A Mathematical Model of Covid-19 Transmission Between Regions with Symptomatic and Asymptomatic Cases

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Abstract— In the early 2020, World Health Organization (WHO) has declared COVID-19 as a pandemic disease. COVID-19 was first discovered in Wuhan, China at the end of 2019. Since the emergence of COVID-19, its spread has been studied by various researchers around the world. The spread of COVID-19 is studied both on the spread between populations and between regions. The spread of disease between regions occurs when a population moves from one area to another. This requires investigation because the spread of the disease can occur from one region to another, so studies of regional factors are needed. In this study, the COVID-19 epidemic model has been established. The model describes the spread of the disease between regions. In the model, the population which is infected with COVID-19 is divided into two categories. The first one is called an asymptomatic patient. Asymptomatic patients are those who are infected or exposed to COVID-19 but have no detectable or significant symptoms in these patients. So that the patient is not considered ill, and the patient can infect healthy people. The second one is called a symptomatic patient. This patient causes symptoms that the patient is exposed to COVID-19. Thus, it is assumed that patient can be given treatment such as quarantine, so the patient is not to be able to transmit the disease to others. It is also assumed that asymptomatic patients can move to other areas and transfer the disease to others, but not symptomatic patients. This study aims to determine the dynamics of the spread of the COVID-19 epidemic with asymptomatic cases between regions and to identify the factors that influence them. The basic reproduction number (\mathcal{R}_0) of the model is sought to help identify the factors. Partial Rank Coefficient Correlation (PRCC), one of the methods of sensitivity analysis, is also used to identify key parameters that affect the model solution. Numerical simulations are used to show the behavior of the solution.

Index Terms—Asymptomatic; Basic Reproduction Number; COVID-19; Movement of Population; Dynamical System; Sensitivity Analysis.

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I. INTRODUCTION

CORONAVIRUS disease 2019 (COVID19) was first detected in Wuhan, China in December 2019 [1]. Worldwide, there were 6.3 million confirmed cases and 380,000 deaths as of June 3, 2020 [2]. Severe Acute Respiratory Syndrome Coronavirus 2 (SARSCoV2) is a virus that causes COVID-19 [3]. The disease attacks the human respiratory system [4], [5]. The spread of the virus can be through droplets/saliva that comes out with sneezing or coughing [6]. The spread can also be through the eye tissue if exposed to these droplets so that the transmission is very quickly spreading [7].

To reduce the prevalence of COVID19, we need a policy on the risk of infection. As the virus spreads through the droplets, it is necessary to avoid contact between healthy and infected people to avoid the spread of disease. Selfquarantine should be carried out by the infected person to prevent the infected person from spreading the disease [8]. However, because some people are asymptomatic, they are less effective in controlling the spread of the disease. They are called asymptomatic cases [9].

In epidemiological problems, the knowledge of the spread of diseases in a population, mathematics has an important role in controlling the disease. Hence a lot of mathematical models were developed to uncover this knowledge. One of the mathematical applications on epidemiological problems is the deterministic model. There have been many epidemiological models developed by various researchers to determine the behavior of COVID-19. A Generalized SEIR-COVID-19 Model was constructed by Peng et al. for the China territory [10]. Meanwhile, the Fractional Time-Delay Dynamic System was used by Chen et al. to examined COVID-19 cases in China [11]. Shao et al. used the Basic Reproductive Number (\mathcal{R}_0) of COVID-19 to identify factors influencing the spread of COVID-19 using the Statistical Time Delay Dynamic System Model [12]. A dynamic model was used to research the effect of Malaysia's restricted or quarantine areas by Altahir et al. [13]. Asymptomatic cases against the spread of COVID-19 are also studied by Peirlinck et al. [14].

The spreading process of the disease in a population group can also be seen from its spread between regions. An area whose population has been infected with the disease can spread to other areas. The spread can occur due to population movement between regions such as migration, travel, or tourism that occurs between these regions. The effect of migration on disease spread has also been studied

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Fig. 1 Schematic Diagram of the COVID-19 Model

by many researchers [15]-[24].

