

Predictive Modelling of COVID-19 Pandemic Evolution in Nigeria

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Abstract

COVID-19 is a pandemic that has defined human life, shutting down economic activities. Various measures have been implemented to curb its spread. However, in many places, confirmed cases have continued to increase. Many believe that unless its vaccine is discovered, the pandemic has come to stay. This article aims to develop a model for the evolution of the total confirmed cases, which in the early stage increase exponentially and in the later stage flatten out.

Following the balance equation modelling and employing assumptions similar to the typical pandemic modelling, an exponential model was developed. In order to describe the whole trajectory of the pandemic, following the general trend of COVID-19 data, the exponential model was modified with an inverse exponential expression, comparable to the Arrhenius Equation in chemical reaction engineering. After parameter estimation, the resulting model was validated using data from Italy and Nigeria. The model predictions compare reasonably well with the data.

The model was then employed to predict the future of COVID-19 in Nigeria. The final equilibrium total confirmed cases would be 81,292 and the time for the country to record very low new daily cases would be in March 2021.

1. Introduction

Coronavirus disease 2019, popular known by its abbreviated form COVID-19 is a recent virus infection and a global pandemic currently ravaging the whole world (Ong et al., 2020; WHO, 2020^a). As of 16 August, 2020, the global confirmed cases of people who had contracted the disease were in excess of 21 million; more than 13.5 million had recovered and nearly 774,000 dead, leaving slightly above 7 million people as active carriers of the virus and COVID-19 patients (WHO, 2020^b). These cases were reported in 188 countries out of the 195 countries of the world in less than a year, rising from the few initial cases of the disease reported in Hubei City of China in November 2019 (CSSE, 2020; Aljazeera, 2020). Research shows that the initial cases in China occurred by zoonosis, bat-to-human transmission, while first cases in other parts of the world occurred by cross border migration, classified as imported cases (Sun et al, 2020). Then the imported cases transmitted locally before metamorphosing into community transmission. After about 300 days since inception, new covid-19 cases in China occurred sporadically and in clusters and the country was approaching the end of the pandemic (WHO, 2020c). Countries such as New Zealand have almost attained the status of being covid-19 free while some countries in Africa and Europe experience prolonged phase of community transmission (Rohatgi, 2020; Cobore et al., 2020). Qualitatively, the evolution of the pandemic is described as no cases, zoonosis or imported cases, local and community transmissions, cluster of cases, sporadic cases and COVID-19 free status.

Understanding the disease evolution is one of the critical strategies for the prevention and control of the pandemic, the reduction of related mortality and minimization of economic impact; prevention

and control measures to be adopted depend on the evolution stage (WHO, 2020d and e). These measures include active case finding, signs and symptoms checking, laboratory testing, contact tracing, and patients' isolation. Others are travel restrictions, border closures, clinical management, and community engagement. At the inception of the pandemic, China deployed active case finding, signs and symptoms checking, and laboratory testing to locate COVID-19 active cases in Hubei City where the disease was contracted via zoonotic transmission (WHO, 2020d). Several countries enforced self-isolation, isolation centres, and contacts' tracing for the imported cases, their relatives and associates. Border closures also controlled the imported cases while territory isolation and total lockdown restricted local transmission. The community engagement, a further measure to curb local and community transmission, involves aggressive campaigns and publicity for social distancing, use of sanitizers, face masks and infrared thermometers. With the introduction of these various measures, analyses of epidemiologic data and transmission dynamics would show effectiveness in curbing and even stamping out the pandemic.

Mathematical modelling is a tool that can be used to describe pandemic transmission dynamics; analyse impact and effectiveness of various prevention and control measures; and estimate key transmission and severity parameters (Wang et al., 2020). Since the beginning of the pandemic, various studies on mathematical modelling have been published. Some focus on statistical and stochastic analyses of epidemiologic data (Sun et al., 2020) while some draw analogies for descriptive analyses of the evolutionary trend as obtained for example in the SEIR (Susceptible-Exposed-Infectious-Recovered) modelling (Sun and Li, 2020; Nwalili et al., 2020). The latter modelling is a variant of balance equation modelling widely employed in chemical reactions engineering, where rate constant values determine rates of reaction and increase with temperature according to the Arrhenius equation (Fogler, 2004). As COVID-19 data and trend change rapidly, new studies based on recent information and modelling, not only valid for the early stage of the pandemic but also for the entire time trajectory, should be sustained.

Key COVID-19 epidemiologic data include total confirmed cases, recovered cases, daily recorded cases and death cases. Others include tested samples, days since the last recorded case and transmission classification (WHO, 2020a). The most important variable is the total confirmed cases; it shows the proportion of the population infected with the disease as well as a measure of the pandemic impact on the economy. Further, the total confirmed cases comprise active, dead and recovered cases; alongside epidemiologic statistical data, these component cases can be estimated from total confirmed cases. Also, with the total confirmed cases represented by a function of time, its first derivative becomes an equation that would yield new recorded cases. A model for the total confirmed cases would therefore be informative in describing key indicators of the pandemic.

The objective of this article is to develop a model for the COVID-19 pandemic using the balance equation modelling in chemical reactions engineering and considering two components of the population of a country: total confirmed cases and the rest. From the world's COVID-19 data as a whole and those of individual countries and territories as of August 16, 2020, proportions of total confirmed cases were less than 1 % of total human populations (WHO, 2020a; UN, 2020). In mathematical modelling therefore, the uninfected population can be assumed to be constant. Following this assumption, the developed model is subsequently simplified, yielding an exponential equation. As its name suggests, with a constant-value coefficient, this equation diverges exponentially, capturing only the early part of the pandemic, but not the whole pandemic time trajectory. Instead of a constant value, a variable coefficient that changes with time, to capture various infection prevention and control interventions at different times aimed at flattening the pandemic time curve, is introduced. The time function can assume different forms. However, its introduction should yield a

model that can describe the entire pandemic time trajectory as witnessed in countries nearing the end of COVID-19. Using data from these countries, an inverse exponential time function able to arrest the exponential divergence and vanish it at infinite time, was justified, validated and used in the model. This model was subsequently employed for the Nigerian COVID-19 pandemic to determine key indicators such as the expected final equilibrium value of the total confirmed case, the maximum daily recorded case and the corresponding time; the estimated time for the daily recorded cases to be insignificant (for example, considering values in the order of one new case in 10 million people).

Thus, the article comprises six sections. Section 2 follows this introductory section and develops an exponential model capable of describing the early part of the pandemic. Section 3 modifies the exponential model and estimates parameter values in describing the pandemic using COVID-19 data from China and Italy. Subsequently, Section 4 employs COVID-19 data from Nigeria to validate the modified model. Looking into the future, Section 5 predicts the end of COVID-19 in Nigeria. Finally, Section 6 reports the conclusions.

2. Exponential model

In this section, we adopt the balance modelling approach to develop a model for the total confirmed cases of COVID-19. These cases comprise active, recovered and dead cases. By implication, we divide the human population into two compartments: healthy population (those who have never contracted the disease) and confirmed cases. These two compartments are those simply required to develop an expression for total confirmed cases. The compartments can be three in the SIR (Susceptible-Infectious-Recovered) modelling or four in the SEIR modelling (Beckley et al., 2013).

As in the latter, the following assumptions apply. The population in each compartment is described by a continuous function. Furthermore, the region under investigation is closed. Thus, cross-border migration is neglected. Finally, each population evolves by interacting with the other.

Thus, the number of confirmed cases is described as:

$$\frac{dP}{dt} = k_F P P_H \quad (1)$$

where P is the number of confirmed cases per unit area; P_H is the area density of the healthy population; and k_F (measured in m^2 per day) is the pandemic spreading rate constant.

