The sensitivity of Covid-19 spread model parameter: an effort to point out the importance of the detection program

R Ratianingsih¹, H Hajar¹, A A Rahmah¹ and A I Jaya¹∗
¹ Mathematics Study Program, Tadulako University, Palu, Indonesia
*Email: jayaindraagus@gmail.com

Abstract: The pandemic of covid-19 has been spread in entire the world. Unfortunately, some regions in Indonesia are ignoring the detection program as an important prevention in control the disease. This research notice some parameters that play a role in the behaviour of covid-19 spread model. The parameters describe the level and rate of the transition and interaction behaviour of the variables, the number of susceptive, unsympthom, quarantined, infected and recovered population with respect to time. The reproduction number, governed from the matrix generation of the mathematical model, shows that the parameters determine the disease spread status. The mathematical model is governed from the disease spread diagram that derives a nonlinear partial differential equation system. The reproduction number is nothing but the thresh hold of the spread disease. To keep the disease spread to be controllable, the reproduction number of the model have to be arranged less than the thresh hold. The appearance of the parameters interpret that the detection program in important to be pointed out.

1. Introduction
In early 2020, the world was shocked by the incidence of severe infections with unknown causes, which began with a report to the World Health Organization (WHO) that there were 44 severe pneumonia patients in an area, namely Wuhan City, Hubei Province, China at 2019. On January 10, 2020, the cause was identified and the genetic code was obtained, namely the new coronavirus [1]. World Health Organization name the new virus Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) and the name of the disease as Coronavirus Disease 2019 (Covid-19). The serious impact of the spread of Covid-19 can be seen from the number of victims that continues to increase over time. Recent reports from WHO globally have noted that more than 15 million people have been infected with the disease with no less than 600 thousand among them die. The spread of the Corona virus that has spread to all parts of the world has various impacts on the lives of living things around the world [2].

Covid-19 can spread very quickly and has spread to almost all countries, including Indonesia, in just a few months. It makes several countries implement policies to enforce it lockdown in order to prevent the spread of the Corona virus. In Indonesia, the first Covid-19 case was confirmed on Monday 2 March 2020 when President Joko Widodo announced that two Indonesians had tested positive for the Corona virus, it was a 31-year-old woman and her mother [3].

Covid-19 is mainly spread through respiratory droplets secreted by someone who is coughing or has other symptoms such as fever or feeling tired. Many people infected with Covid-19 experience only mild symptoms, especially in the early stages. Therefore, Covid-19 can be transmitted from people who have only mild symptoms, such as a mild cough, but feel well. Several reports suggest that people
without symptoms can transmit the virus [2]. People without symptoms are those who do not show symptoms of Covid-19, but have had close contact with people who have tested positive for Covid-19. Based on the information from the researchers, this group has a big role in the spread of Covid-19 so that individuals from without symptoms class need to carry out a rapid test [4].

The SOQIR model will be constructed to direct the involvement of all population groups that build their dynamic system. This study only discusses the spread of Covid-19 through the interaction of the population of people without symptoms in Palu City and only discusses disease-free conditions against models created by the authors. The mathematical model is built on existing facts and assumptions by taking into account the interactions between populations that play a role in the spread of Covid-19. Then an analysis of the mathematical model is carried out so that the equilibrium point is obtained. Next, determine the basic reproduction number \( R_0 \). To simulate deployment disease represented by a model of asymptomatic person interaction on the spread of Covid-19 math software Maple13 used to describe the growth curve of each model constructing variable.

2. Materials and method

In 2010, Mishra and Jha developed the SEIQRS epidemic model (Susceptible-Infected-Quarantined-Recovered-Susceptible). This model uses a constant population growth rate and uses a bilinear infection incidence rate. In this model, the infection rate is only influenced by the interaction between susceptible individuals (S) and infected individuals (I). In the model, infected individuals recover immediately without being quarantined first. A similar study was conducted by Wang, et al. (2014) with the SEIQRS model by modifying the model studied by Mishra and Jha by dividing the infection rate into two types, namely the first infection rate depends on the interaction between susceptible individuals (S) and latent individuals (E) and the rate of second infection depends on the interaction between susceptible individual (S) and infected individual (I).