However, previous researchers have not studied many cases of the COVID-19 spreading model with asymptomatic cases between regions. The spread between these regions needs to be studied, considering the spread of the disease can be suppressed by minimizing contact between residents of regions who have not been affected by COVID-19 cases with residents of regions who have been affected by COVID-19 cases. Asymptomatic case factors also need to be researched further because asymptomatic patients are not aware that they have COVID-19. So that asymptomatic patients still travel or move to various regions.

From the above-stated literature, the writers are interested to create an epidemiological model of COVID-19 with symptomatic and asymptomatic cases between regions using a dynamic system approach. The numerical simulation is used to show the behavior solution of the model.

II. MODEL FORMULATION

This COVID-19 dynamical model assumes that the population of each region is divided into five compartments, namely: populations that are susceptible to disease (Susceptible), populations that have contracted the disease but are still in the latent stage (Exposed), populations that have been infected but do not cause symptoms (Asymptomatic), populations that have been infected and cause symptoms (Symptomatic) and populations that have recovered (Recovered). This model has been represented by a schematic diagram in Figure 1 with parameter description shown in Table 1. For model population movement, it is assumed that between regions are interconnected so that each region can go directly to other regions without the need to pass through other regions. This can be illustrated in Figure 2.

The system of differential equations (1) for the spread of COVID-19 between regions with asymptomatic cases are as follows:

$$\begin{aligned} \frac{dS_i}{dt} &= \pi_i - \beta_i S_i I a_i - d_i S_i + \delta R_i + \sum_{j=1}^n m s_{ij} S_j - S_i \sum_{j=1}^n m s_{ij} \\ \frac{dE_i}{dt} &= \beta_i S_i I a_i - (\alpha_i + d_i) E_i + \sum_{j=1}^n m e_{ij} E_j - E_i \sum_{j=1}^n m e_{ij} \\ \frac{dIa_i}{dt} &= q_i \alpha_i E_i - (\gamma_i + d_i + \nu_i) I a_i + \sum_{j=1}^n m i_{ij} I a_j - I a_i \sum_{j=1}^n m i_{ij} \\ \frac{dIs_i}{dt} &= (1 - q_i) \alpha_i E_i - (\gamma_i + d_i + \theta_i) I s_i + \nu_i I a_i \\ \frac{dR_i}{dt} &= \gamma_i (I a_i + I s_i) - (d_i + \delta_i) R_i + \sum_{j=1}^n m r_{ij} R_j - R_i \sum_{j=1}^n m r_{ij} \end{aligned}$$

by defining parameters in Table 1 and $\sum_{j=1}^{n} ms_{ij} = 1$, $\sum_{j=1}^{n} me_{ij} = 1$, $\sum_{j=1}^{n} mi_{ij} = 1$ dan $\sum_{j=1}^{n} mr_{ij} = 1$.



Fig. 2 Illustration of Regional Connectedness with Graph

Symbol	DESCRIPTION
π_i	The birth rate in the region <i>i</i>
d_i	Rate of death in the region <i>i</i>
β_i	Rate of infection of the region <i>i</i>
α_i	The rate of change from the latent phase to
	the infected phase in the region <i>i</i>
q_i	The probability of latent populations
	becoming asymptomatic populations in the
	region <i>i</i>
$1 - q_{i}$	The probability for latent populations to
	become symptomatic populations in the
	region <i>i</i>
γ_i	Rate of recovery in the region <i>i</i>
$ heta_i$	Rate of death from disease in the region <i>i</i>
δ_i	The rate of R_i change to S_i in the region <i>i</i>
ν_i	The rate of Ia_i change to Is_i in the region <i>i</i>
ms _{ij}	Parameters movement of susceptible
-	populations from region <i>i</i> to region <i>j</i>
me _{ij}	Parameters movement of latent
	populations from region <i>i</i> to region <i>j</i>
mi _{i i}	Parameters movement of asymptomatic
-	populations from region <i>i</i> to region <i>j</i>
mr _{ij}	Parameters movement of recovered
	populations from region <i>i</i> to region <i>j</i>

