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Analysis of the Effects of Foreign Travelers and Immigrants on Omicron Transmission in Indonesia

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Abstract

The Indonesian government wanted to determine the transmission of the Omicron virus via immigrants and foreign tourists in Indonesia. Hence, the Omicron transmission Susceptible–Infectious–Recovered model, with parameters of foreign travelers and immigrants was constructed. Then, using the next-generation matrix method, it was discovered that when the number of foreign travelers and immigrants

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who entered Indonesia (a) is constant and the number of foreign travelers who leave Indonesia (c) varies, the basic reproductive number is $R_0 = 5.6$. Conversely, when the number of foreign travelers and immigrants entering Indonesia (a) varies and the number of foreign travelers leaving Indonesia (c) is constant, the basic reproductive number is $R_0 = 6.7$.

1 Introduction

The Omicron variant (B.1.1.529) of COVID-19, known for its rapid spread and increased transmissibility, emerged in December 2021 and quickly reached numerous countries [1, 2, 3]. Its exponential growth led the WHO to designate Omicron as a Variant of Concern (VOC) [4]. This study focuses on the impact of foreign travelers and immigrants on Omicron transmission in Indonesia. Jakarta has been the primary entry and exit point for foreign visitors and immigrants to Indonesia. On December 8, 2021, the virus first appeared in the country when a Nigerian traveler infected three homestead workers, subsequently leading to eight additional cases among travelers from various countries, including Britain, the USA, Congo, and Malaysia. The Indonesian Minister of Health officially confirmed Omicron's presence on December 16, 2021 [1, 5]. Notably, 75% of the 725 reported Omicron cases in Indonesia originated from foreign travelers and immigrants [6].

While previous studies have examined COVID–19 and Omicron outbreaks in Indonesia using various mathematical models [7, 8, 9], our approach differs. In this study, we present a modified SIR mathematical model tailored to account for parameters related to foreign travelers and immigrants. This model is designed to calculate the basic reproduction number, a key metric for understanding the virus's potential transmission. Moreover, it enables the simulation of parameter values for foreign travelers and immigrants, aiding in estimating the maximum allowable numbers to prevent the virus from spreading and causing an epidemic.

2 Method

The Omicron SIR epidemic model, incorporating foreign travelers and immigrants, utilized actual Omicron case data from Jakarta between December 16, 2021 and May 31, 2022 [10]. Two equilibrium points were identified: endemic and disease-free, assuming no subpopulation changes in each compartment. The basic reproduction number was computed using the next-generation method based on the infected compartment submodel [11]. The

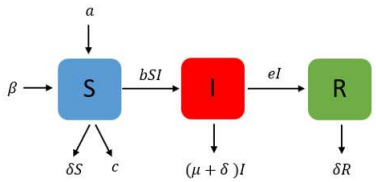


Figure 1: SIR model scheme with parameters of foreign travelers and immigrants.

stability of the disease-free equilibrium point was established using the eigenvalue theorem and the Jacobian matrix, while the stability of the endemic equilibrium point was determined using the polynomial stability theorem. Numerical simulations, varying parameter values for incoming and outgoing foreign travelers and immigrants, were conducted using MAPLE software to analyze virus propagation.

3 Results and Discussion

3.1 SIR Omicron Model Formulation

The SIR model for Omicron spread in Indonesia comprises three compartments: Vulnerable (S), Infected (I), and Recovered (R). It accounts for foreign travelers and immigrants, births, natural deaths, Omicron-related deaths, and recoveries. Infected immigrants and tourists were assumed unable to enter Indonesia. The model allows individuals to transition between compartments, and recovery confers immunity to reinfection. Figure 1 illustrates the schematic of Omicron transmission in Indonesia. Based on the scheme in Figure 1, changes in the number of individuals in each compartment could be expressed through the following SIR model:

$$\begin{aligned} \frac{dS}{dt} &= \beta + a - c - \delta S - bSI, \\ \frac{dI}{dt} &= bSI - (\delta - \mu - e)I, \\ \frac{dR}{dt} &= eI - \delta R. \end{aligned} \tag{3.1}$$

3.2 Determination of the Equilibrium Point

If it was assumed that the number of individuals in each compartment does not change (constant), $\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$, then two equilibrium points

(disease-free and endemic) can be obtained from the following system:

$$\beta + a - c - \delta S - bSI = 0, \tag{3.2}$$
$$bSI - (\delta + \mu + e)I = 0, \tag{3.3}$$
$$eI - \delta R = 0. \tag{3.4}$$

Table 1: Definitions, estimated value and chance of each variable and parameter.