On the other hand, the healthy population, which decreases by interacting with confirmed cases of COVID-19 and increases by the cumulative effect of other factors such as birth and death, is described as:

$$\frac{dP_H}{dt} = -k_F P P_H + k_G P_H \quad (2)$$

where k_G is the demographic population growth rate. While the coronavirus disease decreases the healthy population by the first term on the right-hand side of Eq. (2), by the second term, population growth increases it. Although it has been declining, the world population growth rate for the period 2010 to 2015 was still positive at 1.2% (UN, 2016). The healthy population growth due to other factors and the decrease due to the impact of COVID-19 are therefore assumed to cancel out, thereby making the healthy population constant. Thus, Eq. (2) becomes:

$$\frac{dP_H}{dt} = -k_F P P_H = 0; \quad P_H = B \text{ (a constant)} \quad (3)$$

By substituting Equation (3) into equation (1), the latter can be integrated to yield:

$$\ln(P/P_0) = k_F B t; P_F = P_0 e^{(Kt)} \quad (4)$$

where $K = k_F B$; it is a pseudo-exponential rate constant. Its value indicates how fast the disease spreads.

Eq. (4) is a simple population growth model, illustrating that the confirmed cases of COVID-19 increase exponentially for any positive value of K and suggesting that eventually, everyone in the healthy population becomes infected. However, due to various infection prevention and control measures, the disease exponential spread can be reduced such that more than 90 % of the population escape the infection. In order to reflect this in the equation, K must be modified so that its value vanishes at infinite time. The modification can be written as:

$$\frac{dP}{dt} = f(t) P; \quad f(t) = \frac{dP/dt}{P} \quad (5)$$

where $f(t)$ is a function of time with k_F and B embedded.

A further analysis of COVID-19 data will help in determining the functional form of $f(t)$. This analysis is performed in the following section.

3. Modified model

In this section, we modify the exponential model developed in Section 2 to describe the entire trajectory of the COVID-19 pandemic and then employ it for the predictions of COVID-19 cases in Italy. In the following, we first demonstrate the equation that best describes the evolution of the pandemic.

Figure 1 shows the time evolution of COVID-19 confirmed in China (WHO, 2020^a). This profile is typical of the disease. In the early part, dP/dt at the numerator on the y -axis variable ($dP/(Pdt)$) is finite and begins to rise while P at the denominator is small. Their combination yields a large value. As P increases exponentially, the y -axis variable decreases exponentially with time, thus the profile.

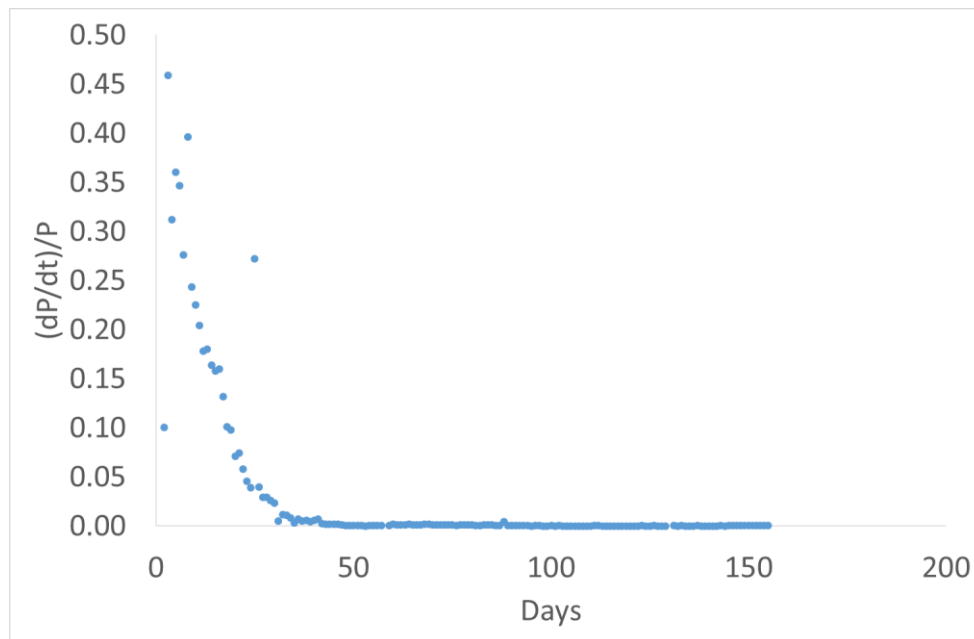


Figure 1: Rate of Covid-19 cases with time using data from China. Data from WHO (2020^a).

Thus, for the modelling of the spread of COVID-19, we write:

$$\frac{dP}{dt} = K_0 e^{-at} P \quad (6)$$

where K_0 (measured in per day) is the disease infection rate constant, and a (measured in per day) is an exponential constant, which accounts for the changes in the rate constant with time. The rate constant along with the exponential term resembles the Arrhenius Equation in chemical kinetics for the effect of temperature on reaction rates; refer to Fogler (2004) or other texts on chemical reactions engineering for details.

The modified model in Eq. (6) is the rate of change of the confirmed cases with time. By integrating this equation, we can obtain the total confirmed cases of COVID-19 at any time. As it is, the equation yields the new recorded cases at any time. Further differentiation yields an expression for the maximum new recorded case. The integration is obtained as follows.

Rearranging Eq. (6), we have:

$$\frac{dP}{P} = K_0 e^{-at} dt \quad (7)$$

Integration yields:

$$\ln P = -\frac{K_0}{a} e^{-at} + C \quad (8)$$

where C is the integration constant, obtained as follows:

$$C = \ln P_0 + \frac{K_0}{a} e^{-at_0} \quad (9)$$

where t_0 can be taken as the first day of the index case P_0 , the initial condition. Thus, the integral is:

$$P = e^{\left[\frac{K_0}{a}(e^{-at_0} - e^{-at}) + \ln P_0\right]} \quad (10)$$

On the other hand, the differentiation of Eq. (6) yields:

$$\frac{d}{dt} \left(\frac{dP}{dt} \right) = \frac{d}{dt} (K_0 e^{-at} P); \frac{d^2 P}{dt^2} = -K_0 a e^{-at} P + K_0 e^{-at} \frac{dP}{dt}; \frac{d^2 P}{dt^2} = -K_0 a e^{-at} P + K_0^2 e^{-2at} P \quad (11)$$

At the peak increase in daily confirmed cases corresponding to time t_p , Eq. (11) is zero as:

$$\frac{d^2 P}{dt^2} = -K_0 a e^{-at_p} P + K_0^2 e^{-2at_p} P = 0; a = K_0 e^{-at_p} \quad (12)$$

The time for the peak daily increase is:

$$t_p = \frac{1}{a} \ln \frac{K_0}{a} \quad (13)$$

Values of K_0 and a are required to use this model. These can be obtained by fitting the model to some data and validating it with some other data as follows. Rearranging Eq. (6), we obtain:

$$\ln \left(\frac{dP/dt}{P} \right) = \ln K_0 - at \quad (14)$$

COVID-19 data with P as total confirmed cases with time are required to calculate the values of K_0 and a . For this reason, we employ COVID-19 data for the first 150 days of the pandemic in Italy, a country that has gone through almost all the stages in the evolution of the pandemic (WHO, 2020^a). Data for the first 100 days are used for parameter estimation while the remaining data are used for model validation. For the parameter estimation, Figure 2 shows a linear correlation of the data.

