

A SIAR Model Approach to the Impact of *Mudik* Tradition on Covid-19 Transmission in Indonesia

Darsih Idayani^{1✉}, Asmara Iriani Tarigan², Selly Anastassia Amellia Kharis³,
Heny Kurniawati⁴

^{1, 2, 3} Mathematics Study Program, Faculty of Science and Technology, Universitas Terbuka, Indonesia

⁴ Biology Study Program, Faculty of Science and Technology, Universitas Terbuka, Indonesia

✉ Corresponding Author : Darsih Idayani (e-mail: darsih@ecampus.ut.ac.id)

Article Information

Article History

Received : June 08, 2025

Revised : June 24 2025

Published : July 12, 2025

Keywords:

Mathematics modelling;

SIAR;

Covid-19;

Mudik tradition.

ABSTRACT

In Indonesia, on March 2, 2020, the government announced the first case of Covid-19. Preventing the COVID-19 spread in Indonesia is challenging because the people are very diverse, and not everyone has the same understanding of the transmission of COVID-19. In addition, the Indonesians has *mudik* tradition, going home yearly on Eid al-Fitr. This study developed an epidemic model of Covid-19 spread *SIAR* by adding migration factors to represent the *mudik* tradition. The disease-free equilibrium point, the endemic equilibrium point, and its stability were determined. Numerical simulations were done using Covid-19 transmission data to analyze the trend of symptomatic and asymptomatic infected subpopulations. The results show that the dynamic characteristics of Covid-19 cases were semi-stable in compartments *S*, *I*, and *A*. This condition means that *S*, *I*, and *A* will rise at a certain time. In a disease-free situation, the susceptible subpopulation *S* is stable at a certain value. At the same time, other subpopulations are stable at almost zero and at zero. The susceptible subpopulation *S* in a disease-free situation is larger than during an epidemic. The number of people in disease-free conditions is smaller than those in epidemic conditions. In addition, migration at a certain level can increase the spread of Covid-19.

INTRODUCTION

The SARS-CoV-2 coronavirus outbreak centered in Hubei Province, PRC has overspread to many countries in early 2020 (Cucinotta & Vanelli, 2020). In January 2020, a global health emergency announced by the WHO Emergency Committee based on the information of growth rate of Covid-19 cases in China and other countries (Velavan & Meyer, 2020). In Indonesia, the government announced the first Covid-19 case on March 2, 2020, with two positive Covid-19 patients. However, some experts say that Indonesia responded late to this incident. Indonesia's late response threatened the health of citizens (Olivia et al., 2020). Setiati & Azwar (2020) said that, in Indonesia, at the end of March 2020, the death rate reached 8,9% due to Covid-19.

The government has done many things to prevent the transmission of Covid-19, including tightening the appeal to stay at home, reducing the spread of the disease with regional quarantine, improving health services, and increasing the availability of personal protective equipment. During the new normal, the government also appealed to people who were forced to leave their homes to wear masks, use hand sanitizers, and maintain distance to minimize the Covid-19 spread. In

addition, the government is carrying out vaccinations to decrease the Covid-19 transmission risk which has been carried out since early January and is targeted to be completed in March 2022.

Preventing the Covid-19 transmission in Indonesia has its challenges because the Indonesian population is very diverse, and not everyone has the same understanding of the spread of Covid-19. In addition, the Indonesian have *mudik* tradition, going home every year on Eid al-Fitr. *Mudik* is done en masse, so there will be many crowds if *mudik* is conducted during Eid. To decrease the risk of Covid-19 transmission, the government has banned *mudik* in 2020 and 2021. However, some still force themselves to carry out the *mudik* tradition on the grounds of visiting family in their hometowns.

The spread of Covid-19 can be modeled using mathematical disease transmission modeling. Mathematical modeling can describe a physical system or real problem in a mathematical statement so that the problem can be understood comprehensively. Panovska-Griffiths (2020) stated that mathematical models can be used to figure out the spread of Covid-19 by exploring different scenarios. However, mathematically figuring out the Covid-19 spread is not enough to solve the problem. Other mathematical models are needed to answer further questions, such as how to stop the transmission of the disease. At least, with mathematical modeling, the Covid-19 spread can be predicted before there is a spike in the number of people infected before making decisions.

Several studies related to the mathematical model of Covid-19 spread have been conducted. Khrapov & Loginova (2020) modified a differential equations system formulated based on the SIR model to develop a mathematical model of the Covid-19 coronavirus. Nag (2020) used a modified Lotka-Volterra model to form a dynamic model of the healthy-infected population. Joyosemito & Nasir (2021) used a dynamic modeling approach to analyze Covid-19 cases in Indonesia. Fauzia (2021) added an inpatient compartment (*H*) to the *SIR* model to construct a mathematical model of outspread of Covid-19. Hasan et al. (2022) developed a mathematical model to analyze quantitatively the effect of large-scale social restriction in Jakarta from 10 April to 4 June 2020. Furthermore, Chen et al. (2020) and Hu et al. (2021) proposed enhanced model, which will be referred to as the *SEIR* (Susceptible–Exposed–Infectious–Recovered) model with population migration.

Therefore, in this study, mathematical modeling of *SIAR* (Suscepted – Infected – Asymptomatic – Recovered) was carried out by adding the influence of *mudik* tradition parameters. The *SIAR* model is suitable to represent the spread of Covid-19 because it is in line with its characteristics, i.e. there are susceptible, symptomatic, and asymptomatic infected and recovered subpopulations. In addition, migration parameters can be added to this model as a representation of the *mudik* tradition. The disease-free and endemic equilibrium points and their stability were analyzed. A comparative analysis of several cases was carried out in numerical simulations using Maple software to see how the *mudik* tradition affects the spread of Covid-19, i.e. the number of infected and asymptomatic subpopulations.