Var.	Definitions	Est. Value for t=0	Chance	Source
N	Total population	10,609,681	1	[12]
S	Total vulnerable population	10,598,666	0.998962	-
I	Total infected population	6015	0.000567	[10]
R	Total recovered population	5000	0.000471 268	Assumption
β	Birth rate	0.00156		[13]
a	Incoming foreign travelers & imm.			
c	Exiting foreign travelers			
δ	Natural death rate	0.000028		[14]
b	Omicron transmission rate	0.0162		Assumption
μ	Omicron-death rate	0.000109		[15]
e	Omicron-recovered rate	0.00606		Assumption

3.2.1 Disease-free equilibrium point

This equilibrium point represents the condition in which there were no infected individuals in the population ($I = 0$). Then, using Equation 3.2, the number of susceptible individuals in disease-free conditions is

$$S = (\beta + a - c)/\delta = S^0, \tag{3.5}$$

with S^0 indicating the number of susceptible individuals in disease-free conditions. Moreover, under the same conditions, using Equations 3.4 and 3.5, the disease-free equilibrium point can be restated as

$$E^0 = (S^0, I^0, R^0) = (\frac{\beta + a - c}{\delta}, 0, 0). \tag{3.6}$$

3.2.2 Endemic equilibrium point

The equilibrium point when $I \neq 0$ indicates the condition of the virus spreading in a population [16]. Assuming $S = S^*, I = I^*, R = R^*$, the number of

susceptible individuals (S^*) is obtained using Equation 3.3 as follows:

$$S = \frac{(\delta + \mu + e)}{b} = S^*. \tag{3.7}$$

Then, by substituting Equation 3.7 into Equation 3.3 and from Equation 3.4, the endemic equilibrium point can be written as

$$\begin{aligned} E^* &= (S^*, I^*, R^*) \\ &= \left(\frac{(\delta + \mu + e)}{b}, \frac{(\beta + a - c)b - \delta(\delta + \mu + e)}{b(\delta + \mu + e)}, \frac{eI^*}{\delta} \right). \end{aligned} \tag{3.8}$$

3.3 Basic Reproduction Number

The basic reproductive number R_0 is a number that represents the average number of infected people as a result of contracting one infected individual [11]. This number can be obtained by constructing the nextgeneration matrix from the infected subsystem $\frac{dI}{dt}$ of Equation 3.1. The Jacobian matrix for obtaining the disease-free equilibrium point E_0 from the subsystem is

$$J_{E^0} = [bS^0 - (\delta + \mu + e)] = \left[\frac{b\,\beta + a - c}{\delta} \right] + [-(\delta + \mu + e)] = T + \Sigma$$

where T is the transmission matrix that depicts the genesis of a new infection, and Σ is the transition matrix that explains the change from the infected condition to the recovered state, including death [17]. The next-generation matrix is expressed as $\Sigma^{-1} = \left[\frac{-1}{(\delta+\mu+e)} \right]$, and the next-generation matrix is expressed as follows:

$$\begin{aligned} K &= -T\Sigma^{-1} = -\left[\frac{b(\beta + a - c)}{\delta} \right] \left[\frac{-1}{(\delta + \mu + e)} \right], \\ &= \left[\frac{b(\beta + a - c)}{\delta(\delta + \mu + e)} \right] = R_0. \end{aligned} \tag{3.9}$$

The next-generation matrix size of 1 x 1 is the basic reproduction number directly from the matrix components.

Theorem 1 The disease-free equilibrium point E^0 from Equation 3.1 can be locally asymptotically stable if it satisfies the condition of $R_0 < 1$.

Proof. Based on [18] using the characteristic equations, the eigenvalues of the Jacobian matrix for disease-free equilibrium points J_{E0} were obtained

from

$$\begin{vmatrix} -\delta-\lambda & -\delta\frac{(\beta+a-c)}{\delta} & 0 \\ 0 & b\left(\frac{(\beta+a-c)}{\delta}\right)-(\delta+\mu+e)-\lambda & 0 \\ 0 & e & -\delta-\lambda \end{vmatrix} = 0$$

$$\lambda_1 = -\delta, \lambda_2 = b\frac{(\beta+a-c)}{\delta} - (\delta+\mu+e), \text{and } \lambda_3 = -\delta. \tag{3.10}$$

For λ_2, two possibilities were applied; namely, $\lambda_2 < 0$ and $\lambda_2 > 0$. The condition of $\lambda_2 < 0$ can occur if $b\frac{(\beta+a-c)}{\delta} - (\delta+\mu+e) < 0 \leftrightarrow R_0 < 1$.