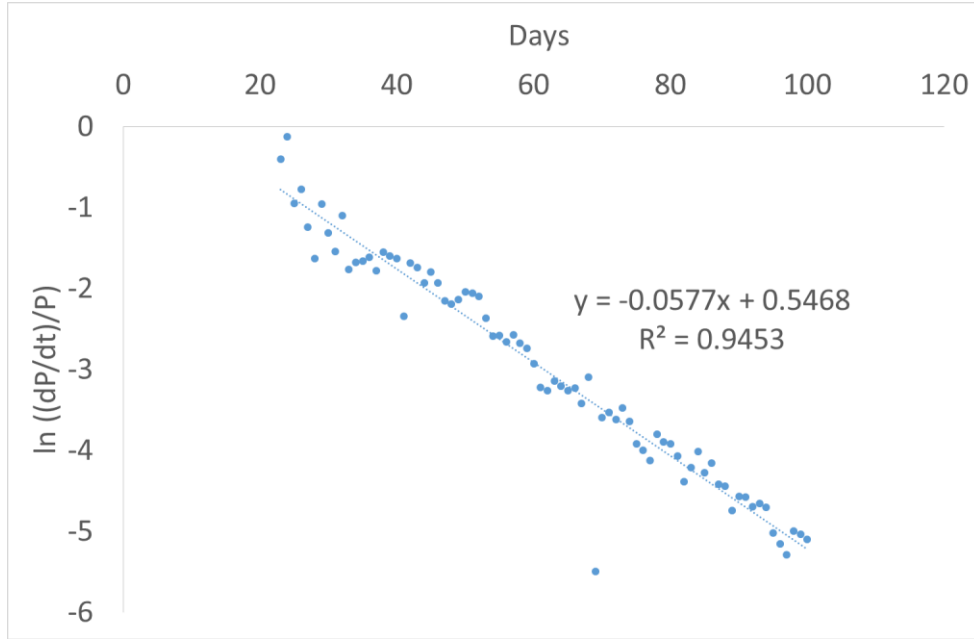


Figure 2: Parameter estimation for modified model 1 using the data from Italy. Data from WHO (2020^a).

In comparison with Eq. (14),

$$a = 0.0577; K_0 = e^{0.5468} = 1.728 \quad (15)$$

Using these values, the evolutions of P and dP/dt for the remaining data can be estimated. While P is given by Eq. (10), dP/dt in terms of time can be obtained by substituting the latter equation for P in Eq. (6) as follows.

$$\frac{dP}{dt} = K_0 e^{-at} e^{\left[\frac{K_0}{a}(e^{-at_0} - e^{-at}) + \ln P_0\right]} \quad (16)$$

For the COVID-19 data of Italy, when $t_0 = 1$, $P_0 = 2$. Thus:

$$P = 2e^{\frac{K_0}{a}(e^{-a} - e^{-at})} = 2e^{9.4766(e^{-0.0577} - e^{-0.0577t})} \quad (17)$$

and

$$\frac{dP}{dt} = 2K_0 e^{-at} e^{\frac{K_0}{a}(e^{-a} - e^{-at})} = 1.0936e^{-0.0577t} e^{9.4766(e^{-0.0577} - e^{-0.0577t})} \quad (18)$$

For the validation of the Eqs (17) and (18), we employed the remaining COVID-19 data of Italy. Figures 3A and B show how the predicted total confirmed cases and daily confirmed cases from modified model 2 compare with the data.

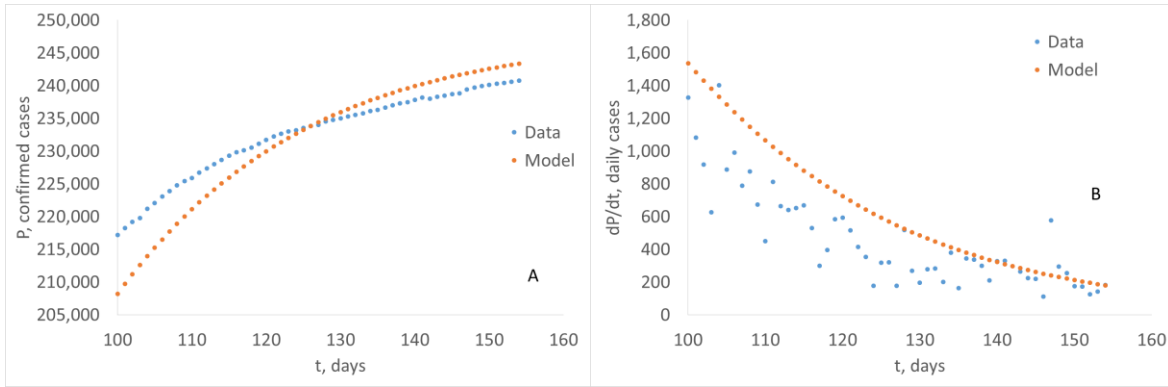


Figure 3: Validation of the modified model 2 using 100 to 150 days of Italy Covid-19 data and the correlation parameters obtained from the first 100 days – A: total confirmed cases and B: daily confirmed cases. Data from WHO (2020^a).

By manually fitting the model to the data, better predictions were obtained with $\alpha = 0.04257$ and $K_0 = 0.5209$. See Figure 4. These predictions suggest that the original values were at a suboptimal point.

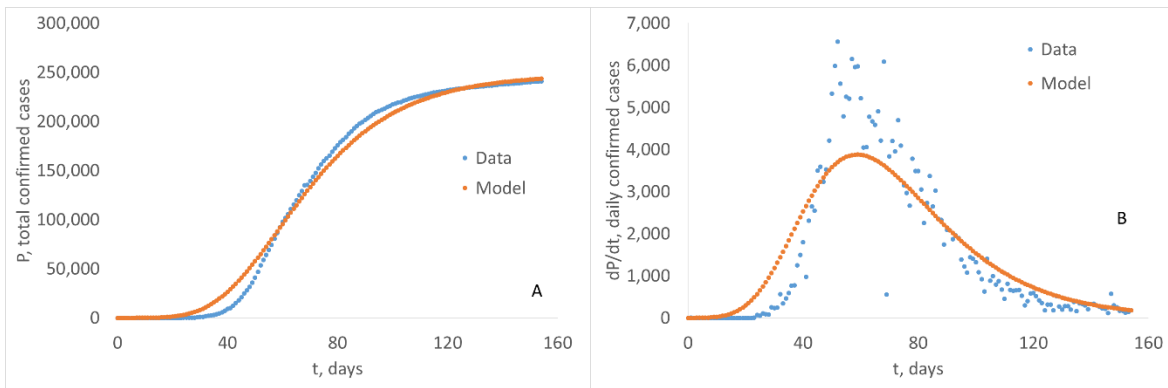


Figure 4: Validation of the modified model 2 using Italy Covid-19 data and the parameters manually adjusted to $\alpha = 0.04257$ and $K_0 = 0.5209$ – A: total confirmed cases and B: daily confirmed cases. Data from WHO (2020^a).

4. Model validation

Above procedures were followed to predict Nigeria's COVID-19 cases. The first 100 data points were used to obtain the parameters: K_0 and α in Eq. (14). Figure 5 shows the correlation.

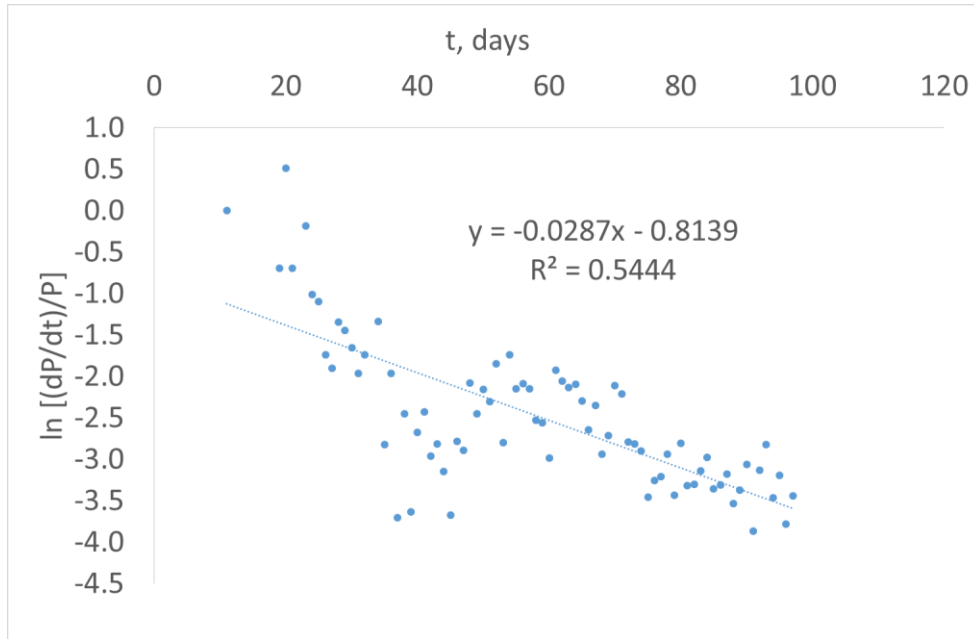


Figure 5: Parameter estimation for modified model 1 using the data from Nigeria. Data from NCDC (2020).