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For i = 1..n, dynamic model for the total population in region *i* as follows:

$$\frac{dN_i}{dt} = \pi_i - d_i N_i - \theta_i Is_i + \sum_{j=1}^n ms_{ij} S_j - S_i \sum_{j=1}^n ms_{ij} + \sum_{j=1}^n me_{ij} E_j - E_i \sum_{j=1}^n me_{ij} + \sum_{j=1}^n mi_{ij} Ia_j - Ia_i \sum_{j=1}^n mi_{ij} + \sum_{i=1}^n mr_{ij} R_j - R_i \sum_{j=1}^n mr_{ij}$$
(2)

If $H(t) = \sum_{i=1}^{n} N_i$ then the dynamic model for the total population is

$$\frac{dH}{dt} = \Pi - \sum_{i=1}^{n} d_i N_i - \theta_i \sum_{i=1}^{n} Is_i$$
(3)

All parameters of the COVID-19 models with asymptomatic cases between regions as in the models (1) - (3) are non-negative.

III. MODEL ANALYSIS

A. Positivity of Solution

Lemma 1: Suppose the initial value of the system (1) are:

 $S_{i}(0) \geq 0, E_{i}(0) \geq 0, Ia_{i}(0) \geq 0, Is_{i}(0) \geq 0, R_{i}(0) \geq 0$ then the solution of the system (1) is in the $\Omega = \{(S_{i}, E_{i}, Ia_{i}, Is_{i}, R_{i}) \in \mathbb{R}^{5n}_{+} : S_{i} \geq 0, E_{i} \geq 0, Ia_{i} \geq 0, Is_{i} \geq 0, R_{i} \geq 0, H \leq \frac{\Pi}{d_{min}}\}$ **Proof** From the first equation in the model (1), the equation can be written as follows:

$$\frac{dS_i}{dt} = \pi_i - \beta_i S_i I a_i - d_i S_i + \delta R_i + \sum_{j=1}^n m s_{ij} S_j$$

$$-S_i \sum_{j=1}^n m s_{ij}$$
(4)

$$\frac{dS_i}{dt} \ge -(\beta_i Ia_i + d_i + \sum_{j=1}^n ms_{ij})S_i + (\delta R_i + \sum_{j=1}^n ms_{ij}S_j)$$
(5)

Inequality (5) can be solved as follows:

$$dS_i \ge e^{-\int Qdt} \int \left(\delta R_i + \sum_{j=1}^n m S_{ij} S_j\right) e^{\int Qdt} dt \ge 0$$
(6)

with $Q = (\beta_i Ia_i + d_i + \sum_{j=1}^n ms_{ij})$. By using the same way, hence $E_i \ge 0$, $Ia_i \ge 0$, $Is_i \ge 0$, $R_i \ge 0$. So, it is proven that the model only has a positive solution.

The form of the inequality can be obtained from Equation (3) as follows:

$$\frac{dH}{dt} = \Pi - d_i \sum_{i=1}^n N_i - \theta_i \sum_{i=1}^n Is_i \tag{7}$$

$$\frac{dH}{dt} \ge \Pi - \sum_{i=1}^{n} d_i N_i \ge \Pi - d_{min} H \tag{8}$$

where
$$d_{min} = \min(d_i)$$
. Thus the solution to inequality (8) is

$$H(t) > \frac{\prod}{1 + C} e^{-d_{min}t}$$
(9)

$$H(t) \ge \frac{1}{d_{\min}} + C_1 e^{-a_{\min}t} \tag{9}$$

where C_1 is a constant. So,

$$\lim_{t \to \infty} \sup H(t) \le \frac{\Pi}{d_{\min}} \tag{10}$$

Thus, it is proven that the model has limited solutions \blacksquare .

