Jurnal Theorems (*The Original Reasearch Of Mathematics*)
Volume 10, Number 1, July 2025
URL: http://ejournal.unma.ac.id/index.php/th

e-ISSN: 2528-102X
p-ISSN: 2541-4321

ESTIMATION OF THE EFFECTIVE REPRODUCTION NUMBER (RT) FOR THE COVID-19 PANDEMIC IN JAKARTA: A MATHEMATICAL MODELLING APPROACH

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Article Info:
Received 2025-05-28
Revised 2025-06-27
Accepted 2025-07-04

How to Cite:
Maharesi, Retno., & Widyatmini , Widyatmini. (2025). Estimation of the Effective Reproduction Number (Rt) for the COVID-19 Pandemic in Jakarta: A Mathematical Modelling Approach. *Jurnal Theorems (The Original Research of Mathematics)*, *10*(1), 1-12.

ABSTRCT

A reproduction number that is less than 1 for 14 consecutive days is widely recognized as an essential indicator to assess whether epidemic conditions can be brought under control. This paper reveals how this indicator can be applied to evaluate the dynamics of an epidemic both at the early stage and toward its end within a specific region. The effective reproduction number (Rt), obtained based on the SIR (Susceptible, Infectious, and Removed) model and formulated through a finite difference equation, serves as a practical tool to assess the controllability level of an epidemic. Furthermore, by utilizing contact tracing data provided by the Government for COVID-19 suspects, the value of this indicator can be estimated accurately using the developed mathematical formulation. In this study, data were sourced from the official COVID-19 File History of DKI Jakarta, covering the period from July 24 to August 7, 2020. The calculated Rt values were then compared with those reported in similar studies to validate the findings. Differences in outcomes can be attributed to several factors, including variations in methodology, differences in time frames used for sampling, distinct regional epidemic characteristics, government-implemented social restriction policies of varying intensity, as well as vaccination strategies and public compliance levels. These influencing factors underscore the importance of context-specific analysis in using Rt as a reliable indicator for epidemic control evaluation

Keywords: Effective reproduction number, basic reproduction number, Covid-19 pandemic, finite difference methods.

INRODUCTION

The basic epidemiological mathematical model SIR (Susceptible-Infected-Recovered) underlies various methods of analysing epidemic conditions in an area affected by an infectious disease outbreak. The method of analysing the condition of an outbreak is often carried out using the simulation method of the SIR model. The reproduction number is an indicator that can be directly used by health authorities to assess the epidemic conditions in their work area as per WHO guidelines (World Health Organization [WHO], 2020) regarding contact tracing in the context of the COVID-19 pandemic. The use of the SIR

(Susceptible-Infectious-Removed) model in epidemiological modelling is grounded in its theoretical simplicity and practical relevance. It provides a foundational framework for understanding how infectious diseases spread within a population by categorizing individuals based on their disease status. The SIR model captures essential dynamics such as transmission and recovery rates, which are crucial for estimating key indicators like the effective reproduction number (Rt). Moreover, it aligns with compartmental modeling theory in epidemiology, which helps in simplifying complex biological interactions into mathematically tractable forms. Compared to more complex models such as SEIR or agent-based models, SIR remains widely applicable for early-stage outbreaks and regions with limited data availability, making it a preferred choice for initial epidemic assessment and public health decision-making.

The implementation of the SIR model requires a number of simplifications through a number of assumptions so that it is possible to obtain a solution from the system of equations. Furthermore, the ordinary differential equation in the SIR model is converted into a finite-difference equation to derive the effective reproduction number formula. From this formulation, a formula can then be produced to estimate the maximum percentage of the subpopulation that has been infected. Based on the formula obtained, then with the data from the COVID-19 test survey available on the DKI government's COVID-19 website, the basic reproduction number value along with an estimate of the proportion of the population infected with COVID-19 can be obtained.

