Contemporary Mathematics
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Research Article

Initial Growth Rate and Model Performance for COVID-19 in Nigeria

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Received: 11 October 2024; **Revised:** 16 December 2024; **Accepted:** 17 December 2024

Abstract: While numerous statistical models have been used to analyze the spread of COVID-19 in Nigeria, focusing on factors such as active cases and deaths, there is a gap in understanding the impact of initial parameter choices within these models. This study investigates the impact of initial growth rate parameter choices on the performance of different population growth models in fitting cumulative COVID-19 cases in Nigeria. By comparing Gompertz, logistic, Richard's, modified Gompertz and Morgan-Mercer-Flodin models, the study aims to determine the most appropriate model for analyzing the spread of the disease. Using data from Our World in Data (OWID), the models were fitted to the S-shaped curve observed in the cumulative case data. The performance of the models was evaluated using convergence efficiency, measured by the number of iterations required to converge and the convergence tolerance achieved, and model fit criteria such as log-likelihood, Bayesian Information Criterion (BIC) and Akaike Information Criterion (AIC). The results show that the Gompertz model consistently outperforms other models in terms of both efficiency and convergence tolerance. This suggests that the Gompertz model is a more appropriate choice for future research using population growth models to analyze the spread and impact of infectious diseases in Nigeria.

***Keywords*:** gompertz, logistic, growth rate, COVID-19, iteration, pandemic

MSC: 92D30, 62P10

1. Introduction

The emergence of COVID-19 in late 2019, originating in China, rapidly escalated into a Global health threats, causing a public health emergency to be declared by the World Health Organization in January 2020. The virus caused significant illness and death across continents, with Africa, the Americas, and Europe experiencing rapid case growth [1]. Beyond its health impact, United Nations [2] warned of COVID-19's potential for widespread political, social, and economic disruption.

According to [3], the trend of the COVID-19 pandemic in Nigeria shows that there was an increase in community transmission. A partial relaxation of the lockdown in mid-2020 triggered an increase in the cases of COVID-19 pandemic by about 60 percent and the corresponding increase in recorded deaths by about 33 percent.

The proclivity of the COVID-19 pandemic to generate shocks, causes economic fluctuations which has negative impact on both the macro and microeconomic variables in the country [4].

DOI: https://doi.org/10.37256/cm.6220255889

1.1 *The role of epidemiological models in understanding and predicting disease spread*

Epidemiological models are powerful tools for representing disease outbreaks mathematically. These models integrate data from experiments, field studies, and expert knowledge on infection dynamics and disease control. This allows researchers to address uncertainties in decision-making regarding human disease control strategies [5]. Modeling proves particularly useful when conducting experiments or when field research is impractical [6]. Additionally, it can be applied retrospectively to past outbreaks, helping identify alternative control methods [7]. The history of mathematical modeling in epidemiology stretches back to the 1760s, with the work of Daniel Bernoulli [8]. The field gained further momentum with the rise of dynamical systems techniques in the 1920s [9]. Since the mid-20th century, mathematical epidemiology has seen significant conceptual and technological advancements [10]. The emergence of new infectious diseases, such as swine and avian influenza, has further highlighted the importance of this field [10, 11]. As the threat of infectious diseases continues, the need for innovative and realistic statistical models to understand and predict their spread becomes increasingly critical.

Epidemiological models serve a multitude of purposes in analyzing and managing infectious disease outbreaks. By examining the effects of various parameters within the model, researchers can predict the potential spread of an epidemic [10]. These predictions inform crucial decisions regarding public health interventions, such as immunization campaigns, treatment protocols, and other control measures. Mathematical models go beyond simple prediction. They provide a powerful tool for justifying and analyzing the spread of diseases, including emerging global threats [12]. This allows public health officials to proactively develop and manage public health plans based on a deeper understanding of the outbreak's dynamics. Furthermore, models enhance our ability to understand the intricacies of disease behavior [13]. They help us identify relationships between factors at different scales and even uncover previously unknown aspects of the disease by leveraging existing knowledge [14]. Importantly, models provide valuable insights into the limitations and potential errors inherent in predictions, allowing for a more nuanced understanding of future disease outbreaks [15].

Developing effective models involves navigating a crucial balance between three key factors: accuracy, transparency, and flexibility. **Accuracy:** A model's ability to faithfully represent the real world is paramount. Increased accuracy often comes with increased model complexity, incorporating more details about the system being modeled [14]. However, this complexity can introduce challenges. **Transparency:** A model's inner workings should be clear and understandable. This allows researchers to interpret the results and assess the model's validity. A model that is a "black box" may produce accurate predictions but limit our ability to trust those predictions. **Flexibility:** Real-world scenarios are rarely static. A model's ability to adapt to changing circumstances is crucial. Flexibility allows researchers to evaluate different control strategies and forecast disease levels under various conditions [14]. However, excessive flexibility can lead to models that are overly complex and difficult to interpret.

