

## Predictive Mathematical Modelling of the Total Number of COVID-19 Cases for Indonesia

Abubakar M. Umar<sup>1</sup> and Mohd Yunus Abd Shukur<sup>2\*</sup>

<sup>1</sup>Department of Biological Sciences, Faculty of Science, Gombe State University,  
P.M.B. 027, Gombe, Nigeria.

<sup>2</sup>Department of Biochemistry, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia,  
43400 UPM Serdang, Selangor, Malaysia.

\*Corresponding author:

Prof. Dr. Mohd Yunus Shukur,  
Department of Biochemistry,  
Faculty of Biotechnology and Biomolecular Sciences,  
Universiti Putra Malaysia,  
43400 UPM Serdang, Selangor,  
Malaysia.

Email: [mohdyunus@upm.edu.my](mailto:mohdyunus@upm.edu.my)

### HISTORY

Received: 18<sup>th</sup> July 2020  
Received in revised form: 25<sup>th</sup> July 2020  
Accepted: 28<sup>th</sup> July 2020

### KEYWORDS

COVID-19  
total infection  
pandemic  
mathematical model  
MMF

### ABSTRACT

In the current article, we showcase various growth models like Von Bertalanffy, Baranyi-Roberts, Morgan-Mercer-Flodin (MMF), modified Richards, modified Gompertz, modified Logistics and Huang in the fitting and analysis of the COVID-19 epidemic trend as of 15 July 2020 in Indonesia in the form of the total number of SARS-CoV-2 infections. The MMF model was proved as the suitable model with the highest adjusted  $R^2$  value and lowest RMSE value. The Accuracy and Bias Factors values were near to unity (1.0). The parameters obtained from the MMF model consist of maximum growth rate ( $\mu_m$ ) (log) of 0.025 (95% CI from 0.020 to 0.028), curve constant ( $\delta$ ) that affects the inflection point of 0.770 (95% CI from 0.691 to 0.849), lower asymptote value ( $\beta$ ) of 0.297 (95% CI from 0.229 to 0.365) and maximal total number of cases ( $y_{max}$ ) of 4,634,469 (95% CI from 1,967,886 to 15,417,005). The MMF forecast that the total number of cases in Indonesia on the coming 15<sup>th</sup> of August and 15<sup>th</sup> of September 2020 will be 113,179 (95% CI of 103,477 to 123,790) and 154,235 (95% CI of 136,542 to 174,220), respectively. The predictive capability of the model applied in this paper is likely a reliable tool for epidemiologist to monitor and evaluate the severity of COVID-19 death cases in Indonesia in few months to come. Undoubtedly, the models will be reexamined after every few months in the event unwarranted phenomena lead to an exponential increase or wave of new infection.

### INTRODUCTION

The SARS-CoV-2 virus is the agent responsible for the world pandemic COVID-19 that is still devastating to human being with the present death tolls above half a million individuals with more than 10 million persons left ill. The respiratory ailment, Covid-19, is a current universal health issue that spread into many countries so far. A great task of global researchers is to find cure and vaccines against Covid-19 [1]. Global societies and markets have remained a near-complete stoppage for the first time in a near history due to this virus. The virus belongs to the family of coronavirus (CoV), that is responsible for the zoonotic infections over the past decades on many occasions [2]. In the fall of 2019, SARS-CoV-2 first emerged near Wuhan City, in the People's Republic of China [2–5].

To date there is no therapeutic treatments available for corona virus, and therefore the pandemic overcome healthcare facilities of even well-equipped countries. The only prevention measure rely only on interaction

tracing, isolation of infected persons and distancing [6]. Due to extensive effects of deleterious pandemic on the well-being and economy of the world, it is cognizance to study the trend of transmission of COVID 19 and this can be realistic using mathematical tools. Mathematical modelling is quite significant in prediction and comprehension a pandemic such as COVID 19 [7].