The linear equation, however, poorly correlates the data.

In comparison with Eq. (14),

$$a = 0.0287; K_0 = e^{-0.8139} = 0.4431 \quad (19)$$

For the COVID-19 data of Nigeria, when $t_0 = 1, P_0 = 1$. Thus:

$$P = e^{\frac{K_0}{a}(e^{-a} - e^{-at})} = e^{15.439(e^{-0.0287} - e^{-0.0287t})} \quad (20)$$

and

$$\frac{dP}{dt} = K_0 e^{-at} e^{\frac{K_0}{a}(e^{-a} - e^{-at})} = 0.4431 e^{-0.0287t} e^{15.439(e^{-0.0287} - e^{-0.0287t})} \quad (21)$$

For the validation of the Eqs (20) and (21), we employ COVID-19 data for 100 to 125 days since the index case in Nigeria. Figures 5A and B show how the predicted total confirmed cases and daily confirmed cases from the modified model compare with the data.

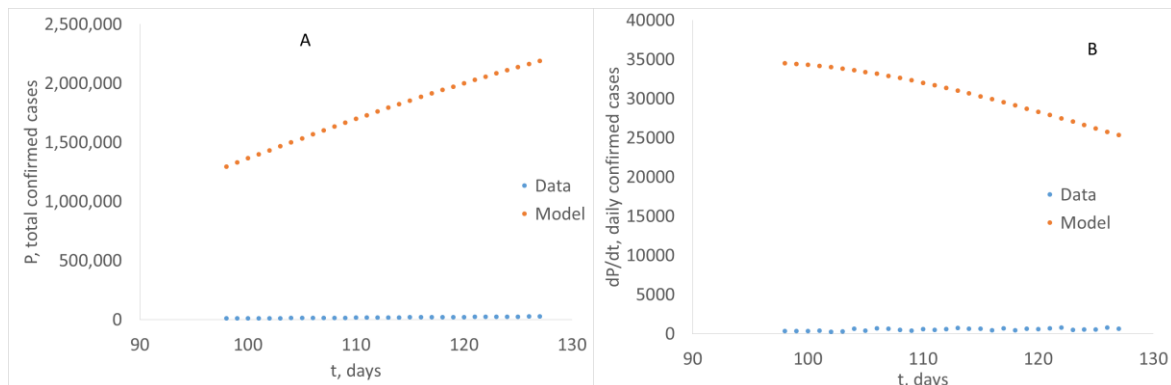


Figure 6: Validation of the modified model 2 using 80 to 130 days of Nigeria Covid-19 data and the correlation parameters obtained from the first 80 days – A: total confirmed cases and B: daily confirmed cases. Data from NCDC (2020).

Because of the poor correlation in Figure 5, the predictions in Figures 6A and B are poor. We therefore resort to manual fitting. The initial values for the manual fitting were

$$a = 0.01829 \text{ and } K_0 = 0.1867 \quad (22)$$

These initial values were obtained by assuming the peak of the curve of dP/dt being the highest recorded new case of 790 occurring at $t_p = 127 \text{ days}$ with $P = 27110$ and $P_0 = 1$ from the Nigeria COVID-19 data and solving the nonlinear equations of Eqs. (10) and (13) simultaneously.

With the values in Eq. (22), Figures 7A and B show how the predicted total confirmed cases and daily confirmed cases from the modified model compare with the data.

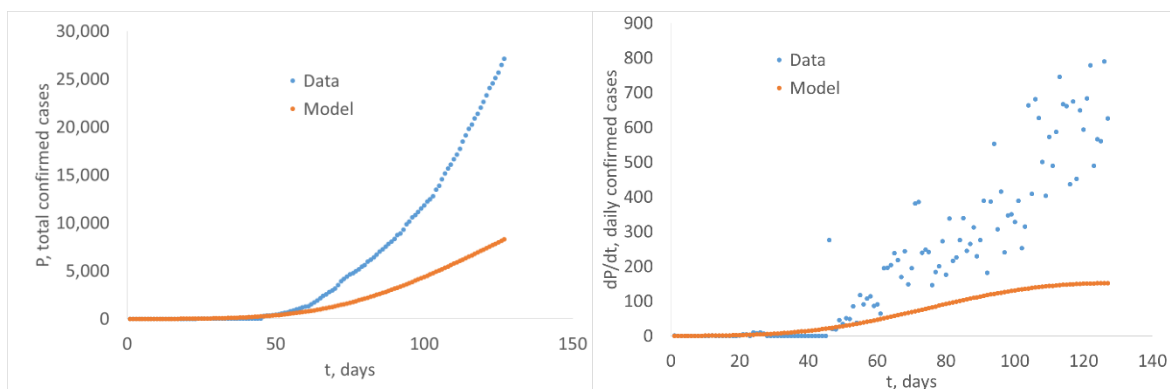


Figure 7: Validation of the modified model using Nigeria Covid-19 data and the parameters obtained by simultaneously solving t_p and P ($t = 127$; $P = 27110$) – A: total confirmed cases and B: daily confirmed cases. Data from NCDC (2020).

By manually fitting the model to the data, better predictions were obtained with $a = 0.01829$ and $K_0 = 0.2106$. See Figure 8.

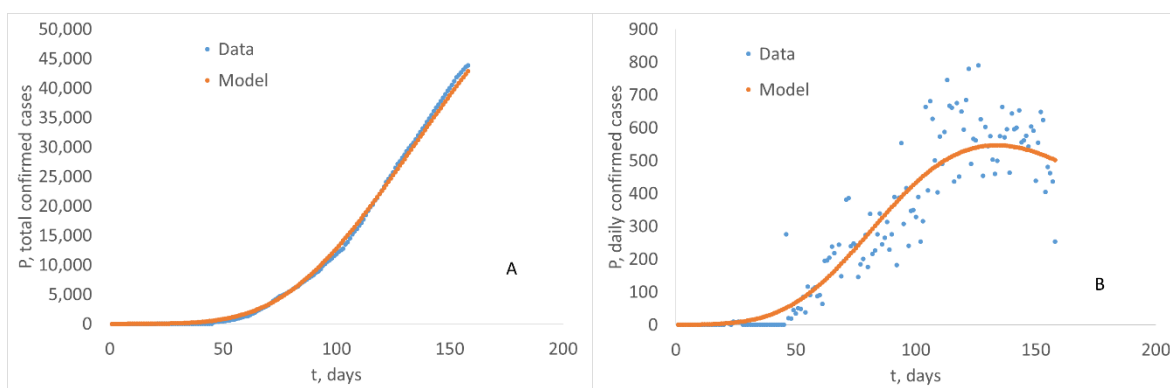


Figure 8: Validation of the modified model 2 using Nigeria Covid-19 data and the parameters manually adjusted to $a = 0.01829$ and $K_0 = 0.2106$ – A: total confirmed cases and B: daily confirmed cases. Data from NCDC (2020).

As shown, we have been able to model the covid-19 cases for Nigeria. This model with the parameter values can be used to predict the evolution daily cases and total confirmed cases.

5. Future predictions

This section further tests model predictions of the Nigerian COVID-19 data using the month of July and analyses the model for key indicators of the pandemic.

In predicting the Nigerian COVID-19 data beyond 125 days after the index case, the model in Eq. (20) along with the parameter values in Eq. (22) were first used for July 03 – August 02, 2020. Figure 9 shows the comparison between the data and model predictions.