The purpose of this study is to derive the effective reproduction number (Rt) formula using a difference equation adaptation of the classical SIR model, utilizing daily data of COVID-19 cases collected by the DKI Jakarta Health Department. This Rt formula is used to assess the dynamics of the epidemic in real time, determine the risk status of the outbreak (controlled or not), and provide evidence-based policy recommendations. This approach allows for the evaluation of the effectiveness of public health interventions through monitoring Rt that is responsive to changes in the proportion of the susceptible population and the transmission rate. This study extends the continuous SIR model to a discrete form that is compatible with daily data, while validating its application in a real context (DKI Jakarta). Rt estimation based on difference equations is more flexible for limited data compared to traditional methods such as serial intervals.

SIR Model

The classic SIR model is one of the epidemic models initially introduced by W. O. Kermack and A. G. Mc Kendrick in 1927. The model aims to describe the dynamics of the spread of infectious diseases through three subpopulations: susceptible individuals, infected individuals, and individuals who recover or die (removed). This simple but effective model explains how diseases spread and decline in a population, assuming that contact between susceptible and infected individuals occurs randomly. The classic SIR epidemic model describes the spread of disease from a group of susceptible individuals who then become infected due to direct or indirect contact. Furthermore, the group of infected individuals who are able to survive the disease recover or die after undergoing the duration of infection and enter the removed group.

The population is divided into three classes of individuals, namely:

1. Susceptible individuals are healthy individuals who can be infected with the virus,
2. Infectious individuals are individuals who are infected and can transmit the virus to other individuals in the population.
3. Removed individuals are individuals who have recovered or died from a viral infection. The recovery can be permanent or otherwise.

The removal method is a process of moving an infected population into a healthy population that can be done through isolation, immunization, recovery or through death. The mathematical model in epidemiology has been widely developed by (Brauer & Carlos-Chavez, 2001). In the SIR model, the basic assumptions used include: 1) The population in the epidemic area is considered fixed and closed, meaning there is no population movement through birth, death, immigration, or emigration. 2) The birth and death rates are considered constant and balanced. 3) Viral infection can cause recovery or death, and individuals who recover will not be reinfected (lifelong immunity). 4. Individuals who have recovered from a viral infection are not infected again because they have a lifelong immune system, 5. Each individual has the possibility of making contact with other individuals in the population. 6. Infected individuals are assumed to be able to recover with a constant chance over time. 7. The population is homogeneous.

The variables and parameters used are related to the total population $N= N_S+ N_I+ N_R$ of the population individuals are in the following categories:

1. S represents the susceptible subpopulation at time t, $0< N_S/N \leq 1$,
2. I represents the infectious individual subpopulation at time t, $0\leq N_I/N \leq 1$,
3. R represents the removed individual subpopulation at time t, $0\leq N_R/N \leq 1$,
4. The constant β represents the contribution to the rate, namely the number of infected per unit time due to contact with infectious individuals,
5. The constant v represents the removed rate, namely the number of recoveries plus deaths per unit time from infectious individuals per capita

The following is comprised formulation of the system of differential equations for the classical epidemic model:

$$\frac{dS}{dt} = -\beta SI, \frac{dI}{dt} = \beta SI - vI, \qquad \frac{dR}{dt} = vI. \tag{1}$$

This differential equation model is quite intuitive, where the first equation describes the rate of change of susceptible individuals (S) proportional to the number of contacts that occur between susceptible and infected individuals. The more contacts that occur, the greater the rate of infection in the population. The decrease in the number of susceptible individuals who have not been infected per unit time is proportional to the total number of contacts of the infected subpopulation N_I with the susceptible subpopulation of individuals infected with N_S.

