On Analysis of Effectiveness Controlling Covid-19 with Quarantine and Vaccination Compartments in Indonesia

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Abstract. The COVID-19 pandemic has spread throughout the world, including Indonesia, where Indonesia is a country with a population of around 271,3 million people with high human mobility. The very high mobility makes the spread more quickly. Today the Indonesian government has been distributing the vaccination for residents. Indonesia's announcement about the vaccination has been started in January 2021. Therefore, in this paper will be assessed the effect of vaccination and quarantine to control the spread of COVID-19 in Indonesia. The method used is $SEVIQR$ with compartments development of vaccinations and quarantines. Numerical simulation results show that the decline in the number of the infected population at month 12 of the initial vaccination, while the population increased healing on day 140, and a stable population at month 18.

1. Introduction

The COVID-19 pandemic, which has spread throughout the world, including Indonesia, is still a concern today. This is because Indonesia is a country with a population of 271.3 million people with high mobility around humans. Very high mobility makes it spread faster. Therefore, it takes the right way to control the spread of COVID-19. Various policies have been set by the government to control the spread of COVID-19 in Indonesia, ranging from establishing health protocol policies in accordance with WHO, providing various health facilities for patients affected by the Coronavirus, as well as implementing social policies that have developed into Large-Scale Social Restrictions or in Indonesia known as PSBB, in several regions in Indonesia [1]. In addition, a vaccination program was also implemented to suppress the spread of COVID-19 in Indonesia in line with the issuance of a Presidential Decree on October 6, 2020 regarding the provision of vaccines and the implementation of a vaccination program to combat the COVID-19 pandemic in Indonesia [2].

Many authors have conducted research on mathematical modeling to determine the dynamics of distribution and estimates of the national and global spread of COVID-19 with various compartments, including implemented the Susceptible Exposed Infectious Recovered Model based on data recorded from December 31, 2019 to January 28, 2020 [3]. Other research also

found that COVID-19 had a modest reproduction rate of around 2.68 and have reported a value of 3.1 for reproduction rates based on SEIR model fitting data, using the assumption of daily time increments with a Poisson distribution [4].
Other research also developed a deterministic compartmental model involving clinical disease progression, human epidemiologic status, and degree of involvement [5]. In other hand, there is research that found the number of reproductive controls might be 6.47. Interaction techniques such as touch and efficient simplified control of quality control and risk of transmission [6]. To predict disease, Imai, et al. carried out computer simulations of possible routes of infection in Wuhan with an emphasis on communication between individuals.
Recently in 2021, built a mathematical epidemic model for the outbreak of the new COVID-19 coronavirus. New considerations for evaluating and controlling the COVID-19 outbreak build on the SEIQR Pandemic Model using real data on the spread of COVID-19 in Saudi Arabia [4]. Based on the description above, in this study a mathematical model of the spread of COVID-19 with the SVIQR epidemic model will be formed, where the population class in the model is divided into five compartments, namely susceptible (S), vaccinated (V), infected (I), quarantine (Q), as well as recovered (R). This model was chosen with the aim of knowing the effect of vaccination and quarantine on controlling the spread of COVID-19 in Indonesia. This research is expected to provide a mathematical analysis of the effectiveness of vaccination and quarantine policies in minimizing the impact of the spread of COVID-19 in Indonesia.

2. The Spread of COVID-19 with SVIQR Compartments Model

In this paper, we will discuss about the spread of COVID-19 with $SVIQR$ compartments epidemic model where the population in the model is divided into five compartments, there are susceptible (S), vaccinated (V), infected (I), quarantine (Q), and recovered (R) classes. The model of the $SVIQR$ epidemic on COVID-19 is below:

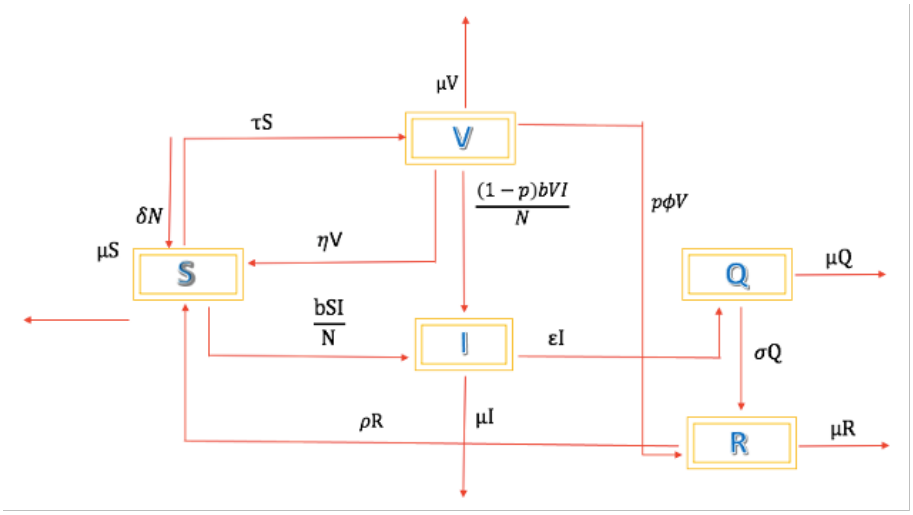

Figure 1. Flowchart of COVID-19 Mathematical Model with $SVIQR$ Compartment

The $SVIQR$ model is a development of the basic SIR model. Susceptible population in this model is assumed to be constant and closed, so there is no additional population that enter to the community due to displacement such as immigration, emigration and others. The rate of susceptible population increases and become infected if they come in to contact with individual who infected with COVID-19.

From the flowchart above, we can formulate the differential equation models for the spread of COVID-19 using $SVIQR$ compartment as follow:

$$\frac{dS}{dt} = \delta N + \rho R + \eta V - \tau S - \frac{bSI}{N} - \mu S \tag{1}$$

$$\frac{dV}{dt} = \tau S - \eta V - \mu V - p\phi V - \frac{(1-p)bVI}{N} \tag{2}$$

$$\frac{dI}{dt} = \frac{bSI}{N} + \frac{(1-p)bVI}{N} - \varepsilon I - \mu I \tag{3}$$

$$\frac{dQ}{dt} = \varepsilon I - \mu I - \sigma Q \tag{4}$$

$$\frac{dQ}{dt} = \sigma Q + p\phi V - \rho R - \mu R \tag{5}$$

With $S(0) > 0$,$V(0) > 0$,$I(0) > 0$,$Q(0) > 0$, and $R(0) > 0$. Based on information that we get from usnews.com, there are cases where someone who has received the vaccine can actually be exposed the COVID-19. Therefore, a new compartment was developed, that is vaccinated population that obtained from the addition of susceptible and exposed populations who have been vaccinated, both the first and second stages of vaccines.
Vaccination is divided into two stages, first stage and second stage. Population that has received vaccine from both first and second stages is categorized into vaccinated population. In vaccinated population, individual that fail after receiving the first or second stage of the vaccine, included in the infected population, while the population that succeed in first or second stage, it means that there is no COVID-19 infection during the specified model time, is categorized into recovered population.
We assumed that infected population will recover from the COVID-19 by given special treatment and entering them to quarantine population, then at a certain time, the quarantine population will enter to recovered population with natural immunity. Population that enters to recovered population with vaccines or natural immunity, will return to susceptible population if the immunity period has expired because it is assumed that individual can re-infected. The rate from recovered to the susceptible population is as long as the vaccine immunity period has expired, which is approximately 6 months. Defined δN is the rate of increase in population or birth rate. Note that:

$$N(t) = S(t) + V(t) + I(t) + Q(t) + R(t) \tag{6}$$

$$\frac{dN}{dt} = \delta N - \mu N \tag{7}$$

Since it assumed that birth rate (δ) and death rate (μ) are same, so we assume that $\frac{dN}{dt} = 0$, and we get $N = \frac{\delta}{\mu}$, it is mean that population in the model is constant. Thus, the $SVIQR$ mathematical model can be scaled into the following equation:

$$\frac{dS}{dt} = \delta + \rho R + \eta V - (\tau = bI + \mu)S \tag{8}$$

$$\frac{dV}{dt} = \tau S - (\eta + \mu + p\phi + (1-p)bI)V \tag{9}$$

$$\frac{dI}{dt} = (bS + (1-p)bV - \varepsilon - \mu)I \tag{10}$$

$$\frac{dQ}{dt} = (\varepsilon - \mu)I - \sigma Q \tag{11}$$

$$\frac{dR}{dt} = \sigma Q + p\phi V - (\rho + \mu)R \tag{12}$$

Parameter δ is rate of the increases in susceptible population due to the natural birth rate. Transmission rate β is probability of infected with the number of direct contacts between susceptible and infected individuals per time. Parameter μ is death rate, in this case death due to virus infection, so deaths because other incident are ignored. The rate of infected population being included in quarantine population is expressed by parameter α, while the recovery rate to recovered population from infected population is expressed by parameter ε.