RESEARCH METHODS

In this study, the first thing that was done was a literature study related to the theories of mathematical models of disease spread, the Covid-19 transmission in Indonesia, and the *mudik* tradition. In addition, it was also studied how to conduct numerical simulations using the help of Maple software. This literature study was sourced from literature books, journals, proceedings, and related online articles. Furthermore, data collection was carried out using the documentation method from various sources such as <https://bnpb-inacovid19.hub.arcgis.com/>, <https://covid19.go.id/>, and <https://github.com/CSSEGISandData/COVID-19>. The data includes the number of healthy populations, the population exposed to Covid-19 (positive), the recovered population, and the deceased population. Furthermore, epidemiological parameters such as infection and recovery rates based on Gao et al. (2021), Gumel et al. (2021), and Winardi et al. (2022). Regarding the parameters of *mudik*, the level of population movement was sought from Sekretariat (2022), which would affect the level of interaction between the positive population

and the recovered and healthy population. The data was analyzed, interpreted concerning the current phenomenon, and compared with others.

Next, mathematical modeling of the Covid-19 spread, *SIAR* model, is carried out by adding *mudik* parameters. After that, the disease-free equilibrium point, the basic reproduction number, the endemic equilibrium point, and its stability are determined. Validation of the model, in the form of a system of differential equations, is performed through numerical simulation. Numerical simulation is done by running the model with relevant input data and comparing the simulation results with observation data. In this study, the numerical simulations are carried out by comparing several cases with different *mudik* parameters to see their effect on the infected and asymptomatic populations using Maple software. Maple has facilities for algebra, calculus, linear algebra, graphics, numerical calculations to arbitrary precision, and many other things (Thompson, 2017). This software is suitable for use in numerical simulations of the spread of the Covid-19 model in the form of a system of differential equations. The last one, the simulation results are compared and analyzed so that appropriate conclusions can be drawn.

RESULTS AND DISCUSSION

Covid-19 Transmission Model

In this study, the disease spread model is the *SIAR* model, which considers the *mudik* tradition factor. There are several assumptions in forming the Covid-19 *SIAR* disease transmission model. The first assumption is that all individuals in the population are initially susceptible populations. The second assumption is that the population is homogeneous, namely that each individual has the same contact proportion as other individuals. The third assumption is that the virus infects susceptible individuals who have contact with infected individuals (symptomatic) or asymptomatic individuals indirectly or directly. The last assumption is that recovering individuals have high immunity and will no longer be susceptible.

The population is notated by N , divided into four compartments. Susceptible, denoted by S is a subpopulation of suspected individuals or susceptible. Infected (symptomatic), denoted by I is a subpopulation of individuals infected with symptoms of Covid-19. At the same time, asymptomatic, denoted by A is a group of individuals who are infected but do not show symptoms. The last compartment is recovered, denoted by R , a group of recovered individuals.

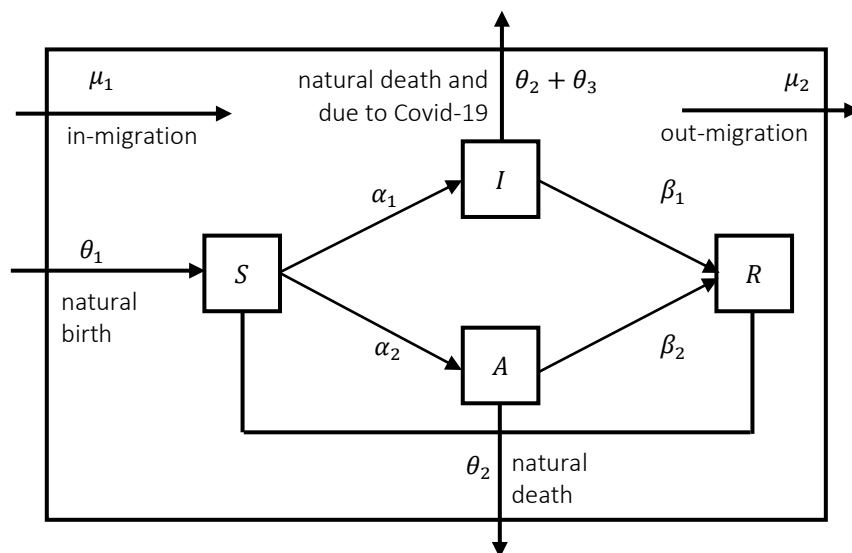


Figure 1. Flowchart of the *SIAR* model compartments with migration

The transformation of individuals in the *SIAR* model is described in Figure 1. The asymptomatic subpopulation (A) will not die due to Covid-19. However, the infected

subpopulation (I) may die from Covid-19 infection. The number of individuals in each compartment or subpopulation at the time t is $S(t)$, $I(t)$, $A(t)$, and $R(t)$. Suppose the total population at the time t is the sum of all compartments as follows.

$$N(t) = S(t) + I(t) + A(t) + R(t) \quad (1)$$

There are several parameters in the SIAR model. The disease transmission rate from the susceptible subpopulation to the infected subpopulation is denoted by α_1 . The rate of disease transmission from the susceptible subpopulation to the asymptomatic subpopulation is denoted by α_2 . The rate of recovery of the infected population is denoted by β_1 . The rate of recovery of the asymptomatic population is denoted by β_2 . In addition, there are natural birth parameters denoted by θ_1 , natural deaths denoted by θ_2 , and deaths due to Covid-19 denoted by θ_3 . Related to population movement, in-migration is denoted by μ_1 and out-migration is denoted by μ_2 . Migration in and out of the population can represent the *mudik* activities.