In a large population N, if the average number of contacts of one infected individual is κ people per unit time, with the proportion of successful virus transmission, τ then the amount of decrease in the number of susceptible individuals infected to become infected per unit time in an epidemic area is:

$$\kappa\tau N_I \frac{N_S}{N} \tag{2}$$

By exchanging $N_S = S$ and $N_I = I$, the rate of decline of subpopulation S follows equation (1), namely$\frac{dS}{dt} = -\beta SI$, for $\beta = \frac{-\kappa\tau}{N}$. The first differential equation describes that the number of uninfected individuals decreases during the epidemic period, which is indicated by the coefficient β of contact between infected and susceptible subpopulations having a negative sign.

The second equation states that the change in the number of individuals infected with the virus per unit time is proportional to the effective contacts that transmit the virus minus the number of individuals eliminated from the population either due to recovery or death from the virus infection in a unit time. In the second equation v is the proportion of individuals who die or recover from the infected subpopulation I per unit time. So the average duration of the virus infection is calculated by: $D = 1/v$. For example, if the removal rate $v = 0.1$ per day, then D = 10 days, which is the time required for one individual to be free from infection either by recovery or death. From the second equation, an epidemic condition occurs if the growth rate of the number of infected individuals is positive.

The effective reproduction number R_e changes over time depending on the factors that influence its change. At the beginning, namely t = 0, the above value is written as R_0, which is the basic reproduction number: $R_0 = \frac{\hat{e}\tau S(0)}{vN} > 1$,, with $S(0) = N-1$ because the number of infected individuals at $t = 0$ is $I(0) = 1$. For a large population, the value of $(N-1)/N \cong 1$ is the probability that each individual can be infected at the start of the epidemic. As a result, $R_0 \cong \frac{k\tau}{v}$. Hence $R_0 = \frac{\kappa\tau}{v} = \frac{b}{v} > 1$ indicates the expected value of the number of individuals in the susceptible subpopulation infected at the start of the epidemic by one person who is first infected.

Based on the formulation of $Re(t)$, it can be interpreted that the SIR Model in epidemiology as further studied by (Weiss, 2013):

1. The duration of D virus infection can be reduced by carrying out treatment therapy or prevention of virus attacks on susceptible individuals.
2. The value of ⍰, namely the frequency of contact between individuals in the population per unit of time can be reduced by limiting the occurrence of public crowds on various occasions.

3. The number of susceptible individuals in the population S(t) can be minimized by vaccination.
4. Virus transmissibility, can be minimized by behaving not to touch the mucous membranes of the eyes, nose and mouth and using masks, protective glasses.

If the vaccine for Covid19 is still nil, then the first three aspects above are a form of health protocol that is carried out to control the spread of the virus.

The basic reproduction number (R_0) and effective reproduction number (R_e) are important metrics in understanding and predicting the dynamics of COVID-19 transmission. R_0 describes the average number of new cases generated by a single infected individual in a fully susceptible population, while R_e takes into account factors such as public health interventions and changes in social behaviour (Fraser et al., 2009). Several studies have attempted to estimate the reproduction number of COVID-19 at different stages of the outbreak and under different intervention scenarios. Kucharski et al. (2020) assessed the impact of non-pharmaceutical interventions on the reproduction number in Europe, finding that policies such as mobility restrictions and school closures significantly reduced the R_e value. Additionally, Cori et al. (2013) developed a method for estimating the reproduction number in real time, which has been widely applied in recent epidemic studies.

A systematic review by Alimohamadi et al. (2020) compiled reproductive number estimates from early COVID-19 studies, showing that the initial R_0 values varied between 2 and 3, depending on the location and estimation method. Li et al.’s (2020) study on COVID-19 transmission dynamics in Wuhan confirmed that population mobility played a significant role in influencing the spread of the virus. In the context of travel restriction policies, Chinazzi et al. (2020) showed that such interventions had a substantial effect on reducing the spread of COVID-19 in China. Data-driven approaches to understanding virus transmission have also been used in epidemiological analyses. Buckee et al. (2020) explored how mobile phone data could be used to estimate the impact of travel restrictions on human movement and the spread of COVID-19 in the UK. Accurate, data-driven estimates of the COVID-19 reproductive number are essential for designing effective mitigation strategies. Modelling that takes into account temporal and spatial factors can help inform public health policies to more appropriately control outbreaks (Fraser et al., 2009; Cori et al., 2013).

