COMPARISON OF PHENOMENOLOGICAL GROWTH MODELS IN PREDICTING CUMULATIVE NUMBER OF COVID-19 CASES IN EAST JAVA PROVINCE, INDONESIA

ISNANI DARTI[1,*], UMMU HABIBAH[1], SUCI ASTUTIK[2], WURYANSARI MUHARINI KUSUMAWINAHYU[1],

MARSUDI[1], AGUS SURYANTO[1]

[1]Biomathematics Research Group, Department of Mathematics, Faculty of Mathematics and Natural Sciences,

University of Brawijaya, Jl. Veteran Malang 65145, Indonesia

[2]Department of Statistics, Faculty of Mathematics and Natural Sciences, University of Brawijaya,

Jl. Veteran Malang 65145, Indonesia

Abstract: In this paper, five phenomenological (Richards, a generalized Richards, Blumberg, Tsoularis & Wallace, and Gompertz) models are implemented to predict the cumulative number of COVID-19 cases. The five phenomenological models are in the form of ordinary differential equations with a few number of model parameters. The model parameters of each model were calibrated by fitting the model with the reported cumulative number of COVID-19 cases in East Java Province from March 25 until October 31, 2020 via nonlinear least square method. We compare the performance of the five phenomenological models by measuring four performance metrics, namely the root mean square error (RMSE), the mean absolute error (MAE), the coefficient of determination (R^2) and the Akaike information criterion (AIC). When calibrating the cumulative number of cases, the five models perform very well, which are indicated by their high coefficient of determination ($R^2 > 0.999$). However, a comparison of the four-performance metrics shows that Tsoularis & Wallace performed the best followed by a generalized Richards model. The prediction for the final size of the COVID-19 epidemic in East Java according to the Tsoularis & Wallace model

[*]Corresponding author

E-mail address: isnanidarti@ub.ac.id

is $K = 78\,002$. Both Richards and Gompertz models tend to underestimate the final size of the epidemic, while the Blumberg model tends to overestimate. The five models estimate the peak of the COVID-19 epidemic in East Java has been occurred on August 13-14, 2020. Using the predicted cumulative number of cases, we determine the daily new cases of COVID-19 in East Java. Based on the four-performance metrics, it appears that the five phenomenological models predict new daily cases of COVID-19 equally well.

1. INTRODUCTION

In late 2019, the Wuhan Municipal Health Commission reported some cases of unusual viral pneumonia [1], which were then identified as an impact of the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The World Health Organization (WHO) named the disease as 2019 coronavirus disease (COVID-19). COVID-19 is a highly contagious disease [2]. With a lot of international travel, COVID-19 can quickly spread around the world. Therefore, WHO declared the global outbreak of COVID-19 as a pandemic on March 11, 2020 [3].

The first COVID-19 case in Indonesia was reported on 2 March 2020 [4]. About a month later, the pandemic has spread to all provinces in Indonesia. East Java becomes one of the provinces in Indonesia with the highest cases of COVID-19. The first recorded case of COVID-19 in East Java occurred on March 17, 2020, when it was reported that six people in Surabaya had been confirmed to have COVID-19 [5]. As of 31 October 2020, the cumulative number of cases in East Java was 52 465 cases (or 12.79% of the total cases in Indonesia). Of the cases reported in East Java, 46 464 people have recovered and 3 752 people have died [6]. As of this writing, the COVID-19 outbreak is still ongoing and continues to spread, although implementation of some control measures have been carried out.

The increasing number of COVID-19 cases has encouraged the development of mathematical modelling to help people understand the behavior of the COVID-19 epidemic. Currently, there are various mathematical models describing the dynamics of the COVID-19 epidemic available in literatures. In general, mathematical models are grouped into mechanistic compartment models and phenomenological models. The mechanistic compartment model takes into account the assumptions of physical or biological mechanisms in explaining the dynamics of disease transmission [7]. Epidemiological models based on a mechanistic approach include SIR epidemic

models and its development, which can be in the form of first order differential equations [8-13] or fractional differential equations [14-15]. Phenomenological models have been applied to generate growth curves of infectious diseases from the observed epidemic data, without mechanistic assumptions nor biological mechanisms incorporated in the transmission dynamics of disease [16-18].

