Modeling and Prediction of COVID-19 with a Large Scale Social Distancing

Yudi Ari Adi[1], Meksianis Z. Ndii[2]

[1]Department of Mathematics, Faculty of Applied Science and Technology, Ahmad Dahlan University, Yogyakarta, Indonesia.
[2]Department of Mathematics, Faculty of Sciences and Engineering, University of Nusa Cendana, Kupang-NTT, Indonesia.

Korespondensi; Yudi Ari Adi, Email: yudi.adi@math.uad.ac.id

Abstrak

Coronavirus 2019 (COVID-19), yang kasusnya dimulai di Cina, dalam kurun waktu dua bulan telah menyebar dengan cepat ke lebih dari 114 negara dan territorial. Pemahaman tentang dinamika penularan Covid-19 sangat penting untuk menentukan kebijakan dan strategi dalam pengobatan dan pengendalian penyebaran penyakit ini. Dalam makalah ini, disusun model matematika yang menggambarkan dinamika penularan penyakit menggunakan model matematika deterministik dengan menggunakan data penyebaran COVID-19 di Jakarta, Indonesia dari 3 Maret 2020, hingga 10 April 2020. Model berbentuk Sistem persamaan diferensial yang selanjutnya dilakukan analisis matematika dan simulasi numerik. Hasil simulasi menunjukkan bahwa tanpa intervensi, angka reproduksi penyebaran Covid-19 di Provisi Jakarta sekitar 1,658 dan jika Pembatasan Sosial Berskala Besar (PSBB) diimplementasikan, maka angka reproduksinya turun menjadi 1,40. Lebih lanjut, epidemi diperkirakan akan berakhir sekitar akhir November 2020 dengan kasus puncak pada pertengahan Juni 2020 dengan jumlah orang yang dikonfirmasi positif terinfeksi mencapai sekitar 9.000 jiwa. Dari hasil pemodelan ini, disimpulkan bahwa untuk meminimalkan penularan penyakit, perlu menerapkan kebijakan dan kontrol yang lebih ketat.

Kata Kunci: Covid-19; Model matematika; PSBB; kestabilan

Abstract

Coronavirus disease 2019 (COVID-19) which was initiated in China, has spread rapidly in more than 114 countries and territories over the last two months. An understanding of the dynamics of Covid-19 transmission is very important to determine policies and strategies in the treatment and control of the spread of this disease. In this paper, we formulated a mathematical model that describes the transmission dynamics of the disease using a deterministic mathematical model and the model is validated against data from Jakarta, Indonesia from March 3, 2020, to April 10, 2020. Mathematical analysis and numerical simulations are presented. We found that without intervention, the reproduction number is around 1.658 and the reproduction number declines to 1.40 if large scale social distancing is implemented. Furthermore, the end time of epidemic is predicted to be around the end of November 2020 with peak cases around mid-June 2020 and the number of confirmed infected individuals is around 9,000. To minimize the transmission of the diseases, it is necessary to enforce strict policies and controls.

Keywords: Covid-19; mathematical model; PSBB; stability

Introduction

An outbreak of Covid-19 has attracted worldwide attention. It has shocked people around the world. WHO has declared COVID-19 as a pandemic on March 11, 2020, after the disease became an epidemic in more than 114 countries and regions around the world. This disease spreads very quickly in the US and European countries, such as Spain, Italy, and Germany. Based on Worldometers data, as of April 15, 2020, there were 2,076,502 confirmed cases worldwide, with 140,791 death and 510,122 recovered. Most cases occurred in the US with 652,477 confirmed positive cases, with 32,712 deaths and 89,535 cures. Whereas in Indonesia, there were 3,512 cases with 469 dead and 1818

recovering, especially in Jakarta Province, there were 1,810 positive cases with 82 deaths and 155 recovering [1].