Indonesia is regarded as the fourth most populated nations of the globe, and therefore predicted to suffer immensely due to covid-19 pandemic as compared less populated nations [8]. The early cases of covid-19 in Indonesia was reported on March 2, 2020 with two confirmed cases. It increases to 1285 cases across 30 provinces. Jakarta, West Java, Banten, East Java and Central Java were the provinces with the highest pandemic [9]. At the end of March 2020, the number of cases increases to 1528 and 136 number of deaths were recorded. The country's case fatality rate (CFR) was quite higher than reported cases of China where the pandemic started (8.9% against 4%) [10]. In April 2, 2020, Indonesia

recorded 1790 confirmed cases, 113 fresh cases, 170 deaths and 112 recoveries [8]

The growth curve of viruses and microorganisms on substrates such as nutrients or other organisms including humans usually followed a sigmoidal pattern, starting with the lag section just after  $t = 0$ , followed by the logarithmic section and then the organism enters the stationary phase and finally moves to the phase of death or decline. There are various sigmoidal functions to describe the growth curve of organisms, such as Von Bertalanffy, Baranyi-Roberts, modified Richards, modified Gompertz and modified Logistics [11], including Morgan-Mercer-Flodin (MMF) [12]. The valuable parameters of the growth curve include the maximum specified growth rate ( $\mu_m$ ), the lag period and asymptotic values.

COVID-19 pandemic analysis can be carried out using mathematical models including theoretical, quantitative and simulation. Models such as the modified Gompertz, von Bertalanffy and logistics have been utilized to model COVID-19 pandemic [13] with good predictive ability. The objective of this work is to evaluate several available models such as Logistic [11,14], Gompertz [11,15], Richards [11,16], Morgan-Mercer-Flodin (MMF) [17], Baranyi-Roberts [18], Von Bertalanffy [19,20], Buchanan three-phase [21] and more recently the Huang model [22] in fitting and analyzing the COVID-19 epidemic trend in Indonesia as of 15 July 2020 in the form of the total SARS-CoV-2 infection case.

**MATERIALS AND METHODS**

Data were acquired from Worldometer [23] for the total number of infected cases from Indonesia as of 15 July 2020. Data were first converted to logarithmic values, and time zero was used as time after first infected case.

**Statistical analysis**

The statistically significant difference between the models was calculated using different methods including the adjusted determination coefficient ( $R^2$ ), accuracy factor (AF), bias factor (BF), root-mean - square error (RMSE), and corrected AICc (Akaike Information Criterion) as reported by [24]. The RMSE was computed using Eq. (1), where  $Pd_i$  are the values predicted by the model and  $Ob_i$  are the experimental data,  $n$  is the number of experimental data, and  $p$  is the number of parameters of the assessed model.

$$RMSE = \sqrt{\frac{\sum_{i=1}^n (Pd_i - Ob_i)^2}{n - p}} \tag{Eqn. 1}$$

The adjusted  $R^2$  is applied to calculate the inferiority of nonlinear models on the basis of the formula where RMS is Residual Mean Square and  $S_y^2$  is the total variance of the calculated y-variable and calculated as follows;

$$Adjusted (R^2) = 1 - \frac{RMS}{S_y^2} \tag{Eqn. 2}$$

$$Adjusted (R^2) = 1 - \frac{(1 - R^2)(n - 1)}{(n - p - 1)} \tag{Eqn. 3}$$

The Akaike information criterion (AIC) [25] was calculated as follows;

$$AICc = 2p + n \ln \left( \frac{RSS}{n} \right) + 2(p+1) + \frac{2(p+1)(p+2)}{n-p-2} \tag{Eqn. 4}$$

Where  $n$  is the number of data points and  $p$  is the number of parameters of the model. The model with the lowest AICc value is greatly likely to be correct [26].

Accuracy Factor (AF) and Bias Factor (BF) as described by Ross [27] were calculated as follows;

$$Bias\ factor = 10^{\left( \frac{\sum_{i=1}^n \log \left( \frac{Pd_i}{Ob_i} \right)}{n} \right)} \tag{Eqn. 5}$$

$$Accuracy\ factor = 10^{\left( \frac{\sum_{i=1}^n \log \left( \left| \frac{Pd_i}{Ob_i} \right| \right)}{n} \right)} \tag{Eqn. 6}$$

**Fitting of the data**

The data was fitted using as far bacterial growth curve using different growth models (Table 1) using the GraphPad Prism (v 8.0 trial version).