Logistic equation is a classical phenomenological model which consists of two parameters and is given by

$$\frac{dC}{dt} = rC\left(1 - \frac{C}{K}\right), \tag{1}$$

where $C = C(t)$ represents the cumulative number of COVID-19 cases at time t, r is the epidemic growth rate at the early stage, K is the final size of the epidemic, and $\frac{dC(t)}{dt}$ represents the incidence case at time t. Logistic model has been applied to predict the growth of COVID-19 active cases [19-20]. Notice that logistic model (1) describes a symmetrical growth pattern with an exponential growth dynamics at the initial stage, i.e. when $C(t) \ll K$. By considering that the growth rate at the early stage is not always exponential and the S-shape epidemic curve can be asymmetric, the logistic model (1) is extended by many authors. For example, to describe asymmetric growth, Richards [21] introduced a parameter which measures the symmetry deviation about the inflection or turning point. To offer more flexible growth pattern, Chowell et al [17-18] introduced a 'deceleration' parameter which can describe linear, exponential or sub-exponential (e.g., polynomial) growth dynamics. Using the deceleration parameter, Chowell et al [17-18] extended the Richards model to obtain a generalized Richards model. Different type of shape parameter has been introduced by Blumberg [22]. Recently, Tsoularis and Wallace [23] have also proposed a more general logistic model, which can be considered as a combination of the Blumberg model and a generalized Richards model. In the limiting case, the Richards model can be reduced to Gompertz model.

Recently, there has been a lot of literatures on modelling and analysis of the dynamics of COVID-19 transmission based on phenomenological models. These include the application of Richards model [24-27], a generalized Richards model [28-30] and Gompertz model [31-34]. In this paper, five phenomenological models including Richards, a generalized Richards, Blumberg, Tsoularis & Wallace and Gompertz growth models are applied to reproduce the empirical trajectory of COVID-19 epidemic by fitting those models to the reported cumulative number of

COVID-19 cases in East Java, Indonesia. The performance of the five phenomenological models is evaluated through four performance metrics, namely the root mean square error (RMSE), the mean absolute error (MAE), the coefficient of determination (R^2) and the Akaike information criterion (AIC).

2. MATERIAL AND METHODS

2.1. Data

We used data from [6] which is the official Indonesian government website. The website [6] provides daily COVID-19 data for all provinces in Indonesia, including East Java. For our study, we consider daily data set of COVID-19 in East Java, which was taken on November 1, 2020. The data set consists of cumulative number of COVID-19 cases and daily new cases of COVID-19 from March 25 until October 31, 2020. The cumulative number of COVID-19 cases and the daily new cases of COVID-19 in East Java are shown in **Figure 1**.
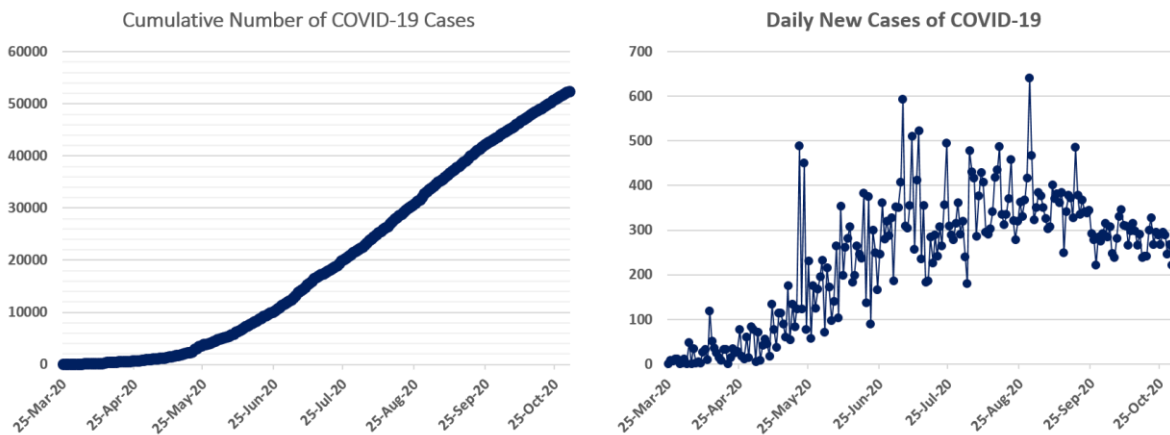

Figure 1. Cumulative number of COVID-19 cases (left) and daily new cases of COVID-19 (right) in East Java, Indonesia.