Based on those parameters, the proposed SIAR model uses ordinary differential equations as follows.

$$\left. \begin{aligned} \frac{dS(t)}{dt} &= \theta_1 + (\mu_1 - \mu_2 - \theta_2 - \alpha_1 I - \alpha_2 A)S(t) \\ \frac{dI(t)}{dt} &= (\mu_1 - \mu_2 - \theta_2 - \theta_3 - \beta_1 + \alpha_1 S)I(t) \\ \frac{dA(t)}{dt} &= (\mu_1 - \mu_2 - \theta_2 - \beta_2 + \alpha_2 S)A(t) \\ \frac{dR(t)}{dt} &= \beta_1 I(t) + \beta_2 A(t) + (\mu_1 - \mu_2 - \theta_2)R(t) \end{aligned} \right\} \quad (2)$$

Equilibrium Point

Point (S, I, A) is an equilibrium point of the system of differential equation (2) if $\frac{dS}{dt} = 0$, $\frac{dI}{dt} = 0$, and $\frac{dA}{dt} = 0$ satisfy. There are two equilibrium points, i.e. the disease-free and the endemic equilibrium points.

1. Disease-free equilibrium point

Disease-free is a condition when all individuals are susceptible and recover, with no infection. However, the recovered subpopulation can be ignored because it does not impact the individuals number in other compartments. If $I = A = 0$, then the point of the disease-free equilibrium (E_0) is obtained. Substitute $I = A = 0$ into $\frac{dS}{dt} = 0$ to obtain $S = -\frac{\theta_1}{\mu_1 - \mu_2 - \theta_2}$. The following is the obtained disease-free equilibrium point.

$$E_0 = \left(-\frac{\theta_1}{p}, 0, 0 \right) \quad (3)$$

with $p = \mu_1 - \mu_2 - \theta_2$.

2. Endemic equilibrium point

Endemic is a condition when the infected subpopulation and asymptomatic subpopulation are greater than zero. If $I, A > 0$, then the endemic equilibrium point (E_1) is obtained. Like the point of disease-free equilibrium, the endemic equilibrium can be acquired from $\frac{dS}{dt} = 0$, $\frac{dI}{dt} = 0$, and $\frac{dA}{dt} = 0$. So the point is acquired as follows.

$$E_1 = \left(\frac{-\theta_1}{p - \alpha_2 A - \alpha_1 I}, \frac{\theta_1}{-p + \theta_3 + \beta_1} + \frac{p - \alpha_2 A}{\alpha_1}, A \right) \quad (4)$$

with

$$A(t) = \frac{p}{k} - \frac{\alpha_1}{k} \left(p + \frac{\alpha_2 \theta_1}{\beta_2 - p} \right) + \frac{\alpha_1 \theta_1}{(\beta_1 + \theta_3 - p)k}$$

and

$$k = (1 - \alpha_1)\alpha_2.$$

Basic Reproduction Number

From the Next Generation Matrix (NGM) method, the basic reproduction number can be obtained (Diekmann et al., 2010; Fosu et al., 2020; Kasbawati, 2009) from the differential equation system (2). In the *SIAR* model, the infected subpopulation of the system is the symptomatic infected (*I*), and the asymptomatic (*A*) compartments. The following is a subsystem of differential equation used.

$$\left. \begin{aligned} \frac{dS(t)}{dt} &= \theta_1 + (\mu_1 - \mu_2 - \theta_2 - \alpha_1 I - \alpha_2 A)S(t) \\ \frac{dI(t)}{dt} &= (\mu_1 - \mu_2 - \theta_2 - \theta_3 - \beta_1 + \alpha_1 S)I(t) \\ \frac{dA(t)}{dt} &= (\mu_1 - \mu_2 - \theta_2 - \beta_2 + \alpha_2 S)A(t) \end{aligned} \right\} \quad (5)$$

The infected subsystem (5) at the disease-free equilibrium point must be linearized with a linear system represented by the Jacobi matrix (*J*). From (5), the Jacobi Matrix is obtained.

$$J_{(S,I,A)} = \begin{bmatrix} \frac{\partial S}{\partial S} & \frac{\partial S}{\partial I} & \frac{\partial S}{\partial A} \\ \frac{\partial I}{\partial S} & \frac{\partial I}{\partial I} & \frac{\partial I}{\partial A} \\ \frac{\partial A}{\partial S} & \frac{\partial A}{\partial I} & \frac{\partial A}{\partial A} \end{bmatrix} = \begin{bmatrix} p - \alpha_1 I - \alpha_2 A & -\alpha_1 S & -\alpha_2 S \\ \alpha_1 I & p - \theta_3 - \beta_1 + \alpha_1 S & 0 \\ \alpha_2 A & 0 & p - \beta_2 + \alpha_2 S \end{bmatrix} \quad (6)$$

The Jacobi matrix (*J*) is decomposed into two matrixes, *F* and *V*, so that $J = F - V$. The *F* is the transmission matrix that describes the emergence of new infections, and *V* is the transition matrix with entries that describe changes in the infected population. Thus we obtain

$$F = \begin{bmatrix} 0 & -\alpha_1 S & -\alpha_2 S \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

dan

$$V = \begin{bmatrix} -(p - \alpha_1 I - \alpha_2 A) & 0 & 0 \\ -\alpha_1 I & -(p - \theta_3 - \beta_1 + \alpha_1 S) & 0 \\ -\alpha_2 A & 0 & -(p - \beta_2 + \alpha_2 S) \end{bmatrix}$$

