

# Prediction of the Spread of Covid-19 in Indonesia Using the SEIRD Model and Hybrid Model with ARIMA Correction

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**Abstract**—Building an SEIRD segmentation model with life dynamics, estimating its parameters, and utilizing the ARIMA model to determine and predict the difference between the SEIRD model solution and the observed and fitted data constitute the machine learning approach used in this study. We use machine learning techniques to accomplish this. A hybrid method is used to process the newly collected data, using the model predictions and the residuals from the data. The historical values of the infected, recovering, and dying populations divided by the confidence intervals serve as the parameters for the SEIRD model, which in turn serve as parameters for the models' applicability. confidence level range. Long-term and short-term estimates with confidence intervals can be provided by the model, which can assess incoming data in real-time.

We tested the model's predictions using actual data on COVID-19 cases in Indonesia. All current models are tested with the maximum allowed deviation during validation using MAE, MSE, MLSE, normalized MAE, and normalized MSE. The findings shown that the features of the current model are highly accurate for infected patients, patients who are recuperating, and patients who have passed away. Governments, business, and policy makers can use the findings of our suggested model to forecast controllable health hazards. This methodology can also be applied to additional research to progress science.

**Keywords**—COVID-19, ARIMA, SEIRD, Hybrid

## I. INTRODUCTION

As of August 2020, World Health Organization (WHO) recorded more than 213 countries have been affected by COVID-19. The number of positive patients is 2 million 397 thousand 216, the dead - 162 thousand 956. In Indonesia, from the time the first case was detected on March 2, 2020 to August 31, 2020, official data released by the Task Force of the National Disaster Management Agency (BNPB) shows positive cases. 174,796 cases of covid-19 and 7,343 patients, 124,185 recovered [1][2].

Previous research with various methods has been carried out a lot either with a time series approach through Autoregressive Integrated Moving Average (ARIMA) singularly [3][4][5], or combined with various other models [6][7]. Thus using the epidemiological approach with the SIR method, as well as its derivatives with an eye on various compartments [8][9][10][11]. Each of those models gets varying results.

What is quite interesting is the approach that does a combination of the SEIRD and ARIMA models using a dynamic Hybrid approach. At least this is the case for Ukraine [12] and California USA [13].

The primary goal of this research is to improve the SIR model, which is often carried out using SEIRD and ARIMA models to account for the residuals between actual and anticipated data. The study's larger and ultimate goal is to provide a trustworthy method for forecasting the course of the epidemic so that decision-makers can implement various anti-Semitic measures, appropriate campaigns to reduce and prevent transmission, and targeted actions that take into account the unique characteristics of each region.

## II. PREVIOUS RESEARCH

The previous research related to this study, using relatively the same method is as described above is that carried out by carried out for cases in Ukraine [12] as well as, studies carried out for the case of California United States [13]. Based on SEIRD, LSTM, and GWR models [14], reference [15] switched forced SEIRDV compartmental models to track COVID-19 dissemination and immunization in Italy. Reference [16] identified and estimated COVID-19 with SEIRD epidemic model in California and Japan. Reference [17] models and forecasts COVID-19 confirmed cases in Indonesia using ARIMA and exponential smoothing.

Some of the above studies use different approaches and designs. The most relevant in this study is the integration of SIERD and ARIMA, followed by hybrid dynamics models. The results presented here, and the validation tests performed show quite effective results. What all previous researchers have failed to do is to use a logarithmic scaling method to determine the difference between case numbers so that there appears to be no difference in a given number. And in this study, we showed the corresponding logarithmic scale.

## III. MATERIAL AND METHOD

### A. Dataset

Datasets were obtained from official sources released by BNPB through the [www.covid19.go.id](http://www.covid19.go.id) website. In this study, we used datasets from these sources, starting from March 2, 2020 (initially found covid-19 cases) in Indonesia, and ending until August 31, 2020. So that a total of 183 data were obtained, and became data training. Furthermore, the dataset is used to predict 200 days since the beginning of the COVID-19 incident in Indonesia. In addition, it is also to predict the next 365 days, starting from August 31, 2020.

