Mathematical modeling and analysis of COVID-19 transmission dynamics in Central Java Province, Indonesia

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Abstract. Covid-19 is currently a pandemic that is considered as the biggest global threat that classified as the human-to-human transmissible disease. This pandemic has affected practically all world countries. The aim of this paper is to construct a mathematical model for the spread of the Covid-19 outbreak and analyze its stability. The proposed mathematical model is STQIR (Susceptible, Traced, Quarantine, Infectious, Recovered) model. The form of the model is a nonlinear differential system with five variables. The step of the method i.e., compute the variables positivity, boundedness of solutions, and the basic reproduction number that computed using next generation matrix. Then the basic reproduction number will be used for testing the local stability of the disease free equilibrium using Routh Hurwitz criteria to examine its epidemiological relevance. This work also investigate the sensivity of the model with respect to the variation of each one of its parameters and is tested in application to the recent data on Covid-19 outbreak in Central Java Province, Indonesia.

1. Introduction
Coronavirus disease 2019 or Covid-19 is an infectious disease caused by Severe Acute Respiratory Syndrome Coronavirus 2 or SARS-CoV-2 that first identified on December 2019 in Wuhan, China and officially declared as pandemics by World Health Organisation (WHO) on Mach 11, 2020 [1-4]. Covid-19 is classified as the human-to-human transmissible disease by the mucus that spread-out through the mouth or nose when the infected people cough, sneeze, or talking.

Based on the data that reported on the official website of World Health Organisation in early September, 2020 there are more than 26 million cases of confirmed infections, with more than 0,86 million deaths cases all around the world. By September 5, 2020, Indonesia contribute 187,537 cases of confirmed infections, with 7,832 death cases and 134,181 recovered patiences. This pandemic not only gives notorious effect on people’s health but also psychological distress, economic loses and other negative impact on daily activities. But at the same time, in the academic field, several research papers about this outbreak especially modelling and estimating the posible number of people infected by Covid-19 has been published. Modelling is very helpfull to understanding and studying the transmission dynamics of some cases especially in a complex case like this, when there are so many factors should be put on and analysed for it cost to the case.
There are models that can be used for infectious disease just like SIR; the most common model, until the most complex model like a SIRB [5], SEI;[6], and SEIQRV [7] which formed based on the disease. There is a riset that had been done by [8] which studied about the Covid-19 transmission dynamics using a mathematical modeling with a case study of Wuhan, China. They used the SEIPAHRF (Susceptible class, Exposed class, Symptomatic and infectious class, Super-spreaders class, Infectious but asymptomatic class, Hospitalized, Recovery class, and Fatality class) model and the model does fit to the reality that occurred in Wuhan, China. And there is so many riset about Covid-19 that had been done with various models such as SEIR model [9], [10], [11], and SIHR model [12].

To predict the nature of The Covid-19, in this works we develop the STQIR model that stratify a population based on their infection status as a function of time such as susceptible class (S), persons in monitoring/traced (T), patients under surveillance in quarantine (Q), infected class (I), and removed class (R). In this study, we also analyze the model stability of equilibria using the basic reproduction number, then established the result using local analysis and do the numerical simulation using the real data from Central Java.

This work is organized as follows. In section 2, we propose a new model for Covid-19. And then the positivity and boundedness of solution are described in section 3. In the section 4, we analyze the local stability of the model. Then the comparison of the model will be illustrated in section 5 of numerical simulations. We end in section 6 of conclusions and discussion of the results.

2. Model formulation

The diagram of the proposed model is shown in Figure 1. The model is a based on compartment from SEIR model [9] that modified based on the pandemic situation in Indonesia by reducing some compartments that are not related to the situation. We divided the constant total population size N into five epidemiological classes: susceptible class (S), persons in monitoring (T), patients under surveillance in quarantine (Q), infected class (I), and removed class (R).

![Figure 1: The diagram of covid-19 transmission](image)

The compartmental models are stratifying based on the infection status such as the following categorie, i.e. Susceptible is Individual who is able to become infected, Person in monitoring is Individual who had contact with a pathogen and have been monitored, Quarantined is Individual who is under surveillance in quarantine, and Infected is Individual who is infected by a pathogen and is capable of transmitting the virus to others. The compartmental models are The recovered person is individual who was infected with and survived by the virus with no long-term health effects or disabilities.
Table 1. Model parameters and their descriptions

| Notation | Interpretations               | Notation | Interpretations               |
|----------|-------------------------------|----------|-------------------------------|
| $\pi$    | Recruitment rate of S class   | $\rho_2$ | Rate at which traced people become infected |
| $\beta$  | Infection rate                | $\gamma_1$ | Recovery rate of quarantined class |
| $r$      | Rate of people become probable| $\gamma_2$ | Recovery rate of Infected class |
| $\kappa$ | Rate of people become suspect | $\mu$   | Death rate due to the infection |
| $\rho_1$ | Rate at which traced people back to susceptible class | $\tau$ | Natural death rate |