It's important to recognize that achieving perfect accuracy is often impractical. Striking the right balance between these three factors is essential for building a model that is both informative and useful. The quality of data, disease dynamics, and researcher expertise all influence model selection for infectious disease outbreaks [16]. No model perfectly predicts future outcomes, but they offer valuable insights into factors affecting disease spread. Statistical models can reveal patterns of disease spread within specific populations and timeframes. In the context of COVID-19 in Nigeria, researchers have employed various models to understand the pandemic. For instance, Samuel et al. [1] compared the performance of different count data regression models to analyze the relationship between daily cases, cumulative cases, and deaths. Their findings suggest that the Generalized Poisson Regression model outperformed others for active, daily cumulative, and critical cases when dealing with overdispersed data.

Another study by [17] utilized quality control tools to monitor confirmed COVID-19 cases. They employed control charts to reveal that confirmed cases were statistically out of control as of August 18th, 2020. Furthermore, studies have explored time series models for forecasting. Rauf and Hannah [18] applied an ARIMA model to forecast COVID-19 cases in Nigeria, while [19] compared the ARIMA and Gompertz models for confirmed cases and deaths across multiple countries. Their findings suggest that the ARIMA model might be better suited for infections, while the Gompertz model might perform better for mortality rates.

This paper builds on this prior research by deriving the growth models of the Gompertz and logistic and applying it specifically for COVID-19 case of Nigeria, and thereafter, comparing their performances with other S-shaped models namely, modified Gompertz model, Richards model and Morgan-Mercer-Flodin model. Focusing on the period from February 2020 to July 2022, the study examines the cumulative confirmed cases. The main metrics used to compare models include log-likelihood, Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC). Other measures include the number of iterations required for the convergence and achieved convergence tolerance. This analysis aims to inform future research on modeling disease prevalence and mortality using population growth models.

2. Materials and methods

2.1 *Data collection*

This study utilizes cumulative symptomatic COVID-19 cases with lab confirmation for Nigeria for the 30-months epic period in Nigeria (February 2020-July 2022). The data was extracted from OWID (Our World in Data) (https://ourworldindata.org/coronavirus), a comprehensive repository tracking the global pandemic. The plot of the cumulative case data revealed an S-shaped curve (Figure 1). This characteristic growth pattern suggests the suitability of sigmoid growth models, such as the Gompertz and logistic models, for analyzing the spread of COVID-19 cases in Nigeria.

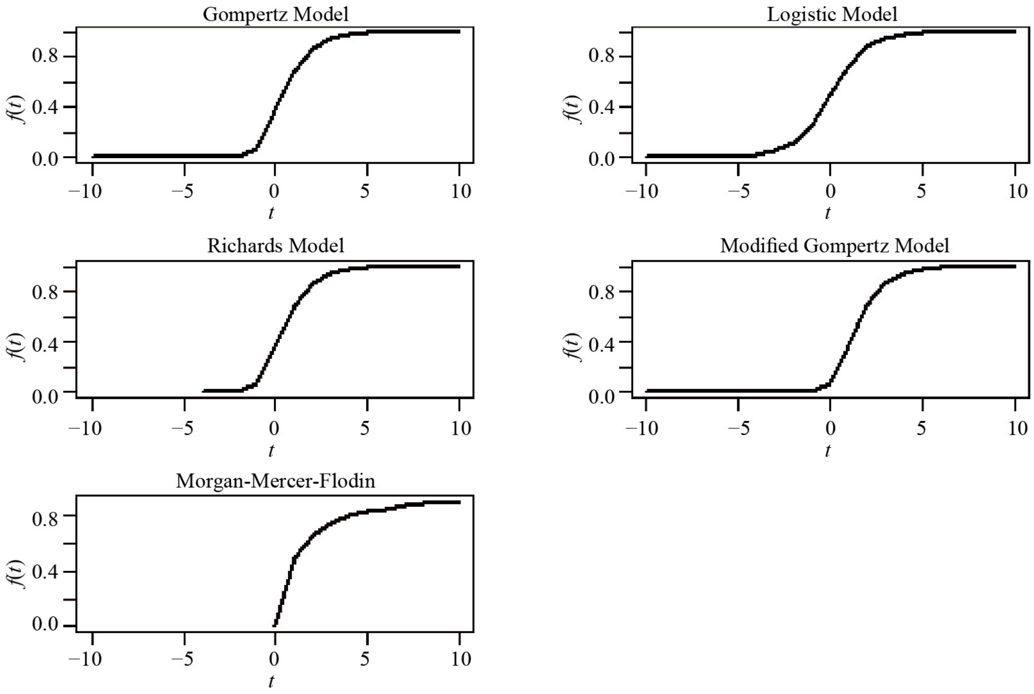

Figure 1. Plot of shapes of the various models under consideration

Growth curve models are equations that describes how the prevalence of a disease or any other phenomenon rises or declines over time. These models differ according to the number of parameters used in the equation. There are many non-linear models that have been used to model growth. The most in use are three parameter growth functions (Gompertz, modified Gompertz and logistic) and four-parameter equations (Richards, and Morgan-Mercer-Flodin). In this study, these five non-linear growth models were used to model the prevalence of COVID-19 pandemic in Nigeria.