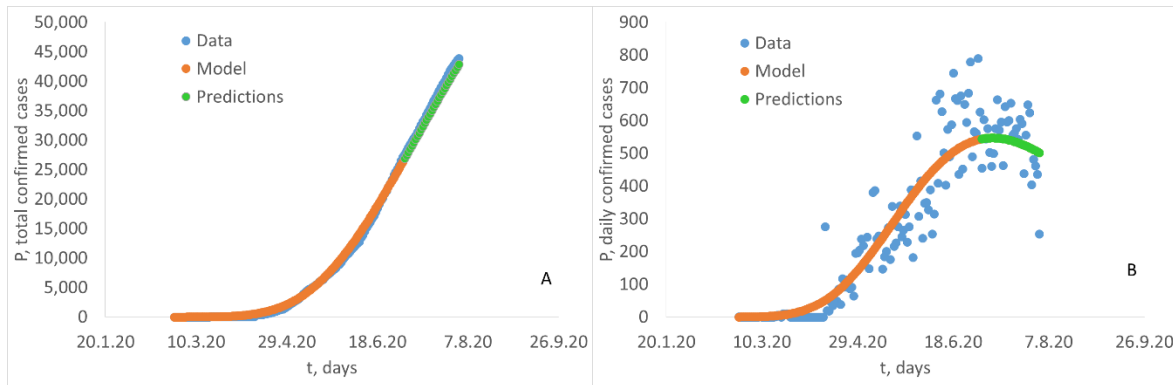


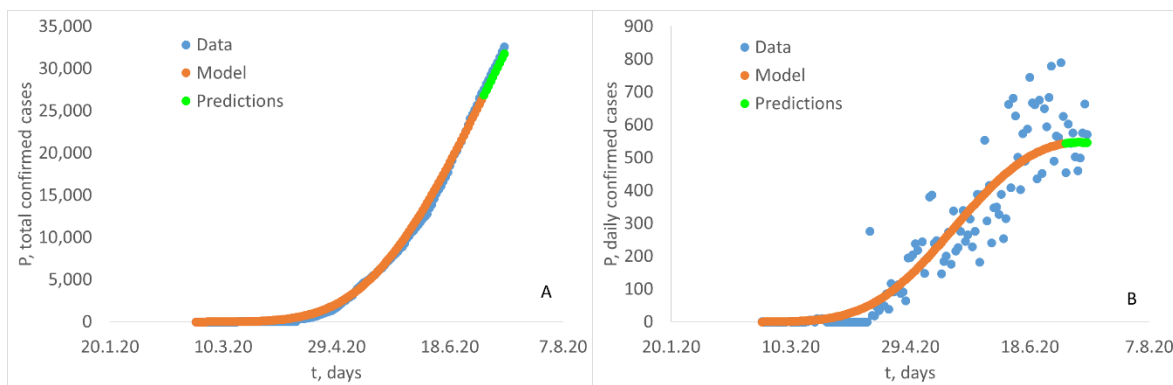
Figure 9: Model predictions of the COVID-19 cases in Nigeria for the period July 03 – August 02, 2020 highlighted in green; A: Total confirmed cases, B: New daily recorded cases. Data from NCDC (2020).

The model predictions are almost identical with the data for the total confirmed cases and have good fitting with the data for the daily recorded cases. To fit the new daily recorded cases better, a sinusoidal function should be included in the model as the data appear to oscillate around the predictions. However, this inclusion would lead to a more complex model.

In order to further track the predictions, the data are analysed weekly as follows:

Week 1 (July 03 – July 12)

Eqs (20) – (22) were subsequently used to predict the total confirmed cases and new daily recorded cases in Nigeria for the period 121 – 130 days after the index case, corresponding to July 03 – July 12, 2020. Figure 10 shows the comparison between the data and model predictions.



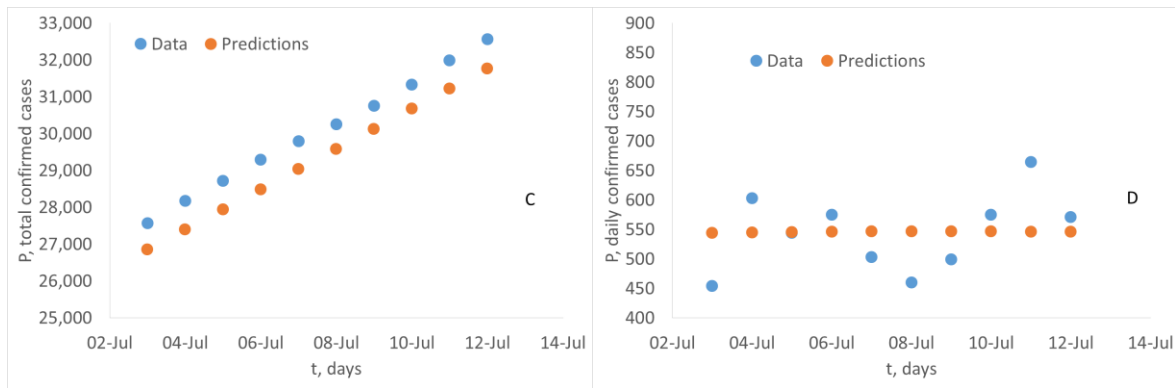


Figure 10: Model predictions of the COVID-19 cases in Nigeria for the period July 03 – July 12, 2020 highlighted in green; A: Total confirmed cases, B: New daily recorded cases; C: Predictions in A magnified, D: Predictions in B magnified. Data from NCDC (2020).

As shown, for the total confirmed cases, the predictions increase in a similar pattern as the real data. On the other hand, for the new daily recorded cases, the model predictions do not change significantly within the period of observation. The predictions appear to be almost at a constant value while real data oscillate around it (see quadrants C and D in Figure 10).

While keeping the value of K_0 constant at 0.2106, to obtain better predictions of the total confirmed cases with values almost identical with the real cases, the value of the parameter α was manually adjusted to 99.65% of the original value, i.e. $\alpha = 0.01823$. The value of K_0 is kept constant as the spreading rate function by analogy compares with the Arrhenius Equation, where the pre-exponential factor must be a constant value. Figure 11 shows the new predictions.

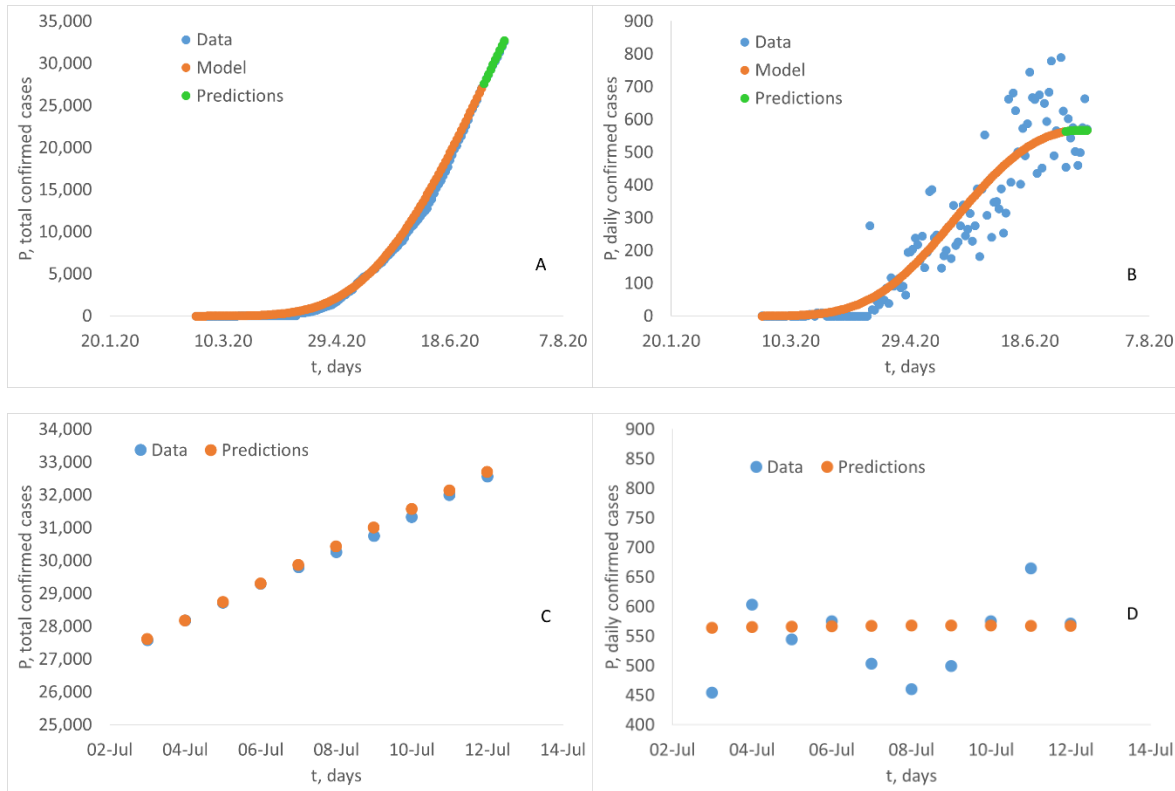


Figure 11: New model predictions of the COVID-19 cases in Nigeria for the period July 03 – July 12, 2020 highlighted in green with $\alpha = 0.01823$; A: Total confirmed cases, B: New daily recorded cases; C: Predictions in A magnified, D: Predictions in B magnified. Data from NCDC (2020).