The developed mathematical model is STQIR model, as follows.

\[
\begin{aligned}
\frac{dS}{dt} &= \pi + ST(\kappa \rho_1 - \beta r) - S\beta(1 - r) - S\tau \\
\frac{dT}{dt} &= ST(\beta r - \kappa \rho_1) - T\kappa \rho_2 - T\kappa(1 - \rho_1 - \rho_2) - T\tau \\
\frac{dQ}{dt} &= S\beta(1 - r) + T\kappa(1 - \rho_1 - \rho_2) - Q\gamma_1 - Q(\mu + \tau) \\
\frac{dI}{dt} &= T\kappa \rho_2 - I\gamma_2 - I(\mu + \tau) \\
\frac{dR}{dt} &= Q\gamma_1 + I\gamma_2 - R\tau \\
\end{aligned}
\]

(2.1)

With the initial condition $S(0) > 0, T(0) > 0, Q(0) > 0, I(0) \geq 0, R \geq 0$ where the parameters are given in Table 1.

3. Positivity and boundedness of solutions
This model is a transmission model of Covid-19 in a closed population (N) that divided into five classes; susceptible (S), traced (T), quarantine (Q), infected (I), and Removed class. Therefore, it is important to prove that all the variables are non-negative for all time $t \geq 0$.

**Theorem 3.1.** The closed region $\Omega = \{(S, T, Q, I, R) \in \mathbb{R}^5_+: N < \frac{\pi}{\tau}\}$ is positively invariant set for the model (2.1).

**Proof:**
Let $N(t) = S(t) + T(t) + Q(t) + I(t) + R(t)$ with $S(0) > 0, T(0) > 0, Q(0) > 0, I(0) \geq 0, R \geq 0$.

From the model (2.1), we have:

\[
\begin{aligned}
\frac{dN}{dt} &= \frac{dS}{dt} + \frac{dT}{dt} + \frac{dQ}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\
&= \pi - \tau N - \mu(Q + I) \\
\end{aligned}
\]

(3.1)

Which is,

\[
\frac{dN}{dt} \leq \pi - \tau N \\
\]

(3.2)

By integrating the inequality (3.2) using the initial condition, we obtain
\[ N(t) \leq N(0)e^{-\tau t} + \frac{\pi}{\tau} (1 - e^{-\tau t}) \]

Letting \( t \) tends to infinity, asymptotically we get and \( N(t) \leq \frac{\pi}{\tau} \).
Therefore, \( \Omega \) is positively invariant of the model (2.1) so that the model is relevant both mathematically and epidemiologically.

4. Basic reproduction number
The basic reproduction number holds a crucial role in the analysis of an infectious disease. Its used to describe the average number of the new infection due to a sick individual and is denoted by \( R_0 \). If \( R_0 > 1 \), it means that one infected people can produce more than one secondary infection. In this case, the disease-free equilibrium is unstable so that it can caused the epidemic outbreaks. But if the \( R_0 < 1 \), the disease-free equilibrium (DFE) will be locally asymptotically stable and the situation is under control.
Since the model (2.1) has DFE \( E_0 (S^0, T^0, Q^0, I^0, R^0) = \left( \frac{\pi}{(\beta(1-\tau)+\bar{\tau})}, 0, 0, 0, 0 \right) \), so the basic reproduction number can be found analytically using next generation matrix. The \( R_0 \) can be computed by considering the below generation matrices \( FV^{-1} \), where
\[
F = \begin{pmatrix} S(\beta r - \kappa \rho_1) & 0 \\ 0 & S(1) \end{pmatrix} \text{ and } V = \begin{pmatrix} \kappa \rho_2 + \kappa (1 - \rho_1 - \rho_2) + \tau & 0 \\ -\kappa \rho_2 & \gamma_2 + \mu + \tau \end{pmatrix}
\]
Therefore, the spectral radius of \( FV^{-1} \) is
\[
R_0 = \frac{\pi (\beta r - \kappa \rho_1)}{(\beta (1-\tau) + \bar{\tau})(\kappa (1 - \rho_1) + \tau)}
\]