B. Fixed Point Analysis and \mathcal{R}_0

A fixed point or equilibrium point is obtained when each rate of population growth in the system (1) is zero. It is a condition of equilibrium where the population does not increase or decrease.

At a non-endemic point, which is defined as $P^0 = (S^0, E^0, Ia^0, Is^0, R^0)$, with $S = (S_1, ..., S_n), E = (E_1, ..., E_n)$, $Ia = (Ia_1, ..., Ia_n), Is = (Is_1, ..., Is_n), R = (R_1, ..., R_n)$. The value of the compartment associated with the disease is zero so that the value of the $E^0 = 0$, $Ia^0 = 0$, $Is^0 = 0$ and $R^0 = 0$. So, that the system of equations (1) become

$$\frac{dS_i}{dt} = \pi_i - d_i S_i + \sum_{j=1}^n m S_{ij} S_j - S_i \sum_{j=1}^n m S_{ij} = 0$$
(11)

By using the matrix operation, the equation (11) can be written as

$$\frac{dS}{dt} = diag(\pi) - diag(d)S - M_s S = 0$$
(12)

with $d = (d_1, ..., d_n)^T$, $\pi = (\pi_1, ..., \pi_n)^T$ and M_s is a transition matrix for susceptible populations with entry $M_s(i,j) = -ms_{ij}$ if $i \neq j$ and $M_s(i,i) = -\sum_{j=1}^n ms_{ji}$. To get a value S^0 , the equation (12) needs to be solved so that the equation (12) becomes

$$diag(\pi) - (diag(d) + M_s)S = 0$$
(13)

$$diag(\pi) = (diag(d) + M_s)S \tag{14}$$

$$S = (diag(d) + M_s)^{-1} diag(\pi)$$
(15)

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Then the non-endemic point value on the model (1) is $P^0 = (S^0, 0, 0, 0, 0)$ with S^0 meet the equation (15).

With the help of next-generation matrix method, we can obtain the Basic Reproduction Number (\mathcal{R}_0) of the COVID-19 model with asymptomatic cases between regions. To get the next generation matrix, it is necessary to group the infected compartments, there are $E_1, \ldots, E_n, Ia_1, \ldots, Ia_n$, Is_1, \ldots, Is_n . Then by using the method [25] the transmission matrix *F* and the disease transition matrix *V* are

$$F = \begin{bmatrix} 0 & G & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} V_1 & 0 & 0 \\ V_2 & V_3 & 0 \\ V_4 & V_5 & V_6 \end{bmatrix}$$
(16)

where $G, V_1, V_2, V_3, V_4, V_5$, and V_6 are block matrices with a size of $n \times n$. The form of Matrix G is as follows

$$G = \begin{bmatrix} \beta_1 S_1^0 & 0 & \dots & 0\\ 0 & \beta_2 S_2^0 & 0 & 0\\ \vdots & 0 & \ddots & \vdots\\ 0 & 0 & \dots & \beta_2 S_3^0 \end{bmatrix}$$
(17)

Suppose M_E is a transition matrix for latent populations with entries $M_E(i,j) = -me_{ij}$ if $i \neq j$ and $M_e(i,i) = -\sum_{j=1}^n me_{ji}$. M_I is a transition matrix for asymptomatic populations with entries $M_I(i,j) = -mi_{ij}$ if $i \neq j$ and $M_i(i,i) = -\sum_{j=1}^n mi_{ji}$. Then the form of the matrix V_1, V_3 , and V_6 are

$$V_1 = diag(\alpha_i + d_i) - M_E \tag{18}$$

$$V_3 = diag(\gamma_i + d_i + \nu_i) - M_I \tag{19}$$

$$V_6 = diag(\gamma_i + d_i + \theta_i)$$
⁽²⁰⁾

As for the matrix shape V_2 , V_4 , V_5 are

$$V_2 = diag(q_i a_i) \tag{21}$$

$$V_4 = diag((1 - q_i)a_i)$$
⁽²²⁾

$$V_5 = diag(v_i) \tag{23}$$

Matrix V_1, V_2 , and V_3 are irreducible block matrices so that they all have positive inverse. Then the inverse of the Matrix F is

$$V^{-1} = \begin{bmatrix} V_1^{-1} & 0 & 0 \\ V_3^{-1}V_2V_1^{-1} & V_3^{-1} & 0 \\ V_6^{-1}V_5V_3^{-1}V_6^{-1}(V_2 + V_4)V_1^{-1} & V_6^{-1}V_5V_3^{-1}V_6^{-1} \end{bmatrix}$$
(24)

