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ANALYZING AND ESTIMATING PARAMETERS OF COVID-19 TRANSMISSION WITH VACCINATION IN INDONESIA

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Abstract: This study analyzes the Susceptibles Infected Recovered Death (SIRD) epidemic model of COVID-19 transmission by considering vaccination in Indonesia. The SIRD epidemic mathematical model divided the population into four compartments, including susceptible compartment, infected compartment, recovered compartment, and death compartment. The model is analyzed for stability of disease free equilibrium and endemic equilibrium. The basic reproduction number corresponding to the stability of the model is determined. The parameters of the model are estimated from COVID-19 data in Indonesia by using the least squares method. The effect of vaccination on infection cases is examined using multiple linear regression. Based on the analytical results and numerical simulations show that the endemic equilibrium point is stable. The basic reproduction is obtained $R_0 = 2$. It can be concluded that the disease is spreading in the population which means there are infected individuals in the population although models suggest that the vaccine reduces transmission rates in the population.

Keywords: SIRD epidemic model; stability analysis; reproduction number; regression analysis.

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1. INTRODUCTION

Coronavirus Disease 2019 (COVID-19) is a new type of disease that has never been identified before in humans. Coronaviruses are viruses that cause diseases ranging from mild to severe symptoms. There are two types of coronaviruses that can cause infection with severe symptoms, namely Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS) [2]. The virus that causes COVID-19 is called Sars-CoV-2. In Indonesia, the first COVID-19 case was found on March 2, 2020, with two confirmed cases [4]. Until now, COVID-19 cases are still being reported with new variants emerging.

One of the efforts to prevent the spread of COVID-19 is through vaccination. Starting from the beginning of 2021 until now, COVID-19 vaccines have been distributed to the entire population of Indonesia. The administration of these vaccines is considered the most appropriate solution to reduce and break the chain of COVID-19 transmission. COVID-19 vaccination also helps maintain productivity and reduce social and economic impacts. The COVID-19 vaccination is carried out after ensuring its safety and effectiveness [2].

One way to understand the phenomenon of infectious disease spread is through mathematical modeling, known as epidemiological mathematical models. Mathematical modeling is widely used in epidemiological studies to provide an understanding of the characteristics and spread of disease. Research on mathematical model of COVID-19 is essential in aiding the understanding and controlling of the pandemic [6,7]. The first mathematical epidemic model, the SIR (Susceptible, Infected, Removed) model, was developed by W. O. Kermack and A. G. McKendrick [11]. This model divides the population into three main compartments, namely Susceptible (S), Infected (I), and Recovered (R). This model helps understand how the number of infected individuals changes over time and how the interactions between these three compartments impact the spread of the virus. Furthermore, in the mathematical model of epidemiology, the threshold parameter (basic reproduction number, denoted as R_0 , represent the average number of individuals who get infected by an already infected individual in a population. This parameter indicates whether the population is free or still affected by disease [12], [13].

There has been a lot of research on mathematical models of the spread of infectious diseases, especially COVID-19. Diagne et al. [1] discussed the mathematical model of COVID-19 with vaccination and treatment. Furthermore, Yundari and Nur'ainul [5] discussed the analysis of the impact of vaccination on new cases of COVID-19 and recovery using the VAR model in Kalimantan. Munaqib et al. [8] developed the spread of COVID-19 model and its simulation with vaccination, implementation of health protocols, and treatment. Arora et al. [9] developed a mathematical model based on COVID-19 to study and manage disease outbreaks by effect of vaccination with regard to its efficacy and percentage. Dynamical of COVID-19 model with vaccination in Saudi Arabia is analyzed by Algarni et al [10].

This study discussed the model of COVID-19 transmission in Indonesia by considering vaccination. The model has reformulated the SIR model by adding the death compartment in the population. The dynamic of the reformulated model is analyzed by analyzing stability around the equilibrium point. The basic reproduction number corresponding to the stability of the model is determined. Furthermore, the model is implemented on daily COVID-19 case data in Indonesia. Furthermore, this study will analyze multiple regression to see the relationship between vaccination policies and COVID-19 infection cases.

2. PRELIMINARIES

2.1. Estimating Parameters Model of COVID-19 Transmission

Mu'tamar et al. [3] discussed the SIR model with vaccination and parameter estimation using the least squares method for COVID-19 cases in Pekanbaru City. This COVID-19 spread model divides the population into three groups of individuals, namely susceptible is a group of individuals who are susceptible to the disease; infected is a group of individuals infected with the disease; recovered is a group of individuals who have recovered. Yavuz and Haidar [14] considered a mathematical model susceptible exposed SEIQVR of COVID-19 disease. The model parameters are estimated using the least squares curve fitting method, and numerical simulations are performed by using these estimated values. Taghizadeh and Djafari [15] considered the SEIR

(Susceptible-Exposed-Infectious-Removed) model for studying COVID-19. Estimation of the parameters of the model using the observed data by using nonlinear least squares (NLS) optimization and a Bayesian estimation method.