Difference equations provide a robust framework for deriving the R_0 of COVID-19 by considering the complexity of transmission dynamics, including asymptomatic cases and public health interventions. This approach allows for a more adaptive analysis of discrete epidemiological data. Mathematical modelling using difference equations has been an effective approach to analyse the transmission dynamics of COVID-19, including in estimating the basic reproduction number (R_0). This reproduction number is a key parameter that describes the potential for disease spread, where $R_0 > 1$ indicates that the epidemic will continue to grow, while $R_0 < 1$ indicates a decline in cases (Tang et al., 2020). Discrete-time models, such as SEIR (Susceptible-Exposed-Infectious-Recovered) and its variants, are often used to predict the spread of COVID-19 by considering daily or weekly time intervals. Elbousty & Rida (2020) developed a discrete model based on difference equations that integrates intervention factors such as social distancing and quarantine. In this model, R_0 is derived from a next-generation matrix constructed based on the transmission rate and the infectious period. Lakshmi & Narayanan (2021) extended the discrete SEIR model by including asymptomatic cases to produce a system of difference equations. Din et al. (2021) analysed the effect of interventions (such as lockdown and vaccination) by modifying parameters in the difference equations. They showed that mobility restrictions significantly reduced R_0. Khan et al. (2020) also emphasized that discrete models are more flexible in accommodating real-time policy changes than continuous models.

METHODS

From various library sources, mainly conference papers and epidemiology textbooks related to the SIR (Susceptible-Infectious-Removed) model, elaboration was carried out to obtain solutions to the problems in this study. The sequential steps of the study are as follows: Investigation of the dimensions of the equations contained in the SIR model, in an effort to help interpret the quantities in its mathematical formula.

Derivation of the effective reproduction number formula followed by the derivation of the formula to estimate the percentage of the maximum infected subpopulation using the finite-difference equation form for the SIR model, as well as the relationship between the effective reproduction number and the estimated maximum size of the susceptible population and those already infected with the virus.

The SIR model application uses secondary data from the DKI Jakarta Covid-19 File History website to model the spread of the disease from the beginning to the end of the pandemic. Calculations (R_e) and contact tracing results are used to describe the dynamics of the spread of the virus in the population. Furthermore, the results are compared with the results of similar studies by other researchers.

FINDINGS

In the section explaining that from the SIR model, the reproduction number based on the formation of a finite-difference equation system can be generated to be applied to survey data. A better understanding related to an epidemic can be seen from the community's compliance in implementing all health protocols that support the four aspects as described in the previous section. The basic reproduction number formula R0 is:

$$R_0 = D\kappa\tau\frac{S(0)}{N} = D\kappa\tau, \text{ dengan } S(t) = N - I(t),\ S(0) = N\text{-}1,\ I(0) = 1,\ t_0 \leq D\ . \qquad (2)$$

Compared with the basic reproduction number indicator R0, the effective reproduction number R_e is more useful in describing the epidemic conditions over time. This article presents the derivation of the R_e formula for the contact tracing data of the DKI Jakarta Covid19 task force using the results of