Then NGM is the multiplication of *F* by the inverse of *V*, namely $G = FV^{-1}$. Next, $\det(\lambda I - G) = 0$ is sought to obtain

$$\left(\lambda + \frac{\alpha_2^2 SA}{(p - \alpha_1 I - \alpha_2 A)} + \frac{\alpha_1^2 SI}{(p - \alpha_1 I - \alpha_2 A)(p - \theta_3 - \beta_1 + \alpha_1 S)} \right) \lambda^2 = 0$$

and eigenvalues

$$\lambda_1 = 0, \lambda_2 = 0, \lambda_3 = -\frac{\alpha_2^2 SA}{(p - \alpha_1 I - \alpha_2 A)} - \frac{\alpha_1^2 SI}{(p - \alpha_1 I - \alpha_2 A)(p - \theta_3 - \beta_1 + \alpha_1 S)}$$

The basic reproduction number R_0 is obtained from the spectral radius or the largest eigenvalue. Then, obtained

$$R_0 = -\frac{\alpha_2^2 SA}{(p - \alpha_1 I - \alpha_2 A)} - \frac{\alpha_1^2 SI}{(p - \alpha_1 I - \alpha_2 A)(p - \theta_3 - \beta_1 + \alpha_1 S)} \quad (7)$$

Stability Analysis of Disease-Free Equilibrium Point

The differential equations system (2) is a nonlinear differential equations system. The stability analysis can be obtained based on the eigenvalues of the Jacobian matrix. Substitute the disease-free equilibrium points (3) into the Jacobian matrix (6) to obtain

$$J = \begin{bmatrix} p & \frac{\alpha_1 \theta_1}{p} & \frac{\alpha_2 \theta_1}{p} \\ 0 & p - \theta_3 - \beta_1 - \frac{\alpha_1 \theta_1}{p} & 0 \\ 0 & 0 & p - \beta_2 - \frac{\alpha_2 \theta_1}{p} \end{bmatrix} \quad (8)$$

The eigenvalues of the Jacobian matrix (8) are obtained from

$$\det(\lambda I - J) = 0$$

$$(\lambda - p) \left(\lambda - p + \theta_3 + \beta_1 + \frac{\alpha_1 \theta_1}{p} \right) \left(\lambda - p + \beta_2 + \frac{\alpha_2 \theta_1}{p} \right) = 0 \quad (9)$$

Then, the eigenvalues are obtained as follows.

$$\lambda_1 = p, \lambda_2 = p - \theta_3 - \beta_1 - \frac{\alpha_1 \theta_1}{p}, \lambda_3 = p - \beta_2 - \frac{\alpha_2 \theta_1}{p}$$

All the constants and coefficients in (9) will be positive if $R_0 < 1$. It leads to a condition that there is no change in the sign from one term to the next. Based on the Descartes' rule, in a polynomial equation, there are no roots or solutions of the equation that will be positive if there is no change in the sign (Drucker, 1979). It means that the eigenvalues λ_1 , λ_2 , and λ_3 obtained from equation (9) will be negative.

The constants and coefficients will be negative if $R_0 > 1$. It leads to a condition that there is a single change in sign from the positive second term to the negative third term. Based on the Descartes' rule, in a polynomial equation, if there is a single change in sign, then there will be a solution or roots of the equation that will be positive (Drucker, 1979). It means that one of the eigenvalues λ_1 , λ_2 , or λ_3 will be positive.

Thus, all the Jacobian matrix eigenvalues around the equilibrium point will have negative value if $R_0 < 1$. So, in this state, the equilibrium point will be locally asymptotically stable. On the contrary, there is a positive eigenvalue if $R_0 > 1$. So, in this state, the equilibrium point becomes unstable and will appear a new equilibrium point.

Numerical Simulation

Numerical simulation of the Covid-19 spread model, *SIAR*, was conducted to prove the disease-free equilibrium point, the endemic equilibrium point, and their stability. The numerical simulation was performed utilizing Maple, a mathematics software, with parameters determined from estimation or derived from data collection from various sources, including previous studies. The data are population, birth rate, deaths rate, migration data, etc.

Numerical simulation of the system of differential equation (2) towards the disease-free equilibrium point was conducted with the population of Indonesia in 2021 (N), which is 272.682.500 (BPS, 2022). Table 1 describes all the parameters used in the numerical simulation.

Tabel 1. The parameters value

Parameter	Definition	Value	Source
N	Population	272.682.500	(Winardi et al., 2022)
μ_1	In-migration rate	0,024	(Sekretariat, 2022)
μ_2	Out-migration rate	0,024	assumed the same as μ_1
θ_1	Natural birth rate	0,0025	(Sekretariat, 2022)
θ_2	Natural death rate	0,0047	(Winardi et al., 2022)

Parameter	Definition	Value	Source
θ_3	Death rate due to Covid-19	0,00112667	(Winardi et al., 2022)
α_1	Susceptible subpopulation rate who are symptomatic infected	1/14	(Gumel et al., 2021)
α_2	Susceptible subpopulation rate who are infected asymptomatic infected	1/14	assumed the same as α_1 (Gao et al., 2021)
β_1	The rate of recovery people from symptomatic infected subpopulation	0,03230667	(Winardi et al., 2022)
β_2	The rate of recovery people from asymptomatic infected subpopulation	0,03230667	assumed the same as γ_1

1. Numerical simulation of the disease-free equilibrium point

Numerical simulation of the equation system (2) when getting near the disease-free equilibrium point is completed according to the parameter values in Table 1. In the simulation, the $S(t)$, $I(t)$, and $A(t)$ initial values are required. $S(0) = 0,5$, $I(0) = 0,2$, and $A(0) = 0,3$ are the initials values.

