_2 + \mu)}{(\phi + \theta_1 + \gamma_1 + \mu) (\sigma_2 \mu (\alpha_1 + \alpha_2 + \sigma_1 + \mu) + \mu (\alpha_1 \alpha_2 + \mu (\alpha_1 + \alpha_2 + \sigma_1 + \mu)))} \quad (10)$$

With the R_0 that is stated in equation (10), the equilibrium points can be expressed as follows:

1.) Disease free equilibrium point $E_0 = (s_0, v_{10}, v_{20}, 0, 0, 0)$, where

$$s_0 = \frac{R_0 (\phi + \theta_1 + \gamma_1 + \mu)}{\beta}$$

$$v_{10} = \frac{\alpha_1 s_0}{(\alpha_2 + \sigma_1 + \mu)}$$

$$v_{20} = \frac{\alpha_1 \alpha_2 s_0}{(\alpha_2 + \sigma_1 + \mu) (\sigma_2 + \mu)}$$

Since all parameter values are positive, so it is known that a disease-free equilibrium point exists and is positive in the $R_0 < 1$ or $R_0 > 1$ conditions.

2.) Endemic equilibrium point $E^* = (s^*, v_1^*, v_2^*, i^*, q^*, r^*)$, where:

$$s^* = \frac{\phi + \theta_1 + \gamma_1 + \mu}{\beta}$$

$$v_1^* = \frac{\alpha_1 s^*}{(\alpha_2 + \sigma_1 + \mu)}$$

From the equation (6), the transmission (F) and transition (V) matrix are obtained:

$$F = \begin{pmatrix} \beta s_0 & 0 \\ 0 & 0 \end{pmatrix} \quad (7)$$

$$V = \begin{pmatrix} (\phi + \theta_1 + \gamma_1 + \mu) & 0 \\ \phi & -(\theta_2 + \gamma_2 + \mu) \end{pmatrix} \quad (8)$$

Furthermore, the calculation of FV^{-1} obtained:

$$FV^{-1} = \begin{pmatrix} \frac{\beta s_0}{(\phi + \theta_1 + \gamma_1 + \mu)} & 0 \\ 0 & 0 \end{pmatrix} \quad (9)$$

Because the basic reproduction number is the largest eigen value of the next generation matrix, then from equation (9) we get a basic reproduction number which is presented in equation (10).

$$v_2^* = \frac{\alpha_1 \alpha_2 s^*}{(\alpha_2 + \sigma_1 + \mu) (\sigma_2 + \mu)}$$

$$i^* = \frac{\Lambda}{(\phi + \theta_1 + \gamma_1 + \mu)} \left(\frac{R_0 - 1}{R_0} \right)$$

$$q^* = \frac{\phi i^*}{(\theta_2 + \gamma_2 + \mu)}$$

$$r^* = \frac{\gamma_1 i^* + \gamma_2 q^*}{\mu}$$

Since all parameter values are positive, it is known that the endemic equilibrium point exists and is positive when $R_0 > 1$.

4. Equilibrium Point Stability Analysis

Stability analysis was carried out by looking at the real part of the eigenvalues from the linearization of the system of equations (2) with the Jacobian matrix, then substitution of the equilibrium points for stability analysis was carried out. The Routh-Hurwitz criterion is used to make it easier to determine the stability of the

equilibrium point. The Jacobian matrix of equation (2) is presented in equation (11).

$$J(E) = \begin{pmatrix} J_{11} & \sigma_1 & \sigma_2 & -\beta s & 0 & 0 \\ \alpha_1 & J_{22} & 0 & 0 & 0 & 0 \\ 0 & \alpha_2 & J_{33} & 0 & 0 & 0 \\ \beta i & 0 & 0 & J_{44} & 0 & 0 \\ 0 & 0 & 0 & \phi & J_{55} & 0 \\ 0 & 0 & 0 & \gamma_1 & \gamma_2 & -\mu \end{pmatrix} \quad (11)$$

where

$$J_{11} = -\beta i - (\alpha_1 + \mu)$$

$$J_{22} = -(\alpha_2 + \sigma_1 + \mu)$$

$$J_{33} = -(\sigma_2 + \mu)$$

$$J_{44} = \beta s - (\phi + \gamma_1 + \theta_1 + \mu)$$

$$J_{55} = -(\gamma_2 + \theta_2 + \mu)$$

Furthermore, the equilibrium point is substituted for stability analysis in equation (11) and the eigenvalues are sought to determine the stability.