2.2. Models

There are many phenomenological models known in the literatures that have been used to describe dynamics of population, including for several infectious disease outbreaks. In this paper, our data will be fitted to five types of phenomenological models and then we determine the best-fit model among those models by choosing the best performance metrics in the calibration process. In the following Sub-sections, we review the considered phenomenological models.

2.2.1. Richards Growth Model

Richards growth model extends the logistic model (1) by introducing parameter a which adjusts the symmetrical deviation of the S-shaped curve as follows

$$\frac{dC}{dt} = rC\left(1 - \left(\frac{C}{K}\right)^a\right). \tag{2}$$

Notice that if $a = 1$ then the Richards model (2) recovers to the logistic equation (1). The solution of model (2) is given by

$$C(t) = K\left(1 - e^{-art}\left(1 - \left(\frac{K}{C_0}\right)^a\right)\right)^{-\frac{1}{a}}, \tag{3}$$

where $C_0 = C(0)$. It is clear that $\lim_{t \to \infty} C(t) = K$. By setting $d^2C/dt^2 = 0$, we can find that at the turning point (where the growth rate is maximum), the cumulative number of cases is $C_p = K\left(\frac{1}{1+a}\right)^{\frac{1}{a}}$. Turning point is a point at which the cumulative number of cases attains its inflection point and the incidence curve reaches its maximum. Hence, the turning point indicates the occurrence of the epidemic peak.

2.2.2. A Generalized Richards Growth Model

For the second model, we consider a generalized Richards growth model, which is given by the following differential equation

$$\frac{dC}{dt} = rC^p\left(1 - \left(\frac{C}{K}\right)^a\right). \tag{4}$$

p is known as the 'deceleration of growth' parameter which captures different early stages of the epidemic, where $p \in [0,1]$. In the limiting cases, the incidence of cases grows exponentially when $p = 1$ and it remains constant if $p = 0$. If $0 < p < 1$, then the incidence of cases shows a sub-exponential growth pattern. At the turning point, the cumulative number of cases is $C_p = K\left(\frac{p}{a+p}\right)^{\frac{1}{a}}$. The generalized Richards model (4) reduces to the Richards model (2) for $p = 1$ and it reduces to the logistic equation (1) for $p = 1$ and $a = 1$.

2.2.3. Blumberg Growth Model

We next consider the Blumberg growth model, which can also be considered as one of generalization of logistic growth equation. The differential equation form of the Blumberg model is

$$\frac{dC}{dt} = rC^p \left(1 - \frac{C}{K}\right)^\gamma, \tag{5}$$

where γ is the shape parameter. It is clearly seen that the logistic equation is a special case of the Blumberg model, namely when $p = \gamma = 1$. Blumberg growth model is also known as the hyper-logistic equation. The explicit analytical solution of equation (5) does not always exist. The cumulative number of cases at the turning point can be determined by setting $d^2C/dt^2 = 0$. In this way, we obtain $C_p = K \frac{p}{p+\gamma}$.

2.2.4. Tsoularis & Wallace Growth Model

A more general growth model has been introduced by Tsoularis & Wallace, namely

$$\frac{dC}{dt} = rC^p \left(1 - \left(\frac{C}{K}\right)^a\right)^\gamma. \tag{6}$$

The Tsoularis & Wallace growth model reduces to a generalized Richards model for $\gamma = 1$ and recovers the Blumberg model for $a = 1$. The general analytical solution of equation (6) cannot be written in an explicit form. However, we can determine the cumulative number of cases at the turning point by setting the second derivative of $C(t)$ to be zero. Here we get $C_p = K \left(\frac{p}{p+a\gamma}\right)^{\frac{1}{a}}$. By choosing suitably parameter values, we can show that the cumulative number of cases at the turning point of the Tsoularis & Wallace model coincides with those of Richards, generalized Richards and Blumberg models. Tsoularis & Wallace have shown that the solution of model (6) satisfies

$$\lim_{n\to\infty} C(t) = K, \tag{7}$$

showing that the cumulative number of cases will converge to the final epidemic size K. Since this property is valid for any parameter values and all previous models (Richards, generalized Richards and Blumberg models) are special cases of the Tsoularis & Wallace model, it can be deduced the solution of those models also converge to K.

