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# Comparison of various epidemic models on the COVID-19 outbreak in Indonesia

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***Abstract – This paper compares four mathematical models to describe Indonesia's current coronavirus disease 2019 (COVID-19) pandemic. The daily confirmed case data are used to develop the four models: Logistic, Richards, SIR, and SEIR. A least-square fitting computes each parameter to the available confirmed cases data. We conducted parameterization and sensitivity experiments by varying the length of the data from 60 until 300 days of transmission. All models are susceptible to the epidemic data. Though the correlations between the models and the data are pretty good (>90%), all models still show a poor performance (RMSE>18%). In this study case, Richards model is superior to other models from the highest projection of the positive cases of COVID-19 in Indonesia. At the same time, others underestimate the outbreak and estimate too early decreasing phase. Richards model predicts that the pandemic remains high for a long time, while others project the pandemic will finish much earlier.***

***Keywords*** *– COVID-19; SEIR; SIR; Richard; Logistic*

## I. INTRODUCTION

The first human cases of coronavirus diseases (COVID-19) caused by the novel severe acute respiratory syndrome coronavirus (SARS-CoV-2) were first reported by officials in Wuhan City, China, in December 2019. A wholesale food market in Wuhan city was believed as the source of this outbreak or played a role in the initial amplification of the pandemic. The President of Indonesia announced that COVID-19 was confirmed to have spread in the country on March 2, 2020, and spread to all provinces by April 9, 2020. The spread of COVID-19 has impacted various aspects of life for the Indonesian people. One strategy of the Indonesian government to prevent the spread of COVID-19 is to establish a Large-Scale Social Restriction (LSSR/PSBB) policy. Several restrictions are applied, such as restrictions on religious activities and activities restrictions in public facilities, schools, and workplaces.

Moreover, the Indonesian government obliges people to implement health protocols (mask-wearing, hand-washing, social distancing). The government also makes improvements strategies in the health system, especially in 3T (testing, tracing, and treatment) and in COVID-19 vaccination. However, for more than a year COVID-19 pandemic has occurred in Indonesia. There are no signs that the transmission can be controlled. Based on Worldometers data in mid-January 2021, Indonesia became the highest positive case of COVID-19 in Southeast Asia and the fourth highest in Asia. Besides, the death case is also the third highest in Asia. The Indonesian government is still endeavoring to accelerate the COVID-19 pandemic handling.

The spread of COVID-19 in many regions has been investigated in recent studies. In 2020, Putra and Abidin [1] modeled the spread of COVID-19 in South East Asia using a compartment model, namely the SEIR model. The SEIR model is also used to model the outbreak and the dynamic of COVID-19 in Croatia [2], Italy [3], [4], and Wuhan [5], [6]. Soewono [7] also implemented the SEIR model to investigate the COVID-19 spread in Wuhan, Diamond Princess, and Jakarta-cluster in the beginning time.

Another compartment model, the SIR model, was well implemented in the COVID-19 transmission in China, Italy, and France [8]. Simpler growth models such as the classical logistic or generalized logistic model called Richards model are also used to describe the spread in Guangdong and Zhejiang [9]. The logistic model has been applied for COVID-19 cases to forecast the movement of the outbreak in China [10] and other infected countries, such as Kuwait [11], Cuba [12], and India [13]. Wu et al. [14] calibrated the logistic model to the reported infected cases in China and 33 other countries in USA, Europe, Japan, and Turkey. They classified them based on the level of outbreak progress. Wang et al. [15] stated that the peak of the global outbreak would happen in late October by summarizing the modeling results for the world, Brazil, Russia, India, Peru, and Indonesia. Nuraini et al. [16] applied Richards model to model the early stage of the transmission of COVID-19 in Indonesia, resulting in a vast overestimation. This shortcoming may be due to the limited data and under-reported cases in the early phase.

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Nevertheless, an overestimation prediction is good for preparedness during a pandemic.

This paper aims to simulate the dynamics of COVID-19 in Indonesia based on four epidemic models: the SEIR, SIR, Logistic, and Richards. It compares and evaluates the model's performances based on the limited confirmed cases data. Four models were fitted with optimized parameters to estimate the number of infected individuals over time. The comparison of four epidemic models was carried out to determine the projection results for each model, then compared with the actual data on daily cases.