To find the endemic equilibrium state of the model, we set
\[
\frac{dS}{dt} = 0, \frac{dT}{dt} = 0, \frac{dQ}{dt} = 0, \frac{dI}{dt} = 0, \frac{dR}{dt} = 0 \tag{4.1}
\]
Since the \( R \) equation in system (2.1) has no relation with the other equations, so we can reduce the system into:
\[
\begin{align*}
\frac{dS}{dt} &= \pi + ST(\kappa \rho_1 - \beta r) - S\beta (1 - \tau) - S\tau \\
\frac{dT}{dt} &= ST(\beta r - \kappa \rho_1) - T\kappa \rho_2 - T\kappa (1 - \rho_1 - \rho_2) - T\tau \\
\frac{dQ}{dt} &= S\beta (1 - \tau) + T\kappa (1 - \rho_1 - \rho_2) - Q\gamma_1 - Q(\mu + \tau) \\
\frac{dI}{dt} &= T\kappa \rho_2 - I\gamma_2 - I(\mu + \tau)
\end{align*} \tag{4.2}
\]
To solve the system (4.2), we get the endemic equilibrium state \( E_1 (S^*, T^*, Q^*, I^*) \)
Where,
\[
\begin{align*}
S^* &= (\kappa - \kappa \rho_1 + \tau) / (\beta r - \kappa \rho_1) \\
T^* &= \pi \beta r - \pi \kappa \rho_1 + \pi T^2 \rho_1 - \pi T^2 \rho_1^2 + T\kappa \rho_1 \tau - T\beta r k + T\beta r k \rho_1 - T\beta r \tau - \beta \kappa + \beta \kappa \rho_1 - \beta \tau + \beta r k - \beta r k \rho_1 + \beta \tau - \kappa + \kappa \rho_1 \tau - \tau^2 \\
Q^* &= (\beta \kappa - \beta \kappa \rho_1 + \beta \tau - \beta r k + \beta r k \rho_1 - \beta \tau + T\beta r k - T\beta r \kappa \rho_1 + T\beta^2 \rho_1^2 - T\kappa \rho_2 \beta r + T^2 \rho_2^2) / (\gamma_1 \beta r - \gamma_1 \kappa \rho_1 + \beta \tau \mu - \kappa \rho_1 \mu + \beta \tau - \kappa \rho_1 \tau) \\
I^* &= (T\kappa \rho_2) / (\gamma_2 + \mu + \tau)
\end{align*}
\]
From the expressions of the \( E_1 \) it is obvious that the endemic equilibrium will exist only when \( R_0 > 1 \). And we got the Jacobian matrix of the system at any equilibrium point in \( J \).
\[ J = \begin{bmatrix} T(\kappa \rho_1 - \beta r) - \beta (1 - r) - \tau & S(\kappa \rho_1 - \beta r) & 0 & 0 \\ T(\beta r - \kappa \rho_1) & S(\beta r - \kappa \rho_1) - \kappa \rho_2 - \kappa (1 - \rho_1 - \rho_2) - \tau & 0 & 0 \\ \beta (1 - r) & \kappa (1 - \rho_1 - \rho_2) & -\gamma_1 - \mu - \tau & 0 \\ 0 & \kappa \rho_2 & 0 & -\gamma_2 - \mu + \tau \end{bmatrix} \]

(4.3)

4.1. Stability Analysis of the equilibrium point

In this section we will establish the stability and bifurcation condition of the equilibrium states. The nature of \( E_0 \) will be established in Theorem 4.1 and Theorem 4.2 for the \( E_0 \).

**Theorem 4.1.** Let \( R_0 = \frac{\pi (\beta r - \kappa \rho_1)}{(\beta (1 - r) + \tau)(\kappa (1 - \rho_1) + \tau)} \). The disease free equilibrium will be locally asymptotically stable if \( R_0 < 1 \) and unstable if \( R_0 > 1 \).

**Proof:**

The Jacobian of the system at the disease free equilibrium point with \( E_0 = \left( \frac{\pi}{(\beta (1 - r) + \tau)}, 0, 0, 0 \right) \) at the (4.2) is,

\[ J(E_0) = \begin{bmatrix} -\beta (1 - r) - \tau & \frac{\pi (\kappa \rho_1 - \beta r)}{(\beta (1 - r) + \tau)} & 0 & 0 \\ 0 & \frac{\pi (\beta r - \kappa \rho_1)}{(\beta (1 - r) + \tau)} - \kappa \rho_2 - \kappa (1 - \rho_1 - \rho_2) - \tau & 0 & 0 \\ \beta (1 - r) & \kappa (1 - \rho_1 - \rho_2) & -\gamma_1 - \mu - \tau & 0 \\ 0 & \kappa \rho_2 & 0 & -\gamma_2 - \mu + \tau \end{bmatrix} \]