The SARS-CoV-2 virus has an average incubation period of 5.1 to 5.8 days and starts showing symptoms around 11.5 to 15.6 days [2]. The SARS-CoV-2 virus can spread from person to person mainly through drops coming out of the mouth when coughing or talking [3, 4, 5, 6]. Unlike other diseases, not all patients who are positive for COVID-19 are experiencing symptoms of pain. WHO states that about 85% of positive cases of infection are reported to have mild symptoms or even no symptoms of pain, but can transmit the virus to others [7]. One intervention procedure to control the spread of COVID-19 is to avoid encounters or interactions with many people so that the risk of transmission is reduced. Various regions have made various efforts to prevent the spread of this disease, from social distance, physical distance, to locking as did Italy. One way to prevent the spread of COVID-19 is to isolate people suspected of being exposed to COVID-19 for at least 14 days [8]. In Indonesia, the government requests physical distance to maintain a safe distance, which in its implementation, some regions implement policies to limit the movement of people. The policy is very dependent on the discipline of citizens in doing physical distance. To put more pressure on the development of COVID-19, several provinces in Indonesia, preceded by the Jakarta province, imposed large-scale Social Restrictions (PSBB) regulations. PSBB is limiting certain activities of the population in such a way that the possibility of the spread of Covid-19 can be prevented. The Jakarta province has implemented PSBB starting April 10, 2020.

Mathematical modeling of epidemics has been widely used to study the spread of disease, such as for SARS epidemiological diseases in [9, 10]. Several mathematical models of the spread of COVID-19 have been developed, especially in China, such as in [11, 12, 13, 14]. Recently, based on Richards Curve, Nuning et al. [15] predict that in Indonesia, the number of cases of COVID-19 disease will reach more than 8000 cases and will end in April 2020. From various mathematical modeling of the spread of COVID-19 that has been developed, no model was found that considers susceptible groups that carry out physical distance programs as the implementation of Large-Scale Social Restrictions (PSBB). Therefore, in this study, a mathematical model of the spread of COVID-19 was built taking into account the policy of the PSBB rules in susceptible groups. The purpose of this study is to provide a mathematical analysis of the extent to which the effectiveness of the PSBB policy on the success of suppressing the transmission and spread of COVID-19.

The Model and Basic Properties of Solution

We develop a mathematical model of COVID-19 by dividing the population into six compartments, namely susceptible, $S(t)$, restricted susceptible, $S_r(t)$, under monitoring, $O(t)$, under surveillance, $P(t)$, confirmed infected, $I(t)$, and recovered, $R(t)$ individuals. The total population size is $N(t) = S(t) + S_r(t) + O(t) + P(t) + I(t) + R(t)$. The schematic diagram of the model is depicted in Figure 1.

Susceptible populations increase from the entry of individuals into communities, including new births, immigration, and emigration at a constant Λ recruitment rate. Susceptible populations can be infected through contact between susceptible and positively confirmed infected individuals. Before being confirmed positive infection, susceptible individuals who make contact with infected people will be categorized as individuals in care who have not tested positive or under surveillance (P). The transmission coefficient from the susceptible population to the under surveillance population is β. Susceptible populations also decrease due to maintaining social distance or PSBB at the rate α and natural mortality at rate μ. In addition, susceptible individuals who travel or are in areas where the spread of COVID-19 will fall into the category of individuals under monitoring (O). In this model, the rate of change from S to O is denoted by c.

The restricted susceptible individuals are generated from susceptible individuals who apply the physical distance rules or PSBB at rate α. Assuming that physical distance is not perfect, restricted susceptible individuals can also be in the under surveillance population through contact with an infected person. In this case, the transmission coefficient of β is multiplied by $(1-p)$, where $0 \leq p \leq 1$ is the level of transmission effectiveness that is influenced by individual discipline in complying

with PSBB rules, maintaining physical distance, and the governments assertiveness of those who violate the PSBB rules. Note that $p = 0$ indicates that no individual adheres to the PSBB rules.
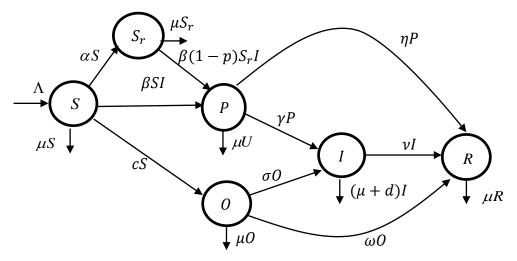

Figure 1. Schematic diagram for the transmissions of COVID-19 with PSBB.