Week 2 (July 13 – July 19)

While the value of K_0 was kept constant at 0.2106 corresponding to its fitting value of the first 125 days, and that of α being 0.01823, corresponding to its fitting value for Week 1 above, the model was used to predict the Nigerian COVID-19 cases for week 2 in the period July 13 – July 19, 2020. Figure 12 shows the comparison between the data and model predictions.

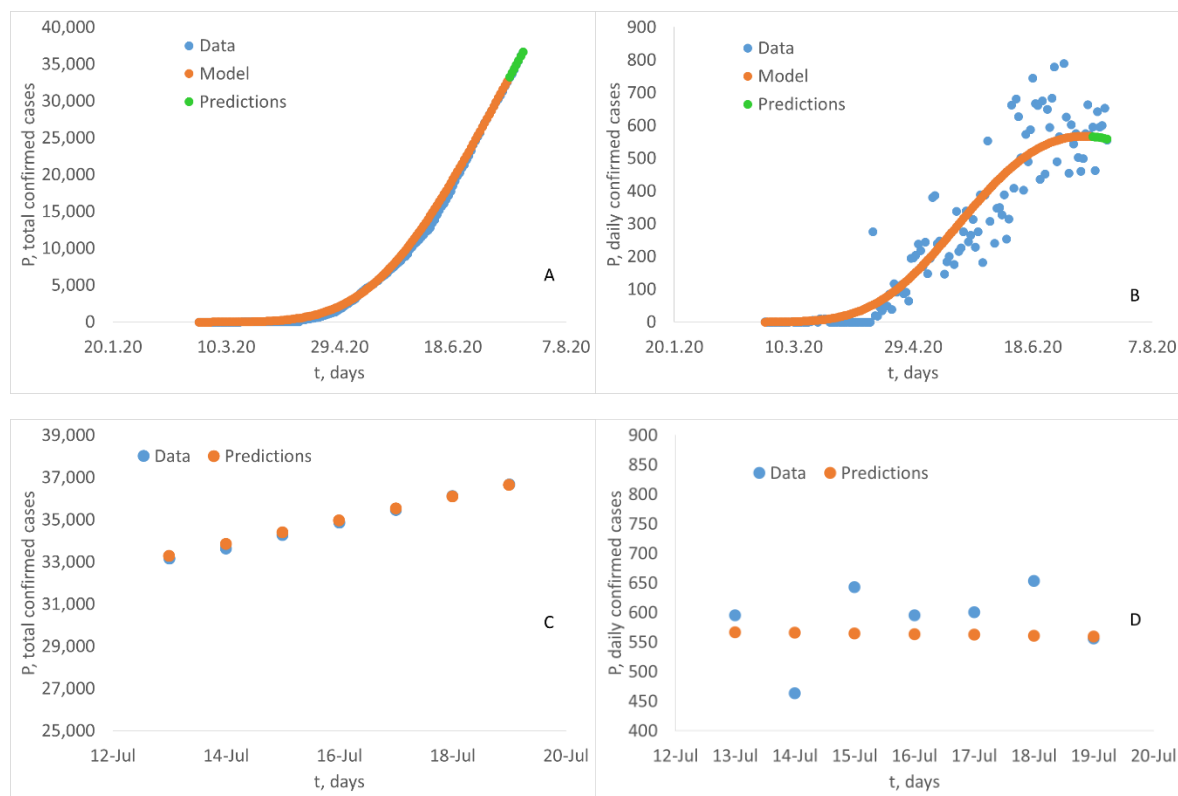


Figure 12: New model predictions of the COVID-19 cases in Nigeria for the period July 13 – July 19, 2020 highlighted in green with $\alpha = 0.01823$; A: Total confirmed cases, B: New daily recorded cases; C: Predictions in A magnified, D: Predictions in B magnified. Data from NCDC (2020).

As shown, for the total confirmed cases, the predictions show excellent agreement with the data. On the other hand, for the daily recorded cases, the model predictions do not change significantly within the period of observation while the data continue to display an oscillatory pattern.

Week 3 (July 20 – July 26) and Week 4 (July 27 – August 02)

For Weeks 3 and 4, the procedure and parameter values for week 2 above apply. Figures 13 and 14 show the comparison between the data and model predictions.

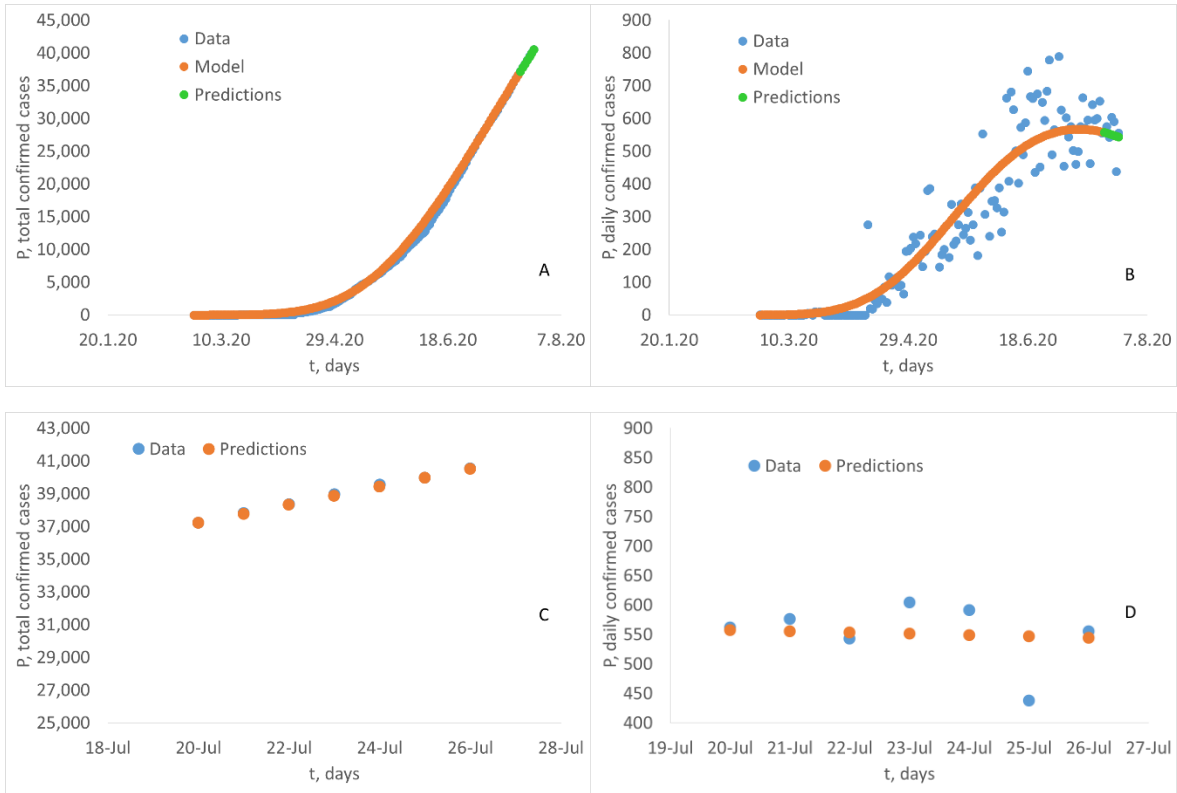


Figure 13: New model predictions of the COVID-19 cases in Nigeria for the period July 20 – July 26, 2020 highlighted in green with $\alpha = 0.01823$; A: Total confirmed cases, B: New daily recorded cases; C: Predictions in A magnified, D: Predictions in B magnified. Data from NCDC (2020).