2.2.5. Gompertz Growth Model

For the last model, we consider Gompertz growth model. The Gompertz model can be derived from the Richards model, i.e. by taking the limiting case as follows

$$
\begin{aligned}
\frac{dC}{dt} &= \lim_{a \to 0} \frac{r}{a} C \left(1 - \left(\frac{C}{K} \right)^a \right) \\
&= \lim_{a \to 0} \frac{r}{a} C \left(1 - \exp\left(a \ln \frac{C}{K} \right) \right) \\
&= \lim_{a \to 0} rC \left(-\ln \frac{C}{K} - \frac{a}{2} \left(\ln \frac{C}{K} \right)^2 + \mathcal{O}(a^2) \right) \\
&= rC \ln \frac{K}{C}.
\end{aligned}
\tag{8}
$$

The closed form of analytical solution of the Gompertz equation is given by

$$
C(t) = K \exp\left\{ \ln\left(\frac{C_0}{K} \right) \exp(-rt) \right\}, C(0) = C_0.
\tag{9}
$$

Clearly that $\lim_{n \to \infty} C(t) = K$. Furthermore, at the turning point, the cumulative number of cases is $C_p = K/e$, where e is the natural number.

2.3. Model Fitting

In this paper, all five growth models will be fitted to the observed data of cumulative number of COVID-19 cases in East Java to estimate the model parameters. The fitting is performed via nonlinear least-square technique, i.e. by finding the set of model parameters $\widehat{\Theta}$ which minimizes the following sum of squared differences

$$
\sum_{i=1}^{N} \left(C(t_i) - \hat{C}(t_i; \widehat{\Theta}) \right)^2,
\tag{10}
$$

where $C(t_i)$ represents the observed data of cumulative number of COVID-19 cases at time t_i, $\hat{C}(t_i; \widehat{\Theta})$ denotes the related solution of the model with parameter $\widehat{\Theta}$ and N is the number of data points. To obtain the solution of each growth model in our study, we implement the fourth-order Runge-Kutta method using the first observed cumulative number of cases as the initial value. The models fitting in this work was performed using a built-in MATLAB function *lsqcurvefit*.

To evaluate the performance of each model, the root mean square error (RMSE), the mean absolute error (MAE), the coefficient of determination (R^2) and the Akaike information criterion (AIC) are calculated according to the following formulae

$$RMSE = \sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(C(t_i) - \hat{C}(t_i; \widehat{\Theta})\right)^2}, \tag{11}$$

$$MAE = \frac{1}{N}\sum_{i=1}^{N}\left|C(t_i) - \hat{C}(t_i; \widehat{\Theta})\right|, \tag{12}$$

$$R^2 = 1 - \frac{\sum_{i=1}^{N}\left(C(t_i) - \hat{C}(t_i; \widehat{\Theta})\right)^2}{\sum_{i=1}^{N}(C(t_i) - \bar{C})^2}, \tag{13}$$

$$AIC = N\ln\left(\frac{\sum_{i=1}^{N}\left(C(t_i) - \hat{C}(t_i; \widehat{\Theta})\right)^2}{N}\right) + 2P, \tag{14}$$