3. The Spread of COVID-19 with $SVIQR$ Compartments Model

The basic assumption used in this research as follows: total population constant; birth rate and death rate are same; infected individuals can recover from the COVID-19 after quarantine; recovered individuals can reinfected; There are only natural deaths, deaths from other causes are ignored; All individuals who enter the recovered population have acquired immunity for 6 months and after 6 months they will return to the susceptible population at a rate ρ.

4. Compartments and Parameter Description

Notation of each compartment on Differential Equation Model (or Equation (x)) can be seen at Table 1.

Table 1. Compartment Description

Compartment	Description
`S(t)`	Susceptible
`V(t)`	Vaccinated
`I(t)`	Infected
`Q(t)`	Quarantine
`R(t)`	Recovered

Therefore, the parameters that included on Differential Equation Model (or Equation (x)) contained at Table 2.

5. Determination of Basic Reproduction Number (R_0)

Basic reproduction number (R_0) defined as the expected number of cases resulting from a single patient having the ability to transmit the disease at the time when virus enters an all-healthy population, during the infectious period. In other words, the quantity is a multiple factor (multiplication factor) of the initial case. Basic reproduction number (R_0) as the expected number of secondary cases per primary case in population. In mathematical concepts, this quantity has threshold value of 1. If $R_0 > 1$ is obtained, this indicates that during the infection period, more than one secondary case has been produced from one primary case. But on the other hand, if $R_0 < 1$ then during the infection period, the interaction does not produce secondary cases from the primary case.

This basic reproduction number is a dimensionless quantity and generally a bifurcation point of a system. This stability change is occurred at the threshold value $R_0 = 1$ where the local stability changes from non-endemic conditions to endemic conditions. In general, the value of

Table 2. Parameter Description

x	Description
δ	Recruitment rate
b	Transmission 1 rate (susceptible $\rightarrow$ infected)
ρ	Reinfection rate (individual vaccine immunity term inverse)
μ	Natural death rate
ε	Transmission 2 rate (infected $\rightarrow$ quarantine)
τ	Vaccination rate average
σ	COVID-19 recovery rate
η	Vaccine immunity term average
ϕ	Vaccination effectiveness transition rate
p	Vaccination success proportion

R_0 can be obtained by searching for the existence conditions of the endemic equilibrium point of the system or from the stability of the non-endemic equilibrium point or the stability of the endemic equilibrium point. In this paper, for determining R_0 we use the Next Generation Matrix (NGM) method.

$$\frac{dV}{dt} = \tau S - (1-p)bVI - p\phi V - \mu V \tag{13}$$

$$\frac{dI}{dt} = bSI + (1-p)bVI - \varepsilon I - \mu I \tag{14}$$

$$\frac{dV}{dt} = \tau S - (\eta + \mu + p\phi + (1-p)bI)V \tag{15}$$

$$\frac{dI}{dt} = (bS + (1-p)bV - \varepsilon - \mu)I \tag{16}$$

The matrix is decomposed into $\mathbf{F} - \mathbf{V}$

$$\mathbf{F} = \begin{pmatrix} (1-p)bVI \\ bSI + (1-p)bVI \end{pmatrix} \tag{17}$$

$$\mathbf{V} = \begin{pmatrix} -\tau S + p\phi V + \mu V \\ \varepsilon I + \mu I \end{pmatrix} \tag{18}$$

And the define Jacobian matrix

$$Jac_{\mathbf{F}} = \mathbb{F} = \begin{pmatrix} -(1-p)bI & -(1-p)bV \\ (1-p)bI & bS + (1-p)bV \end{pmatrix} \tag{19}$$

$$Jac_{\mathbf{V}} = \mathbb{Z} = \begin{pmatrix} p\phi + \mu & 0 \\ 0 & \varepsilon + \mu \end{pmatrix} \tag{20}$$

Substitution of non-endemic equilibrium point $(S, 0, V)$ to Jacobian matrix

$$\mathbb{F} = \begin{pmatrix} 0 & -(1-p)bV \\ 0 & bS + (1-p)bV \end{pmatrix} \tag{21}$$

$$\mathbb{Z} = \begin{pmatrix} p\phi + \mu & 0 \\ 0 & \varepsilon + \mu \end{pmatrix} \tag{22}$$