2.2 *Derivation of gompertz and logistic growth models*

The Gompertz model, developed by Benjamin Gompertz in 1825, was originally used to analyze mortality rates and the “exhaustion of a man’s power to avoid death” as he aged. This model can be applied to situations where growth initially slows, then rapidly accelerates, before finally reaching an asymptote. The Gompertz model is based on an idea about how death rates change with age, represented by differential equation:

$$\frac{\mathrm{d}p}{\mathrm{d}t} = c\ln\left(\frac{k}{p}\right)p, \tag{1}$$

where p is the population, c is a constant and k is a carrying capacity. Equation (1) can be solved using variable separation, leading to expression:

$$\frac{\mathrm{d}p}{\ln\left(\frac{k}{p}\right)p} = c\mathrm{d}t. \tag{2}$$

Integrating (2) and letting $u = \ln\left(\frac{k}{p}\right) = \ln k - \ln p$, we then obtain the derivative $\mathrm{d}u/\mathrm{d}p$

$$\frac{\mathrm{d}u}{\mathrm{d}p} = 0 - \frac{1}{p} = -\frac{1}{p}. \tag{3}$$

Hence, $\mathrm{d}u = -\frac{\mathrm{d}p}{p}$

$$\mathrm{d}p = -p\mathrm{d}u.$$

On substituting u and $\mathrm{d}p$ in Equation (2) with their solutions, then integrating, we have

$$\int -\frac{p\mathrm{d}u}{up} = -\int \frac{\mathrm{d}u}{u} = \int c\mathrm{d}t$$

$$-\ln|u| + c_1 = ct + c_2, \tag{4}$$

$-\ln|u| = ct + C$, where $C = c_2 - c_1 =$ constant.

$$\ln|u| = -ct - C. \tag{5}$$

Exponentiating Equation (5) gives:

$$e^{\ln|u|} = e^{-ct-C}. \tag{6}$$

Therefore

$$u = De^{-ct}. \tag{7}$$

where $D = \pm\, e^{-C}$ (a constant). Hence,

$$\ln\left(\frac{k}{p}\right) = De^{-ct}. \tag{8}$$

In order to obtain D, we let the original population at a given time $t = 0$ be $p(0) = p_0$

$$D = \ln\left(\frac{k}{p_0}\right). \tag{9}$$

Putting Equation (9) in (8) yields

$$\ln\left(\frac{k}{p}\right) = \ln\left(\frac{k}{p_0}\right) e^{-ct}. \tag{10}$$

Exponentiating both sides of (10) P is obtained as follows

$$e^{\ln\left(\frac{k}{p}\right)} = e^{\ln\left(\frac{k}{p_0}\right)e^{-ct}}$$

$$\frac{k}{p} = e^{\ln\left(\frac{k}{p_0}\right)e^{-ct}}$$

$$p = ke^{-\ln\left(\frac{k}{p_0}\right)e^{-ct}}.$$

Since p is a function of time, t, the above equation can, therefore be written as

$$p(t) = ke^{-\ln\left(\frac{k}{p_0}\right)e^{-ct}}, \tag{11}$$

which is the Gompertz population growth function/model.

Let $b = \ln\left(\frac{k}{p_0}\right)$, Equation (11) therefore simplifies as

$$f(t) = ke^{-be^{-ct}}, \tag{12}$$

where k is the population carrying capacity, b is the displacement along the x-axis, while c is the population growth rate.

Pierre Verhulst developed the logistic model, which shares a key concept with the Gompertz model, i.e., the carrying capacity (K). This value represents the upper limit of a population's growth. Similar to the Gompertz model, the logistic model predicts that populations will increase when below K and decrease when exceeding K. The core assumption of the logistic model is that the rate of population change $\left(\frac{\mathrm{d}y}{\mathrm{d}t}\right)$ is proportional to the current population (y) multiplied by the difference between the carrying capacity (K) and current population (y). This relationship can be mathematically expressed by differential equation $\frac{\mathrm{d}y}{\mathrm{d}t} = y\left(1 - \frac{y}{k}\right)$.