Under surveillance individuals arise as a result of the interaction between susceptible individuals and infected individuals at the rate β then decreased by the development of infected populations at a rate σ. The confirmed infected also come from the under monitoring individual that confirmed positif in a rate σ. The confirmed infected population is diminished by disease induced death at a rate d. The under monitoring, under surveillance, and confirmed infected populations are decrease by recover at rate ω, η, and ν, respectively. In addition, populations in all compartments are assumed to suffer natural death at a rate μ. The parameters used and descriptions are listed in Table 1.

Table 1. Parameter used and descriptions.

Parameter	Description
Λ	Recruitment rate of susceptible humans
α	Restricted coverage rate
β	Transmission rate of susceptible to under surveillance
c	Transmission rate of susceptible to under monitoring
μ	Natural mortality rate
p	The efficacy of PSBB
σ	Recruitment rate of confirmed infected from under monitoring
ω	Recovery rate of under monitoring
ν	Recovery rate of confirmed infected
γ	Recruitment rate of confirmed infected from under surveillance
η	Recovery rate of under surveillance
d	Mortality rate of confirmed infected

Our model is thus given by the following equations:

$$\frac{dS}{dt} = \Lambda - \alpha S - \beta S I - \mu S - cS, \tag{1}$$

$$\frac{S_r}{dt} = \alpha S - \beta(1-p)S_r I - \mu S_r, \tag{2}$$

$$\frac{dO}{dt} = cS - (\mu + \sigma + \omega)O, \tag{3}$$

$$\frac{dP}{dt} = \beta SI + \beta(1-p)S_r I - (\mu + \gamma + \eta)P, \tag{4}$$

$$\frac{dI}{dt} = \gamma P + \sigma O - (\mu + v + d)I, \tag{5}$$

$$\frac{dR}{dt} = \eta P + vI + \omega O - \mu R. \tag{6}$$

In this model, it is assumed that the recovered individuals do not reacquired Coronavirus infection. Next, since the recovered population does not appear in the first five equations of the model, the rest of the paper will consider only equations (1)-(5).

In the following theorem, we verify that all solutions of Equations (1)-(5) with nonnegative initial conditions remain nonnegative for $t \geq 0$.

Theorem 2.1   *The set*

$$\Omega = \left\{ (S, S_r, O, P, I) \in \mathbf{R}_+^5 : S + S_r + O + P + I \leq \frac{\Lambda}{\mu}, \ S \leq \frac{\Lambda}{\mu + \alpha + c}, S_r \leq \frac{\alpha\Lambda}{\mu(\mu + \alpha + c)} \right\}$$

is a positively invariant and attracting set for Equations (1) (5).

Proof. From Equation (1), we get

$$\frac{dS}{dt} = \Lambda - \alpha S - \beta SI - \mu S - cS \leq \Lambda - (\alpha + \mu + c)S.$$

Thus, following the standard comparison argument we get $0 \leq \lim_{t\to\infty} \sup S(t) \leq \frac{\Lambda}{\mu + \alpha + c}$.

Similarly, from Equation (2), we get $0 \leq \lim_{t\to\infty} \sup S_r(t) \leq \frac{\alpha\Lambda}{\mu(\mu + \alpha + c)}$.

Since $N(t) = S(t) + S_r(t) + P(t) + P(t) + I(t) + R(t)$, we get

$$\frac{dN}{dt} = \Lambda - dI - \mu N \leq \Lambda - \mu N.$$

Thus we have $0 \leq \lim_{t\to\infty} \sup N(t) \leq \frac{\Lambda}{\mu}$, so all solutions of (1)-(5) are ultimately bounded and inside the region Ω.