After substituting the disease-free equilibrium point (E_0) in equation (11), the eigenvalues are obtained as follows:

$\lambda_1 = \mu$, $\lambda_2 = -(\gamma_2 + \theta_2 + \mu)$, $\lambda_3 = \beta s_0 - (\phi + \gamma_1 + \theta_1 + \mu)$, and eigenvalue $\lambda_{4,5,6}$ are the solution to the equation

$$(\lambda + (\alpha_1 + \mu))(\lambda + (\alpha_2 + \sigma_1 + \mu))(\lambda + (\sigma_2 + \mu)) + \alpha_1 \alpha_2 \sigma_2 - \alpha_1 \sigma_1 (\lambda + (\sigma_2 + \mu)) = 0.$$

It is clear that the value of λ_1, λ_2 , and λ_3 are negative. By using Routh Hurwitz's criteria for a polynomial to the power of 3 it is concluded that the value of λ_4, λ_5 , and λ_6 are negative when $R_0 < 1$ is fulfilled. From the process of analyzing the stability of the disease-free equilibrium point by looking at the eigenvalues obtained and R_0 described in equation (10), it is concluded that the disease-free equilibrium point will be locally asymptotically stable in the $R_0 < 1$ condition, and unstable in the $R_0 > 1$ condition.

After substituting the endemic equilibrium point in equation (11), the eigenvalues are obtained as follows:

$\lambda_1 = \mu$, $\lambda_2 = -(\gamma_2 + \theta_2 + \mu)$, and eigen values $\lambda_{3,4,5,6}$ are the solution to the equation

$$0 = (\lambda + \sigma_2 + \mu)((\lambda(\lambda + \beta i^* + \alpha_1 + \mu)(\lambda + \alpha_2 + \sigma_1 + \mu) + \beta i^*(\lambda + \alpha_2 + \sigma_1 + \mu)(\phi + \theta_1 + \gamma_1 + \mu) - \lambda \alpha_1 \sigma_1)) + \lambda \alpha_1 \alpha_2 \sigma_2$$

It is clear that the values of λ_1 , and λ_2 are negative, and by using Routh Hurwitz's criteria for polynomials to the power of 4, it is concluded that the values of $\lambda_3, \lambda_4, \lambda_5$, and λ_6 are negative in the $R_0 > 1$ condition. From the process of analyzing the stability of the endemic equilibrium point (E^*) which was carried out by looking at the eigenvalues obtained and the R_0 that described in equation (10), it was concluded that the endemic equilibrium point would be locally asymptotically stable when $R_0 < 1$.

5. Numerical Simulations

Next, a numerical simulation of the mathematical model that has been formed is carried out to illustrate the existence and stability of the obtained equilibrium points. Numerical simulation is carried out by providing initial parameter values which are presented in Table 1.

Table. 1 Parameter values used for numerical simulation

Symbol	Value	Reference
Λ	0.2276	Assumption
μ	0.2276	Assumption
β	0.85	(Din & Algehyne, 2021)
σ_1	0.648	(Yalçın et al., 2022)
σ_2	0.347	(WHO, 2020)
γ_1	0.3302	(Tang et al., 2020)
γ_2	0.1162	(Tang et al., 2020)
θ_1	0	Assumption
θ_2	0	Assumption

The goal of numerical simulation is to examine how variations in the values of ϕ, α_1 , and α_2 affect the value of R_0 , the presence of an equilibrium point, and the stability of those points. Given various ϕ, α_1 , and α_2 values, the value of the obtained R_0 , and the established equilibrium points those are shown in Table 2.

It is known from Table 2 that by giving some values of ϕ, α_1 , and α_2 , changes in the value of the given parameter influence the value of the obtained equilibrium points, where the greater the values of ϕ, α_1 , and α_2 given, the smaller the value

of R_0 . Furthermore, simulations are carried out to see how the dynamics of individual growth in each class are illustrated based on the parameter values in Tables 2. This numerical simulation is carried out by giving initial values to the sub $S(0) =$

$0.28, V_1(0) = 0.137, V_2(0) = 0.525, I(0) = 0.058, Q(0) = 0$, dan $R(0) = 0$. The simulation results obtained are presented in Figure 2 until 7.