where $\bar{C}$ is the average of the observed data of cumulative number of COVID-19 cases and P is the number of model parameters.
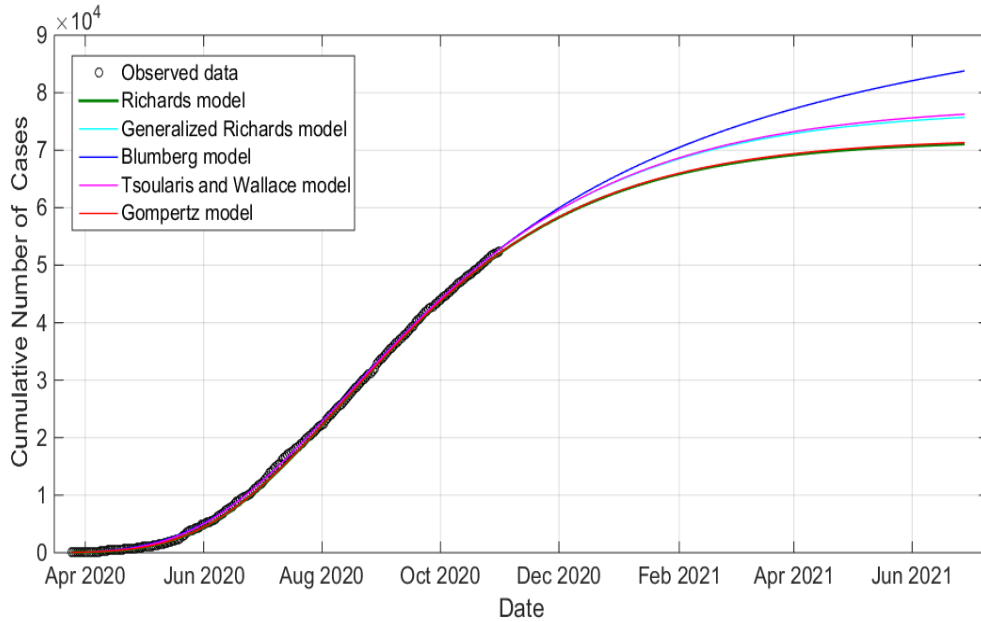
3. RESULTS AND DISCUSSION

Figure 2. The observed data and predicted values calculated for the cumulative number of COVID-19 cases in East Java using five different growth models.

As mentioned before, the five growth models are fitted to the observed cumulative number of COVID-19 cases in East Java using the built-in MATLAB function *lsqcurvefit*. For the calibration, we use data set from March 25 until October 31, 2020. When applying the function *lsqcurvefit*, we

need an initial guess as well as lower and upper bounds for each parameter. The initial guess, the lower and upper bounds used in the model fitting and the estimated value for each parameter are shown in Table 1. From this table, we see that the final epidemic size of the Richards model, a generalized Richards model, Blumberg model, Tsoularis & Wallace model and Gompertz model are respectively 71 855, 77 169, 107 392, 78 002, and 72 102. Roughly speaking, the final epidemic size estimated by the Richards is almost the same as that by the Gompertz model, while the final epidemic size estimated by the generalized Richards model is comparable to that by the Tsoularis & Wallace model. The final size of epidemic obtained by the Blumberg model is far larger than those obtained by other models. It is found that the Richards and Gompertz models have a tendency to underestimate the final epidemic size (K), while the Blumberg model tends to overestimate the value of K. Thus, the final epidemic sizes estimated by the Richards/Gompertz models and that by the Blumberg model can respectively be used as lower and upper bounds of the future scenarios. The behavior of the Richards model in predicting the final size of the epidemic is consistent with the results in [28, 35].

Using the corresponding estimated parameter values, we solve each model and compare the result with the observed cumulative number of COVID-19 cases. Figure 2 shows that in the calibration period, all models fit well with the observed data. In Figure 2 we also plot the 8-month (240 days) ahead forecasts of cumulative number of COVID-19 cases in East Java using all five models. It is seen that the cumulative number of cases for each model is monotonically increasing and is convergent to the corresponding final epidemic size (K). Moreover, the deceleration parameter of a generalized Richards, Blumberg and Tsoularis & Wallace models are estimated to be $0 < p < 1$, which indicates that the dynamic of epidemic growth in the early stage is not exponential but sub-exponential.