## II. RESEARCH METHODS

### A. Dataset

The confirmed case data were collected from the official website of Gugus Tugas COVID-19 of the Ministry of Health of Indonesia[1]. We used 300 days of daily confirmed cases data from March 2, 2020 until December 26, 2020, as model forcing. The number of populations in Indonesia is based on the results of the 2020 population census from the Central Bureau of Statistics (BPS)[2], i.e., 270.203.917 people. At the end of the explanation, we used daily test data from KawalCOVID19[3] to see the relationship between the number of daily tests and cases.

### B. Epidemic models

Four basic epidemic models, namely logistic, Richards, SIR, and SEIR, are implemented to describe the dynamics of COVID-19 in Indonesia. Each epidemic model consists of five model simulations. Model simulations 1 to 5 (written as S1, S2, S3, S4, and S5) use 60, 120, 180, 240, and 300 days of confirmed cases of COVID-19 data, respectively.

*Logistic model*

For decades, the use of logistic regression analysis has been widely applicable to epidemiology studies [17], [18]. The logistic model proposed by Pierre-François Verhulst (1804–1849) and developed by other mathematicians in the following years [19] is a common S-shaped curve (sigmoid) describing the dynamics of the infected individuals being controlled by the growth rate and population density. It is formulated in (1) where $r$, $K$ are real numbers. The variable $C(t)$ is the cumulative infected persons by time $t$, $r$ is the growth rate, and $K$ is the final epidemic size. If $C_0=C_0>0$ is the initial number of infected cases, then the analytic solution for (1) is expressed in (2).

$$0 \le \beta, \gamma \le 1 \qquad (1)$$

$$C(t;r,K)=K(1+A\exp(-rt))^{-1}, A=\frac{K-C_0}{C_0} \qquad (2)$$

King et al. [20] found that deterministic models are appropriate with cumulative cases, lead to biased parameters, and overestimate and underestimate the inconstancy of parameters. Therefore, in this study, we adopted to use the daily new confirmed cases.

*Richards model*

Richards model is an extension of the logistic model by adding a scale factor $a$, which measures the deviation from the symmetric simple logistic curve. Richards or generalized logistic model is widely used in epidemiology modeling, including the COVID-19 outbreak [14], [21]. This model was introduced by Richards [22] and is defined as (3) where $r$, $K$ are real numbers and $a$ is a positive real number. The general solution for this differential equation is expressed in (4).

$$\frac{dC}{dt}=rC\left(1-\left(\frac{C}{K}\right)^{a}\right) \qquad (3)$$

$$C(t;r,K,a)=K(1+a\exp(-r(t-t_m)))^{-1/a} \qquad (4)$$

The $C(t)$ represents the cumulative of infected cases at time $t$, $r$ is the initial infection rate, $K$ is the final epidemic size which is the asymptotic total number of infections over the whole epidemics, $t_m$ is a lag phase, and $a$ is a scaling parameter. The flexibility of Richards model is due to the scaling parameter $a$. If $a=1$, then it becomes the logistic model, and if $a$ converges to zero, then the model converges to the Gompertz model [21].

*SIR model*

Susceptible-Infected-Recovered (SIR) model is the simplest deterministic (compartment) model that predicts the behavior of an epidemic outbreak [23]. It follows ordinary differential equations as expressed in (5)-(8) with the initial condition $S(0)\ge 0$, $I(0)\ge 0$, and $0 \le \beta, \gamma$.

$$\frac{dS}{dt}=-\beta\frac{SI}{N} \qquad (5)$$

$$R_0=\frac{\beta}{\gamma} \qquad (6)$$

$$\frac{dR}{dt}=\gamma I \qquad (7)$$

$$N=S+I+R \qquad (8)$$

This model considers only three compartments in the population ($N$), namely the susceptible compartment $S(t)$ represents the number of people who are susceptible or have not contacted the disease, the infected compartment $I(t)$ shows the number of people who have

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[1] https://covid19.go.id/peta-sebaran-covid19 (Accessed: Feb. 17, 2021)