2.2. Real Data

The SIRD model was implemented for COVID-19 cases in Indonesia. The data used in this study were data from COVID-19 cases in Indonesia from June 14th to August 31st, 2021. The total population of Indonesia is obtained from the website of the Indonesian Central Bureau of Statistics. The data collected is the daily increase in positive (infected), recovered, and death cases. Meanwhile, the vaccine data is limited to the second dose.

2.3. Stability Analysis Methods

Determining the stability of a system of differential equations can be known through the solutions of that system. In a linear system of differential equations, the solution can be determined, whereas in a nonlinear system of differential equations, the solution is difficult to ascertain. Therefore, the solution of a nonlinear system of differential equations can be approximated linearly.

Definition 1: An equilibrium point (critical point, fixed point, or stationary point) is a point that satisfies the equation $\dot{\mathbf{x}} = \mathbf{f}(\mathbf{x}) = \mathbf{0}$.

Definition 2: Let $f: \mathbb{R}^n \rightarrow \mathbb{R}^n$ be a differentiable and continuous function on a set $D \subset \mathbb{R}^n$ and $\mathbf{x}^* \in \mathbb{R}^n$. The Jacobian matrix around \mathbf{x}^* is denoted J , is defined as follows

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \dots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \dots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_n}{\partial x_1} & \frac{\partial f_n}{\partial x_2} & \dots & \frac{\partial f_n}{\partial x_n} \end{bmatrix}. \quad (1)$$

Definition 3: J is the $n \times n$ Jacobian matrix, which has k eigenvalues $\lambda_1, \lambda_2, \dots, \lambda_k$ where $k \leq n$.

1. If $Re(\lambda_i) < 0$, for $i = 1, 2, \dots, n$ then the equilibrium points \mathbf{x}^* are asymptotically stable.
2. If $Re(\lambda_i) \leq 0$, for $i = 1, 2, \dots, n$ then the equilibrium points \mathbf{x}^* are stable.

3. If there are eigenvalues of the Jacobian matrix that have positive real parts, then the equilibrium points \mathbf{x}^* are unstable.

2.3. Least Square Method

The least squares method is a method for determining the estimated values minimizing the sum of squared residuals for the simple linear regression and the multiple linear regression, respectively.

$$\sum_{i=1}^n U_i^2 = \sum_{i=1}^n (Y_i - \alpha - \beta X_i)^2, \quad (2)$$

for

$$\sum_{i=1}^n U_i^2 = \sum_{i=1}^n (Y_i - \beta_1 X_{1i} - \beta_2 X_{2i} - \beta_3 X_{3i} - \beta_p X_{pi})^2, \quad (3)$$

Furthermore, in simple linear regression and multiple linear regression analysis, there are several prerequisites that need to be fulfilled, namely the classical assumption test (the normality test, the multicollinearity test, the heteroskedasticity test, the autocorrelation test) and the goodness-of-fit test.

3. MAIN RESULTS

3.1. Stability Analysis SIRD Model

The SIRD model of COVID-19 transmission contains four compartments in the population, namely the susceptible compartment, the infected compartment, the recovered compartment, and the death compartment. This model is the result of a reformulation of the SIR model by adding a compartment death with vaccination using the following assumptions, population is constant, population is closed which means there is no population entry and exit, each individual has the same chance of being infected with COVID-19 disease, only COVID-19 disease exists in the population, COVID-19 vaccine is given to each individual with vaccination rate θ , individuals in the susceptible population can migrate to the infected population due to contact between susceptible individuals and infected individuals with an infection rate β , individuals is recovery cannot turn back to susceptible, there is only death from COVID-19 with a death rate μ , infected individuals move to

the recovered population with a recovery rate of γ . Based on the assumptions, the COVID-19 transmission model with vaccination in Indonesia consideration can be seen in the compartment diagram in Figure 1.