Table. 2 Various of parameter values used for numerical simulation

α_1	α_2	ϕ	R_0	Equilibrium Points
0	0	0	1.52	$E_0 = (1, 0, 0, 0, 0, 0)$ dan $E^* = (0.65, 0, 0, 0.14, 0, 0.20)$
0.1	0.1	0.1	1.15	$E_0 = (0.89, 0.09, 0.015, 0, 0, 0)$ dan $E^* = (0.77, 0.079, 0.013, 0.045, 0.013, 0.073)$
0.2	0.2	0.2	0.89	$E_0 = (0.79, 0.14, 0.051, 0, 0, 0)$
0.3	0.3	0.3	0.71	$E_0 = (0.72, 0.18, 0.095, 0, 0, 0)$
0.4	0.4	0.4	0.57	$E_0 = (0.65, 0.20, 0.14, 0, 0, 0)$

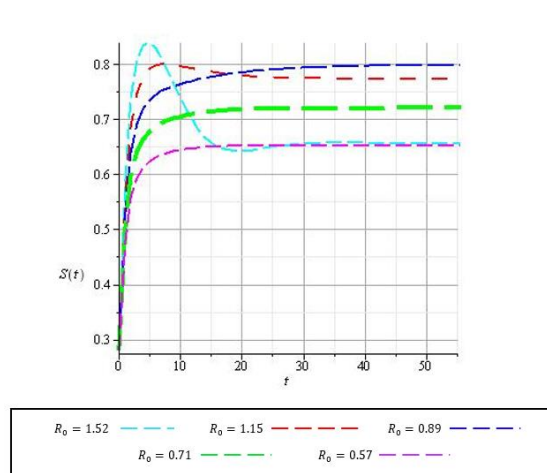


Figure 2. Dynamics of the class S

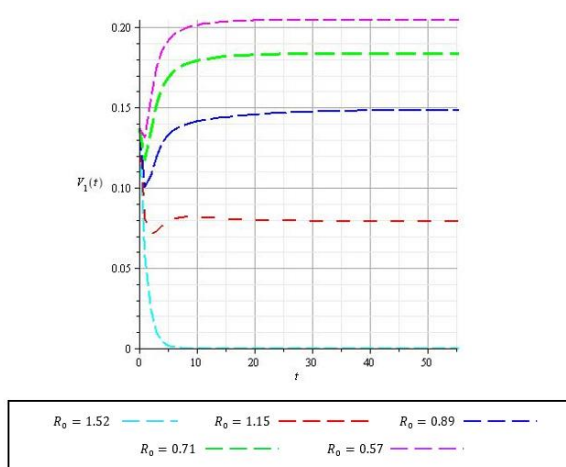


Figure 3. Dynamics of the class V_1

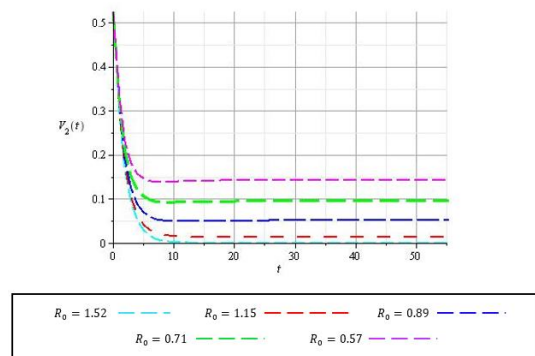
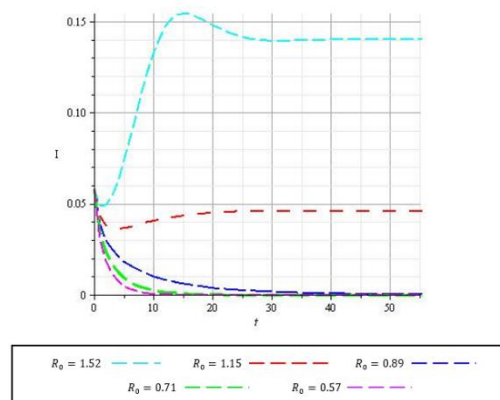
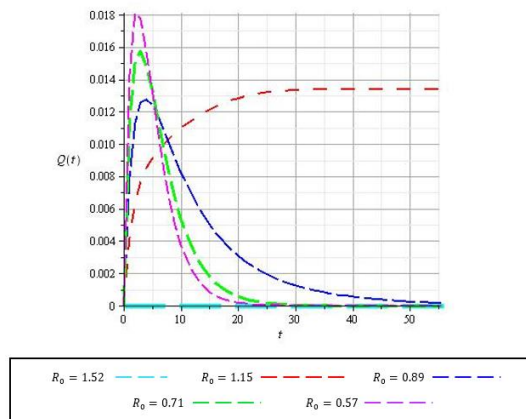
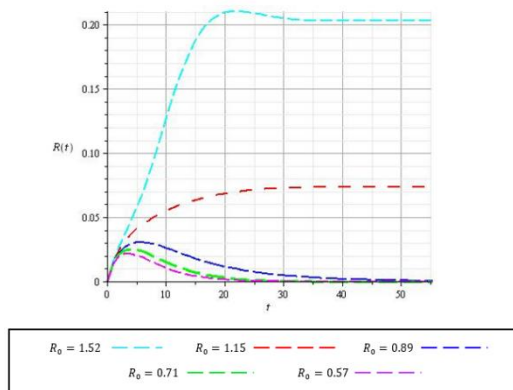