[2] https://www.bps.go.id/pressrelease/2021/01/21/1854/hasil-sensus-penduduk-2020.html (Accessed: Feb.17, 2021)

[3] https://kawalcovid19.id/ (Accessed: Mar. 11, 2021)

been infected and can spread the disease, the recovered compartment *R(t)* are people who have been infected and recovered from the disease, also cannot be infected again, in the certain time *t*. The transition rate between susceptible (*S*) and infected (*I*) is indicated by contact rate ($\beta$). The transition rate between infected and recovered, is $\gamma$, which has the meaning of the rate of recovery. If the duration of the infection is denoted D, then $\gamma$=1/D, since an individual experiences one recovery in D units of time. Since gamma is interpreted as transition rate (in the term of probability), its range is between 0 and 1 [24].

The dynamics of the infectious compartment depends on the ratio of the expected number of new infections in the susceptible compartment, which is called by basic reproduction number ($R_0$) and expressed in (9). If the $R_0$ less than 1 then the population of infected cannot grow. An epidemic occurs if the number of infected individuals increases or $R_0$ greater than 1. In general, the greater the $R_0$, the more difficult to control the epidemic [25].

$$R_0 = \frac{\beta}{\gamma} \tag{9}$$

*SEIR model*

Susceptible-Exposed-Infected-Recovered (SEIR) model is an extension of the SIR model by adding an exposed (E) compartment to make the model more realistic because the virus needs an incubation period to transmit to humans. The basic SEIR model is written in terms of differential equation as expressed in (10)-(14), with the initial condition $S(0) \geq 0$, $E(0) \geq 0$, $I(0) \geq 0, R(0) \geq 0$, and $0 \leq \beta, \gamma, \sigma \leq 1$.

$$\frac{dS}{dt} = -\beta \frac{SI}{N} \tag{10}$$

$$\frac{dE}{dt} = \beta \frac{SI}{N} - \sigma E \tag{11}$$

$$\frac{dI}{dt} = \sigma E - \gamma I \tag{12}$$

$$\frac{dR}{dt} = \gamma I \tag{13}$$

$$N = S + E + I + R \tag{14}$$

In this model, one more compartment is added to the population described in the SIR model, namely the exposed compartment *E(t)* is the people who have been infected but have not yet been infectious in a specific time *t*. This stage of condition occurs between susceptible and infected compartments. The parameter of this compartment $\sigma$ regulates the lag between having undergone an infectious contact and showing symptoms. This parameter takes people from the exposed compartment to the infected compartment [4].

*Optimization problem*

For each epidemic model, we defined an optimization problem to estimate the best parameters, which specify the model by a least-square method [26]. Given a set of $N$ data measurements $Y_i, i \in 1, N$, which are to be fitted to a model *f(x)*, where $x$ is a vector of parameter values, we minimize the square of the difference between the data measurements and the values of the model to give an estimate of the parameters $\tilde{x}$. The minimization problem is defined as (15). Thus, the estimated $\tilde{x}$ is the solution of the system in (16) and (17).

$$\tilde{x} = \min_{x} \sum_{i=1}^{N} \left(Y_i - f(t_i, x)\right)^2 \tag{15}$$

$$\frac{\partial}{\partial x} \sum_{i=1}^{N} \left(Y_i - f(t_i, x)\right)^2 = 0 \tag{16}$$

$$\sum_{i=1}^{N} \left(Y_i - f(t_i, x)\right) \frac{\partial f(t_i, x)}{\partial x} = 0 \tag{17}$$

### C. Evaluation method

We evaluated the model by measuring normalized root mean square error (NRMSE) and Pearson correlation (*corr*) to determine the fit of the model to the confirmed cases of COVID-19 data using (18) and (19), where $x$ is the model calculation and $y$ is the confirmed cases data. NRMSE measures the difference in the number of daily cases calculated by the model and has been confirmed. The Pearson correlation coefficient measures the linear relationship between result data from the model and confirmed data. We applied these two evaluation methods to make the model results more robust.

$$NRMSE = \frac{RMSE}{\bar{y}} \tag{18}$$

$$corr(X, Y) = \frac{\sum (x - \bar{x})(y - \bar{y})}{\sqrt{\sum (x - \bar{x})^2 (y - \bar{y})^2}} \tag{19}$$

## III. RESULTS AND DISCUSSION

### A. Parameter estimation

In this section, the least-squares method is applied to estimate the parameters of each epidemic model to fit the actual situation of the COVID-19 daily case data. The optimized parameters of each model are presented in Table 1 through Table 6.