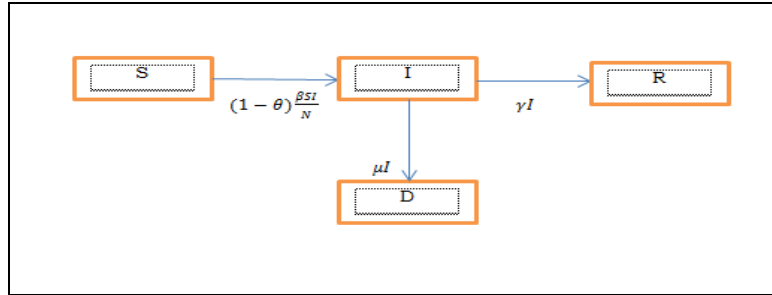


Figure 1. Compartment Diagram of The SIRD Model

The SIRD model of COVID-19 transmission with vaccination in Indonesia is modeled in the following system of differential equations.

$$\begin{aligned}
 \frac{dS}{dt} &= -(1 - \theta) \frac{\beta SI}{N}, \\
 \frac{dI}{dt} &= (1 - \theta) \frac{\beta SI}{N} - \gamma I - \mu I, \\
 \frac{dR}{dt} &= \gamma I, \\
 \frac{dD}{dt} &= \mu I.
 \end{aligned} \tag{4}$$

There are two equilibrium points that describe the state of the model (1), the first one is the disease-free equilibrium point ($I = 0$), which is a condition where the population is free from disease and the second one is the endemic equilibrium point ($I > 0$), which is a condition where there are still individuals infected with the disease in the population. The disease-free equilibrium point of system (1) is

$$E^0 = (S^0, 0, 0, 0), \tag{5}$$

and the disease endemic equilibrium point of system (1) is

$$E^* = (S^*, I^*, R^*, D^*) = \left(\frac{\gamma + \mu}{(1 - \theta) \frac{\beta}{N}}, I^*, R^*, D^* \right). \tag{6}$$

Stability of the equilibrium points depend on the Jacobian matrix. Jacobian matrix for the disease-

free equilibrium is

$$J^0 = J^* = \begin{bmatrix} 0 & -\frac{\beta S^0}{N}(1-\theta) & 0 & 0 \\ 0 & \frac{\beta S^0}{N}(1-\theta) - \gamma - \mu & 0 & 0 \\ 0 & \gamma & 0 & 0 \\ 0 & \mu & 0 & 0 \end{bmatrix}. \quad (7)$$

The eigenvalues for disease-free are obtained as follows, $\lambda_{1,2,3} = 0$ and $\lambda_4 = (\beta S^0 - \beta S^0 \theta - \gamma - \mu)$. Since $\lambda_{1,2,3} = 0$, the stability of the disease-free equilibrium point depends on λ_4 . If $\lambda_4 < 0$ then the equilibrium point E^0 is stable, otherwise if $\lambda_4 > 0$ then the equilibrium point E^0 is unstable.

Jacobian matrix for the endemic disease equilibrium point is

$$J^* = \begin{bmatrix} \frac{\beta S^*}{N}(-1+\theta) & -\gamma - \mu & 0 & 0 \\ -\frac{\beta S^*}{N}(-1+\theta) & 0 & 0 & 0 \\ 0 & \gamma & 0 & 0 \\ 0 & \mu & 0 & 0 \end{bmatrix}. \quad (8)$$

The eigenvalues for the endemic disease are obtained as follows $\lambda_{1,2} = 0$, $\lambda_{3,4} = \frac{1}{2}(-\frac{\beta I^*}{N}(1-\theta) \pm \sqrt{D})$ where $D = (\frac{\beta^2 I^{*2} - 2\beta^2 I^{*2} \theta + \beta^2 I^{*2} \theta^2 - 4N\beta I^* \mu + 4N\beta I^* \theta \gamma + 4N\beta I^* \theta \mu - 4N\beta I^* \gamma}{N})$. Since $\lambda_{1,2} = 0$, the stability of the endemic equilibrium point depends on the value of $\lambda_{3,4}$.

- If $D < 0$ then $\lambda_{3,4}$ is complex, because $(-\frac{\beta I^*}{N}(1-\theta))$ is negative, then the real part of $\lambda_{3,4}$ is negative, it means that the equilibrium point E^* is stable.
- If $D > 0$ then $\lambda_{3,4}$ is real number of different sign, it means that the equilibrium point E^* is unstable.
- If $D = 0$ then $\lambda_{3,4}$ is repeated negative numbers, it means that the equilibrium point E^* is stable.

Furthermore, the basic reproduction number is determined by assuming $\frac{dI}{dt} > 0$ in model (1) as follows

$$\frac{\beta SI}{N}(1-\theta) - (\gamma + \mu)I > 0,$$

$$\left(\frac{\beta S}{N} (1 - \theta) - (\gamma + \mu) \right) I > 0,$$

$$\frac{\beta S(1 - \theta)}{N(\gamma + \mu)} > 1.$$

It can be concluded that

$$R_0 = \frac{\beta S(1 - \theta)}{N(\gamma + \mu)}. \quad (9)$$

If $R_0 < 1$ then the disease-free equilibrium point E^0 is stable which means disease does not spread (disappear) in the population and If $R_0 > 1$ then the endemic equilibrium point E^* is unstable.