Furthermore, it can be easily verified that the model given by Equations (1)-(5) always has a unique disease-free equilibrium, which we will denote by E_0, obtained by setting the right-hand side of Equations (1)-(5) equal to zero, and it is given by

$$E_0 = \left(\frac{\Lambda}{\mu + \alpha + c}, \frac{\alpha\Lambda}{\mu(\mu + \alpha + c)}, 0, 0, 0 \right).$$

It is clear that E_0 attracts the region

$$\Omega_0 = \{ (S, S_r, O, P, I) \in \Omega : O = P = I = 0 \}.$$

Next, we will compute the basic reproduction number, R_0 of the model and analyze the stability of the disease-free equilibrium. The basic reproduction number defined as the expected number of secondary cases that result from one newly infected individual introduced into a completely susceptible individual [16]. Here, we compute the effective reproduction number, denoted by R_e, to describe the average number of secondary infections generated by primary cases in a community under specified controls such as PSBB. By applying the procedure of next-generation matrix described in [16], we have

$$\mathcal{F} = \begin{bmatrix} cS \\ \beta SI + \beta(1-p)S_r I \\ 0 \end{bmatrix}$$

and

$$\mathcal{V} = \begin{bmatrix} (\mu + \sigma + \omega)O \\ (\mu + \eta + \gamma)P \\ -\gamma P - \sigma O + (\mu + v + d)I \end{bmatrix}.$$

The next-generation matrix is defined as FV^{-1} with F and V are both the Jacobian matrices of $\mathcal{F}$ and $\mathcal{V}$ evaluated at the disease-free equilibrium point. After simple calculations, we found that FV^{-1} has a single nonzero eigenvalue corresponding to the spectral radius of FV^{-1} which represents the effective reproduction number of the model, denoted by R_e. So we have

$$R_e = \frac{\beta \gamma \Lambda (\mu + (1-p)\alpha)}{\mu(\mu+\gamma+\eta)(\mu+v+d)(\mu+\alpha+c)}. \tag{7}$$

From the formula R_e, we have the basic reproduction number, R_0 that obtained for $\alpha = 0$, that means that there are no individual that enters to restricted susceptible populations. In other word, there are no policies such as physical distancing or PSBB.

Now, we analyze the stability of the disease-free equilibrium point. The stability determined by the signs of the real part of eigenvalues of the Jacobian matrix at the equilibrium point. The disease-free equilibrium is locally asymptotically stable if and only if all eigenvalues of the Jacobian matrices have negative real parts. We have the following theorem.

Theorem 2.2   *The disease-free equilibrium point E_0 is locally asymptotically stable if $R_e < 1$ and unstable if $R_e > 1$.*

Proof. To prove this theorem we evaluation the Jacobian matrix of Equations (1)- (5) at the disease-free equilibrium point, $E_0 = (\frac{\Lambda}{\mu+\alpha+c}, \frac{\alpha\Lambda}{\mu(\mu+\alpha+c)}, 0,0,0)$, and we find a characteristic polynomial as

$$(\lambda + \mu)[(\lambda + \Lambda)(\lambda + K)(\lambda^2 + a_1\lambda + a_2)] + L(\lambda + M) = 0, \tag{8}$$

where

$$K = \mu + \sigma + \omega, a_1 = (\mu + \gamma + v) + (\mu + v + d),$$

$$a_2 = (\mu + \gamma + v)(\mu + \eta + d)\left(1 - \frac{\beta\gamma\Lambda(\mu+(1-p)\alpha)}{\mu(\mu+\gamma+\eta)(\mu+v+d)(\mu+\alpha+c)}\right),$$

$$L = \frac{c\beta\sigma\Lambda}{(\mu+\sigma+\omega)}, \quad M = \mu + \gamma + \eta.$$

Thus, Equation (8) will has strictly negative real root if $a_2 > 0$. So, all of the eigenvalues are negative if

$$1 - \frac{\beta\gamma\Lambda(\mu + (1 - p)\alpha)}{\mu(\mu + \gamma + \eta)(\mu + v + d)(\mu + \alpha + c)} > 0$$

or

$$1 - R_e > 0.$$

Hence, the disease-free equilibrium E_0 is locally asymptotically stable if $R_e < 1$ and unstable if $R_e > 1$.

Theorem 2 shows that COVID-19 will be eliminated from the community if $R_e < 1$. It has an important public health implications, especially in an effort to stop the spread of COVID-19.