**Table 1.** Models used in this study.

Model	p	Equation
Modified Logistic	3	$y = \frac{A}{1 + \exp \left[ \frac{4\mu_m}{A} (\lambda - t) + 2 \right]}$
Modified Gompertz	3	$y = A \exp \left\{ -\exp \left[ \frac{\mu_m e}{A} (\lambda - t) + 1 \right] \right\}$
Modified Richards	4	$y = A \left\{ 1 + v \exp(1+v) \exp \left[ \frac{\mu_m}{A} (1+v) \left( 1 + \frac{1}{v} \right) (\lambda - t) \right] \right\}^{\left( \frac{-1}{v} \right)}$
Morgan-Mercer-Flodin (MMF)	4	$y = y_{max} - \frac{(y_{max} - \beta)}{1 + (\mu_m t)^\delta}$
Baranyi-Roberts	4	$y = A + \frac{1}{\mu_m} \ln \left( e^{-\mu_m x} + e^{-h_0} - e^{-\mu_m x - h_0} \right)$ $-\ln \left( \frac{1 + \frac{\mu_m x + 1}{\mu_m} \ln \left( e^{-\mu_m x} + e^{-h_0} - e^{-\mu_m x - h_0} \right)}{e^{(y_{max} - A)}} \right)$
Von Bertalanffy	3	$y = K \left[ 1 - \left( \frac{A}{K} \right)^3 \exp \left( -\frac{\mu_m x}{3K} \right) \right]^3$
Huang	4	$y = A + y_{max} - \ln \left( e^A + \left( e^{y_{max} - A} \right) e^{-\mu_m B(x)} \right)$ $B(x) = x + \frac{1}{\alpha} \ln \frac{1 + e^{-\alpha(x-\lambda)}}{1 + e^{\alpha \lambda}}$
Buchanan Three-phase model	3	Y = A, IF X < LAG Y = A + K(X-λ), IF λ ≤ X ≤ X <sub>MAX</sub> Y = Y <sub>MAX</sub> , IF X ≥ X <sub>MAX</sub>

Note:  
 A= maximum no of cases lower asymptote;  
 $y_{max}$ = maximum no of cases upper asymptote;  
 $\mu_m$ = maximum specific growth rate;  
 v= affects near which asymptote maximum no of cases occurs.  
 $\lambda$ =lag time  
 e = exponent (2.718281828)  
 t = time after first case is reported  
 $\alpha, \beta, \delta$  and k = curve fitting parameters  
 $h_0$  = a dimensionless parameter quantifying the initial physiological state of the reduction process. The lag time ( $h^1$ ) or ( $d^1$ ) can be calculated as  $h_0 = \mu_m$   
 When data at time zero is 0 (Day after 1<sup>st</sup> case log 1=0 for COVID-19) the MMF is reduced to a 3-parameter model

**RESULTS AND DISCUSSION**

All the curves tested indicated visually satisfactory fitting with the exclusion of the Buchanan-3-phase model which indicated non-satisfactory curve (Figs 1 to 8). The most suitable performance was the MMF model having the lowest value for RMSE, AICc and the uppermost value for adjusted  $R^2$ . The AF and BF values were equally excellent for the model with their values nearer to unity (1.0). The lowest performance was the modified logistics model (Table 2). The coefficients for the MMF model are presented in Table 3. The Predictions of COVID-19 pandemic for Indonesia based on the MMF model are presented in Table 4.

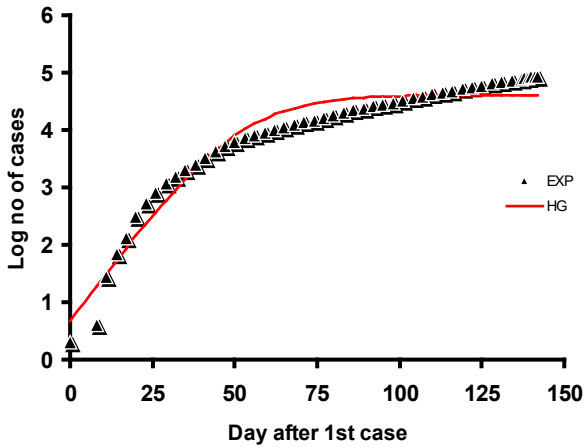


Fig. 1. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the Huang model.

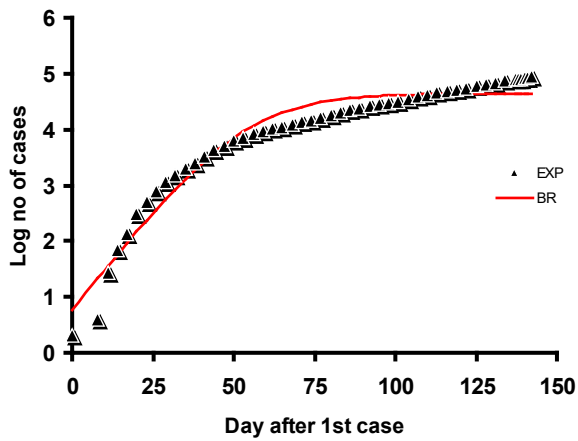


Fig. 2. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the Baranyi-Roberts model.