And the characteristic roots of the Jacobian at \( J(E_0) \) are

\[ X_1 = 0 \]

\[ X_2 = -\gamma_1 - \mu - \tau \]

\[ X_3 = -\gamma_2 - \mu - \tau \]

\[ X_4 = -\frac{\pi (-\kappa \rho_1 \tau + \beta r \kappa - \beta r \kappa \rho_1 + \beta r \tau - \kappa^2 \rho_1 + \kappa^2 \rho_1^2)}{-\tau^2 - \beta r \kappa \rho_1 + \beta r \tau + \kappa \rho_1 \tau + \pi \beta r - \pi \kappa \rho_1 + \beta \kappa \rho_1 - \beta \tau + \beta r \kappa - \beta \kappa - \kappa \kappa} (1 - R_0) \]

\[ + \frac{\pi (-\kappa \rho_1 \tau + \beta r \kappa - \beta r \kappa \rho_1 + \beta r \tau - \kappa^2 \rho_1 + \kappa^2 \rho_1^2)}{-\tau^2 - \beta r \kappa \rho_1 + \beta r \tau + \kappa \rho_1 \tau + \pi \beta r - \pi \kappa \rho_1 + \beta \kappa \rho_1 - \beta \tau + \beta r \kappa - \beta \kappa - \kappa \kappa} \left( 1 + \frac{\pi (\beta r - \kappa \rho_1)}{(\beta + \beta r - \tau)(\kappa - \kappa \rho_1 + \tau)} \right) \]

Since the \( X_2 \) and \( X_3 \) is negative so the last root will be negative if \( R_0 < 1 \). Therefore, based on Routh Hurwitz criteria, the disease free equilibrium \( (E_0) \) is locally asymptotically stable if \( R_0 < 1 \) and unstable if \( R_0 > 1 \).

Manifold center theory can be used to determine the local behaviour of the dynamic model by investigating at the flow on a low dimensional manifold, i.e., instead of doing with an \( n \)-dimensional system, we can just work with a \( c \)-dimensional one so that we can reduce the full \( n \)-dimensional system into a \( c \)-dimensional system, with \( n < c \). A center manifold for the system can be represented as follows:

\[ \frac{dy}{dt} = f(0, \phi), f: \mathbb{R}^n \times R \rightarrow \mathbb{R}^n \text{ and } f \in C^1(\mathbb{R}^n \times \mathbb{R}) \]
Theorem 4.2. Let \( R_0 = \frac{\pi(b \tau - \kappa \rho_1)}{(\beta(1 - r) + \pi)(\kappa(1 - \rho_1) + \pi)} \). The endemic equilibrium state \( E_1(S^*, T^*, Q^*, I^*) \) is stable if \( R_0 > 1 \) and unstable if \( R_0 < 1 \).

**Proof:**

Local stability of the endemic equilibrium states will be proved with Manifold Center Theory. Will be assumed that the equilibrium point is around the bifurcation point, so that \( R_0 = 1 \) with \( \beta \) as the chosen bifurcation parameter,

\[
\beta^* = \frac{\pi \kappa \rho_1}{\pi \tau - \kappa \rho_1 + \tau^2},
\]

then one of the eigenvalue vanishes. \( w \) will given as the right eigen vector that denoted by \( w = [w_1 \ w_2 \ w_3 \ w_4]^T \), where \( f(E_0, \beta^*), w = 0 \).

\[
w_1 = \left( -w_2 (r \tau^2 + \pi \tau r + 2r \kappa \rho_1 - r \pi \kappa \rho_1 - 2 \kappa^2 \rho_1 r + \kappa \pi r + \kappa^2 r + \kappa^2 \rho_1^2 r - \tau^2 + 2 \kappa \rho_1 r - 2 \tau \kappa - \kappa^2 + 2 \kappa^2 \rho_1 - \kappa^2 \rho_1^2) / (\pi (\kappa \rho_1 - \tau \kappa \rho_1 + \tau r)) \right)
\]

\[
w_2 = w_2
\]

\[
w_3 = \left(-w_2 \left( - \pi \tau r - \pi \rho_1 \rho_2 r + \pi \kappa \rho_1 \pi + \pi \kappa \rho_1 \tau + \pi \kappa \rho_1 \rho_2 - r \tau \kappa - 2 \tau \kappa r^2 + 2 \tau \kappa^2 \rho_1 \right)
\]

\[
w_4 = (\kappa \rho_1 w_2) / (\gamma_2 + \mu + \tau)
\]

And then the \( v \) which is the left eigen vector is denoted by \( v = [v_1 \ v_2 \ v_3 \ v_4]^T \), where \( v \ \left( f(E_0, \beta^*) = 0 \right) \) with \( v_1 = 0, v_2 = v_2, v_3 = 0, \) and \( v_4 = 0 \).