Define invers of matrix $\mathbb{Z}$

$$\mathbb{Z}^{-1} = \begin{pmatrix} \frac{1}{p\phi+\mu} & 0 \\ 0 & \frac{1}{\varepsilon+\mu} \end{pmatrix} \tag{23}$$

The next generation matrix

$$\mathbb{F}\mathbb{Z}^{-1} = \begin{pmatrix} 0 & -(1-p)bV \\ 0 & bS + (1-p)bV \end{pmatrix} \begin{pmatrix} \frac{1}{p\phi+\mu} & 0 \\ 0 & \frac{1}{\varepsilon+\mu} \end{pmatrix} \tag{24}$$

$$\mathbb{F}\mathbb{Z}^{-1} = \begin{pmatrix} 0 & \frac{-(1-p)bV}{\varepsilon+\mu} \\ 0 & \frac{bS+(1-p)bV}{\varepsilon+\mu} \end{pmatrix} \tag{25}$$

So, we get eigenvalue $\mathbb{F}\mathbb{Z}^{-1}$ as below:

$$\lambda_1 = \frac{b(-pV + 2V)}{\varepsilon + \mu} \tag{26}$$

$$\lambda_2 = 0 \tag{27}$$

$$R_0 = max\{\lambda_i\} = \frac{b(-pV + 2V)}{\varepsilon + \mu} \tag{28}$$

From the results above, it can be interpreted that in this case, each an individual is able to transmit the virus to as many as $\frac{b(-pV+2V)}{\varepsilon+\mu}$ individuals. In this model, if we get $\frac{b(-pV+2V)}{\varepsilon+\mu} > 1$, indicates that during the period of infection, more than one secondary case has been produced from one primary case, so define this is endemic case because of large transmission or each individual can affect as many as $\frac{b(-pV+2V)}{\varepsilon+\mu}$ other individuals exposed to the virus. While if we get $\frac{b(-pV+2V)}{\varepsilon+\mu} < 1$, then during the period of infection occurs, the interaction does not produce secondary cases from the primary case, so it is impossible for an endemic to occur because transmission is very small or each individual is unable to infect other individuals.

6. Local Stability Analysis of Equilibrium Point

Equilibrium point is obtained when the rate of change each population is zero, when $\frac{dS}{dt} = \frac{dV}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = 0$ [7]. $SVIQR$ mathematical model has two points of equilibrium, non-endemic equilibrium point (E_1) and the endemic equilibrium point (E_2). Non endemic equilibrium point is $E_1 = (S_1, V_1, 0, 0, R_1)$.

$$S_1 = \frac{\delta(\mu + \rho)N(p\phi + \eta + \mu)}{\mu(\mu p\phi + p\phi\rho + p\phi\tau + \eta\mu + \eta\rho + \mu^2 + \mu\rho + \mu\tau + \rho\tau)} \tag{29}$$

$$V_1 = \frac{N\delta\tau(\mu + \rho)}{\mu(\mu p\phi + p\phi\rho + p\phi\tau + \eta\mu + \eta\rho + \mu^2 + \mu\rho + \mu\tau + \rho\tau)} \tag{30}$$

$$R_1 = \frac{p\phi N\delta\tau}{\mu(\mu p\phi + p\phi\rho + p\phi\tau + \eta\mu + \eta\rho + \mu^2 + \mu\rho + \mu\tau + \rho\tau)} \tag{31}$$

The SVIQR mathematical model is non-linear differential equation systems. Then, to analyze the stability required linearization using Jacobian matrix. Local stability of a system can be

determined by the eigenvalues of the Jacobian matrix form. Analysis of non-endemic equilibrium point E_1 is determined by substituting the equilibrium point of E_1 into Jacobian matrix.

$$J = \begin{pmatrix} -\tau - \frac{bI}{N} - \mu & \eta & -\frac{bS}{N} & 0 & \rho \\ \tau & -p\phi - \eta - \mu - \frac{(1-p)bI}{N} & -\frac{(1-p)bV}{N} & 0 & 0 \\ \frac{bI}{N} & \frac{(1-p)bI}{N} & \frac{bS}{N} + \frac{(1-p)bV}{N} - \varepsilon - \mu & 0 & 0 \\ 0 & 0 & \varepsilon - \mu & -\sigma & 0 \\ 0 & p\phi & 0 & \sigma & -\mu - \rho \end{pmatrix} \tag{32}$$

Furthermore, the characteristic equation can be formed by $det(\lambda I - J_1)0$ and we get five λ as roots of equation.