Figure 4. Dynamics of the class V_2



Gambar 5. Dynamics of the class I

Gambar 6. Dynamics of the class Q Gambar 7. Dynamics of the class R

The simulation results show that changes in the values of ϕ , α_1 , and α_2 resulted in significant changes in the number of individuals in each sub-population. The number of individuals in the infected class related to the transmission of covid-19 that occurs. Higher values of ϕ that are given will obtain a lower infectious individual. As the number of infectious individuals who are quarantined increases, the contact of infectious individuals with susceptible individuals will decrease, and the transmission of covid-19 will also decrease. Increasing values of α_1 , and α_2 will also decrease the number of infectious individuals because immunity will prevent those susceptible individuals be infected with covid-19 when in contact with infectious individuals. The number of infected individuals influences the number of individuals in the recovered class because of the

recruitment of recovered individuals in the recovery of infectious individuals

The number of individuals in the V_1 and V_2 classes depend on the number of vaccinated individuals. Increasing individuals receiving both the first and second doses of vaccination will reduce the transmission of covid-19 in the population due to the presence of immunity from individuals, so they are not susceptible to contracting covid-19. The number of individuals in the quarantined class is affected by the number of infectious individuals that are quarantined. More infectious individuals who are quarantined will obtain a lower number of covid-19 in the population because the quarantine will stop contact between infectious and susceptible individuals so that transmission can be stopped. It is known that when $R_0 < 1$, the system will be stable at the disease-free equilibrium point, this means that if the state of $R_0 < 1$, the covid-19 in the population will gradually disappear. Meanwhile, when in a state $R_0 > 1$, the system will be stable at the endemic equilibrium point. Which means that when in a state $R_0 > 1$, the disease will remain in the population indefinitely.

CONCLUSIONS

Based on the research that has been done, the mathematical model in the case of the spread of the covid-19 with the existence of double-dose vaccination and quarantine, we obtained a basic reproduction number R_0 , and two equilibrium points. The equilibrium points are the disease-free equilibrium point (E_0), which is locally asymptotically stable when $R_0 < 1$, and the endemic equilibrium point (E^*), which is locally asymptotically stable when $R_0 > 1$.

Furthermore, after numerical simulations were carried out, it was found that boosting the vaccination, both the first and second doses, and raising the proportion of quarantined individuals would result in a lower R_0 value and would reduce the transmission of covid-19 on the population. To achieve a disease-free state in the population, it is

necessary to achieve an $R_0 < 1$, so the way that needs to be done is to boost the vaccination, so that individuals have immunity. Another thing that needs to be done is to raise the quarantine for infectious individuals, and this can be maximized by intensifying testing and tracking so that individuals who can transmit covid-19 can be detected earlier, so they can be quarantined faster and can't make contact with susceptible individuals.

This study only focuses on prevention in the form of giving double-dose vaccines and quarantine, so it is necessary to carry out further research by adding consideration of other factors that can influence the spread of covid-19 in the population, such as vaccinations booster or the establishment of mandatory wearing masks.

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