In the Logistic model, the more days in the model simulation, the smaller $r$ and the higher $K$, as shown in Table 1. The decreasing value of the growth rate agrees with the actual condition that the transmission is very rapid initially and slightly slowed down afterward. Meanwhile, the value of parameter $K$ referring to the final epidemic size underestimates the actual epidemic condition significantly.

Similar to the Logistic model results, Richard's model shows a decrease in the growth rate and an increase of $K$ (Table 2). The largest value of $r$ is 0.07 only at the beginning. The more days, the growth rate does not change. The more extended data we used makes the model tend to be a Gompertz model [21].

**Table 1**. Parameters of Logistic model

| Model | $r$ | $K$ |
|---|---|---|
| S1 | 0.11 | 12,703.33 |
| S2 | 0.04 | 95,043.00 |
| S3 | 0.03 | 246,163.34 |
| S4 | 0.02 | 733,210.09 |
| S5 | 0.02 | 986,803.55 |

**Table 2**. Parameters of Richards model

| Model | $r$ | $a$ | $K$ |
|---|---|---|---|
| S1 | 0.07 | 0.35 | 16,751.00 |
| S2 | 0.01 | 0.00 | 381,441.03 |
| S3 | 0.01 | 0.04 | 682,131.59 |
| S4 | 0.01 | 0.00 | 4,401,372.99 |
| S5 | 0.01 | 0.00 | 2,689,916.12 |

**Table 3.** Parameters of SIR model with $0 \le \beta, \gamma \le 1$

| Model | $\beta$ | $\gamma$ | $R_0$ | NRMSE (%) |
|---|---|---|---|---|
| S1 | 0.99 | 0.88 | 1.13 | 84.05 |
| S2 | 0.99 | 0.93 | 1.06 | 72.09 |
| S3 | 0.99 | 0.95 | 1.04 | 78.79 |
| S4 | 0.99 | 0.96 | 1.03 | 82.27 |
| S5 | 0.99 | 0.97 | 1.02 | 78.21 |

**Table 4.** Parameters of SEIR model with $0 \le \beta, \gamma \le 1$

| Model | $\beta$ | $\gamma$ | $\sigma$ | $R_0$ | NRMSE (%) |
|---|---|---|---|---|---|
| S1 | 0.19 | 2E-12 | 0.99 | inf | 75.00 |
| S2 | 0.18 | 0.03 | 0.90 | 6.0 | 64.36 |
| S3 | 0.19 | 0.06 | 0.73 | 3.2 | 72.39 |
| S4 | 0.12 | 1.7E-11 | 0.99 | inf | 75.29 |
| S5 | 0.19 | 0.06 | 0.42 | 3.2 | 73.81 |

**Table 5.** Parameters of SIR model with $0 \le \beta, \gamma$

| Model | $\beta$ | $\gamma$ | $R_0$ | NRMSE (%) |
|---|---|---|---|---|
| S1 | 97.49 | 97.32 | 1.002 | 41.52 |
| S2 | 29.01 | 28.92 | 1.003 | 47.23 |
| S3 | 15.45 | 15.38 | 1.005 | 49.01 |
| S4 | 8.58 | 8.25 | 1.040 | 40.74 |
| S5 | 5.87 | 5.83 | 1.007 | 59.23 |

**Table 6.** Parameters of SEIR model with $0 \le \beta, \gamma$

| Model | $\beta$ | $\gamma$ | $\sigma\ (10^6)$ | $R_0$ | NRMSE (%) |
|---|---|---|---|---|---|
| S1 | 81.94 | 81.72 | 7.8 | 1.003 | 33.22 |
| S2 | 24.68 | 24.52 | 6.6 | 1.007 | 41.04 |
| S3 | 13.28 | 13.14 | 0.6 | 1.011 | 41.43 |
| S4 | 7.54 | 7.42 | 1,705.3 | 1.016 | 34.77 |
| S5 | 5.20 | 5.09 | 46.8 | 1.022 | 52.71 |