Since V^{-1} is a block lower triangular matrix, it can be written with a matrix block FV^{-1} as well. So, the \mathcal{R}_0 for the system is spectral radius of the matrix $GV_3^{-1}V_2V_1^{-1}$, namely

$$\mathcal{R}_0 = \rho(GV_3^{-1}V_2V_1^{-1}) \tag{25}$$

By solving the equation (16) the value \mathcal{R}_0 is

$$\min_{i=1.n} \frac{q_i \alpha_i \beta_i S_i^\circ}{(\alpha_i + d_i)(\gamma_i + d_i + \nu_i)} \le \mathcal{R}_0$$

$$\le \max_{i=1.n} \frac{q_i \alpha_i \beta_i S_i^0}{(\alpha_i + d_i)(\gamma_i + d_i + \nu_i)}$$
(26)

If the value of $M_S = 0$ then the equation (26) can be formed into

$$\min_{i=1..n} \frac{q_i \alpha_i \beta_i \pi_i}{d_i (\alpha_i + d_i)(\gamma_i + d_i + \nu_i)} \leq \mathcal{R}_0$$

$$\leq \max_{i=1..n} \frac{q_i \alpha_i \beta_i \pi_i}{d_i (\alpha_i + d_i)(\gamma_i + d_i + \nu_i)}$$
(27)

Then the value \mathcal{R}_0^i , i.e., the value \mathcal{R}^0 for each region is

$$\mathcal{R}_0^i = \frac{q_i \alpha_i \beta_i \pi_i}{d_i (\alpha_i + d_i)(\gamma_i + d_i + \nu_i)}$$
(28)

C. Numerical Simulation

Numeric simulation in this article uses parameter values and the starting value of compartments presented in Table 2.

Table 2	Parameter	Value
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Symbol	Quantity
π_i	10^7 3×10^7 2×10^7
,	$70 \times 365'$ $70 \times 365'$ 70×365
a_i	
P	70 × 365 Variable
ρ_i	1
α_i	
	5.1
q_i	0.6
ν_i	0.05
γ_i	0.12
θ_i	0.05
δ_i	1
L.	120
ms _{ii}	Variable
me _{ii}	Variable
mi_{ij}	Variable
mr_{ij}	Variable

1) Population Dynamics without Movement Factor

It is assumed that no movement occurred from one region to the others. That means the value of $M_s = 0, M_E =$ $0, M_I = 0$, and $M_E = 0$. Suppose $\beta_1 = 2.5 \times 10^{-8}$, $\beta_2 =$ $5 \times 10^{-8}, \beta_3 = 1 \times 10^{-8}$ and for other parameters equal to those in Table 4.2. To perform numerical simulations, the model is given the starting value for each compartment i.e.: $S_1(0) = 10^7, S_2(0) = 3 \times 10^7, S_3(0) = 2 \times 10^7, E_1(0) =$ $E_2(0) = E_3(0) = 0, Ia_1(0) = Ia_2(0) = Ia_3(0) =$ $10^6, Is_1(0) = Is_2(0) = Is_3(0) = 0, R_1(0) = R_2(0) =$ $R_3(0) = 0$



Fig. 3 Comparison Graph of The Number of Asymptomatic Cases

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To find out if a disease can be disappearing or not in each region, we can use the value \mathcal{R}_0 obtained from the equation (19). The values of \mathcal{R}_0 in each region are $\mathcal{R}_0^1 = 0.8819$, $\mathcal{R}_0^2 = 5.2918$, and $\mathcal{R}_0^3 = 0.7055$. The value \mathcal{R}_0 in region 2 is greater than 1 but the value \mathcal{R}_0 in region 1 and region 3 is less than 1. This indicates that in the region of 2, the diseases remain in the population or endemic while in region 1 and region 3 diseases will gradually disappear in the region. This can be seen in Figure 3, Figure 4, and Figure 5.