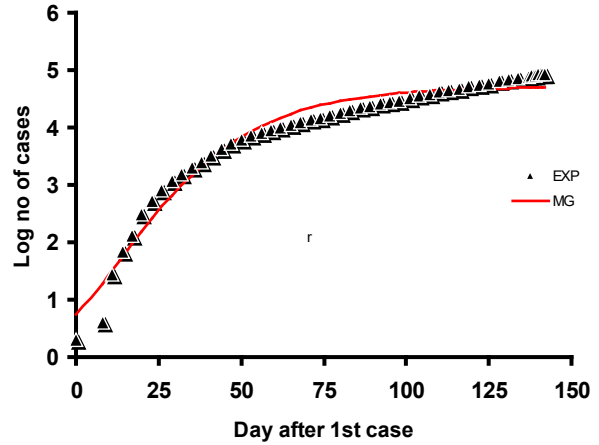


Fig. 3. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the modified Gompertz model.

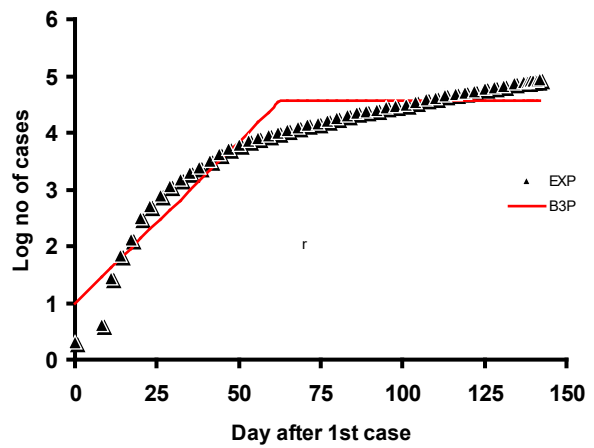


Fig. 4. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the Buchanan-3-phase model.

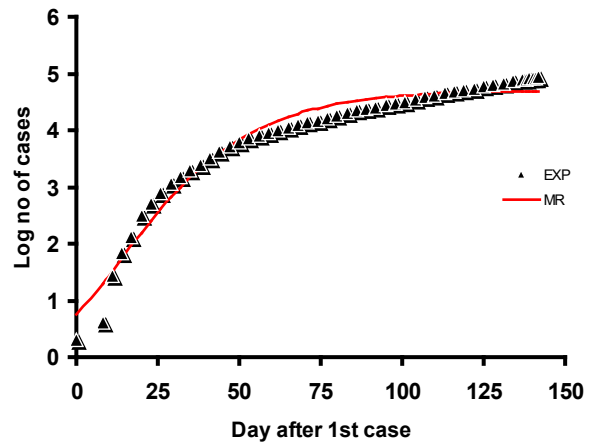


Fig. 5. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the modified Richard model.

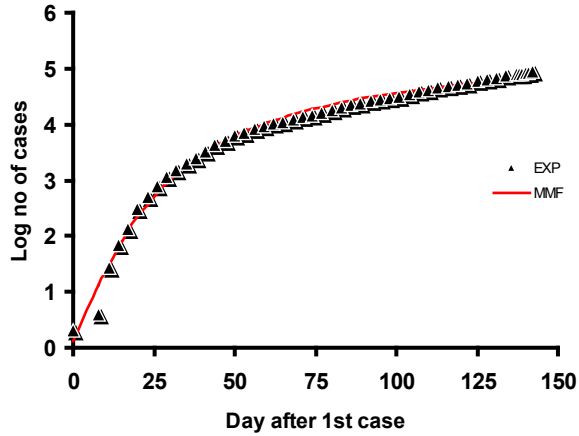


Fig. 6. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the MMF model.