Simulation Results and Discussions

In this section, we carry out numerical simulations using parameter values from data released by the Government of Indonesia from March 3, 2020, to April 10, 2020 (https://www.covid19.go. Indo). In particular, we look at data from the Jakarta province which first applied the PSBB policy. The

associated parameters are estimated using available data with several assumed to get more realistic simulation results as described below.
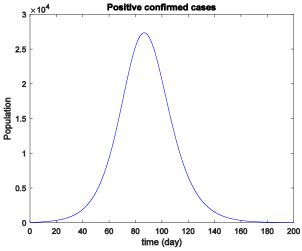
We estimate the parameter $\Lambda = 403$ per day. It based on the data of Central Bureau of Statistics (BPS) that the total Jakarta province population is 10,645,000 with average life-expectancy 72.4 years (http://www.bps.go.id). It follows that the natural death rate, $\mu = \frac{1}{72.4 \times 365} = 0.0000378$ per day.

The parameters α, β, and c measure the rate of restricting, under monitoring, and under surveillance individuals. In the initial phase of COVID-19, we can take the parameters $\alpha = 0, \beta = 0$, and $c = 0$ in our model. After the Government recognized the positive COVID-19 patients, then government began to implement a physical distancing rules. Consequently, we set the value of α, β, and c switching to some constant value. Since there are no available data, we chose these parameter values such that the results obtained are realistic. It is reasonable to assume that $\alpha \geq c \geq \beta$ because detecting restricted individuals seem easier than detecting under monitoring individuals, and detecting under monitoring individuals easier than detecting under surveillance individuals. For this purpose, we assume that $0.01 \leq \alpha \leq 0.4$ per day, $3.78 \times 10^{-5} \leq c \leq 1.0 \times 10^{-2}$ per day and $3.78 \times 10^{-6} \leq \beta \leq 3.78 \times 10^{-3}$ per day.

During this time, the Government through the Task Force for the Acceleration of Handling COVID-19 only provides death data updates for patients who have positive confirmed. In this model, we do not consider the under monitoring and under surveillance individuals die because of COVID-19. However, we consider that the under monitoring and under surveillance individuals as well as the confirmed individuals can recover from this disease. The incubation period of COVID-19 is between 5.1 to 15.6 days and the average disease duration is 21 days [15]. Based on the historical data COVID-19 case in Jakarta province up to April 10, 2020, the mortality rate is about 8.6 % and the recovery rate is about 4.53 %. Therefore it is reasonable to assume that both of the parameter σ and γ are lie between 0.064 to 0.196 per day and the disease mortality rate is lie in the interval $0.045 \leq d \leq 0.086$. Meanwhile, under monitoring individuals who were stated to have finished monitoring is around 86 %, while under surveillance individuals who were declared cured reached 54.8 %. This number is increasing day by day. Therefore, we assume that the parameter values of ω, η, and ν are between 0.045 to 0.86 per day.

For simulation purposes, we use the set of parameter values $\Lambda = 403, \alpha = 0.14, \beta = 1.4 \times 10^{-5}, \mu = 3.78 \times 10^{-4}, c = 0.005, \sigma = 0.05, \eta = 0.86, \omega = 0.82, \gamma = 0.08, \nu = 0.21$, and $d = 0.086$, with all in units day^{-1}, and we chose transmission effectiveness $p = 0.6$, before PSBB policy at April 10, 2020 (days 39th). It should be noted that the Jakarta province reported the first positive case of COVID19 on 3 March 2020, in which there were 3 positive patients.

Figure 2 shows the simulation result of I for the first 200 days of COVID-19 disease. It can be seen that at the peak of epidemic, the number of confirmed infected individuals is about 27.300 cases which reach at days 86th (May, 27,2020). In Figure 3, we provide four scenarios after the 39th day by considering the implementation of the PSBB rules taken by the Jakarta provincial government. Scenario 1, if the PSBB rule does not change the rate of spread of COVID-19, while in scenario 2 the application of the PSBB rule results in an increase in the effectiveness of physical distance p from 0.6 to 0.65. Next, in scenario 3 we set $p = 0.662$, and in scenario 4 we set $p = 0.68$. We also compared the predicted positive COVID-19 case from the simulation results with real cases of infected people confirmed for the first 50 days, starting from March 3, 2020, to April 21, 2020, see Figure 4. From the comparison with the real case in Figure 4, we deduce that the implementation of the PSBB rule has succeeded in suppressing the transmission of COVID 19. This is indicated by the increasing effectiveness of social distancing, which in this model is expressed by p. Furthermore, assuming that the PSBB rules have succeeded in increasing the effectiveness of physical distancing from 0.6 to 0.662, the COVID-19 outbreak in Jakarta will reach its peak on day 105 (mid of June 2020) with about 9000 cases of confirmed positive. Figure 5 shows the prediction of confirmed positive cases of COVID-19 in Jakarta province with and without the effects of PSBB. If there are no significant changes, then it is estimated that the COVID epidemic in Jakarta will stop at the end of November 2020.