$$\lambda_1 = -\mu - \tau \tag{33}$$

$$\lambda_2 = -p\phi - \eta - \mu \tag{34}$$

$$\lambda_3 = \frac{(1-p)b\delta\tau(\mu+\rho)}{\mu(\mu p\phi + p\phi\rho + p\phi\tau + \eta\rho + \mu^2 + \mu\rho + \mu\tau + \rho\tau)} \tag{35}$$

$$\lambda_4 = -\sigma \tag{36}$$

$$\lambda_5 = -\mu - \rho \tag{37}$$

The equilibrium point of a system is stable if the roots of characteristic equation of a Jacobian matrix have eigenvalues with real negative part. If $\lambda_i < 0$ then the equilibrium point E_1 of the model is stable asymptotically. But, if $\lambda_i > 0$ then the equilibrium point E_1 of the model is unstable.

From the result above, we get that $\lambda_1 = -\mu - \tau$, where μ is positive number and τ is positive number too, so the real part of the first eigen is negative. From the next eigenvalue, $\lambda_2 = -p\phi - \eta - \mu$ where p is positive number, ϕ is positive number and η is positive number too, so the real part of the second eigenvalue is negative. Because we choose the values of all compartments are positive, whereas the values of first and second eigenvalue are negative, so the eigen value $\lambda_3, \lambda_4, \lambda_5$ are negative too. Thus, the model equation has each of the eigenvalue is negative. So, it can be concluded that E_1 is a local asymptotic stable point.

7. Numerical Simulation

In this chapter we discuss about numerical simulation using software. Parameter values that we used are parameter values when endemic condition ($R_0 > 1$). Numerical simulation aimed to determine the predict of future conditions based on several scenario vaccination and quarantine were made. The initial value used is based on assumption from real condition in Indonesia which is then scaled in Table 3. Therefore, the parameter values on Differential Equation Model contained at Table 4.

Based on the results, we concluded that vaccinated compartment and quarantine compartment give a positive effect on the spread of COVID-19 in human. The conclusion can be seen from the graphic results above that determined the mathematical model of COVID-19 with vaccinated and quarantine better than population without vaccinated and quarantine.

Table 3. Compartment Value

Compartment	Description	Value
S(t)	Susceptible	0.9187814
V(t)	Vaccinated	0.038274
I(t)	Infected	0.0429456
Q(t)	Quarantine	0.0429456
R(t)	Recovered	0.0812196

Table 4. Parameter Value

x	Description	Value
δ	Recruitment rate	$\frac{1}{70\times365}$
b	Transmission 1 rate (susceptible $\rightarrow$ infected)	0.1
ρ	Reinfection rate (individual vaccine immunity term inverse)	$\frac{1}{270}$
μ	Natural death rate	$\frac{1}{70\times365}$
ε	Transmission 2 rate (infected $\rightarrow$ quarantine)	$\frac{1}{14}$
τ	Vaccination rate average	$\frac{1}{365}$
σ	COVID-19 recovery rate	$\frac{1}{27}$
η	Vaccine immunity term average	$\frac{1}{365}$
ϕ	Vaccination effectiveness transition rate	0.65
p	Vaccination success proportion	0.99

8. Conclusion

The population class in $SVIQR$ epidemic model for COVID-19 divided into five compartments. The susceptible population, the vaccinated population, the infected population, the quarantine population and the recovered population that has natural immunity and vaccine immunity. Based on the diagram transmission, $SVIQR$ model of COVID-19 can be determined with this differential equation, $\frac{dS}{dt} = \delta + \rho R + \eta V - (\tau = bI + \mu)S$; $\frac{dV}{dt} = \tau S - (\eta + \mu + p\phi + (1-p)bI)V$; $\frac{dI}{dt} = (bS + (1-p)bV - \varepsilon - \mu)I$; $\frac{dQ}{dt} = (\varepsilon - \mu)I - \sigma Q$; $\frac{dR}{dt} = \sigma Q + p\phi V - (\rho + \mu)R$. Basic reproduction number for this model is $R_0 = max\{\lambda_i\} = \frac{b(-pV+2V)}{\varepsilon+\mu}$, it can be represented that if we get $R_0 = max\{\lambda_i\} = \frac{b(-pV+2V)}{\varepsilon+\mu} > 1$, indicates more than one secondary case has been produced from one primary case, so define this is endemic case. While if we get $R_0 = max\{\lambda_i\} = \frac{b(-pV+2V)}{\varepsilon+\mu} < 1$, so it is impossible for an endemic to occur because transmission is very small or each individual is unable to infect other individuals.

9. References

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