$$\frac{\mathrm{d}y}{\mathrm{d}t} = ry\left(1 - \frac{y}{K}\right) \tag{13}$$

where r is constant and positive. When $y < K$, $\frac{\mathrm{d}y}{\mathrm{d}t}$ is positive, y increases, but when $y > K$, $\frac{\mathrm{d}y}{\mathrm{d}t}$ is negative, on the other hand, and y decreases. The variable separable method is used to solve the differential equation above. This gives:

$$\frac{1}{y\left(1 - \frac{y}{K}\right)}\mathrm{d}y = r\mathrm{d}t. \tag{14}$$

Integrating

$$\int \frac{1}{y\left(1 - \frac{y}{K}\right)}\mathrm{d}y = \int r\mathrm{d}t.$$

Solving the left hand side of the equation into partial fractions gives

$$\frac{1}{y\left(1 - \frac{y}{K}\right)} = \frac{A}{y} + \frac{B}{1 - \frac{y}{K}}. \tag{15}$$

Eliminating the denominators will give:

$$1 = A\left(1 - \frac{y}{K}\right) + By = A - \frac{A}{K}y + By. \tag{16}$$

Simplifying Equation (16) gives $A = 1$ and $B = \frac{1}{K}$.
On substituting for A and B in (16), we have:

$$\frac{1}{y\left(1 - \frac{y}{K}\right)} = \frac{1}{y} + \frac{1/K}{1 - \frac{y}{K}} = \frac{1}{y} + \frac{1}{K - y}. \tag{17}$$

Hence,

$$\int \frac{\mathrm{d}y}{y\left(1 - \frac{y}{K}\right)} = \int \frac{\mathrm{d}y}{y} + \int \frac{\mathrm{d}y}{K - y} = \ln y - \ln|K - y| = \ln\left|\frac{y}{y - K}\right|.$$

We obtain the final equation as:

$$\ln\left|\frac{y}{y-K}\right| = rt + C. \tag{18}$$

Simplifying the equation gives

$$y = \frac{K}{1 + Ae^{-rt}}, \tag{19}$$

where A = constant.

Equation (19) is the logistic population growth model, with the graph of the model being asymptotic to the y-axis on the left, and to the right, $y = K$. The graph of the model is symmetrical around the point where the population is equal to half ($K/2$) of the carrying capacity.

Other models investigated in this work include the modified Gompertz model, Richards model and Morgan-Mercer-Flodin model as given in the following equations according to [20].

Richards model:

$$y = A\left[1 + (\delta - 1)\exp\left(-k(t - l)\right)\right]^{\frac{1}{1-\delta}}. \tag{20}$$

Morgan-Mercer-Flodin model:

$$y = A - \frac{A - B}{1 + (kt)^{\delta}}. \tag{21}$$

Modified Gompertz model:

$$y = A\ \exp[-\exp(B - Ct)], \tag{22}$$

where y is the cumulative COVID-19 cases at time t; A is the asymptote when t approaches infinity; k is the growth rate; l is the time at inflection point; δ is the parameter that controls and B is the lower asymptote.

2.3 *Impact of initial parameter values*

In non-linear modeling, selecting appropriate initial values for model parameters is crucial. The chosen optimization algorithm, in this case, the Gauss-Newton method implemented with the nls function from R's minpack library, estimates these parameters using a least squares approach. However, these algorithms require initial guesses for the parameter values. This study explores how varying the initial values of the growth rate parameters affects the performance of the models under consideration. We investigated a range of initial values, starting from 0.0001 and increasing with uniform steps of 0.0001, 0.001, 0.01, 0.1, and 1.0. Performance was evaluated based on two key metrics:

1. **Number of iterations to convergence:** This indicates how computationally efficient the model is for a given set of initial values. A lower number of iterations signify better efficiency.
2. **Convergence tolerance:** This measures how closely the estimated parameters align with the true parameters. A lower tolerance value suggests a more robust convergence.

The models were fitted to the data using these varying initial values, and both the number of iterations and convergence tolerance were recorded. This analysis aimed to identify the model that demonstrates superior efficiency (fewer iterations) while also exhibiting greater robustness in terms of convergence tolerance across diverse initial values. The study utilizes R software in carrying out the plots and analysis.

2.4 *Model selection*

This study employed three model selection criteria namely, the Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC) and the log likelihood (LL).

2.4.1 *Information criteria and goodness of fit measure*

To assess model fit, we use information criteria such as the Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC). The Akaike Information Criterion is given as

$$AIC = 2k - 2ln(\widehat{L}), \tag{23}$$

where $k =$ number of estimated parameters in the model $\widehat{L} =$ the maximum value of the likelihood function of the model. However, if the sample size is small, then some correction is often necessary. The corrected AIC is given as

$$AIC_c = 2k - \ln\left(\widehat{L}\right) + \frac{2k(k+1)}{n-k-1}, \tag{24}$$

where $k =$ number of estimated parameters in the model $\widehat{L} =$ the maximum value of the likelihood function.