Let \( S = y_1, T = y_2, Q = y_3, I = y_4 \) with \( f_1 = \frac{dy_1}{dt}, f_2 = \frac{dy_2}{dt}, f_3 = \frac{dy_3}{dt}, f_4 = \frac{dy_4}{dt} \), we got

\[
a = \sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 f_k}{\partial y_i \partial y_j} \left( \frac{\pi}{\beta(1 - r) + \tau}, 0, 0, 0 \right)
\]

\[
= v_1 w_1 w_2 \frac{\partial^2 f_1}{\partial \sigma \partial \tau} + v_2 w_1 w_2 \frac{\partial^2 f_2}{\partial \sigma \partial \tau}
\]

\[
= v_2 \left( \frac{-r(\kappa - \kappa \rho_1 + \tau)}{\kappa \rho_1 - \tau \kappa \rho_1 + \tau} \right) w_2 (\beta \tau - \kappa \rho_1)
\]

\[
b = \sum_{k,i=1}^{4} v_k w_i \frac{\partial^2 f_k}{\partial y_i \partial \beta^*} \left( \frac{\pi}{\beta(1 - r) + \tau}, 0, 0, 0 \right)
\]

\[
= v_1 w_1 \frac{\partial^2 f_1}{\partial \beta^*} + v_1 w_2 \frac{\partial^2 f_2}{\partial \beta^*} + v_2 w_1 \frac{\partial^2 f_2}{\partial \beta^*} + v_2 w_2 \frac{\partial^2 f_2}{\partial \beta^*} + v_3 w_1 \frac{\partial^2 f_3}{\partial \beta^*}
\]

Based on Center Manifold Theory, if \( a < 0 \) and \( b < 0 \), then the endemic equilibrium is locally asymptotically stable so that the system will do the back bifurcation where the endemic equilibrium state is steady when the \( R_0 < 1 \) [13]. Because the \( R_0 < 1 \), so the endemic equilibrium state is locally asymptotically stable.

5. Numerical simulation

Using least square method and by using Maple software, we have estimated the important model parameters using the real cases of Central Java from July, 16th until August, 25th which are given in Table 2.
Table 2. Parameters estimation for Central Java, Indonesia

| Notation | Value   | References |
|----------|---------|------------|
| π        | 0.063   | [14]       |
| β        | 0.99    | Estimated  |
| r        | 0.99    | Estimated  |
| κ        | 0.02057 | Estimated  |
| ρ₁       | 0.037462| Estimated  |
| ρ₂       | 0.008   | Estimated  |
| γ₁       | 0.037462| Estimated  |
| γ₂       | 0.028272| Estimated  |
| μ        | 0.038   | Estimated  |
| τ        | 0.033121| Estimated  |

Figure 2. Model Simulation endemic (R₀ > 1)

In figure 2, we know that the susceptible class is decreasing with time, which means there are many people had contacted the infected people so that they become person in monitoring. Then the person in monitoring class is increasing. It means that there are infected people who transmit the virus for more than one people at period. Therefore there is a large number of infected people over time that can lead to an outbreak in a very short time with R₀ = 1.139512709 > 1. The value of R₀ is determined using the parameters that are estimated in Table 2. Non endemic (disease free) simulation is given in Figure 3. Its can be seen that the outbreak is going to disapeared by the number of T,Q,I that decreasing. Where it means that there is one infected people who only transmit the virus to less than one people at period. So we got R₀ = 0.2090694197 < 1.

6. Conclusion
In this study, we had proposed the STQIR model for Covid-19 outbreak and proved its stability at several analytic. Theoretically its proved that the dynamics transmission depends on the basic reproduction number which have a crucial role for the stability of the system and also all the necessary properties that needed for the epidemiological relevance have also been proved. We have estimated the parameteric values based on the data from Central Java province, Indonesia and the numerical simulation are
established. Where we got $R_0 = 1.139512709$ for the endemic situation and $R_0 = 0.2090694197$ for non-endemic situation. This indicates that mathematical modelling is an efficient method to estimate this kind of pandemic situation if the parameters can be estimated properly.

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