(Susanto et al., 2020) using a simple method in estimating the COVID-19 reproduction number. The second and third differential equation systems of the SIR model are first changed to the form of finite difference equations with a step size of h = 1 sequentially, which can be written by first changing: β = β_n and $v = v_n$, so that:

$$\varDelta I_n = \tau \beta S_n I_n - \tau v I_n, \tag{3}$$

$$\varDelta R_n = \tau v I_n. \tag{4}$$

The sum of Equations (3) and (4) gives: $\varDelta I_n + \varDelta R_n = \tau \beta_n S_n I_n$, so that this result is obtained: $\beta_n = \frac{\varDelta(I_n+R_n)}{\tau S_n I_n}$ and $v_n = \frac{\varDelta R_n}{\tau I_n}$. Changes in writing the basic and effective reproduction numbers using subscripts *n*, is: $R_0(n) = N\frac{\beta_n}{v_n}$, with $R0\frac{S_n}{N}{}_e$. So that a series of equations is obtained as shown by Equation (5):

$$R_e(t) = R_0\frac{S_n}{N} = N\frac{\beta_n}{v_n}\frac{S_n}{N} = \mathrm{N}\frac{\frac{\varDelta(I_n+R_n)}{\tau S_n I_n}}{\frac{\varDelta R_n}{\tau I_n}}\frac{S_n}{N} = \frac{\frac{\varDelta(I_n+R_n)}{\tau S_n I_n}}{\frac{\varDelta R_n}{\tau I_n}}S_n = \frac{\varDelta(I_n+R_n)}{\tau S_n I_n}\frac{\tau I_n}{\varDelta R_n}S_n = \frac{\varDelta(I_n+R_n)}{\tau I_n}\frac{\tau I_n}{\varDelta R_n} = \frac{\varDelta(I_n+R_n)}{\varDelta R_n}$$

$$R_e(t) = \frac{\varDelta I_n}{\varDelta R_n} + \frac{\varDelta R_n}{\varDelta R_n} = 1 + \frac{\varDelta I_n}{\varDelta R_n}. \tag{5}$$

Estimation of the maximum number of infections based on the effective reproduction number R_e obtained by obtaining the solution to the second differential equation of the SIR model as follows: $\frac{dS}{dI} = \frac{-\beta SI}{\beta SI - vI}$, $\frac{dS}{-\beta S}(\beta S - v) = dI$ which is a sparable differential equation, then ,$\frac{(\beta S - v)}{-\beta S}dS = dI$,$-dS + \frac{v}{\beta}\frac{dS}{S} = dI, I(t) + S(t) - v/\beta \ln S = C$. Since the right-hand side is a constant, for each time *t*, we can write:

$$I(t) + S(t) - v/\beta \ln S\,(t) = I(0) + S(0) - v/\beta \ln S\,(0). \tag{6}$$

I_{max} will be obtained if $\frac{dI}{dt} = 0$ then using the second equation we get: $S(t)=v/\beta$. By this way, then Equation (6) can be written as:$I_{max}(t) + \frac{v}{\beta} - v/\beta \ln\frac{v}{\beta} = I(0) + S(0) - v/\beta \ln S\,(0)$, or

$$I_{max}(t) = I(0) + S(0) - v/\beta \ln S\,(0) - \frac{v}{\beta} + v/\beta \ln\frac{v}{\beta}, \tag{7}$$

Equation (7) if expressed using the basic reproduction number is as follows: $R_0 = D\kappa\tau = b/v = N\beta/v, \beta = \frac{R_0 v}{N}$, becomes $I_{max}(t) = I(0) + S(0) - \frac{N}{R_0}\ln S\,(0) - \frac{N}{R_0} + \frac{N}{R_0}\ln\frac{N}{R_0}$.

Hence dividing all segments by N:

$$I_{max}(t)/N = I(0)/N + S(0)/N - \frac{1}{R_0}\ln S\,(0) - \frac{1}{R_0} + \frac{1}{R_0}\ln\frac{N}{R_0}$$

$$I_{max}(t)/N = 1 - \frac{1}{R_0}(1 - \ln S\,(0) + \ln\frac{N}{R_0})$$

$$\frac{I_{max}(t)}{N} = 1 - \frac{1}{R_0}(1 - \ln\frac{N}{R_0} + \ln(N-1)) - \ln\frac{N}{R_0} + \ln(N-1) = \ln(\frac{R_0}{N}(N-1)) = \ln(R_0)$$