Based on the stability theorem reported by [19], as $\lambda_i < 0$ for $i = 1, 2, 3$, the equilibrium point of E^0 is locally asymptotically stable under the conditions of $R_0 < 1$. Conversely, the condition of $\lambda_2 > 0$ occurs if $R_0 > 1$. Therefore, the disease-free equilibrium point of E^0 is unstable.

Theorem 2 If $R_0 > 1$, the endemic equilibrium point E^* is locally asymptotically stable and unstable otherwise.

Proof. As in the proof of theorem 1, using the Jacobian matrix for the endemic equilibrium point E^*, the obtained characteristic equation is

$$\lambda^3 + X\lambda^2 + Y\lambda + Z = 0, \tag{3.11}$$

where

$$\begin{aligned} X &= \frac{\delta(\delta+\mu+e)+(\beta+a-c)b}{(\delta+\mu+e)}, \\ Y &= \frac{\delta b(\beta+a-c)+(\beta+a-c)(\delta+\mu+e)b-\delta(\delta+\mu+e)^2}{(\delta+\mu+e)}, \\ Z &= \delta(b(\beta+a-c)-\delta(\delta+\mu+e)). \end{aligned}$$

Because $X > 0$, $Y > 0$, $Z > 0$, and $XY - Z > 0$, the endemic equilibrium point E^* for System (1) is stable based on the study in [19]. Conversely, if the stability is not fulfilled, then the polynomial is said to be unstable. Furthermore, if $Z > 0$, then $\frac{b(\beta+a-c)}{\delta(\delta+\mu+e)} > 1$ or $R_0 > 1$. According to the polynomial stability theorem, the endemic equilibrium point E^* is locally and asymptotically stable if $R_0 > 1$ and unstable if $Z < 0$; so $R_0 < 1$.

3.4 Numerical Simulation of the Omicron SIR Model

Foreign travelers and immigrants' movement rates were simulated with MAPLE software, while in Table 1 we present the initial and parameter values. Ad-

Table 2: Disease-free equilibrium point values and their eigenvalues

Simulation	$\mathbf{S^0}$	$\mathbf{I^0}$	$\mathbf{R^0}$	λ_1	λ_2	λ_3
1	0.1634	0	0	-0.000028	0.02868871429	-0.000028
2	0.1004	0	0	-0.000028	-3.04521E-05	-0.000028
3	0.0956	0	0	-0.000028	-0.004229857	-0.000028
4	0.1764	0	0	-0.000028	0.034881571	-0.000028
5	0.104	0	0	-0.000028	-0.006196827	-0.000028
6	0.0915	0	0	-0.000028	-0.006197	-0.000028

ditionally, by keeping 'a' fixed at 0.02 and varying 'c' ($c = 0.021489$), Equation 3.1 can be expressed as:

$$\begin{aligned} \frac{dS}{dt} &= 0.000071 - 0.000028S - 0.01628SI \\ \frac{dI}{dt} &= 0.01628SI - 0.006197I, \\ \frac{dR}{dt} &= 0.00606I - 0.000028R \end{aligned} \tag{3.12}$$

Using Equation 3.9, the basic reproduction number R_0 is calculated as $R_0 = 5.629452040$, which exceeds 1 [13], indicating the potential for an outbreak. According to Equation 3.10, the eigenvalues are $\lambda_1 = -0.000028$, $\lambda_2 = 0.034881571$, and $\lambda_3 = -0.000028$, as depicted in Simulation 4 in Table 2. In Theorem 1, we established the instability of the disease-free equilibrium point due to a positive eigenvalue.