The SOQIR model divides a population into five categories, namely, S (Susceptible), O (Without Symptoms), Q (Quarantined), I (Infected), and R (Recovered). Susceptibles are some healthy individuals that have a chance and vulnerable to be infected. While unsymptoms are those, who do not show symptoms of COVID-19, but have had close contact with people who have tested positive for COVID-19. Q is isolated or individually quarantined. Infected is individuals who tested positive for infection, and Recovered is individuals who are declared cured and are assumed to have immunity to the virus but they could be infected again. In this study, a modified SOQIR model is used with the following assumptions:

a. There is an immigration process in the Susceptible subpopulation (S).
b. Individuals in an un-symptoms subpopulation could recover and return to the Susceptive subpopulation.
c. There is an interaction between Susceptive individual population and Quarantined individual.
d. The spread of the disease occurs when there is contact from an individual in a Suscepted class with an infected individual in the un-symptoms (O), Quarantine (Q), and Infected (I) classes.

3. Results and discussion

3.1. The mathematical model

The SOQIR model scheme used to govern the mathematical model could be seen in Figure 1:
The governing equation is a differential equation that represented as follows:

\[
\frac{dS}{dt} = (\alpha + \varepsilon) + \psi R + \tau O - \beta SI - (\gamma O + \theta Q)S - \mu S \tag{1}
\]

\[
\frac{dO}{dt} = \beta SI - (\delta + \tau + \omega)O \tag{2}
\]

\[
\frac{dQ}{dt} = \delta O + (\gamma O + \theta Q)S - (\phi + \sigma + \omega)Q \tag{3}
\]

\[
\frac{dI}{dt} = \phi Q - (\rho + \omega)I \tag{4}
\]

\[
\frac{dR}{dt} = \rho I + \sigma Q - \psi R \tag{5}
\]

Where: \( S + O + Q + I + R = 1 \)

The stated parameters of the system and its description are tabulated in Table 1.

### Table 1. Parameters list

| Parameter | Description |
|-----------|-------------|
| \( \alpha \) | Birth Rate |
| \( \varepsilon \) | Immigration Rate |
| \( \beta \) | Contact Rate |
| \( \delta \) | The ratio of transmission of without symptoms to be quarantined |
| \( \gamma \) | The interaction rate of susceptible and without symptoms |
| \( \theta \) | The interaction rate of susceptible and quarantine |
| \( \phi \) | The transmission rate of quarantine to be infected |
| \( \tau \) | The recovery rate of without symptoms |
| \( \rho \) | The recovery rate of the infected |
| \( \sigma \) | The recovery rate of the quarantine |
| \( \psi \) | The losing rate of immunity |
| \( \mu \) | Mortality rate |
| \( \omega \) | The death rate caused by Covid-19 |

### 3.2. Determining the critical values

The critical point of a system of nonlinear differential equations can be obtained by looking at equations (1) - (5) in a state of stagnation or no change in the population as follows:

\[
\frac{ds}{dt} = 0, \frac{dO}{dt} = 0, \frac{dQ}{dt} = 0, \frac{dI}{dt} = 0, \frac{dR}{dt} = 0.
\]

Such that:

\[
(\alpha + \varepsilon) + \psi R + \tau O - \beta SI - (\gamma O + \theta Q)S - \mu S = 0 \tag{6}
\]

\[
\beta SI - (\delta + \tau + \omega)O = 0 \tag{7}
\]
\[\delta O + (\gamma O + \theta Q)S - (\phi + \sigma + \omega)Q = 0 \]  
\[\phi Q - (\rho + \omega)I = 0 \]  
\[\rho I + \sigma Q - \psi R = 0 \]  

The substitution of \( I = 0 \) to equation (7) that determine the disease-free equilibrium point gives the zero value of \( O \) such that equation (8) also gives the zero value of \( Q \). This result leads equation (10) to the zero value of \( R \). Substitute the zero value of \( I, O, Q \) and \( R \) to the equation (6) gives \((\alpha + \varepsilon) - \mu S = 0 \Rightarrow S = \frac{\alpha + \varepsilon}{\mu}\) such that we have the disease-free equilibrium \(\left(\frac{\alpha + \varepsilon}{\mu}, 0,0,0,0\right)\).