## B. SEIRD Model

We employed the SEIRD paradigm in this work, which divides the class Removed into Recovered (designated with (R) and Dead (D). SEIRD evaluates five grades as a result: susceptibility (S), exposure (E), infectiousness (I), recovery (R), and death (D) (D). The total number of N subjects in the research population is given by the sum at any time t.

Consequently,  $N = S + E + I + R + D$  [15]. Fig 1 illustrates the diagram compartment.

The derivation of the system of equations for the SEIRD model is expressed as in (1).

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta}{N} SI \\ \frac{dE}{dt} &= \frac{\beta}{N} SI - \alpha E \\ \frac{dI}{dt} &= \alpha E - \frac{1}{T_1} I \end{aligned} \quad (1)$$

$$\begin{aligned} \frac{dR}{dt} &= \frac{(1-f)}{T_1} I \\ \frac{dD}{dt} &= \frac{f}{T_1} I \end{aligned}$$

N stands for the total population, for the infection rate, for the transition period from infection to infection (i.e., the degree of the incubation period), TI for the mean length of infection, and f for the number of fatalities.

The starting time  $t = t_0$  is used to solve the ODE system, and the values are used to determine  $S(t_0)$ ,  $E(t_0)$ ,  $I(t_0)$ ,  $R(t_0)$ , and  $D(t_0)$ . Using the information T [10], available at that time and aggregated up to the last hour, we calculate the base number of multiplications  $R_0$  as in (2).

$$R_0 = \beta TI. \quad (2)$$

We divide the integration interval to account for the many external factors influencing the outbreak data  $[t_0, T]$   $k = 1$ , in the subinterval  $[tk, tk + 1]$ . . . p and fit the model to the data at each subinterval. The conditions that allow changing the trend of the spread of the outbreak are various restrictions imposed by the Indonesian government, starting from DKI Jakarta from April 10 to June 3, 2020, through the PSBB (Large Scale Social Restrictions) approach, or different protocols related to the SWAB test. The frequency of contacts between Infected and Vulnerable should have decreased as a result of the limits being put in place, hence we modeled the coefficient of  $\beta$  in (1) as a function of diminishing time-dependent (t).

When the function is presumed to have a declining exponential form, a comparable model for the infection rate in the SEIR equation can be established. However, by examining the data's trend, we have demonstrated that exponential  $\beta(t)$  behaves in an excessively quick manner as it decreases, thus we have chosen to describe it as a rational function of decreasing as in (3).

$$\beta(t) = \beta_0 (1 - \rho k(t - tk) / t), t \in (tk, tk + 1] \quad (3)$$

where  $k > 0$  and  $0 = 0$  are present. The SEIRD (SEIRD(rm)) rational model, which is depicted below, serves as the source of the input  $\beta(t)$  (3) to the SEIRD(1) model.

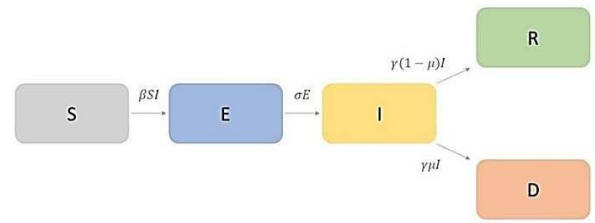


Fig. 1. Diagram compartment of SEIRD model

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta(t)}{N} SI \\ \frac{dE}{dt} &= -\frac{\beta(t)}{N} SI - \alpha E \\ \frac{dI}{dt} &= \alpha E - \frac{1}{T_1} I \\ \frac{dR}{dt} &= \frac{(1-f)}{T_1} I \\ \frac{dD}{dt} &= \frac{f}{T_1} I \end{aligned} \quad (4)$$

The fundamental reproduction number is stated as follows since the infection rate  $\beta(t)$  is dependent on time ( $R_t = \beta(t) TI$ ).

## C. ARIMA Model

A second name for ARIMA is the Box-Jenkins time-winning approach. While long-term forecasting accuracy is not outstanding, ARIMA is excellent for short-term forecasting. Typically, it will remain flat (flat/constant) for a considerable amount of time [18].

When predicting, the ARIMA model fully disregards independent factors. For precise short-term forecasting, ARIMA uses the dependant variables' current and historical values. If the time series' observations are statistically connected to one another, ARIMA is appropriate (dependent).