The results show that R_0 is equal to zero, which is less than 1. Since R_0 is less than 1, the Covid-19 will not transmit or will disappear slowly. It can be said that the population will be free from disease for a particular period. In addition, the disease-free equilibrium point is $E_0 = (0,5319; 0; 0)$. Generally, the subpopulation in each compartment fluctuates for 1000 days. The number of susceptible (S) individual decreases at the initial point in the first 50 days, increases, and stabilizes at point 0,5319. The number of infected (I) and asymptomatic (A) individuals decrease to approach zero and stabilize at zero (see Figure 2).

The population number of each compartment will stabilize at the endemic equilibrium point after the 1000th day. If the total population is $N = 272.682.500$ (see Table 1), then the susceptible population S is 145.039.822. Meanwhile, the proportion of the recovered population can be calculated by $R = 1 - (S + I + A)$, so that the proportion obtained is $R = 0,4681$, and the recovered population is 127.642.678 individuals.

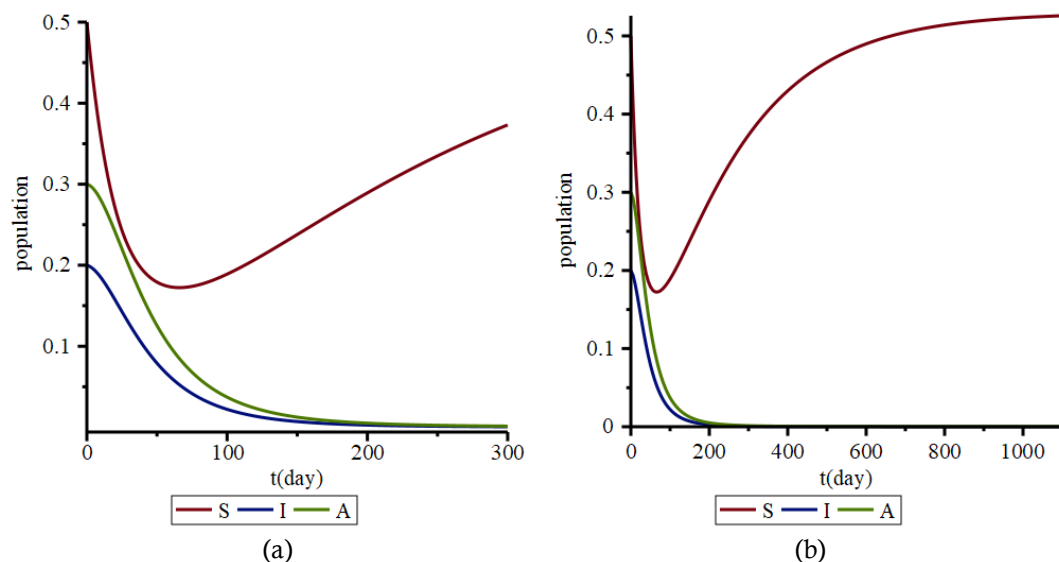


Figure 2. The simulation of equation system (2) toward free-disease equilibrium point: (a) the first 300 days and (b) the first 1000 days

2. Numerical simulation of the endemic equilibrium point

Numerical simulations were performed on the differential equations system (2) as it approached the endemic equilibrium point using the value of parameters in Table 1. The values of α_1 , and α_2 were increased to $\alpha_1 = 0,3$, and $\alpha_2 = 0,4$. In addition, $S(0) = 0,5$, $I(0) = 0,2$, and $A(0) = 0,3$ are the initial values.

The results show that $R_0 = 1,5849$. Since R_0 is greater than 1, the Covid-19 will spread rapidly and become a pandemic. $E_1 = (0,1271; 0,0105; 0,0295)$ is the obtained disease-free equilibrium point. Figure 3 shows the results of a numerical simulation depicting population fluctuations in each compartment during the first 300 days. The susceptible subpopulation S decreases at the initial point, then increases and stabilizes at 0,1271. Meanwhile, the infected subpopulation I increases and decreases on the 10th day until it stabilizes at 0,0105. The asymptomatic subpopulation A increases and decreases on the 10th day but increases again on the 150th day and stabilizes at 0,0295.

The population of each compartment will stabilize at the endemic equilibrium point after day 500th. If the total population is $N = 272,682,500$ (see Table 1), then the susceptible subpopulation is 34.657.946, the infected subpopulation is 2.865.732, the asymptomatic subpopulation is 8.051.343, and the recovered subpopulation is 227.117.254 with a proportion of $R = 0,8329$.

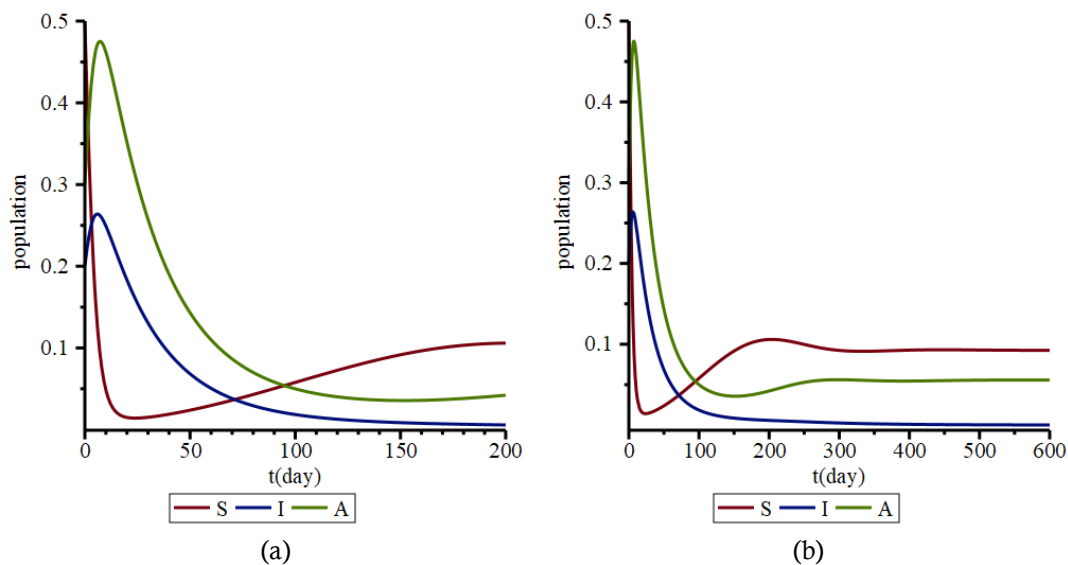


Figure 3. Simulation of the system of equations (2) against the endemic-free equilibrium point: (a) the first 200 days and (b) the first 600 days