Table 3 and Table 4 show the value of the optimized $\beta$ and $\gamma$ of SIR and SEIR models bounded by 0 and 1 as described in section II. In addition, we also add the value of the reproduction number and the error computed by NRMSE. The parameters are calculated under conditions $0 \le \beta, \gamma \le 1$. SIR and SEIR models give very large NRMSE, showing that the model results in a bad performance. Two simulations from the SEIR model seem unrealistic as the reproduction number ($R_0$) value is infinity. Other simulations in SEIR based on $R_0$ show much faster growth than all simulations by the SIR model.

The significant error in SIR and SEIR models motivates us to optimize the models by relieving the condition for the parameters so that we only restrict $\beta, \gamma \ge 0$. Then, the optimized parameters are presented in Table 5 and Table 6. The parameter values of the SIR and SEIR models by only limiting parameters as positive constants. Parameter values that are limited between 0 and 1 produce much higher errors than the parameters without limitation. Even though the selected parameters for SIR and SEIR models do not follow the constraints of the ideal SIR and SEIR models, the model performances seem to be better, and the results will be used for further analysis. Moreover, all simulations by SIR and SEIR models give $R_0$ greater than 1, indicating a transmission is occurring.

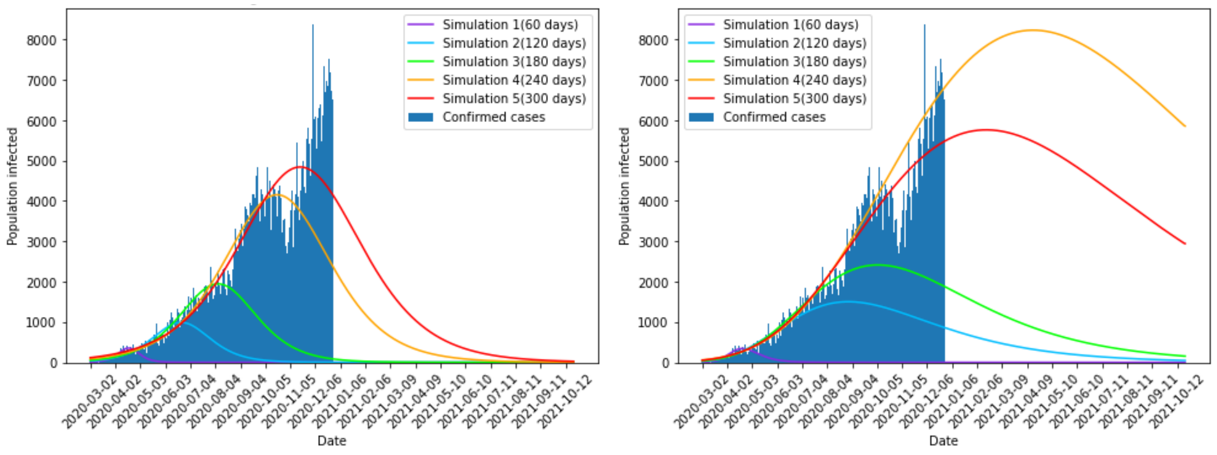
## B. Model fitting

Four epidemic models estimate the daily confirmed cases of COVID-19 in Indonesia (Figure 1). Each model is fitted by five different lengths of the confirmed cases data, namely 60, 120, 180, 240, and 300 days data. The SIR and the SEIR model have a similar projection pattern for each model simulation. The Logistic, the SIR, and the SEIR models have the highest peak of simulation results using 300 days data, while Richards model shows a maximum peak when using 240 days data (Simulation 4). Unlike other models, Richards model simulation using 240 or 300 days of data show that the peak of the projection is around April 2021 and the end of the pandemic is more than 600 days or after October 2021. Other model simulations show an underestimation of the outbreak and estimate too early decreasing phase.