Next, we calculate the cumulative number of COVID-19 cases at the turning point (C_p) for each model using formulae given in Section 2. By substituting the corresponding estimated parameter values into those formulae, we get C_p for each model. C_p can be interpreted as the cumulative number of COVID-19 cases when the peak of the pandemic occurs. Hence, we can numerically estimate the time when the peak of the pandemic occurs (t_p), i.e., by identifying the value of C_p in the curve of cumulative number of cases and determining when C_p occurs. C_p and t_p for each model are shown in Table 2. The Richards model, Blumberg model and Gompertz model estimate the pandemic peak to occur on August 13, 2020, while a generalized Richards

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model and Tsoularis & Wallace model give estimation of the peak of the pandemic to occur on August 14, 2020.

Table 1. Lower and upper bounds and initial guess for each parameter used in the fitting model, and the estimated value of parameter.

Model	Parameter	Lower Bound	Upper Bound	Initial Guess	Estimated Value
Richards	r	0	4	0.5	4
	K	4×10^4	5×10^5	4×10^4	71 855
	a	0	4	1	0.0035
Generalized Richards	r	0	4	0.5	0.2878
	p	0	1	0.5	0.9109
	K	4×10^4	5×10^5	4×10^4	77 169
	a	0	4	1	0.1179
Blumberg	r	0	4	0.5	0.4113
	p	0	1	0.5	0.7268
	K	4×10^4	5×10^5	4×10^4	107 392
	γ	0	4	2	2.1609
Tsoularis & Wallace	r	0	4	0.5	0.3066
	p	0	1	0.5	0.9236
	K	4×10^4	5×10^5	4×10^4	78 002
	a	0	4	1	0.0994
	γ	0	4	2	1.0178
Gompertz	r	0	4	0.5	0.0141
	K	4×10^4	5×10^5	4×10^4	72 104

Table 2. Cumulative number of COVID-19 cases in East Java at the inflection point (C_p) and date when the peak of the pandemic is estimated to occur (t_p).

Model	Richards	Generalized Richards	Blumberg	Tsoularis & Wallace	Gompertz
C_p	26 480	27 485	27 023	27 413	26 525
t_p	13-Aug-20	14-Aug-20	13-Aug-20	14-Aug-20	13-Aug-20

Table 3. Performance metrics calculated from the growth models applied to the observed cumulative number of COVID-19 cases.

Performance metrics	Richards	Generalized Richards	Blumberg	Tsoularis & Wallace	Gompertz
$RMSE$	444.8765	269.0351	333.7896	268.7001	420.7418
MAE	338.1818	211.1503	272.0806	204.7738	318.0247
R^2	0.9996	0.9998	0.9993	0.9998	0.9994
AIC	2576.2458	2480.9201	2701.2065	2474.0672	2674.5726

Table 4. Performance metrics calculated from the growth models applied to the observed daily new cases of COVID-19.

Performance metrics	Richards	Generalized Richards	Blumberg	Tsoularis & Wallace	Gompertz
RMSE	72.2991	71.7784	72.0002	71.7763	72.2463
MAE	48.7937	48.7009	49.0218	48.6833	48.7621
R^2	0.6461	0.6534	0.675	0.6539	0.6742
AIC	1898.2876	1896.9241	1898.1187	1898.9108	1895.7958

Table 3 shows the performance metrics calculated from all five growth models applied to the observed cumulative number of COVID-19 cases in East Java. It is observed that all models studied in this paper show very high R^2 values (> 0.999), indicating all models perform well. Based on the value of R^2, the generalized Richards model and the Tsoularis & Wallace model