3. The effect of *mudik* tradition

Numerical simulations were conducted to observe how the *mudik* tradition influences the transmission of Covid-19, specifically analyzing the changes in the number of symptomatic (I) and asymptomatic (A) infected subpopulations. In this case, population mobility in the *mudik* tradition is considered which is related to several parameters. The parameters related to the *mudik* are the rate of in-migration μ_1 , the rate of out-migration μ_2 , the rate of transmission of susceptible subpopulations becoming infected α_1 and the rate of transmission of susceptible subpopulations becoming asymptotically infected α_2 . Four cases were tested in this simulation (see Table 2). These four cases are presented to see how changes in the *mudik* (migration) rate affect the number of infected and asymptomatic subpopulations. This can also be called a sensitivity analysis. The

impact of the *mudik* practice on changes in the infected subpopulation (I) and the asymptomatic population (A) can be seen in Figures 4 and 5.

Tabel 2. The values of μ_1 , μ_2 , α_1 , and α_2

Case	μ_1 and α_1	μ_2 and α_2
1	0	0
2	0,2	0,3
3	0,4	0,5
4	0,6	0,7

Figure 4 shows the number of infected subpopulation (I) increases from a condition where there is no *mudik* activity (case 1) to a condition where people are carrying out *mudik* (case 2 to 4). In case 1, the number of infected subpopulations immediately decreases until it stabilizes near zero. In case 2 to 4, the number of infected subpopulation increases in the first 10 days, decreases, and stabilizes near zero. However, the number does not approach zero. The higher the number of *mudik* activity, the more people are infected.

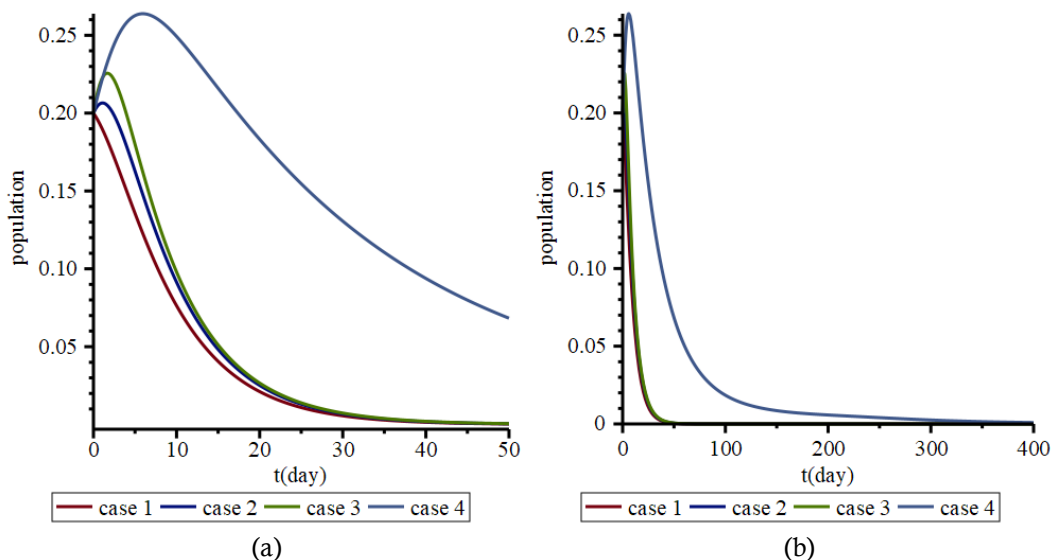


Figure 4. The effect of *mudik* tradition on infected subpopulations (I): (a) the first 50 days, (b) the first 400 days

Figure 5 shows the same trend as the infected population (I). However, the tradition of *mudik* has a more significant impact on the asymptomatic subpopulation (A). Changes occur from when *mudik* is not carried out (case 1) to when *mudik* is carried out (case 2 to 4). In conditions without *mudik* (case 1), the asymptomatic subpopulation immediately decreases and stabilizes near zero. However, when *mudik* is carried out (case 2 to 4), the asymptomatic subpopulation increases in the first 10 days and decreases until it finally stabilizes. However, it does not approach zero. Especially in case 4, before the stabilizes, the number of asymptomatic subpopulations fluctuates. The higher the *mudik* ratio, the more asymptomatic population number.