3.3. Determining the basic reproduction number

Basic reproduction numbers \(R_0\) can be obtained using the Next Generation Matrix method. In equation (1)–(5) shows three infected subpopulations, namely \(O, Q,\) and \(I\) and two uninfected subpopulations, namely \(S\) and \(R\). Furthermore, a matrix can be built containing an average increase in the number of new infected individuals involving the three infected subpopulations.

Supposed that \(x = (O, Q, I)^T\), so that equations (1) – (5) can be written as:
\[
d\frac{dx}{dt} = F(x) - V(x)
\]
where \(F(x)\) is a transmission matrix, which contains the rate of infection of new individuals due to contact, and \(V(x)\) is the transition matrix, a matrix that features the rates of transfer in and out of the infected subpopulation. Those two matrices could be written as:
\[
F(x) = \begin{bmatrix}
\beta SI \\
(\gamma O + \theta Q)S \\
0
\end{bmatrix}
\quad \text{and} \quad
V(x) = \begin{bmatrix}
(\delta + \tau + \omega)O \\
(\phi + \sigma + \omega)Q \\
(\rho + \omega)I
\end{bmatrix} - \begin{bmatrix}
0 \\
0 \\
0
\end{bmatrix}
\]

Then a matrix of \(T(x)\) and \(E(x)\) are the Jacobian matrices of \(F(x)\) and \(V(x)\) evaluated at a disease-free of critical point \(T_0 = \left(\frac{\alpha + \varepsilon}{\mu}, 0,0,0,0\right)\), that are:
\[
T(x) = \begin{bmatrix}
0 & 0 & \beta \frac{\alpha + \varepsilon}{\mu} \\
\gamma \frac{\alpha + \varepsilon}{\mu} & 0 & 0 \\
0 & 0 & 0
\end{bmatrix}
\quad \text{dan} \quad
E(x) = \begin{bmatrix}
\delta + \tau + \omega & 0 & 0 \\
-\delta & \phi + \sigma + \omega & 0 \\
0 & -\phi & \rho + \omega
\end{bmatrix}
\]

The next Generation Matrix is obtained from the multiplication between \(T(x)\) and the inverse of \(E(x)^{-1}\) as follow:
\[
T(x)E(x)^{-1} = \begin{bmatrix}
0 & 0 & \beta \frac{\alpha + \varepsilon}{\mu} \\
\gamma \frac{\alpha + \varepsilon}{\mu} & 0 & 0 \\
0 & 0 & 0
\end{bmatrix} \begin{bmatrix}
\frac{1}{\delta + \tau + \omega} & 0 & 0 \\
\frac{1}{\phi + \sigma + \omega} & 0 & 0 \\
\frac{1}{\rho + \omega} & 0 & 0
\end{bmatrix}
\]
\[
T(x)E(x)^{-1} = \begin{bmatrix}
k \frac{\beta(\alpha + \varepsilon)\phi}{\mu(\rho + \omega)(\phi + \sigma + \omega)} & \beta \frac{\alpha + \varepsilon}{\mu(\rho + \omega)} \\
l \frac{\beta(\alpha + \varepsilon)\phi}{\theta(\alpha + \varepsilon)} & 0 \\
0 & 0
\end{bmatrix}
\]