Table 7 shows the model simulation and the projection results at peak days for each epidemic model. The Logistic, SIR, and SEIR models have the highest peak, around 4842, 6253, and 6060 infected people, respectively. Richards model has the highest peak day in Simulation 4, about 8232 cases. The SIR and SEIR models have similar results based on Figure 1 and Table 7. This similarity is because the SEIR model is a SIR model extension by adding an exposed component as a latent phase when a person is infected with the virus but has not yet had symptoms.

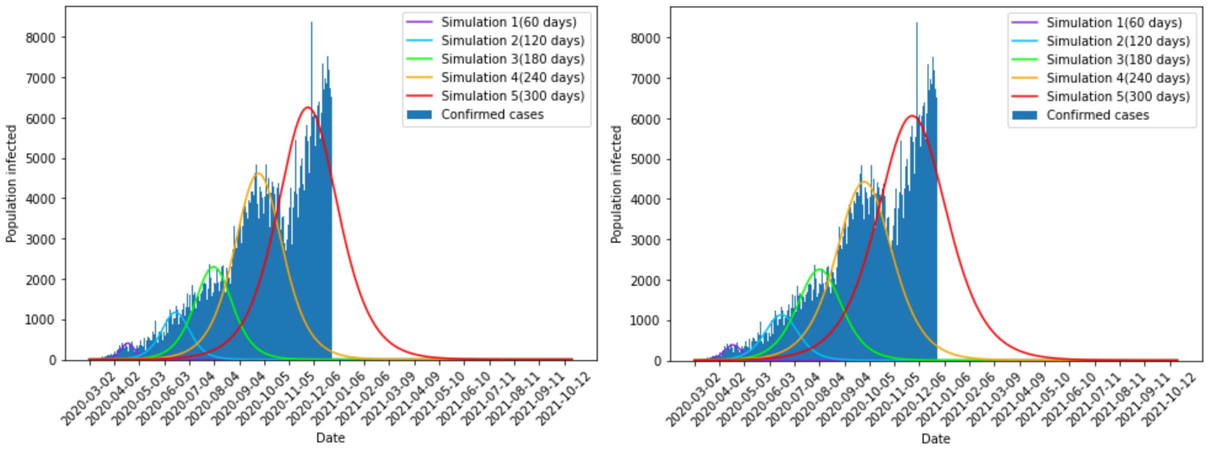
## C. Model performance

The model performances consisting of NRMSE and correlations of all models are shown in Table 8 and Table 9. Richards model has the lowest NRMSE compared to other pandemic models, except for model Simulation 4. Model Simulation 4 in the Logistic model has the lowest value of NRMSE with 18.57%.



(a) Logistic model

(b) Richards model



(c) SIR model

(d) SEIR model

**Figure 1**. The fit of four epidemic models to infected cases

Meanwhile, the highest NRMSE is shown by the SIR Model in model Simulation 5 with a value of 59.23%.

For correlation, most of the simulation models in each epidemic model have a value of more than 90%. The Logistic model has the highest correlation of 97.75% in model Simulation 4. However, Richards model has the highest average correlation of 95.79% compared to the other epidemic models. Richards model is a development of the Logistic model by including an additional scaling factor in the calculations. The lowest correlation value in the SIR model is 85.41% for model Simulation 5.

Richards model has the highest mean of correlation and the lowest mean of NRMSE. Therefore, this model has the best performance compared to other epidemic models. However, based on the NRMSE of four models, they still have large errors. These errors are understandable as the dynamic models only consider a saturated growth with the reduction of cases due to the attempt to avoid contact and the implementation of control measures [27] without considering the uncertainty of the model. External factors such as air quality, temperature, population, and environment may also affect disease transmission. Those might be one of the reasons for the large error in the performance of the basic epidemic model presented in this paper, so justify the importance of external uncertainty factors in modeling the COVID-19 transmission.