The spread of diseases without migration factors can be determined by the value \mathcal{R}_0^i of each region. By using sensitivity analysis, it can be shown that parameters are correlated positively [26]. By using N = 1000 samples and each parameter is assumed to be between 0 until 1 the PRCC value is obtained as in Table 3.

Table 3 PRCC value between parameter and \mathcal{R}_0

Symbol	Quantity
q	0.6476
α	0.0182
β	0.6283
π	0.6392
d	-0.7833
ν	-0.215

Table 3 shows that the probability of latent populations becoming asymptomatic populations (q), rate of infection (β) , and birth rate (π) parameters are positively correlated to \mathcal{R}_0 . That means if the values q, β, π increase then the value of \mathcal{R}_0 increase and if the values q, β, π decrease then the value of \mathcal{R}_0 decrease. The parameters rate of death (d), rate of *Ia* change to *Is* (ν) are negatively correlated to the value \mathcal{R}_0 . That means if values d, ν increase then the value of \mathcal{R}_0 decrease and if values d, ν increase then the value of \mathcal{R}_0 increase. The results showed that to reduce the spread of disease can be done control over parameter values that have a high correlation to the value \mathcal{R}_0^i .



Fig. 4 Graph Comparison of Number of Symptomatic Cases



Fig. 5 Population Graph for Region 2 without Movement Factors

2) Population Dynamic with Movement Factor

It is assumed that there is a movement occurring from one region to another regions. For example, suppose $ms_{ij} = me_{ij} = mi_{ij} = mr_{ij} = 0.2$, if $i \neq j$ and $ms_{ii} = me_{ii} = mi_{ii} = mr_{ii} = 0.6$ and for other parameters is equal to that of Table 2. The initial value given is the same as the previous simulation.



(a)



Fig. 6 Graph of Population Dynamics with Movement Factors

Figures 6(a), 6(b) and 6(c) shows similar patterns between the 3 regions (1,2 and 3) respectively. Also, the entire regions are endemic. This is different from the population dynamics model without movement. Figure 3 and Figure 4 show that region 1 and region 3 of the disease are not endemic while in Figure 7 the disease is endemic in each region. Figure 7(a) and Figure 7(b) show that the asymptomatic population and symptomatic population in Region 1, Region 2, and Region 3 have similar pattern even though each region has difference parameter values. We can also compare Figure 3, 4 and Figure 7(a), 7(b). Those figures show the difference value of asymptomatic and symptomatic population. Different values of the populations indicate the influence or the impact of the movement and spread of disease between regions.



Fig. 7 Graph of Asymptomatic and Symptomatic Case Models with Movement Factor

IV. CONCLUSION

Model of the spread of COVID-19 between regions with asymptomatic cases is influenced by populations that are vulnerable to contracting the disease (Susceptible), populations that have contracted the disease but are still in the latent stage (Exposed), populations that have been infected but do not cause symptoms (Asymptomatic), populations that have been infected and cause symptoms (Symptomatic) and populations that have recovered (Recovered) and the transfer of population between regions. Numerical simulation indicates that the stability of the COVID-19 transmission model between regions with symptomatic and asymptomatic cases is affected by the value of \mathcal{R}_0 . If the value of $\mathcal{R}_0 < 1$, the diseases will decrease over time, and if the value of $\mathcal{R}_0 > 1$, the diseases remain in the population or endemic. The sensitivity analysis shows that parameters q, β, π are positively correlated to the value of \mathcal{R}_0 and parameters d, ν negatively correlated to the value of \mathcal{R}_0 .

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