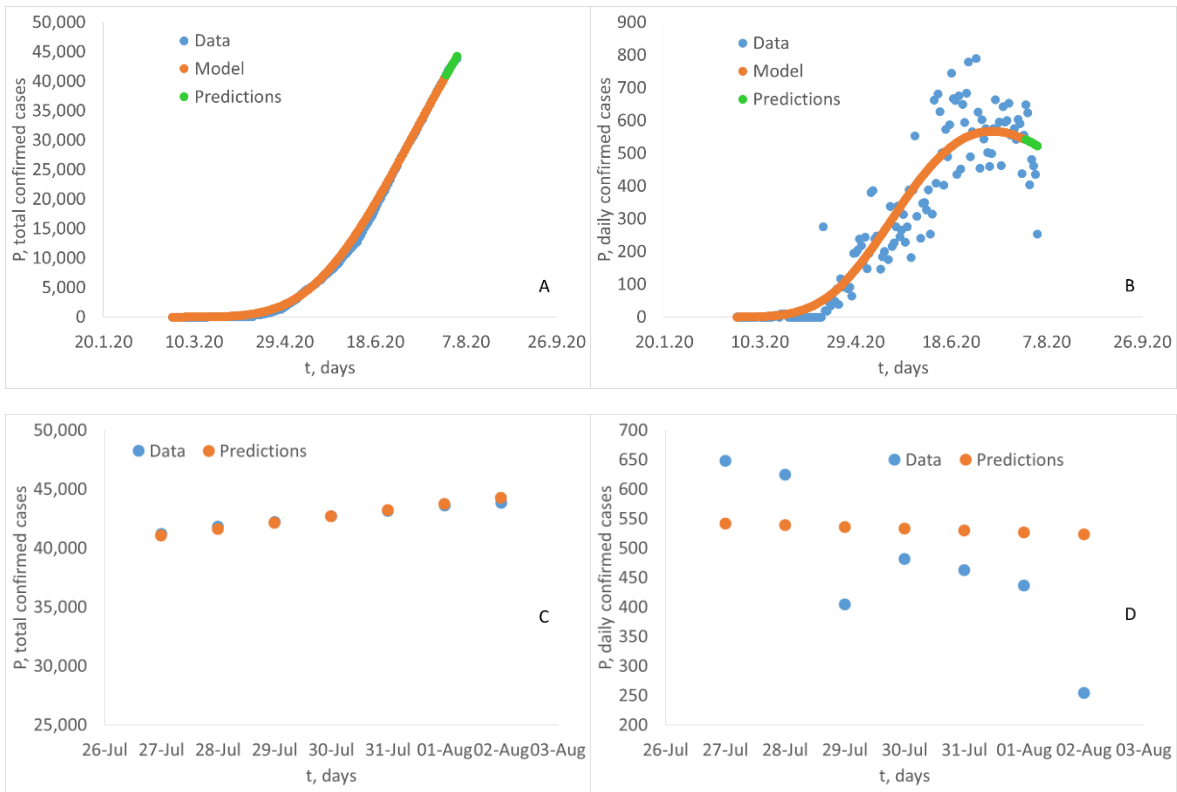


Figure 14: New model predictions of the COVID-19 cases in Nigeria for the period July 27 – August 02, 2020 highlighted in green with $a = 0.01823$; A: Total confirmed cases, B: New daily recorded cases; C: Predictions in A magnified, D: Predictions in B magnified. Data from NCDC (2020).

The model predictions are identical with the data for the total confirmed cases and have excellent fitting with the data for the new daily recorded cases. For this week, the decline in the predicted daily recorded cases is now obvious unlike the apparent horizontal profile of the previous weeks.

Key indicators of the Pandemic

The model can be used to determine the following: the final equilibrium value of P as $t \rightarrow \infty$; the maximum new daily recorded case and the corresponding time; the estimated time for the daily recorded cases to be insignificant (that is, 1 new case in 10 million people).

For the final equilibrium value, using the parameters in Eq. (22), we substitute $t = \infty$ into Eq. (20) as:

$$P = P_0 e^{\frac{K_0}{a}(e^{-a} - e^{-at})} = e^{\frac{0.2106}{0.01829}(e^{-0.01829} - e^{-0.01829 \times \infty})} = 81,292 \text{ confirmed cases}$$

For the maximum daily recorded case, we differentiate Eq. (21) and then equate to zero (the necessary condition for an optimum point):

$$\frac{d}{dt} \left(\frac{dP}{dt} \right) = \frac{d}{dt} (K_0 e^{-at} P); \frac{d^2 P}{dt^2} = -K_0 a e^{-at} P + K_0^2 e^{-2at} P \quad (23)$$

$$\frac{d^2 P}{dt^2} = -K_0 a e^{-at} P + K_0^2 e^{-2at} P = 0; a = K_0 e^{-at} \quad (24)$$

$$t = \frac{\ln \frac{a}{K_0}}{-a} = \frac{\ln \frac{K_0}{a}}{a} \quad (25)$$

Substituting the parameter values,

$$t = \frac{\ln \frac{0.2106}{0.01829}}{0.01829} = 133.6 \cong 134 \text{ days}$$

The corresponding maximum daily rise is:

$$\begin{aligned} \frac{dP}{dt} &= K_0 P_0 e^{-at} e^{\frac{K_0}{a}(e^{-a} - e^{-at})} = 0.2106 \times 1 \times e^{-0.01829 \times 133.6} e^{\frac{0.2106}{0.01829}(e^{-0.01829} - e^{-0.01829 \times 133.6})} \\ &= 546.9 \cong 547 \text{ cases} \end{aligned}$$

Finally, for the estimated time for the daily recorded cases to be very low (that is 1 new per 10 million people or equivalently, below twenty new cases per day in Nigeria), the predicted P is computed until its value is below 20. The corresponding time is 369 days after the index case, which falls on March 01, 2021. Figures show the full pandemic evolution of COVID-19 in Nigeria.

The model reported in the previous reports was used for the predictions of the COVID-19 cases in Nigeria. Figure 15 shows the full pandemic evolution. 'A' shows the total confirmed cases while 'B' shows the new daily cases. In the former, the model predictions are identical to the data while in the latter, the model predictions describe the new cases quite well, thus informing as reasonable the predicted full pandemic evolution.

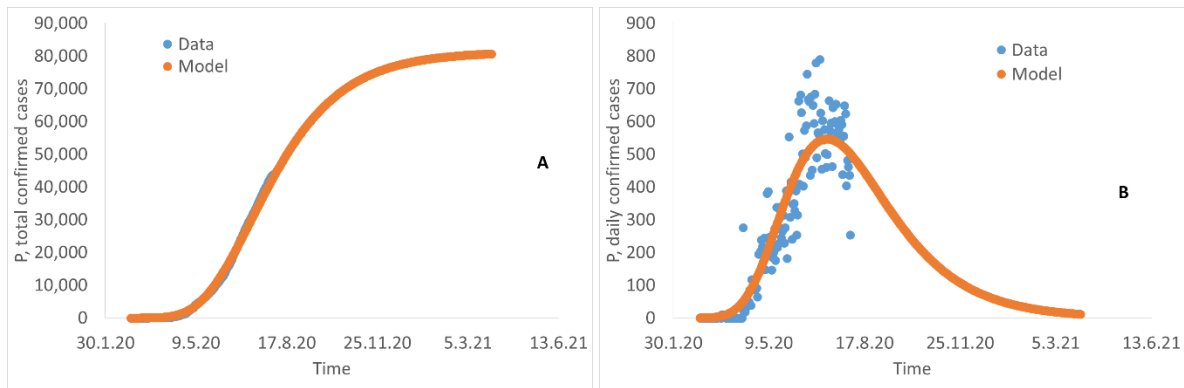


Figure 15: Model predictions of the full pandemic evolution of COVID-19 cases in Nigeria; A: Total confirmed cases B: Daily recorded cases. Data from NCDC (2020).