**Table 7.** Maximum number of confirmed cases based on four pandemic models (in person)

| **Model** | **Peak** | | | | |
|---|---|---|---|---|---|
| | **S1** | **S2** | **S3** | **S4** | **S5** |
| Logistic | 355 | 991 | 1945 | 4153 | 4842 |
| Richards | 342 | 1503 | 2414 | 8232 | 5762 |
| SIR | 403 | 1169 | 2298 | 4616 | 6253 |
| SEIR | 382 | 1130 | 2255 | 4428 | 6060 |

## D. Relationship between daily tests and new cases of COVID-19

According to Figure 2, the number of daily polymerase chain reaction (PCR) swab tests and the number of new positive cases of COVID-19 in Indonesia from March 2 to December 26, 2020, correlate highly with the Pearson correlation value of 93.75%. Since the pandemic began, the number of tests was expected to increase continuously so that more infected people were quarantined and the spread would decrease.

**Table 8**. NRMSE (%) of four epidemic models and confirmed cases of COVID-19

| Model | NRMSE (%) | | | | |
|---|---|---|---|---|---|
| | S1 | S2 | S3 | S4 | S5 |
| Logistic | 28.82 | 28.65 | 24.31 | 18.57 | 33.30 |
| Richards | 27.38 | 25.60 | 20.73 | 20.92 | 25.35 |
| SIR | 41.52 | 47.23 | 49.01 | 40.74 | 59.23 |
| SEIR | 33.22 | 41.04 | 41.43 | 34.77 | 52.71 |

The number of COVID-19 cases decreased at the beginning of November. Unfortunately, this was not a consequence of good control, but there was a long weekend at the end of October when some laboratories were not conducting PCR tests. According to World Health Organization (WHO) standards, the number of tests is 1 per 1,000 people multiplied by the population per week. The government continues increasing testing capacity according to WHO standards [28]. The number of testing increased again and reached 262.568 people per week, or 97% of the WHO standard in the first week of December, still less than the standard value.

Overall, the performance of the four epidemic models is still needed to be optimized. Incorporation of a grey information method for external uncertainty factors to the basic epidemic model as proposed in [27] may improve the model performance. Besides, adding the number of tests in the model should be considered as the number of daily cases of COVID-19 in Indonesia is significantly affected by the number of daily tests. The decrease in daily cases was not due to good control, but to a decrease in daily tests. If the number of conducted tests is still less than the standard value, then the epidemiological curve may not be reliable in describing the actual condition in Indonesia.

## IV. CONCLUSION

This paper presented various model simulations based on four epidemic models, namely the Logistic, Richards, SIR, and SEIR models, to project the pandemic of COVID-19 in Indonesia. Except for Richards model, three other models show that the longer duration of the data is used, the higher the peak of the projection will be. We remark that the SIR and SEIR model performs similarly. Of these four models, the best model performance is Richards model, which has the highest mean of correlation and the lowest mean of NRMSE. Richards model describes the highest projection of the positive cases of COVID-19 in Indonesia. Other epidemic models show an underestimation of the outbreak and estimate too early decreasing phase. Richards model shows the peak of daily cases in April 2021 and the end of the pandemic after October 2021.

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**Table 9**. Correlation (%) of four epidemic models and confirmed cases of COVID-19

| Model | Correlation (%) | | | | |
|---|---|---|---|---|---|
| | S1 | S2 | S3 | S4 | S5 |
| Logistic | 93.61 | 93.72 | 95.57 | 97.75 | 92.44 |
| Richards | 94.26 | 94.98 | 96.74 | 97.26 | 95.69 |
| SIR | 90.19 | 90.71 | 89.32 | 94.79 | 85.41 |
| SEIR | 92.67 | 92.11 | 91.91 | 95.90 | 87.74 |

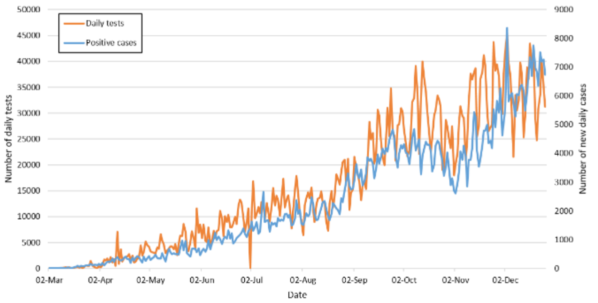

**Figure 2**. The number of daily tests and new cases of COVID-19 in Indonesia from March 2 until December 26, 2020

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