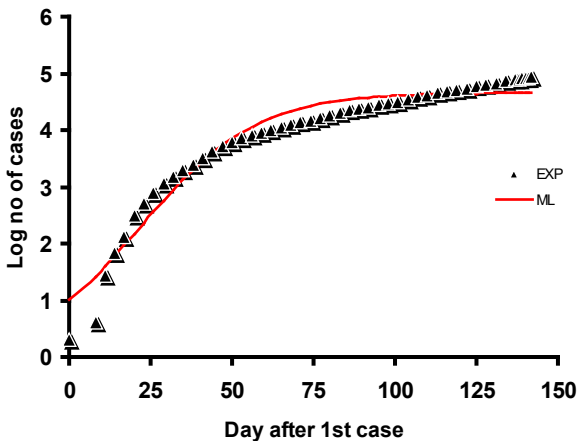


Fig. 7. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the modified logistics model.

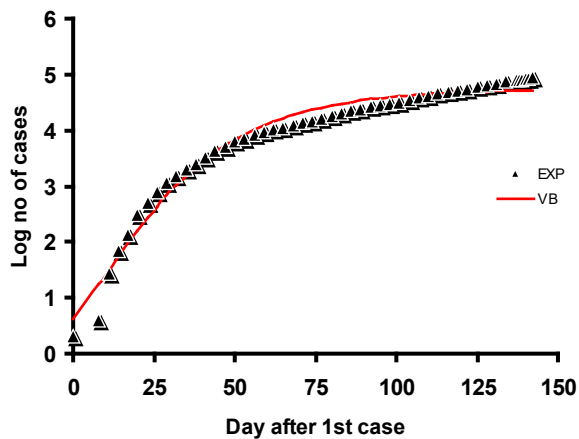


Fig. 8. Total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020 as modelled using the von Bertalanffy model.

Table 2. Statistical tests for the various models utilized in modelling the total no of SARS-CoV-2 cases in Indonesia as of 15<sup>th</sup> of July 2020.

Model	<i>p</i>	RMSE	<i>R</i> <sup>2</sup>	<i>adR</i> <sup>2</sup>	AF	BF	AICc
Huang	4	0.247	0.950	0.945	1.033	1.00	-124.56
Baranyi-Roberts	4	0.245	0.950	0.945	1.031	1.00	-125.26
modified Gompertz	3	0.205	0.964	0.962	1.045	1.00	-146.87
Buchanan-3-phase	3	0.330	0.906	0.900	1.045	1.00	-98.98
modified Richards	4	0.207	0.964	0.961	1.024	1.00	-142.40
MMF	4	0.111	0.990	0.990	1.011	1.00	-204.67
modified Logistics	3	0.252	0.944	0.940	1.029	1.00	-126.21
von Bertalanffy	3	0.185	0.972	0.970	1.022	1.00	-157.04

Note: *p* is no of parameter

Table 3. Coefficients as modelled using the MMF model.

Parameters	Value	95% Confidence interval
$\mu_m$	0.025	0.020 to 0.028
$\delta$	0.770	0.691 to 0.849
$y_{max}$	4,634,469	1,967,886 to 15,417,005
$\beta$	0.297	0.229 to 0.365

Table 4. Predictions of COVID-19 pandemic for Indonesia based on the MMF model.

Prediction	Mean	95% Confidence interval
Maximum number of total cases by the end of COVID-19	4,634,469	1,967,886 to 15,417,005
Maximum number of total cases by 15 <sup>th</sup> of August 2020	113,179	103,477 to 123,790
Maximum number of total cases by 15 <sup>th</sup> of September 2020	154,235	136,542 to 174,220

The parameters obtained from the MMF model include maximum growth rate ( $\mu_m$ ) (log) of 0.025 (95% CI from 0.020 to 0.028), curve constant ( $\delta$ ) that affects the inflection point of 0.770 (95% CI from 0.691 to 0.849), lower asymptote value ( $\beta$ ) of 0.297 (95% CI from 0.229 to 0.365) and maximal total number of cases ( $y_{max}$ ) of 4,634,469 (95% CI from 1,967,886 to 15,417,005). The MMF model predicted that COVID-19 will end about 1,513.53 days (95% CI of 833.58 to 2,193.48) days from 15<sup>th</sup> of July 2020 based on the lower bound of the 95% CI from the calculated maximum number of total cases ( $y_{max}$ ) while the mean and upper 95% CI bound values failed to be predicted by the software for their number of days. The MMF predicted that the total number of cases for Indonesia on the coming 15<sup>th</sup> of August and 15<sup>th</sup> of September 2020 will be 113,179 (95% CI of 103,477 to 123,790) and 154,235 (95% CI of 136,542 to 174,220), respectively. This prediction has to be taken with caution since the model refused to predict the number of days for the mean and upper 95% CI values and the number of days for COVID-19 to end may be greatly larger.