The Bayesian Information Criterion (BIC) is given as

$$BIC = k\ln(n) - 2\ln(\widehat{L}), \tag{25}$$

where $k =$ number of estimated parameters in the model while $\widehat{L} =$ the maximum value of the likelihood function and n is the sample size [3, 21].

3. Results

The collected data were modeled using the five different non-linear population growth models. The aim is to determine a more suitable model using various model selection criteria. The study also examined the models by varying the initial values of growth rate parameters for each model and considering the number of iterations and convergence tolerance of the models. Figure 2 and 3 below shows the plot of the daily cumulative COVID-19 cases in Nigeria.

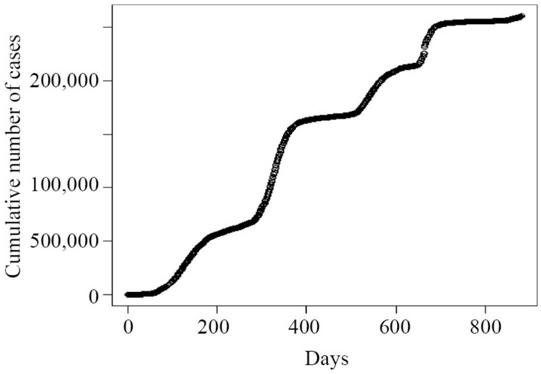

Figure 2. Plot of cumulative confirmed cases of COVID-19

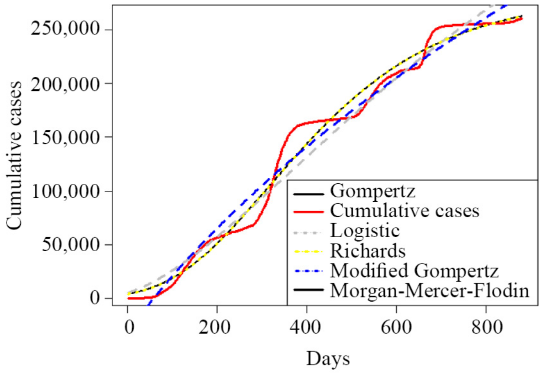

Figure 3. Fitted models on cumulative confirmed cases of COVID-19

Based on the goodness-of-fit metrics presented in Table 1, the Gompertz and modified Gompertz models outperformed the other models, with the logistic model ranking second. These models exhibited the highest log-likelihood values and the lowest Bayesian Information Criterion (BIC) and Akaike Information Criterion (AIC) scores, indicating their superior fit to the data.

Table 1. Performance comparison of fitted models

Models	Log likelihood	AIC	BIC
Gompertz model	−6,407.868*	18,922.04*	18,941.17*
Logistic model	−9,457.021*	19,245.10	19,264.22*
Modified gompertz model	−6,407.868*	18,922.04*	18,941.17*
Richards model	−9,729.541	19,465.08	19,479.43
Morgan-mercer flodin model	−9,659.156	19,326.31	19,345.44

3.1 *Effect of choice of initial value of the growth rate on the performance of models*

The results obtained with different initial values for both models are shown in the Table 1.