Box-Jenkins (ARIMA) models are classified into three groups of mixed ARIMA models, which combine the features of the first two models, and autoregressive (AR) models.

### a. Autoregressive Model (AR)

An ARIMA (p,0,0) model or an autoregressive model of order p (AR(p)) has the following general form:  $X_t = \mu' + \theta_1 X_{t-1} + \theta_2 X_{t-2} + \dots + \theta_p X_{t-p} + e_t[0]$  (5) where:

$\mu' =$  a constant

$\theta_p =$  p-th autoregressive parameter

$e_t =$  error value at the moment -t

### b. Moving Average Model (MA)

Sequential moving average model q(MA(q)) or ARIMA(0,0,q)general's form is written as :

$$X_t = \mu' + e_t - \theta_1 X_{t-1} - \theta_2 X_{t-2} - \dots + \theta_q X_{t-q} \quad (6)$$

where:

$\mu' =$  a constant

$\theta_1$  until  $\theta_q$  is-parameter moving average

$e_{t-k} =$  error value at the time of t-k

### c. Mixed models

1. ARMA Method Following is an example of a typical model for a blend of pure AR(1) and pure MA(1) processes, such as ARIMA (1,0,1) :

$$(1 - \phi_1 B)X_t = \mu' + (1 - \theta_1 B)e_t$$

$$\text{AR (1) MA(1)}$$

$$X_t = \mu' + \theta_1 X_{t-1} + e_t - \theta_1 e_{t-1} \quad (7)$$

2. ARIMA Process, The generic ARIMA (p, d, and q) model is satisfied when anomalies are added to a mixture of ARMA processes. Equation (1,1,1) in the straightforward ARIMA example is :

$$(1 - B)(1 - \phi_1 B)X_t = \mu' + (1 - \theta_1 B)e_t \quad (8)$$

First distinction      AR (1)      MA(1)

#### D. Logarithmic Scale

Various visualization techniques can be used to display graphics that can be viewed in a variety of situations, according to research (Sevi et al., 2020). The most popular technique used during the 2020–2021 pandemic was to depict the cumulative number of COVID–19 cases over time with a straightforward line. These stories are simple to depict and understand, yet their seeming simplicity can be deceptive [19].

In reality, time series charts are created by data analysts using arbitrary decisions. The scale at which the desired variable should be displayed is a crucial decision. Most time series charts have a linear scale set as their default option for the vertical axis. On this scale, the variable grows additively as its value rises. If the value of x is increases up to a value of 1000 units, it will appear flat and hundreds of millions of indigo will be visible on the y-axis. This line chart is typically regarded as the most straightforward and fundamental type of time series data visualization.

Using a logarithmic scale on the vertical axis is another method of displaying time series data [20]. As ARIMA, SEIRD, and hybrid time series models are integrated in the right panel, the variables on this scale are multiplied and increased.

For example, it can be seen that the y-axis is logarithmic scale. If each increment is a division, the actual value is incremented by 10 degrees at a time. A scale of 2 means that 10 is quadratic. The function of the logarithmic scale is to concisely display numerical data over a wide range of data. Data that was previously indistinguishable is clearly visible.

#### E. Hybrid Model

It offers a so-called hybrid dynamic framework and is research-based. A hybrid model built on the SEIRD model and the sophisticated ARIMA model was used in this investigation. Creating a model in the SEIRD department, evaluating the parameters, and calculating and predicting the difference between the SEIRD model solution and the observed data using the ARIMA model are the primary steps of this approach. These variations are utilized to modify the model predictions and provide fresh outcomes [12][13].

The stages of this model are as follows:

1. To start, we wish to narrow the discrepancy between the model output and the observed data by using the historical data to calibrate the SEIRD model parameters. Long-term prediction is handled by this model (in the study it was 200 days and 365 days).

2. Determine the residual between the populations that match the SEIRD model and the observed percentage of infected, recovered, and deceased populations.
3. Create three ARIMA models, one for each of the residuals' time series. In order to provide an accurate prediction mode, this ARIMA model prediction corrects residuals between the SEIRD model and historical data.
4. Validation the resulting model predictions using data from the previous day's infected, recovered, and dead people that were not included when working with the model in the previous step.