3.2. Estimation Parameters

The data is processed using the least squares method is presented in Table 1. A comparison graph is illustrated between the predictive model and the data of the number of positive, recovered, and death COVID-19 cases in Indonesia.

Table 1. Estimation of model parameters by least squares method

Notation	Description	Value
β	Infection rate	0,166
γ	Recovered rate	0,071
μ	Death rate	0,003
θ	Vaccination rate	0,07711

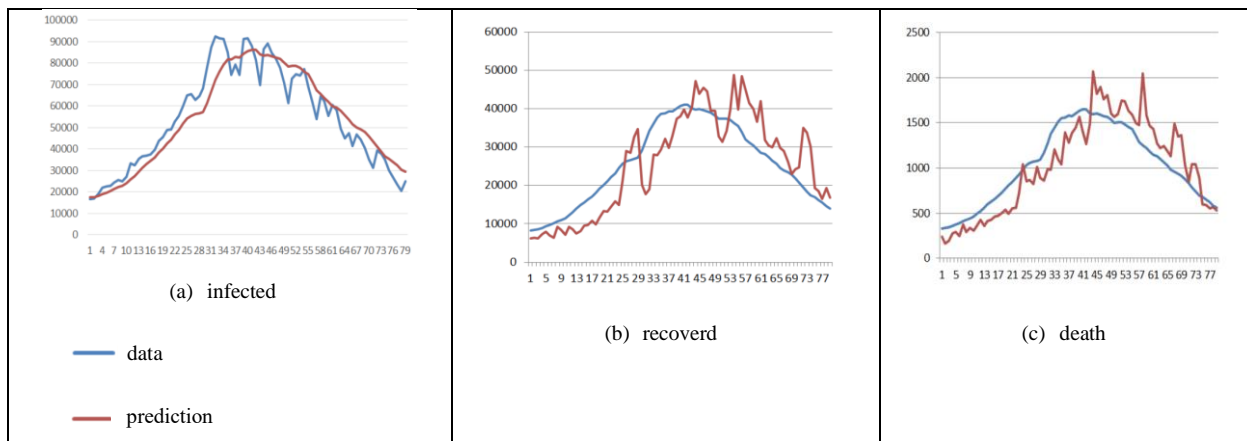


Figure 2. Comparison graph of data and prediction

The reproduction number (R_0) is obtained by substituting the value of parameter in Table 1 to system of equation (5),

$$R_0 = \frac{\beta S(1 - \theta)}{N(\gamma + \mu)}$$

$$R_0 = 2,0441. \quad (10)$$

It can be concluded that COVID-19 spreads in the population.

Furthermore, The estimated model by multiple linear regression is obtained

$$\hat{y} = 126,105 - 87447,136 X_1 + 2,10302 X_2, \quad (11)$$

where X_1 is the number of vaccination cases, X_2 is the number of recovery cases, and \hat{y} is prediction of the number of infected cases. It can be interpreted that for every increase of one vaccination case (X_1), the COVID-19 infection case will decrease by 87447, assuming other variables are constant. For every increase of one case of recovery (X_2), the COVID-19 infection case will increase by 2, assuming other variables are constant.

The last, it is carried out model goodness testing to determine the accuracy of the given predictive model. The result is shown in Table 2 and Table 3.

Table 2. R value squared

S	R-sq	R-sq(adj)	R-sq(pred)
78,11	89,02%	92,4%	92,04%

Table. 2 shows that the R square value is 0,92 which means that the diversity of infections due to COVID-19 can be explained by the estimated model produced by 92,4%. Thus it can be concluded that the regression model of COVID-19 infection cases is the best conjecture model.

Table 3. Anova

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Regression	2	38057395522	19028697761	2785392,21	0,0001
X_1	1	459762	459762	67,30	0,0001
X_2	1	35470874108	35470874108	5192173,29	0,0001
Error	76	519202	6832		
Total	78	38057914724			

Based on Table. 3, it can be obtained that the calculated F value is 2785392.21, while the P-Value is 0,001 which is smaller than 0,05. Thus it can be concluded that this multiple regression model is feasible to use and has a significant value. So based on the R^2 test and the F test, it is concluded that the multiple regression model used is good.

4. CONCLUSIONS

Based on the discussion, it can be concluded that the disease-free equilibrium point is stable and the disease-endemic equilibrium point is stable for certain conditions. The basic reproduction value is obtained $R_0 = 2$, meaning that the disease is still spreading in the population. Finally, it was found that for every one-unit increase in vaccination cases, COVID-19 infection cases will decrease by around 87 infection cases.

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CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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