Table 2. Models performance with varying initial growth rates

	Gompertz model			Modified gompertz model			logistic model			Richards model			Morgan-mercer flodin model		
Initial value for growth rate	No. of itera-tion	Estimate	Convergence tolerance	No. of itera-tion	Estimate	Convergence tolerance	No. of itera-tion	Estimate	Convergence tolerance	No. of itera-tion	Estimate	Convergence tolerance	No. of itera-tion	Estimate	Convergence tolerance
0.0001	-	NaN	-	-	NaN	-	-	NaN	-	6	1.589e-03	3.046e-06	8	2.835e-04	2.548e-06
0.0002	-	NaN	-	-	NaN	-	-	NaN	-	6	1.589e-03	2.759e-07	9	2.835e-04	5.502e-06
0.0003	18	4.649e-03	8.013e-07	-	NaN	-	19	7.756e-03	8.767e-06	6	1.589e-03	5.957e-07	8	2.835e-04	7.501e-06
0.0004	14	4.649e-03	8.351e-07	-	NaN	-	16	7.756e-03	8.758e-06	5	1.589e-03	6.442e-06	-	NaN	-
0.0005	13	4.649e-03	8.884e-07	-	NaN	-	15	7.756e-03	8.695e-06	5	1.589e-03	5.547e-07	-	NaN	-
0.0006	12	4.649e-03	9.297e-07	19	4.649e-03	6.056e-06	14	7.756e-03	8.758e-06	5	1.589e-03	6.344e-07	-	NaN	-
0.0007	11	4.649e-03	9.817e-07	16	4.649e-03	7.782e-06	13	7.756e-03	9.062e-06	5	1.589e-03	6.757e-07	-	NaN	-
0.0008	10	4.649e-03	1.044e-06	15	4.649e-03	7.516e-07	13	7.756e-03	8.873e-06	5	1.589e-03	1.253e-06	-	NaN	-
0.0009	9	4.649e-03	1.117e-06	14	4.649e-03	9.074e-07	12	7.756e-03	9.631e-06	5	1.589e-03	9.98e-07	-	NaN	-
0.0010	8	4.649e-03	1.105e-06	12	4.649e-03	9.663e-07	12	7.756e-03	1.878e-06	5	1.589e-03	3.624e-07	-	NaN	-
0.0020	7	4.649e-03	1.088e-06	7	4.649e-03	2.975e-06	10	7.756e-03	2.373e-06	5	1.589e-03	6.697e-07	-	NaN	-
0.0030	8	4.649e-03	1.502e-06	5	4.649e-03	6.537e-06	10	7.756e-03	2.188e-06	5	1.589e-03	9.159e-06	-	NaN	-
0.0040	7	4.649e-03	3.734e-06	5	4.649e-03	6.905e-07	11	7.756e-03	3.072e-06	7	1.589e-03	4.644e-07	-	NaN	-
0.0050	7	4.649e-03	4.777e-06	5	4.649e-03	5.526e-06	10	7.756e-03	4.785e-06	8	1.589e-03	4.605e-07	-	NaN	-
0.0060	8	4.649e-03	2.118e-06	6	4.649e-03	2.973e-06	11	7.756e-03	1.736e-06	9	1.589e-03	6.965e-07	-	NaN	-
0.0070	10	4.649e-03	4.604e-06	6	4.649e-03	1.82e-06	13	7.756e-03	4.321e-06	9	1.589e-03	4.121e-06	-	NaN	-
0.0080	18	4.649e-03	1.732e-06	6	4.649e-03	6.078e-06	20	7.756e-03	4.421e-06	10	1.589e-03	7.84e-06	-	NaN	-
0.0090	9	4.649e-03	1.735e-06	7	4.649e-03	8.943e-07	11	7.756e-03	3.3e-06	8	1.589e-03	5.786e-06	-	NaN	-
0.0100	8	4.649e-03	2.096e-06	7	4.649e-03	1.499e-06	11	7.756e-03	3.415e-06	10	1.589e-03	3.095e-06	-	NaN	-
0.0200	9	4.649e-03	9.684e-07	7	4.649e-03	1.684e-06	11	7.756e-03	4.089e-06	-	NaN	-	-	NaN	-

Table 2. cont.

	Gompertz model			Modified gompertz model			logistic model			Richards model			Morgan-mercer flodin model		
Initial value for growth rate	No. of itera- tion	Estimate	Convergence tolerance	No. of itera- tion	Estimate	Convergence tolerance	No. of itera- tion	Estimate	Convergence tolerance	No. of itera- tion	Estimate	Convergence tolerance	No. of itera- tion	Estimate	Convergence tolerance
0.0300	9	4.649e-03	8.599e-07	7	4.649e-03	6.847e-06	11	7.756e-03	4.416e-06	-	NaN	-	-	NaN	-
0.0400	9	4.649e-03	1.249e-06	12	4.649e-03	2.415e-06	11	7.756e-03	4.64e-06	-	NaN	-	-	NaN	-
0.0500	9	4.649e-03	1.61e-06	-	NaN	-	11	7.756e-03	4.73e-06	-	NaN	-	-	NaN	-
0.0600	9	4.649e-03	1.958e-06	-	NaN	-	11	7.756e-03	4.752e-06	-	NaN	-	-	NaN	-
0.0700	9	4.649e-03	2.473e-06	-	NaN	-	11	7.756e-03	4.777e-06	-	NaN	-	-	NaN	-
0.0800	9	4.649e-03	1.494e-06	14	4.649e-03	2.721e-06	11	7.756e-03	4.752e-06	-	NaN	-	-	NaN	-
0.0900	12	4.649e-03	1.132e-06	11	4.649e-03	2.136e-06	11	7.756e-03	4.27e-06	-	NaN	-	-	NaN	-
0.1000	-	NaN	-	8	4.649e-03	2.149e-06	11	7.756e-03	9.833e-06	-	NaN	-	-	NaN	-
0.2000	-	NaN	-	8	4.649e-03	9.493e-07	12	7.756e-03	3.281e-06	14	1.742e-01	9.473e-07	-	NaN	-
0.3000	-	NaN	-	8	4.649e-03	8.939e-07	11	7.756e-03	5.664e-06	19	2.752e-01	5.541e-07	-	NaN	-
0.4000	-	NaN	-	7	4.649e-03	6.456e-06	15	7.756e-03	4.216e-06	24	3.939e-01	8.282e-06	-	NaN	-
0.5000	-	NaN	-	10	4.649e-03	1.641e-06	15	7.756e-03	3.733e-06	30	4.802e-01	4.143e-07	-	NaN	-
0.6000	-	NaN	-	12	4.649e-03	6.718e-06	15	7.756e-03	3.646e-06	36	5.755e-01	3.858e-07	-	NaN	-
0.7000	-	NaN	-	12	4.649e-03	7.084e-07	15	7.756e-03	3.561e-06	41	6.745e-01	3.626e-07	-	NaN	-
0.8000	-	NaN	-	11	4.649e-03	1.666e-06	15	7.756e-03	3.47e-06	48	7.750e-01	3.449e-07	-	NaN	-
0.9000	-	NaN	-	10	4.649e-03	8.149e-06	14	7.756e-03	4.346e-06	-	NaN	-	-	NaN	-
1.0000	-	NaN	-	10	4.649e-03	4.273e-06	-	NaN	-	-	NaN	-	-	NaN	-
2.0000	-	NaN	-	-	NaN	-	-	NaN	-	-	NaN	-	-	NaN	-
3.0000	-	NaN	-	-	NaN	-	-	NaN	-	-	NaN	-	-	NaN	-
4.0000	-	NaN	-	-	NaN	-	-	NaN	-	-	NaN	-	-	NaN	-