#### F. Validation

During the validation stage, we estimate the SEIRD model's parameters and gather fresh information that won't be used to fit the ARIMA model. We'll stick to the same standards for quality:

1. Mean Absolute Error (MAE)

The absolute difference between the actual (actual) and projected (predicted) values is averaged to get the mean absolute error (MAE). The MAE formula is used to assess how well statistical models predict the future. Of course, the smallest inaccuracy is the predicted difference.

MAE is expressed as:

$$MAE(y, \hat{y}) = \frac{1}{T} \sum_{t=1}^T |y(t) - \hat{y}(t)| \quad (9)$$

2. Mean Squared Error (MSE)

The difference in actual and anticipated values' mean squared errors is known as the mean squared error (MSE). The prediction error estimate is frequently verified using the root mean square error approach. A low rms error value or an rms error value close to zero indicates that the forecast results are consistent with the actual data and can be used for forecast calculations in future periods.

The MSE is expressed as:

$$MSE(y, \hat{y}) = \frac{1}{T} \sum_{t=1}^T (y(t) - \hat{y}(t))^2 \quad (10)$$

3. Mean Squared Logarithmic Error (MSLE)

The ratio between the actual and anticipated values can be calculated using the root mean square error (MSLE). As the name implies, a variation of the mean squared error is the logarithmic mean squared error. MSLE is only concerned with percentage disparities as a result. Due to the logarithm, MSLE is only concerned with the relative difference, or the percentage difference between the actual and anticipated values. This means that MSLE treats small differences between true and small predictions as roughly equivalent to large differences between true and large predictions.

The MSLE is expressed as:

$$MSE(y, \hat{y}) = \frac{1}{T} \sum_{t=1}^T (\log(y(t) + 1) - \log(\hat{y}(t) + 1))^2 \quad (11)$$

#### 4. Normalized Mean Absolute Error (NMAE)

This statistic is intended to make it easier to compare the MAE of datasets at various scales. The average of the measured data is used as a normalization method by the model performance evaluation tool. The lowest value, or one that is near to zero, is sought in NMAE similarly to MAE.

NMAE is indicated by the formula:

$$NormMAE(y, \hat{y}) = \frac{MAE(y, \hat{y})}{\bar{y}} \quad (12)$$

#### 5. Normalized Mean Squared Error (NMSE)

The fundamental purpose of NMSE is to assess how well behavioral models perform. The normalized mean squared error is the statistic that captures the variance in the data collection (NMSE). Normalization by MSE results ensures that NMSE is not biased towards over- or under-predicted models. Small NMSE values indicate good model performance.

NMSE is expressed as:

$$NormMAE(y, \hat{y}) = \frac{MAE(y, \hat{y})}{\bar{y}} \quad (13)$$

where  $(x)$  is the time series' average value.

The maximum deviation between the two scenarios (optimistic and unfavorable) was also calculated by the researchers using the estimated reference line generated by the ARIMA model. It is a size contrast [19] :

$$MaxMAE(y, \hat{y}) = \frac{|y(t) - \hat{y}(t)|}{y(t)} \quad (14)$$

## IV. RESULT

The results all of the entire model and existing parameters can be described in the following sections.

### A. SEIRD Model

To model we used 183 days of training data coupled with predictions for 365 days, so the following graph (see Fig. 2) was obtained.

For the SEIRD model, we use these parameters:

1.  $N = 273,5$  billion total population (uninfected) (Population of Indonesia 2020)
2.  $\Sigma = 1/4$  (1/day) infection rate after contact (4 days after contact)
3.  $\gamma = 1/9$  The death or recovery rate (1/day) is set to Day 9 because death begins on Day 10.
4.  $f = 0.05$  mortality, 5% of infected individuals die and 95% survive
5.  $\beta = 0.21$  Attack rate that can infect others (contact) (unit:  $1^{-1}$  person $^{-1}$ )

From there, we use the usual differential equations and get as above. For the SIERD prediction model, we did not show actual data for suspect and exposed, so we made a graph

based on only 3 other parameters, namely infected, recovered, and death. So, the graph can look as follows:

### B. ARIMA Model

From the calculations and simulations that we have done with training data totaling 183 data, it can be found that the ARIMA parameters are as follows:

1. INFECTED  
 $p, d, q = (2, 2, 2)$
2. RECOVERED  
 $p, d, q = (3, 2, 2)$
3. DEATHS  
 $p, d, q = (3, 2, 2)$

So that from these parameters, the graph is obtained as follows:

This modeling was obtained from 183 training data, and predictions for the next 365 days. From the ARIMA model on each of the parameters shows a linear graph (see Fig. 3).