The MMF model has never been used to model growth of infectious cases unlike modified Gompertz and logistics. It was developed initially to describe a broad range of nutrient-response relationships in higher organisms [17]. The growth of animals such as rabbits, sheep, horses, microorganisms [28–32], yield of oil palm [33], ethanol [34] and also in finance [35] all have benefitted from this model. The resulting modelling prediction in this work is dependent upon effective lockdown no virus mutations which increases the virus' infection rate. Undoubtedly, the models will be reexamined after every few months in the event these phenomena lead to an exponential increase or wave of new infection to remodel the data so as a better prediction can be achieved.

## CONCLUSION

Conclusively, the findings of this study indicated that, the MMF model was proved to be the best model in modelling the total number of COVID-19 cases for Indonesia based on statistical tests like corrected AICc (Akaike Information Criterion), bias factor (BF), adjusted coefficient of determination ( $R^2$ ) and root-mean-square error (RMSE). The parameters acquired from the MMF model include maximum growth rate ( $\mu_m$ ) (log) of 0.025 (95% CI from 0.020 to 0.028), curve constant ( $\delta$ ) that affects the inflection point of 0.770 (95% CI from 0.691 to 0.849), lower asymptote value ( $\beta$ ) of 0.297 (95% CI from 0.229 to 0.365) and maximal total number of cases ( $y_{max}$ ) of 4,634,469 (95% CI from 1,967,886 to 15,417,005). The MMF predicted that the total number of cases for Indonesia on the coming 15<sup>th</sup> of August and 15<sup>th</sup> of September 2020 will be 113,179 (95% CI of 103,477 to 123,790) and 154,235 (95% CI of 136,542 to 174,220), respectively. The model permits for prediction of total number of cases and this prediction will differ based on several number of factors. Despite this, the predictive capability of the model applied in this study is an influential tool for epidemiologist to monitor and evaluate the harshness of COVID-19 in Indonesia in months to come.