NaN-Not a Number. It implies that the iteration does not produce a real estimate; i.e., an undefined estimate was encountered during iteration, using that particular initial value

Table 2 reveals that both the Gompertz and logistic models share a lower bound of 0.0003 for their initial growth rate parameters (c and r, respectively). However, the upper bound differs: the Gompertz model allows values up to 0.09, while the logistic model can accommodate values as high as 0.90. This indicates greater flexibility in choosing initial values for the logistic model compared to the Gompertz model. Hence, the range of possible initial values for the growth rate of the logistic growth model is $r_i : 0.0003 \leq r_i \leq 0.90$ while that of the Gompertz model is $c_i : 0.0003 \leq c_i \leq 0.09$. Table 1 also shows that for almost every initial value of the growth rate, the Gompertz model had a lower number of iterations before convergence compared to the logistic model. Figure 4 shows the number of iterations for different initial values of the growth rate for the Gompertz and logistic growth models.

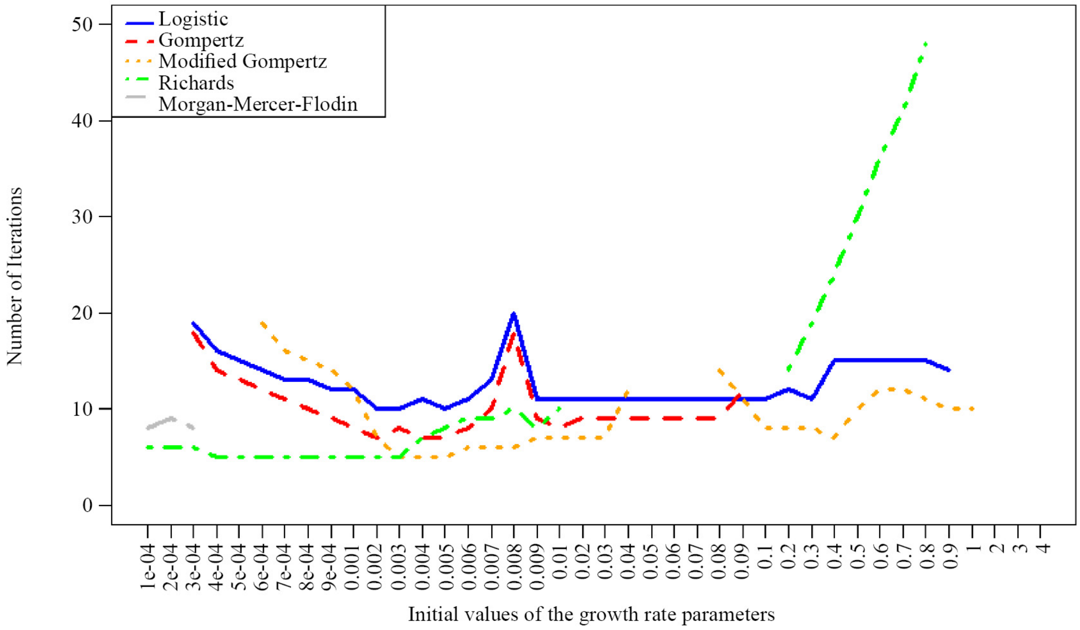

Figure 4. Number of iterations at various initial values of the growth rate for the various models

Figure 4 shows the performance of the models in terms of number of iterations for different initial values of the growth rate parameter. It can be seen from the plot that the Richards model initially converges in less number of iteration. However, the model shows a discontinuity between points 0.01 and 0.1 after which the number of iteration increased rapidly until it exceeded maximum iteration of 50.