### C. Hybrid Model

The results of the Hybrid model, can be displayed as in the following graph (see Fig 4).

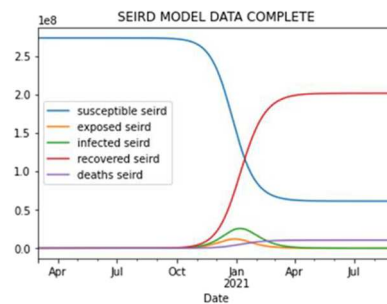


Fig. 2. SIERD model data for all parameters

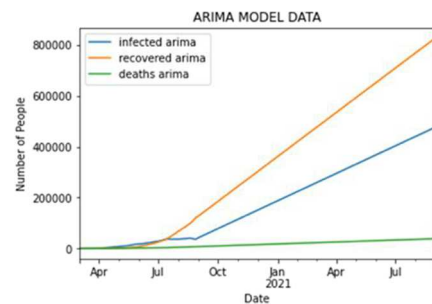


Fig. 3. ARIMA model data for infected, recovered and death

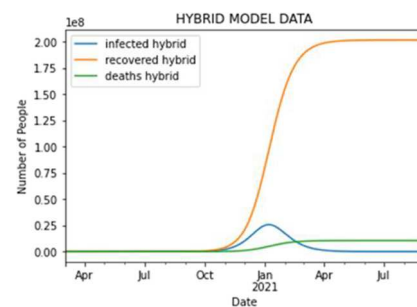


Fig. 4. Hybrid model data for infected, recovered dan death

TABLE I. VALIDATION MAE, MSE, NORMMAE, NORM MSE AND MSLE FOR INFECTED, RECOVERED AND DEATH

The above graph (see Fig. 5) was obtained from the SEIRD model and used ARIMA residue for correction. (Training data uses the first 183 data)

#### D. Logarithmic Scale

For logarithmic scale, the graph (see Fig. 5) can be seen as follows. In logarithmic scale, the y-axis is displayed in logarithmic scale. For each division increment, the actual value increases by a factor of 10 degrees. So, a scale of 2 means that 10 is squared.

Concise display of numerical data over a wide (large) range of data on a logarithmic scale. It clearly shows the difference data, so it does not look like the previous image.

#### E. Validation

The results of the validation test with various test tools as described above (see Table I), using 3 models (SIERD, ARIMA and Hybrid), as well as 3 parameters (infected, recovered and death), obtained the following data:

An essential first step in determining how the final model will function in the future with brand-new data that has never been seen before is validation using each of the techniques listed in the table above. With the addition of real data for the following 365 days, we contrasted this approach using 183 training data. The validation datasets have the same structure because they originate from the same source.

The table above (see Table I) shows that each model considerably varies in all measures of prediction skill for the proportion of infected, recovering, and dying populations. Consequently, the normalized MAE table for ARIMA demonstrates:

1. Only 1.60 percent, on average, separates the actual number of sick people from the population estimate.
2. Only an average of 1.01% separated the actual number of healers from the anticipated number.
3. Only 0.75%, on average, separated the actual number of deaths from the value projected.

While the following Table II shows the maximum deviation (Max Dev):

Additionally, the results of a prediction analysis for the 365 days following the final training day can be displayed as follows:

1. (Max Dev) A probability of 95% indicates that there is a maximum deviation of 250.8% between the expected and actual number of infected people.
2. The highest deviation (Max Dev) with a probability of 95% between the estimated and actual number of recoveries is 80.20%.

3. The largest difference (Max Dev) between the anticipated and actual death rates is 80.6 percent, with a probability of 95%.