$$\frac{I_{max}(t)}{N} = 1 - \frac{1}{R_0}(1 + \ln R_0)$$

Substitution $R_e(t) = 1 + \frac{\Delta I_n}{\Delta R_n}$ from $R_0 = R_e(t)\frac{N}{S(t)}$, for estimating I_{max} with effective reproduction number R_e obtained from Equation (5) to yield Equation (8) as follows:

$$\frac{I_{max}(t)}{N} = 1 - \frac{S_n}{R_e(t)N}\left(1 + ln\left(R_e(t)\frac{N}{S_n}\right)\right). \tag{8}$$

Application to government survey data

Furthermore, the implementation of the first equation can be applied in reality, based on survey data, especially for data removal and the increase in daily positive cases using Equation (5). The effective reproduction number uses testing data from contact tracing. Data for this study were obtained from the DKI Jakarta Covid-19 File History website. As an example of the application of the formula in Equation (5), the following are the results of calculating the Re value for data from July 24 to August 7, 2020.

Table 1. Increase in cases in the early period of Covid 19: July 24-August 7, 2020 in DKI Jakarta

Date	Daily positive cases	Daily recovered cases	Daily death cases	R_e
25/7/2020	393	130	1	4
26/7/2020	378	174	10	3.054348
27/7/2020	472	107	3	5.290909
28/7/2020	412	377	13	2.05641
29/7/2020	585	240	25	3.207547
30/7/2020	299	188	1	2.582011
31/7/2020	432	407	15	2.023697
1/8/2020	374	679	16	1.538129
2/8/2020	379	140	0	3.707143
3/8/2020	489	138	15	4.196078
4/8/2020	466	216	13	3.034934
5/8/2020	357	379	15	1.906091
6/8/2020	597	246	13	3.305019
7/8/2020	658	195	14	4.148325
Average Re				3.146474

Data from the early period of the Covid-19 outbreak provided: an average value of $R_e \approx 3.14$, which means it is still far from the criteria for controlled epidemic conditions, namely $Re \leq 1$. The decrease in the R_e value, apart from participating in health protocols in conditions where vaccines are not yet available, is by increasing the number of tests in contact tracing. The estimated number of susceptible individuals who have not or have been infected provides an overview of the number of people who will be examined in the results of contact tracing suspected of being exposed to the disease. Based on

Equations (8) and (5) with the assumed value of Re = 3.14, a = susceptible to infection and b = proportion infected in the population: $\frac{\mathrm{I_{max}}}{\mathrm{N}} = b < 1, a = \frac{N-1}{N}, b + a \leq 1$

$$b = 1 - \frac{N-I}{3.14N}(1 + ln(3.14\frac{N}{N-I})) = 1 - \frac{a}{3.14}(1 + ln(\frac{3.14}{a})) = 0.369436$$

From the calculation results above with Re = 3.14, in there would be 37% of people left who are susceptible to infection because the percentage of infected people is 1-0.37 = 63% of the total population. As a comparison of the proportion of the population immunized, it was carried out based on research by (Ganasegeran et al., 2021), who conducted a mathematical synthesis related to the reproduction rate and herd immunity in Malaysia. So that the efforts that have been made by the government have been running on par with other countries' governments within the scope of WHO's work.

DISCUSSION

As a comparison based on the availability of information, the following are the results of research at the beginning of the Covid-19 pandemic period conducted by other researchers in Indonesia. The third column presents of how the research area, data source and time taken placed, number 1, 2 and 3 in this column described as bellow:

1. DKI Jakarta, www.covid19.go.id, March 2 to 25, 2020, (Fajar, 2020) estimated the reproduction rate of COVID-19 in Indonesia in his initial research.
2. South Kalimantan, Dinkes. kalsel prov.go.id., April 8 to May 20, 2020, based on the COVID-19 spread model in South Kalimantan developed by (Yulida & Karim, 2020).
3. DKI Jakarta, DKI Jakarta Covid-19 File History and www.covid19.go.id, July 24 to August 7, 2020.