provide best results. Other performance metrics ($RMSE, MAE$ and AIC) suggest the Tsoularis & Wallace model as the most suitable model followed by the generalized Richards model.
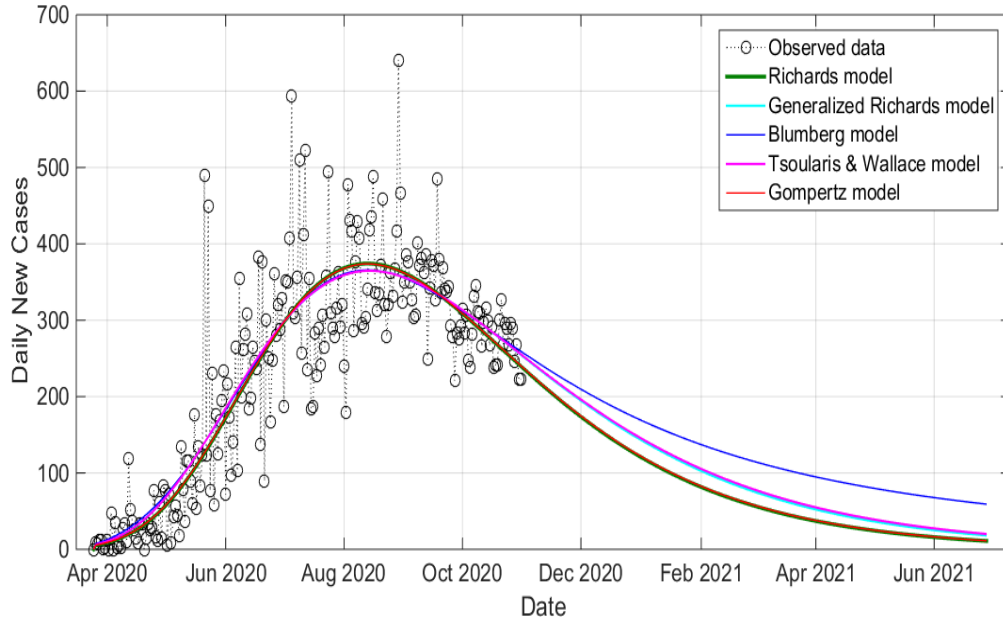

Figure 3. The observed data and predicted values calculated for the daily new cases of COVID-19 in East Java using five different growth models.

Having the curve prediction of cumulative number of COVID-19, we can we predict the new daily cases on the i-th day ($D(t_i)$) by taking the different between the cumulative number of cases on the i-th day and that on $(i-1)$-th day:

$$D(t_i) = C(t_i) - C(t_{i-1}). \tag{14}$$

In **Figure 3**, we compare the actual new daily cases of COVID-19 in East Java with the prediction obtained from all five growth models studied in this paper. We see that the actual data of new daily cases is very scattered and therefore it is not easy to predict. Nevertheless, **Figure 3** shows that all five growth models produce reasonably good predictions of new daily cases of COVID-19. To see how good their prediction, in **Table 4**, we show the goodness of fit statistics calculated from the growth models applied to the daily news cases of COVID-19. It is seen that the determination coefficient (R^2) of all five models are good enough, i.e. $R^2 \approx 0.65$. Furthermore, all performance metrics ($RMSE, MAE, R^2$ and AIC) for all five models for the daily new cases are comparable and difficult to distinguish. This fact indicates that all five models studied in this works perform equally well to predict the daily new cases of COVID-19 in East Java. Furthermore, by observing

Figure 3 we can identify the occurrence of the peak of the epidemic. Based on the predictions of the Richards model, Blumberg model and Gompertz model, the pandemic peak of COVID-19 in East Java is estimated to occur on August 13, 2020, while the generalized Richards model and Tsoularis & Wallace model predict that the pandemic peak occurs on August 14, 2020. Those predictions are consistent with the predictions based on the cumulative number of cases.

4. CONCLUSION

We have implemented phenomenological models to predict the cumulative number of COVID-19 cases in East Java. The studied models are the Richards, generalized Richards, Blumberg, Tsoularis & Wallace and Gompertz models. It is observed that the five studied phenomenological models have very high coefficient of determination ($R^2 > 0.999$), which indicates that those models have very good performance. By comparing the four performance metrics ($RMSE, MAE, R^2$ and AIC), we found that the Tsoularis & Wallace model is the most suitable growth model in predicting the cumulative number of COVID-19 cases in East Java. According to the Tsoularis & Wallace model, the final epidemic size is $K = 78\,002$ and the peak of the epidemic was predicted to occur on August 14, 2020. Using the estimation of the final epidemic size by the Richards and Gompertz models as the lower bound and that by the Blumberg model as the upper bound, the lower and upper bounds of the final epidemic size are approximately 72 000 and 107 400, respectively. We also found that the deceleration parameter for generalized Richards, Blumberg and Tsoularis & Wallace model are $p \approx 0.9$, indicating that the growth dynamic of the early-stage epidemic is sub-exponential.

4. ACKNOWLEDGEMENTS

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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