Get the data for the forecasts for the subsequent 200 days, or 17 days, beginning with the last day of model training:

1. The maximum deviation (max dev) with a probability of 95% between the estimated number of infected and the actual number of infected is 21.25%.
2. (Max dev) The highest deviation with a probability of 95% between the individual predicted and the individual actually recovered is 5.20%.
3. (Max dev) With a probability of 95%, the highest deviation between the anticipated number of fatalities and the actual number of deaths is 4.61%.

From the results of the validation of the maximum deviation (Max Dev) above, it is concluded that for short-term predictions the deviation from ARIMA is smaller, meaning that it is more accurate than long-term predictions. This is also confirmed by this study compared to previous studies.

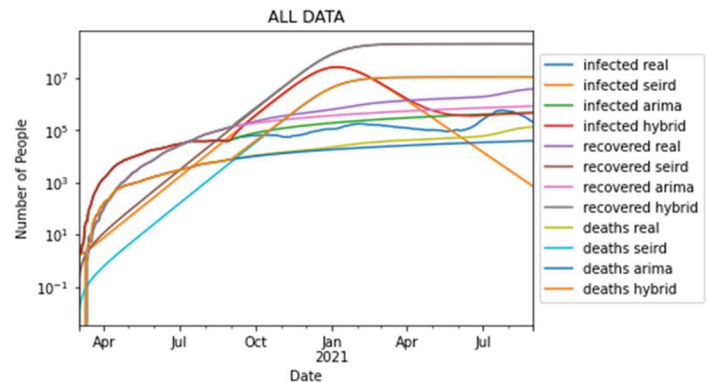


Fig. 5. Logarithmic scale for ARIMA, SEIRD and Hybrid with parameters infected, recovered and death

TABLE II. MAXIMUM DEVIATION 365 DAYS AND 17 DAYS FOR INFECTED, RECOVERED AND DEATH

Category/Measure	Max Dev 365 days	Max Dev 17 days
Infected	2.508054812	0.212562037
Recovered	0.802009699	0.052027312
Death	0.806538425	0.046131768

## V. DISCUSSION AND CONCLUSION

The proposed hybrid model comprises of three ARIMA models that increase prediction accuracy by removing residuals from the dynamic model and a dynamic SEIRD model that simulates the life and mortality dynamics of COVID-19. Unlike solely dynamic models like SIR, SEIR, and SEIRD, the model can make precise forecasts 365 days in advance.

The official COVID-19 statistics for Indonesia were used to test this model. It is clear from the acquired validation findings that the suggested hybrid model performs and predicts well. For health professionals and public officials, the resulting long-term projections are extremely helpful since they provide an overview of the epidemiology of infectious illnesses.

Researchers can anticipate future infection rates, rates of recovery and deaths, as well as the inaccuracy of the estimate under optimistic or pessimistic circumstances, using the short-term forecasts they have acquired. The suggested approach is a powerful tool for analyzing and predicting the dynamics of the COVID-19 pandemic.

There are four significant findings in this study. First, some error tests showed smaller results than previous research because the model's theoretical approach by previous researchers was not compared to factual data. While in this parameter has a small error standard. Second, the population size (N) of 273 million Indonesians in this study was used to model SEIRD and Hybrid. It turned out that the population was too large compared to the actual data. So it is necessary to tune the N (population) parameters in SEIRD modeling in order to get a more suitable model. Third, hybrid using ARIMA-corrected residual SEIRD modeling. This is because ARIMA is not accurate for long-term forecasting. So the hybrid might be worse than SEIRD because the ARIMA correction is worse. Fourth, the results of all error measurements on the Hybrid are smaller than SEIRD because they take the smallest average. This is because the initial conditions of ARIMA still correct SEIRD better. Lastly, the result of Hybrid, while the validation using Maxdev, is greater than SEIRD because it takes the maximum value.

Overall result of this research is better than previous similar studies, which was used the main reference in the study [12] [13]. For future studies we propose: parameter estimation using various algorithms and constraints, tune the machine learning model for optimal results, testing COVID statistical methods in various provinces, develop alternative methods for residual prediction and it is necessary to carry out tuning in the implementation, as an important step in machine learning to produce better models and deviations.

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