where:
\[
x = \frac{\delta}{(\phi + \sigma + \omega)(\delta + \tau + \omega)}
\]
\[
y = \frac{\phi \delta}{(\rho + \omega)(\phi + \sigma + \omega)(\delta + \tau + \omega)}
\]
The $R_0$ value could be found by specifying the largest eigen value of $T(x)E(x)^{-1}$, expressed as $R_0 = \rho(T(x)E(x)^{-1})$, that gives $R_0 = \frac{\beta(\alpha + \varepsilon)\phi\delta + \theta(\alpha + \varepsilon)(\rho + \omega)(\delta + \tau + \omega)}{\mu(\rho + \omega)(\phi + \sigma + \omega)(\delta + \tau + \omega)}$.

3.4. Stability of the disease free point

The stability of the disease free point is satisfied when $|R_0| < 1$ that gives

$$\frac{\beta(\alpha + \varepsilon)\phi\delta + \theta(\alpha + \varepsilon)(\rho + \omega)(\delta + \tau + \omega)}{\mu(\rho + \omega)(\phi + \sigma + \omega)(\delta + \tau + \omega)} < 1$$

Let us consider the case of $\alpha = 0, \omega = 0, \varepsilon = 0$

$$\begin{align*}
\text{a.} & \quad \frac{\beta(\alpha + \varepsilon)\phi\delta + \theta(\alpha + \varepsilon)(\rho + \omega)(\delta + \tau + \omega)}{\mu(\rho + \omega)(\phi + \sigma + \omega)(\delta + \tau + \omega)} < 0 \quad \text{such that we have} \quad \beta(\alpha + \varepsilon)\phi\delta + \theta(\alpha + \varepsilon)(\rho + \omega)(\delta + \tau + \omega) < 0 \\
\text{b.} & \quad \frac{\beta(\alpha + \varepsilon)\phi\delta + \theta(\alpha + \varepsilon)(\rho + \omega)(\delta + \tau + \omega)}{\mu(\rho + \omega)(\phi + \sigma + \omega)(\delta + \tau + \omega)} < 0 \quad \text{such that we have} \quad \beta(\alpha + \varepsilon)\phi\delta + \theta(\alpha + \varepsilon)(\rho + \omega)(\delta + \tau + \omega) < 0 \\
& \quad \text{We come to the requirement of } \beta \text{ as follow} \\
& \quad \beta(\alpha + \varepsilon)\phi\delta < \mu(\rho + \omega)(\phi + \sigma + \omega)(\delta + \tau + \omega) - \theta(\alpha + \varepsilon)(\rho + \omega)(\delta + \tau + \omega) \\
& \quad \beta(\alpha + \varepsilon)\phi\delta < (\mu(\phi + \sigma + \omega) - \theta(\alpha + \varepsilon))(\rho + \omega)(\delta + \tau + \omega) \quad \text{that gives the threshold of } \beta < \frac{(\alpha + \varepsilon)\phi\delta}{(\alpha + \varepsilon)}
\end{align*}$$

3.5. Stability analysis of the critical condition

$T_1 = \left(\frac{\alpha + \varepsilon}{\mu}, \frac{\alpha + \varepsilon}{\mu}, 0, 0, 0, 0\right)$ is a non zero critical condition such that it is necessary to transform the coordinates so that $T_1$ is a zero critical condition in the new coordinates $T_1^* = (0, 0, 0, 0, 0, 0)$. The stability of the critical condition is determined based on the eigenvalue of the Jacobian matrix obtained by linearization as follow

$$J_1 = \begin{bmatrix}
-\mu & \tau - \frac{\gamma(\alpha + \varepsilon)}{\mu} & -\frac{\theta(\alpha + \varepsilon)}{\mu} & -\frac{\beta(\alpha + \varepsilon)}{\mu} & \psi \\
0 & -\delta - \tau - \omega & 0 & 0 & 0 \\
0 & \delta + \frac{\gamma(\alpha + \varepsilon)}{\mu} & -\frac{\theta(\alpha + \varepsilon)}{\mu} & -\phi - \sigma - \omega & 0 \\
0 & 0 & \phi & -\rho - \omega & 0 \\
0 & 0 & \sigma & \rho & -\psi
\end{bmatrix}$$
The Eigen value of $J_1$ is obtained by determining the det$(J_1 - \lambda I) = 0$ as follow:

$$\begin{vmatrix} -\mu - \lambda & \tau - \frac{\omega(a + e)}{\mu} & -\frac{\theta(a + e)}{\mu} & -\frac{\beta(a + e)}{\mu} & \psi \\ 0 & -\delta - \tau - \omega - \lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{vmatrix} = 0$$

det

that gives the characteristic equations in $\lambda$ are as follows

$$(\mu - \lambda)(\psi + \lambda)(a_0 \lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3) = 0$$

(12)

where:

$$a_0 = -\mu^2$$
$$a_1 = (-3\mu^2 - \mu^2 \delta - \mu^2 \tau - \mu^2 \phi - \mu^2 \sigma - \mu^2 \rho + \mu \theta \alpha + \mu \theta \varepsilon)$$
$$a_2 = (-3\mu^2 - \mu^2 \delta - \mu^2 \tau - \mu^2 \phi - \mu^2 \sigma - \mu^2 \rho + \mu \theta \alpha + \mu \theta \varepsilon)$$
$$a_3 = (-\mu^2 - \mu^2 \delta - \mu^2 \tau - \mu^2 \phi - \mu^2 \sigma - \mu^2 \rho + \mu \theta \alpha + \mu \theta \varepsilon)$$

Equation (12) gives two negative eigenvalues $\lambda_1 = -\mu$ and $\lambda_2 = -\mu - \psi$, while the other eigenvalues are difficult to obtain explicitly. It will be shown that the 3rd order of polynomial in $\lambda$ in equation (12) has a negative eigenvalue through the following Routh-Hurwitz Criterion.

| Table 2. Routh Hurwitz Criterion |
|----------------------------------|
| $\lambda^3$ | $a_0$ | $a_2$ |
| $\lambda^2$ | $a_1$ | $a_3$ |
| $\lambda^1$ | $b_1$ | 0 |
| $\lambda^0$ | $c_1$ | 0 |

where $b_1 = \frac{(a_1 a_3) - (a_0 a_2)}{a_1}$ and $c_1 = \frac{(b_1 a_3) - (b_2 a_1)}{b_1}$

For simplicity in terms of computation, an example is carried out as follows:

$$p = \mu$$
$$q = (3\omega + \delta + \tau + \phi + \sigma + \rho)$$
$$r = \theta(\alpha + \varepsilon)$$
$$t = (3\omega^2 + (\delta + \tau + \phi + \sigma + \rho)2\omega + (\delta + \tau + \phi + \sigma)\rho + (\delta + \tau)(\phi + \sigma))$$
$$m = (\delta + \tau + 2\omega + \rho)$$
$$n = \mu(\rho + \omega)(\delta + \tau + \omega)(\phi + \sigma + \omega)$$
$$w = \beta \phi \delta(\alpha + \varepsilon) + \theta(\alpha + \varepsilon)(\delta + \tau + \omega)(\phi + \sigma + \omega)$$
$$v = \beta(\alpha + \varepsilon)\phi(\gamma \alpha + \gamma \varepsilon)$$

Applying the Routh-Hurwitz criterion, the cubic equation of $\lambda$ will have roots with negative real parts if $a_0 < 0$, $a_1 < 0$, $a_3 < 0$, $b_1 < 0$, and $c_1 < 0$ since $p, q, r, t, m, n, w, v < 0$ so that $a_0 < 0$, $a_1 < 0$, $a_3 < 0$, $b_1 < 0$, and $c_1 < 0$ must be:

$$(1 - R_0) > 0 \text{ or } R_0 < 1$$
Since \( p, q, r, t, m, n, w, v < 0 \) the disease-free equilibrium \( T_1 = \left(\frac{\alpha + \varepsilon}{\mu}, 0, 0, 0, 0\right) \), is locally asymptotically stable if \( R_0 < 1 \).