## REFERENCES

- Radiom M, Berret J. Common trends in the epidemic of Covid-19 disease. *Eur Phys J Plus*. 2020;123(2020):1–12.
- Gorbalenya A, Baker S, Baric R, de Groot R, Drosten C, Gulyaeva A, et al. Coronaviridae Study Group of the International Committee on Taxonomy of Viruses. The species Severe acute respiratory syndrome-related coronavirus : classifying 2019-nCoV and naming it SARS-CoV-2. *Nat Microbiol*. 2020;5:536–544.
- Desforges M, Le Coupance A, Dubeau P, Bourgouin A, Lajoie L, Dubé M, et al. Human Coronaviruses and Other Respiratory Viruses: Underestimated Opportunistic Pathogens of the Central Nervous System. *Viruses*. 2020;12(14).
- Hageman J. The Coronavirus Disease 2019 (COVID-19). 49, e99–e100. Vol. 49, *Pediatric Annals*. 2020.
- Segars J, Katler Q, McQueen DDB, Kotlyar A, Glenn T, Knight Z, et al. Prior and novel coronaviruses, Coronavirus Disease 2019 (COVID-19), and human reproduction: what is known? *Fertil Steril*. 2020 Jun;113(6):1140–1149.
- Kissler SM, Tedijanto C, Goldstein E, Grad YH, Lipsitch M. Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. 2020;868(May):860–8.
- Rajagopal K, Hasanazadeh N, Parastesh F, Ismael I, Jafari S, Hussain I. A fractional-order model for the novel coronavirus ( COVID-19 ) outbreak. *Nonlinear Dyn*. 2020;(January).
- Djalante R, Lassa J, Setiamarga D, Sudjatma A, Indrawan M, Haryanto B, et al. Review and analysis of current responses to COVID-19 in Indonesia : Period of January to March 2020 ☆. *Prog Disaster Sci*. 2020;6(2020):100091.
- Tosepu R, Gunawan J, Savitri D, Ode L, Imran A, Lestari H, et al. Correlation between weather and Covid-19 pandemic in Jakarta, Indonesia. *Sci Total Environ*. 2020;725(2020):138436.
- Setiati S, Azwar MK. COVID-19 and Indonesia. *Acta Med Indones - Indones J Intern Med*. 2020;52(1):84–9.
- Zwietering MH, Jongenburger I, Rombouts FM, Van't Riet K. Modeling of the bacterial growth curve. *Appl Environ Microbiol*. 1990;56(6):1875–81.
- Morgan PH, Mercer LP, Flodin NW. General model for nutritional responses of higher organisms. *Proc Natl Acad Sci*. 1975 Nov;72(11):4327–31.
- Jia L, Li K, Jiang Y, Guo X, Zhao T. Prediction and analysis of Coronavirus Disease 2019. *ArXiv200305447 Q-Bio*. 2020 Mar;
- Ricker WE. 11 Growth Rates and Models. 1979. 677 p. (Fish Physiology; vol. 8).
- Gompertz B. On the nature of the function expressiveness of the law of human mortality, and a new mode of determining the value of life contingencies. *Philos TransR Soc Lond*. 1825;115:513 – 585.
- Richards FJ. A flexible growth function for empirical use. *J Exp Bot*. 1959;10:290–300.
- Morgan PH, Mercer LP, Flodin NW. General model for nutritional responses of higher organisms. *Proc Natl Acad Sci*. 1975 Nov;72(11):4327–31.
- Baranyi J. Mathematics of predictive food microbiology. *Int J Food Microbiol*. 1995;26(2):199–218.
- Babák L, Šupinová P, Burdychová R. Growth models of *Thermus aquaticus* and *Thermus scotoductus*. *Acta Univ Agric Silvic Mendel Brun*. 2012;60(5):19–26.
- López S, Prieto M, Dijkstra J, Dhanoa MS, France J. Statistical evaluation of mathematical models for microbial growth. *Int J Food Microbiol*. 2004;96(3):289–300.
- Buchanan RL. Predictive food microbiology. *Trends Food Sci Technol*. 1993;4(1):6–11.
- Huang L. Optimization of a new mathematical model for bacterial growth. *Food Control*. 2013;32(1):283–8.
- Worldometer. COVID-19 Coronavirus Pandemic. <https://www.worldometers.info/coronavirus/#countries>. 2020.
- Halmi M, Shukor M, Johari W, Shukor M. Modeling the growth curves of *Acinetobacter* sp. strain DRY12 grown on diesel. *J Environ Bioremediation Toxicol*. 2014;2:33–37.
- Akaike H. Factor analysis and AIC. *Psychometrika*. 1987;52(3):317–32.
- Motulsky HJ, Ransnas LA. Fitting curves to data using nonlinear regression: a practical and nonmathematical review. *FASEB J Off Publ Fed Am Soc Exp Biol*. 1987;1(5):365–74.
- Ross T, McMeekin TA. Predictive microbiology. *Int J Food Microbiol*. 1994;23(3–4):241–64.
- Santos SA, Souza G da S e, Oliveira MR de, Sereno JR. Uso de modelos não-lineares para o ajuste de curvas de crescimento de cavalos pantaneiros. *Pesqui Agropecuária Bras*. 1999 Jul;34(7):1133–8.
- Topal M, Bolukbasi ŞC. Comparison of nonlinear growth curve models in broiler chickens. *J Appl Anim Res*. 2008 Dec;34(2):149–52.
- Tariq M, Iqbal F, Eyduran E, Bajwa M, Huma Z, Waheed A. Comparison of non-linear functions to describe the growth in Mengali sheep breed of Balochistan. *Pak J Zool*. 2013 Jun;45:661–5.
- Augustine A, Imelda J, Paulraj R, David NS. Growth kinetic profiles of *Aspergillus niger* S14 a mangrove isolate and *Aspergillus oryzae* NCIM 1212 in solid state fermentation. *Indian J Fish*. 2015;62(3):100–6.
- Kemper CM. Growth and development of the brush-tailed rabbit-rat (*Conilurus penicillatus*), a threatened tree-rat from northern Australia. *Aust Mammal*. 2020 Jun;
- Khamis A, Ismail Z, Haron K, Mohammed AT. Nonlinear Growth Models for Modeling Oil Palm Yield Growth. *J Math Stat*. 2005 Sep;1(3):225–33.
- Germec M, Turhan I. Ethanol production from acid-pretreated and detoxified tea processing waste and its modeling. *Fuel*. 2018 Nov;231:101–9.
- Wijeratne AW, Karunaratne JA. Morgan-Mercer-Flodin model for long term trend analysis of currency exchange rates of some selected countries. *Int J Bus Excell*. 2013 Dec;7(1):76–87.