Figure 2. Simulation results of the confirmed infected individuals using the set of parameters $\Lambda = 403, \alpha = 0.14, \beta = 1.4 \times 10^{-5}, \mu = 3.78 \times 10^{-4}, c = 0.005, \sigma = 0.05, \eta = 0.86, \omega = 0.82, \gamma = 0.08, \nu = 0.21$, and $d = 0.086$, and $p = 0.6$.
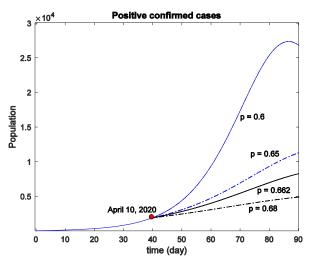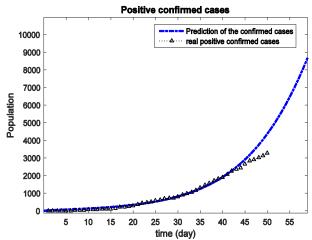

Figure 3. Simulation results of the confirmed infected individuals with different value of parameter p after day 39th.

Figure 4. Comparison of confirmed infected individuals and prediction from simulation results with a set of parameter as in Figure 2. Real data available until April 21, 2020 (days 50).
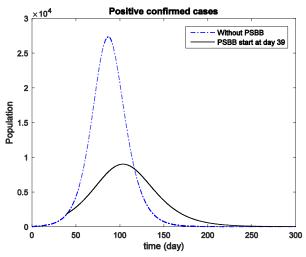
Figure 5. Comparison of prediction COVID-19 without PSBB ($p = 0.6$) and with PSBB after days 39 ($p = 0.662$).
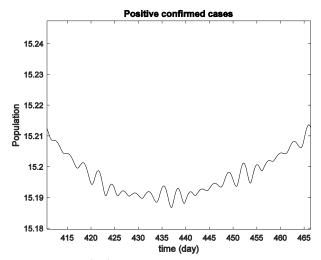

Figure 6. The confirmed positive cases not completely vanished.

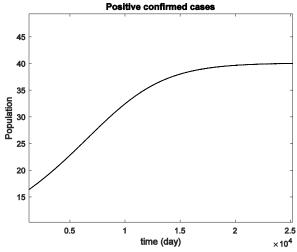**Figure 7**. The confirmed positive case gradually increases to a relatively small number that can be controlled.

We note that, based on the use of the parameter values as in Figure 2, we have an effective reproductive rate for COVID0-19 disease $R_e = 1.658$, greater than one. Likewise if p is increased to 0.662, we still have $R_e = 1.40 > 1$. From theorem 2, we conclude that the disease-free equilibrium

point is not locally asymptotically stable. In fact, from the simulation results, we found that the actual epidemic disease was not completely vanished. The infected population approaches zero and then grows slowly. We can see in Figure 6 and Figure 7, that after the confirmed positive cases reach the lowest number, then the number of cases gradually increases to a certain amount that can be controlled. This is a natural occurrence in many epidemic cases, such as HIV, DHF, malaria, and even SARS. Nevertheless, overall we can say that the epidemic is over.

Conclusion

In this paper, we formulate a mathematical model of the epidemic and predictions of the spread of COVID-19. This is compartment-based epidemic model. We find that this model is biologically meaningful by showing that system solutions are bounded and positive. We have a disease-free equilibrium point and investigate its local stability. We also provide numerical simulations using realistic parameter values. Finally, from the simulation results we estimate that, after the PSBB has been implemented in the province of Jakarta in the prevention and control of COVID-19, the COVID-19 epidemic in Jakarta will peak around mid-June 2020 and will cease after eight months or the end of November 2020.

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