Table 2. R_0 and R_e estimates that have been carried out by other researchers.

Methods	*Ro*	*Re*	Research area, data sources and time
Exponential Growth Rate	-	4.655613	1
Maximum Likelihood	-	4.143258	1
Time Dependent	-	5.667372	1
Bayesian Sequential	-	2.891739	1
Model SIR-1	1.728462	-	1
Model SIR-2	3.0	-	2
Difference equation		3.146474 (Average)	3

Table 2 gives different results due to: Firstly, by differences in the scope of research areas as well as the time of the evaluation towards the reproductive number taken. Secondly, by the risk level of research area coverage 1 namely DKI Jakarta, at that time was higher for exposure to Covid-19 disease as compared to the patients in South Kalimantan which was noted to have lower risk. Thirdly, by the research methods to be used, and lastly due to the time series data used which illustrates the role of the government in controlling the rate of transmission of the outbreak and the level of public understanding of the Covid-19 outbreak.

Changes in the effective reproduction number, based only on the number of susceptible individuals S(t) because the parameters of infection duration D, contact frequency κ and transmissibility τ are assumed to be constant. Data on the addition of Covid-19 cases at the end of the publication period of Covid-19 incidents by the DKI Health Office, the average $R_e \approx$ 1.92. (Fitriyah, 2022) studied the calculation of the basic reproduction number of COVID-19 by considering vaccination. Another study carried by (Armita et al., 2024) found that vaccination applied on a large proportion of the community reduces the ability of the virus to transmit to susceptible individuals, so there is a decrease in positive cases which is reflected in the lower Re(t) value. The value approaches 1, if the number of daily positive cases approaches zero or the number of recoveries or deaths exceeds the number of positive cases.

Table 3. Increase in cases in the final period of Covid 19: August 2022-April 2023 in DKI Jakarta

Date	Daily positive cases	Daily recovered cases	Daily death cases	Re
Aug-22	162	175	0	1.927359
Sep-22	1003	1317	3	1.759566
Oct-22	729	660	1	2.101345
Nov-22	2304	1889	6	2.215831
Dec-22	641	1257	4	1.50849
Jan-23	114	149	1	1.75953
Feb-23	81	79	1	2.0164
Mar-23	154	119	1	2.28456
Apr-23	7	10	0	1.680135
Average Re				1.917024

The main variant of Omicron, a mutation of COVID-19, was present in the world in early 2022. A study by Du et al. (2022) showed that the reproduction rate of the Omicron variant was three times higher than that of the Delta variant. This increased transmissibility is attributed to multiple factors, including Omicron's higher binding affinity to the human ACE2 receptor and its enhanced ability to evade pre-existing immunity, whether from prior infection or vaccination compared to Delta (Liu et al., 2022; He et al., 2021). These characteristics allowed the virus to infect more individuals in a shorter period. Looking at the results of the effective reproduction rate calculation in April 2023, it can be suspected that the Omicron variant was successfully weakened by the gradual vaccination program, which increased population immunity and helped reduce its spread.

CONCLUSION AND SUGGESTION

Massive increases in testing and contact tracing are critical steps in controlling the pandemic, especially in the early days before a vaccine is available. In addition, the SIR model and the calculation of the effective reproduction number R_e provide a strong basis for understanding the pattern of transmission and assessing the effectiveness of mitigation measures. In epidemiological surveys, the calculation of the effective reproduction number is an important tool in decision making. Interventions such as vaccination and social restrictions be continuously monitored and adjusted based on the latest epidemiological data to keep the (R_e) values below 1, so that the rate of disease spread can be controlled effectively. Based on the results of secondary data analysis, it is concluded that the handling of the pandemic in DKI Jakarta has been running well in accordance with the theory of epidemiology.

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