### 3.6. Simulation

The dynamic of the solutions is simulates using Maple13 by providing some parameter values under the \( R_0 \) requirements. Simulations are also conducted by providing some initial value of variables against the critical condition to describe the Covid-19 spread curve in each subpopulation, as shown in Table 3 and Table 4.

#### Table 3. Parameters value

| Parameters | Value | Reference |
|------------|-------|-----------|
| \( \alpha \) | 0.025 | Estimated |
| \( \varepsilon \) | 0.015 | Estimated |
| \( \beta \) | 0.002 | Public Health Office |
| \( \delta \) | 0.44 | Public Health Office |
| \( \gamma \) | 0.30 | Estimated |
| \( \theta \) | 0.30 | Estimated |
| \( \phi \) | 0.21 | Public Health Office |
| \( \tau \) | 0.09 | Estimated |
| \( \rho \) | 0.86 | Public Health Office |
| \( \sigma \) | 1.34 | Public Health Office |
| \( \psi \) | 0.30 | Public Health Office |
| \( \mu \) | 0.04 | Estimated |
| \( \omega \) | 0.35 | Public Health Office |

#### Table 4. The initial value

| Subpopulation | Initial Value | Reference |
|---------------|---------------|-----------|
| \( S(0) \)   | 0.99782       | Central Bureau of Statistics |
| \( O(0) \)   | 0.00134       | Public Health Office |
| \( Q(0) \)   | 0.00059       | Public Health Office |
| \( I(0) \)   | 0.00012       | Public Health Office |
| \( R(0) \)   | 0.00010       | Public Health Office |

Using the initial values, the dynamics of COVID-19 spread through the interaction of un symptoms people at disease-free critical condition. The dynamic are figured with the horizontal axis time \( (t) \) in day unit time, and the vertical axis states the number of \( S, O, Q, I \) or \( R \) population. It means that the figure represents the change of such population with respect to time. Some normalization are needed in order to have a good figure.
Figure 2. The dynamic of subpopulations with respect to time of (a) Susceptible, (b) Unsymptom, (c) Quarantined, (d) Infected, (e) Recovered.
Figure 2.a shows that the number of susceptible individuals increases with respect to time and tend to the carrying capacity in 140 days. The raising number of susceptible individuals at the point to 1. Every healthy individual but susceptible have a very high chance of disease infection. Figure 2.b shows that the number of unsymptoms individual in the first 10 days decreased drastically, due to the transition to be the recovered subpopulation and others are recovering from the symptom.

Figure 2.c also shows that the proportion of quarantine individuals decrease quite drastically, tend to stagnant in 120 days and disappear after 165th days. It is due to the presence of quarantine individuals who recovered from the disease. Figure 2.d shows that the number of infected individuals on the first day decreased drastically, due to a reduction of the number of infected individuals transition that recover from the disease. The figure shows that the disease needs two weeks to extinct. Figure 2.e shows that the number of recovered individuals increases, but within a few days, it will decreases and needs 20 days to keep in the same value. However, this population will eventually disappear over time. The preview condition happens because the basic reproduction numbers $R_0 = 0.15798$ that much less than 1 such that the disease cannot be contagious or and would not come to pandemic condition.

4. Conclusion
From this work, we answer how the covid-19 spread diseases in Palu does not come to pandemic condition. In the case of the interaction rate between the individual of susceptible subpopulation and quarantined $\theta$ could be satisfied, then the interaction rate between the individual of susceptible subpopulation and infected $\beta$ have to be controlled. In otherwise, in case of the interaction rate between the individual of susceptible subpopulation and quarantined $\theta$ could not be satisfied, then the transition rate of the individual of quarantine subpopulation to be the infected subpopulation $\phi$ have to be controlled.

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