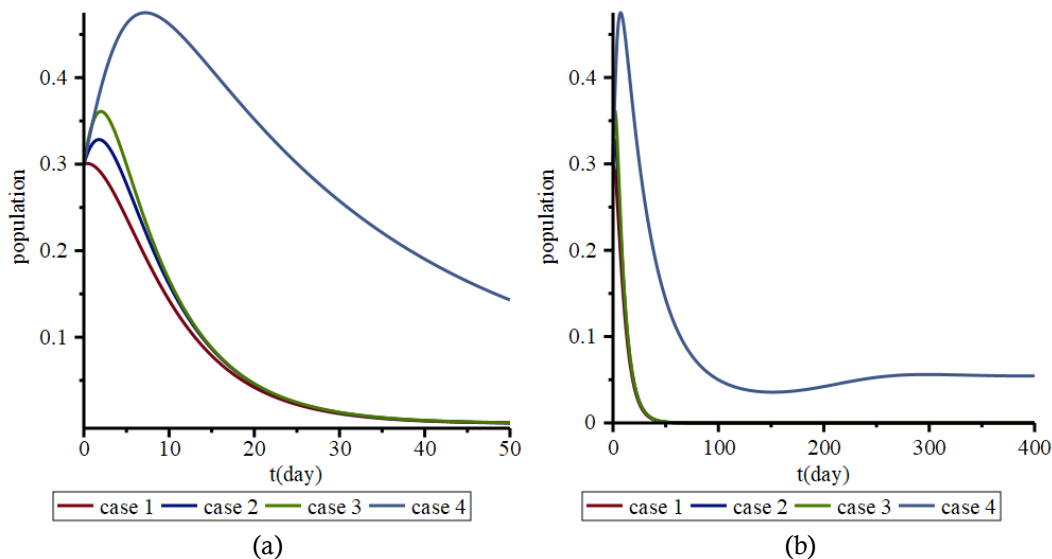


Figure 5. The effect of *mudik* tradition on asymptomatic subpopulations (A): (a) the first 50 days, (b) the first 400 days

Figure 4 and Figure 5 indicate that the higher the *mudik* activity, the greater the number of symptomatic and asymptomatic infected subpopulations. It is in accordance with the result of research by Hu et al. (2021) which states that, in China, the results of the empirical analysis found that population migration and traffic density have a positive impact on the number of infected people. Furthermore, it is also relevant to the Chen et al. (2020) study's result. For the symptomatic population, it indicates that the total number of infected people in the experimental area declines with the migration-in rate reduction.

However, when the *mudik* activity is at point 0,2 or 20% of the susceptible population doing *mudik*, the number of infected people increases moderately. Policymakers can use these results as a consideration. *Mudik* can be done within certain limits. The government can allow *mudik* activities with limitations, a maximum of 20% of the population can do *mudik* in healthy conditions, have been vaccinated, wear masks, and have negative Polymerase Chain Reaction (PCR) swab test results.

In 2021, the government prohibited people from going home during Eid, namely from 6 to 17 May 2021. The number of travelers at that time was 1.5 million people, or 0.55% (Kontan, 2025). However, the increase in Covid-19 cases after Eid increased nationally to 112.22% (Intan, 2021). This is different from the simulation results. If the number of travelers is 0.2 of the population or less, then the number of symptomatic or asymptomatic infected individuals in the subpopulations increases moderately. This difference can be caused by several factors, such as most travelers not complying with the rules regarding maintaining a safe distance, wearing masks, or being vaccinated. In addition, the SIAR model is a simple model of the spread of Covid-19 and has many limitations that can still be developed. With the limitations of the SIAR model representing the spread of Covid-19, several variables, such as vaccination, hospitalization, quarantine, and other related parameters, can be considered for further research while still considering homecoming or migration activities.

CONCLUSION

Based on the previous discussion, it is concluded that the transmission of Covid-19 can be modeled using the SIAR model with migration intervention as an interpretation of the *mudik* tradition practice. The characteristics of the dynamics of Covid-19 cases in S, I, and A are semi-stable. This condition implies that they will rise at a certain time. In disease-free conditions, the susceptible subpopulation is stable at a particular value while other subpopulations are stable

approaching zero. In this condition, the susceptible subpopulation is greater than in epidemic conditions. Conversely, other subpopulations in disease-free conditions are smaller than in epidemic conditions. The *mudik* tradition can increase the transmission of Covid-19 to a certain level. The disease spread can be suppressed by managing the migration or movement of people in and out of the country and cities and controlling population mobility in a city, especially during the *mudik* time. Several variables, such as vaccination, hospitalization, quarantine, and other related parameters, can be considered for further research.

In further research, additional compartments, such as vaccination, quarantine, and death, can be added. Furthermore, variables such as the level of public trust in government can also be added so that the Covid-19 spread model can adjust to real conditions in each country, depending on the unique traditions and people's conditions.

ACKNOWLEDGEMENTS

The authors would like to thank LPPM Universitas Terbuka sincerely for supporting this research through an internal competitive fund.