Figure 5 shows the performance of the various growth models in terms of convergence tolerance for different initial values of the growth rate parameter. From the plot it can be seen that, though there are points where the Richards model showed less convergence tolerance, Gompertz growth model generally had better performance having shown a relatively low convergence tolerance without discontinuity within the range of initial values of the growth rate parameter. This implies that the Gompertz model is most efficient in terms of convergence tolerance.

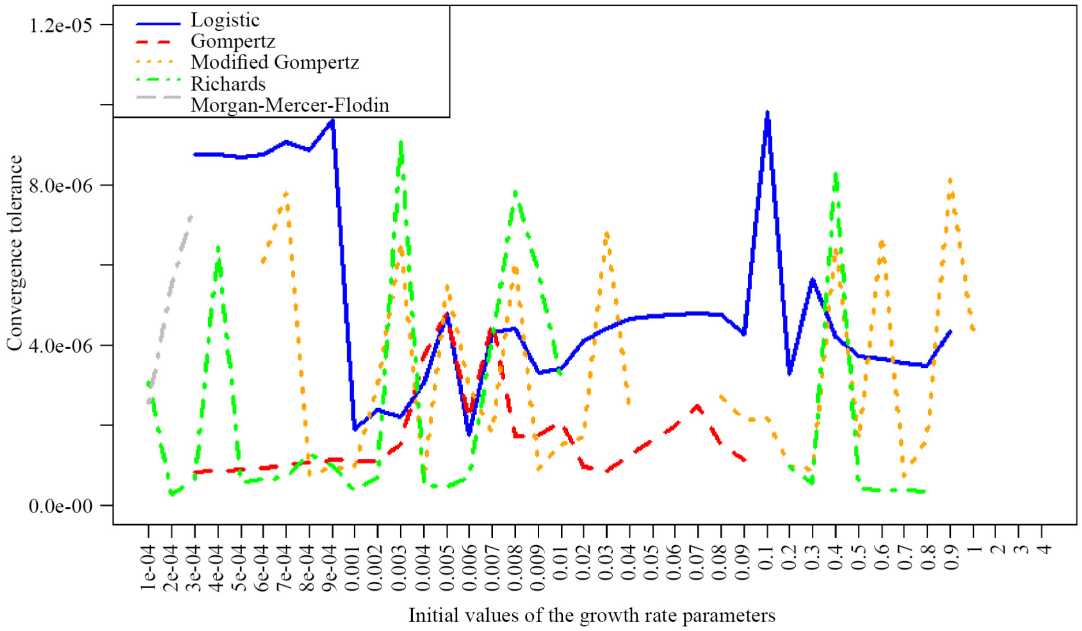

Figure 5. Convergence tolerance at various initial values of the growth rate for the models

4. Discussion

This study investigates the performance of different mathematical models, for fitting the cumulative daily COVID-19 cases in Nigeria from February 2020 to July 2022. The data was obtained from Our World in Data (OWID). Existing studies analyze COVID-19 spread using various models, but the impact of initial parameter choices within these models is not well understood, and is still missing in literature. This study therefore examined the effect of initial parameter choices used in model fitting. In particular, the effect of the initial growth rate parameters on the convergence tolerance and number of iterations of the various models were studied. The study compares these models to see how varying the initial growth rate parameter affects their fit to the data. The study uses cumulative confirmed COVID-19 cases in Nigeria. The models are fitted to the data with varying initial values for the growth rate parameter. Performance was evaluated based on Log likelihood, AIC, BIC, number of iterations required for convergence (efficiency) and convergence tolerance (robustness). The Richards shows to converge in less number of iteration compared to the other models despite showing discontinuity at some points. This implies that the model should be considered when fitting time, memory conservation and other resources are put into consideration. The Gompertz model exhibits lower convergence tolerance across various initial values. This implies that the Gompertz model may be considered when convergence is of necessity in the model fitting process.

5. Conclusions

The Gompertz model outperforms the other models in terms of efficiency and convergence tolerance when fitting cumulative COVID-19 cases in Nigeria. This finding suggests the Gompertz model might be a better choice for future research using population growth models to analyze infectious diseases.

Acknowledgements

Dr. Braimah Joseph Odunayo would like to thank the University of the Free State, Bloemfontein, South Africa, for their support in making this postdoctoral research possible.

Supplementary files

1. Nigeria Lab Confirmed COVID-19 Data set.

Conflicts of interest

Dr. Braimah Joseph Odunayo is a Postdoctoral Research Fellow under the supervision of Professor Fabio Mathias Correa at University of the Free State, Bloemfontein Campus, South Africa. Mr. Edike Nnamdi declares no conflict of interest.

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