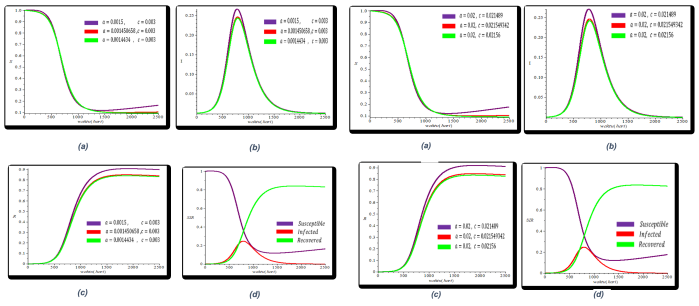
Equation 3.11 yields coefficient values for the characteristic equation: $X = 0.000213606$, $Y = 9.8188110 - 7$, $Z = 2.7347210^{-11}$, with $XY - Z = 1.8238810^{-10}$. Consequently, Theorem 2 affirms that the endemic equilibrium point $X^* = (0.1764, 510 - 4, 0.91)$ from Equation 3.8 is locally and asymptotically stable. This implies that the endemic equilibrium, based on the system of Equation 3.8 with initial values $S(0)$, $I(0)$, and $R(0)$, approaches over time. At the equilibrium point, there are 1,871,548 susceptible, 5,305 infected, and 9,654,810 recovered individuals, out of an initial total population of 10,609,681.

Next, when 'a' varies ($a = 0.0015$) and 'c' is kept constant ($c = 0.003$), the basic reproduction number becomes $R_0 = 6.661518246$, exceeding 1 [11], indicating the potential for an outbreak. For this scenario, the eigenvalues are $\lambda_1 = -0.000028$, $\lambda_2 = 0.02868871429$, and $\lambda_3 = -0.000028$, as observed in Simulation 1 in Table 2. Based on Theorem 1, the disease-free equilibrium

Table 3: Parameter value, endemic equilibrium point, and R_0 value.

Simulation	Parameter Value		S^*	I^*	R^*	R^0
	a	c				
1	0.0015		0.1634	$4.5x10^{-4}$	0.897	6.661518246
2	0.001450658231	0.003	0.1004	$2.3x10^{-4}$	0.8384	1
3	0.0014434		0.0956	$2.1x10^{-4}$	0.8295	0
4		0.021489	0.1764	$5x10^{-4}$	0.91	5.629452040
5	0.02	0.021549341764	0.104	$2.4x10^{-4}$	0.838	1
6		0.02156	0.0915	$2x10^{-4}$	0.8254	0.3190022822

point is unstable because one of the eigenvalues is positive. Additionally, applying Equation 3.11, the coefficient of the characteristic polynomial becomes $X = 0.0001856 > 0$, $Y = 0.00007436 > 0$, $Z = 2.2491952x10^{-11}$, and $XY - Z = 1.378082806x10^{-8} > 0$. The endemic equilibrium point E^* obtained using Equation 3.11 is $E^* = (S^*, I^*, R^*) = (0.1634, 4, 5.10^{-4}, 0.897)$. Hence, E^* locally and asymptotically stable by Theorem 2. This means that Equation 3.13, with initial values of $S(0)$,$I(0)$, and $R(0)$, moves toward the endemic equilibrium point as time (days) passes. According to the equilibrium point E^*, out of the 10,609,681 total initial population, 1,733,622 individuals are susceptible, 4774 individuals are infected, and 9,516,884 individuals have recovered. Eigenvalues in simulations 2, 3, 5, and 6 are negative, indicating that the disease-free equilibrium point is asymptotically stable and does not require further investigation. In Table 3, the threshold values for the virus not to become an epidemic ($R_0 = 1$) and complete eradication ($R_0 < 1$) are listed. In case $R_0 = 1$, if the rate of incoming foreign travelers and immigrants, $a = 0.02$, then the rate of outgoing foreign travelers, $c = 0.021549341764$ (simulation 5). Conversely, when the outgoing foreign travelers $c = 0.003$, the incoming foreign travelers and immigrants $a = 0.001450658231$ (Simulation 2). Then, to make $R_0 < 1$ with $a = 0.02$, $c < 0.021549341764$, Simulation 6 is performed, whereas for $c = 0.003$, $a < 0.001450658231$, Simulation 3 is performed.



Conclusion. The ongoing presence of the COVID-19 pandemic in Indonesia can be attributed to the unrestricted entry and exit of foreign travelers and immigrants. The rate of Omicron virus transmission is directly linked to the inflow and outflow of people. As highlighted by the threshold values in Table 3, the findings from this study offer valuable insights for the government to consider implementing measures to control foreign travelers and immigrants, ultimately curbing the virus's spread.

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