REFERENCES

- BPS. (2022). *Rata-Rata Laju Pertumbuhan Penduduk Menurut Provinsi (Average Population Growth Rate by Province)*. <https://www.bps.go.id/statistictable/2009/02/20/1268/rata-rata-laju-pertumbuhan-penduduk-menurut-provinsi-1971---2022.html>
- Chen, M., Li, M., Hao, Y., Liu, Z., Hu, L., & Wang, L. (2020). The introduction of population migration to SEIAR for COVID-19 epidemic modeling with an efficient intervention strategy. *Information Fusion*, 64, 252–258. <https://doi.org/10.1016/j.inffus.2020.08.002>
- Cucinotta, D., & Vanelli, M. (2020). WHO Declares COVID-19 A Pandemic. In *Acta Biomedica* (Vol. 91, Issue 1, pp. 157–160). Mattioli 1885. <https://doi.org/10.23750/abm.v91i1.9397>
- Diekmann, O., Heesterbeek, J. A. P., & Roberts, M. G. (2010). The Construction of Next-Generation Matrices for Compartmental Epidemic Models. *Journal of the Royal Society Interface*, 7(47), 873–885. <https://doi.org/10.1098/rsif.2009.0386>
- Drucker, D. S. (1979). A Second Look at Descartes' Rule of Signs. *Mathematics Magazine*, 52(4), 237–238. <https://doi.org/10.1080/0025570X.1979.11976790>
- Fauzia, L. A. (2021). Analisis Pemodelan Matematika Penularan Covid-19 dengan Tindakan Rawat Inap di Rumah Sakit (Mathematical Modeling Analysis of Covid-19 Transmission with Hospitalization Actions). *MATHunesa: Jurnal Ilmiah Matematika*, 9(1), 126–132. <https://doi.org/10.26740/mathunesa.v9n1.p126-132>
- Fosu, G. O., Akweitley, E., & Adu-Sackey, A. (2020). Next-Generation Matrices and Basic Reproductive Numbers for All Phases of The Coronavirus Disease. *Open Journal of Mathematical Sciences*, 4(1), 261–272. <https://doi.org/10.30538/oms2020.0117>
- Gao, Z., Xu, Y., Sun, C., Wang, X., Guo, Y., Qiu, S., & Ma, K. (2021). A Systematic Review of Asymptomatic Infections with Covid-19. *Journal of Microbiology, Immunology and Infection*, 54(1), 12–16. <https://doi.org/10.1016/j.jmii.2020.05.001>
- Gumel, A. B., Iboi, E. A., Ngonghala, C. N., & Elbasha, E. H. (2021). A Primer on Using Mathematics to Understand COVID-19 Dynamics: Modeling, Analysis and Simulations. *Infectious Disease Modelling*, 6, 148–168. <https://doi.org/10.1016/j.idm.2020.11.005>
- Hasan, A., Nasution, Y., Susanto, H., Putri, E., Tjahjono, V., Puspita, D., Sukandar, K., Nuraini, N., & Widyastuti, W. (2022). Modeling COVID-19 Transmissions and Evaluation of Large Scale Social Restriction in Jakarta, Indonesia. *Communication in Biomathematical Sciences*, 5(1), 90–100. <https://doi.org/10.5614/cbms.2022.5.1.6>

- Hu, Z., Wu, Y., Su, M., Xie, L., Zhang, A., Lin, X., & Nie, Y. (2021). Population Migration, Spread of COVID-19, and Epidemic Prevention and Control: Empirical Evidence from China. *BMC Public Health*, 21(259), 1–12. <https://doi.org/10.1186/s12889-021-10605-2>
- Intan, G. (2021, June 17). *Satgas: Kenaikan Kasus COVID-19 Pasca Lebaran 2021 Lebih Tinggi dari Tahun Lalu*. VOA Indonesia. <https://www.voaindonesia.com/a/satgas-kenaikan-kasus-covid-19-pasca-lebaran-2021-lebih-tinggi-dari-tahun-lalu/5932653.html>
- Joyosemito, I. S., & Nasir, N. M. (2021). Pendekatan Pemodelan Matematika Dinamis Dalam Analisis Prediksi COVID-19 Sebagai Masukan Kebijakan Pemerintah Indonesia (Dynamic Mathematical Modeling Approach in COVID-19 Prediction Analysis as Policy Input for the Indonesian Government). *Jurnal Pengabdian Kepada Masyarakat UBJ*, 4(1), 1–16. <https://doi.org/10.31599/jabdima.v4i1.455>
- Kasbawati. (2009). Penentuan Nilai R0 dengan Menggunakan Operator The Next Generation (Determining the R0 Value Using the Next Generation Operator). *Jurnal Matematika, Statistika, Dan Komputasi*, 6(1), 59–64. <https://doi.org/https://doi.org/10.20956/jmsk.v7i1.3373>
- Khrapov, P. V., & Loginova, A. A. (2020). Mathematical Modelling of the Dynamics of the Coronavirus COVID-19 Epidemic Development in China. *International Journal of Open Information Technologies*, 8(4), 13–16.
- Kontan, R. (2025, March 20). *Jumlah Pemudik 2016-2025*. Kementerian Perhubungan. <https://pusatdata.kontan.co.id/infografik/83/Jumlah-Pemudik-2016-2025>
- Nag, S. (2020). *A Mathematical Model in The Time of Covid-19*. <https://doi.org/10.31219/osf.io/8n92h>
- Olivia, S., Gibson, J., & Nasrudin, R. (2020). Indonesia in The Time of Covid-19. *Bulletin of Indonesian Economic Studies*, 56(2), 143–174. <https://doi.org/10.1080/00074918.2020.1798581>
- Panovska-Griffiths, J. (2020). Can Mathematical Modelling Solve the Current Covid-19 Crisis? *BMC Public Health*, 20(1). <https://doi.org/10.1186/s12889-020-08671-z>
- Sekretariat. (2022). *273 Juta Penduduk Indonesia Terupdate Versi Kemendagri (273 Million Indonesian Population Updated Version of Ministry of Home Affairs)*. Kementerian Dalam Negeri Republik Indonesia. <https://dukcapil.kemendagri.go.id/phln/read/273-juta-penduduk-indonesia-terupdate-versi-kemendagri>
- Setiati, S., & Azwar, M. K. (2020). COVID-19 and Indonesia. *Acta Medica Indonesiana*, 52(1), 84–89. <https://doi.org/10.1111/tmi.13383>
- Thompson, I. (2017). *Understanding Maple*. Cambridge University Press.
- Velavan, T. P., & Meyer, C. G. (2020). The COVID-19 Epidemic. *Tropical Medicine and International Health*, 25(3), 278–280. <https://doi.org/10.1111/tmi.13383>
- Winardi, W., Karyono, Y., Nugroho, A., Adi, W. P., Budiati, I., Riyadi, Lestari, T. H., Mardiana, Lasma, Sorayan, P. H., & Suswandi. (2022). *Statistical Yearbook of Indonesia 2022*. BPS. <https://www.bps.go.id/id/publication/2022/02/25/0a2afea4fab72a5d052cb315/statistik-indonesia-2022.html>