6. Conclusions

A model for describing the entire trajectory of the COVID-19 pandemic has been developed, demonstrating the exponential increase in the early part and decline resulting from various intervention programs. The balance equation modelling approach and SEIR modelling assumptions were employed in developing an intermediate resulting exponential model. In a similar pattern to the Arrhenius Equation, the model was modified with an inverse exponential term. The resulting model was able to describe the pandemic trend in China and Italy. It could also predict with precision COVID-19 data for Italy and Nigeria. Lastly, the model was used to predict the future of the pandemic in Nigeria if recent gains were sustained.

References

1. Aljazeera, 2020. Coronavirus: Which countries have confirmed cases?, <https://www.aljazeera.com/news/2020/01/countries-confirmed-cases-coronavirus-200125070959786.html>
2. Anubha Rohatgi, 2020. 9 countries including New Zealand are now Covid-19 free. Here's the list, <https://www.hindustantimes.com/world-news/9-countries-including-new-zealand-are-now-covid-19-free-here-s-the-list/story-VANsJu5CZxRyXU2OyrDImO.html>
3. Beckley, Ross; Weatherspoon, Cametria; Alexander, Michael; Chandler, Marissa; Johnson, Anthony; Batt, Ghan S. (2013). "Modeling epidemics with differential equations" (PDF). *Tennessee State University internal report*. Retrieved July 19, 2020.
4. Catherine Wei Min Ong, Giovanni Battista Migliori, Mario Raviglione, Gavin MacGregor-Skinner, Giovanni Sotgiu, Jan-Willem Alffenaar, Simon Tiberi, Cornelia Adlhoch, Tonino Alonzi, Sophia Archuleta, Sergio Brusin, Emmanuelle Cambau, Maria Rosaria Capobianchi, Concetta Castilletti, Rosella Centis, Daniela M. Cirillo, Lia D'Ambrosio, Giovanni Delogu, Susanna M. R. Esposito, Jose Figueroa, Jon S. Friedland, Benjamin Ho Choon Heng, Giuseppe Ippolito, Mateja Jankovic, Hannah Yejin Kim, Senia Rosales Klintz, Csaba Ködmön, Eleonora Lalle, Yee Sin Leo, Chi-Chiu Leung, Anne-Grete Märtson, Mario Melazzini, Saeid Najafi Fard, Pasi Penttinen, Linda Petrone, Elisa Petruccioli, Emanuele Pontali, Laura Saderi, Miguel Santin, Antonio Spanevello, Reinout van Crevel, Marieke J. van der Werf, Dina Visca, Miguel Viveiros, Jean Pierre Zellweger, Alimuddin Zumla, Delia Goletti, 2020. Epidemic and pandemic viral infections: impact on tuberculosis and the lung. A consensus by the World Association for Infectious Diseases and Immunological Disorders (WAidid), Global Tuberculosis Network (GTN) and members# of ESCMID Study Group for

- Mycobacterial Infections (ESGMYC), European Respiratory Journal 2020; DOI: 10.1183/13993003.01727-2020
5. CDC (Centers for Disease Control and Prevention) 2 April 2020. "Contact Tracing for COVID-19, the original on 22 June 2020. <https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/contact-tracing.html> Retrieved 22 June 2020.
 6. [Cabore, J. W.](#), [Karamagi, H. C.](#) [Kipruto, H.](#), [Asamani, J. A.](#), [Droti, B.](#), [Aminata Binetou Wahebine Seydi, A. B. W.](#), [Regina Titi-Ofei](#), [Benido Impouma](#), [Michel Yao](#), [Zabulon Yoti](#), [Felicitas Zawaira](#), [Prosper Tumusiime](#), [Ambrose Talisuna](#), [Francis Chisaka Kasolo](#), and [Matshidiso R Moeti](#)⁸, 2020. The potential effects of widespread community transmission of SARS-CoV-2 infection in the World Health Organization African Region: a predictive model, *BMJ Glob Health*. 2020; 5(5): e002647. Published online 2020 May 25. doi: 10.1136/bmjgh-2020-002647 PMID: PMC7252960
 7. [CSSE \(The Center for Systems Science and Engineering\)](#), at [Johns Hopkins University \(JHU\)](#), 2020. "COVID-19 Dashboard". [ArcGIS](#). [Johns Hopkins University](#). <https://gisanddata.maps.arcgis.com/apps/opsdashboard/index.html#/bda7594740fd40299423467b48e9ecf6>, Retrieved 5 June 2020.
 8. Fogler, H. S., 2004. *Elements of Chemical Reaction Engineering*, Prentice -Hall, Upper Saddle, New Jersey.
 9. NCDC (Nigeria Centre for Disease Control), 2020. COVID-19
 10. [Ning Wang](#), [Yuting Fu](#), [Hu Zhang](#), [Huipeng Shi](#), 2020. An evaluation of mathematical models for the outbreak of COVID-19, *Precision Clinical Medicine*, Volume 3, Issue 2, June 2020, Pages 85–93, <https://doi.org/10.1093/pmedi/pbaa016>
 11. [Peiliang SUN](#), [Kang Li](#), 2020. An SEIR Model for Assessment of Current COVID-19 Pandemic Situation in the UK, License CC BY-NC 4.0, DOI: 10.1101/2020.04.12.20062588
 12. Pengfei Sun, Xiaosheng Lu, Chao Xu, Wenjuan Sun, Bo Pan, 2020. Understanding of COVID-19 based on current evidence, *J Med Virol*. 2020;92:548-551, doi: 10.1002/jmv.25722.
 13. [Samuel Mwalili](#), [Mark Kimathi](#), [Viona Ojiambo](#), [Duncan Gathungu](#) & [Rachel Mbogo](#), 2020. SEIR model for COVID-19 dynamics incorporating the environment and social distancing, *BMC Research Notes* volume 13, Article number: 352 (2020) [Cite this article](#) 570 Accesses [Metrics](#)
 14. UN (United Nations), 2020. World Population Trends, <https://www.un.org/en/observances/world-population-day>
 15. UN (The United Nations) "[World Population Prospects](#)". [esa.un.org](#). Population Division – United Nations. Archived from [the original](#) on 19 September 2016. Retrieved 15 September 2016.
 16. WHO, 2020a, Naming the coronavirus disease (COVID-19) and the virus that causes it, [https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-\(covid-2019\)-and-the-virus-that-causes-it](https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-(covid-2019)-and-the-virus-that-causes-it).
 17. WHO, 2020b. Coronavirus disease (COVID-2019) situation reports, <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports/>
 18. WHO, 2020c. Coronavirus disease 2019 (COVID-19) Situation Report, https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200401-sitrep-72-covid-19.pdf?sfvrsn=3dd8971b_2
 19. WHO, 2020d. Coronavirus disease 2019 (COVID-19) Situation Report – 30, <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports/>

21. [WHO, 2020e, COVID-19 Strategy Update - World Health Organization www.who.int › docs › covid-strategy-update-14april2020](https://www.who.int/docs/default-source/covid-strategy-update-14april2020)

Notations

Notation	Description	Units
a	exponential constant	$1/day$
B	Constant healthy population	$\#/m^2$
K	pseudo-exponential rate constant	$1/day$
K_0	disease infection rate constant	
k_F	pandemic spreading rate constant	m^2/day
P	Number density of confirmed cases	$\#/m^2$
P_H	Area density of the healthy population	$\#/m^2$
r_i	rate of generation of i people per unit area from various events	$\#/(m^2 \cdot t)$
t	Time	$days$
t_p	time for the peak daily increase	$days$

Acknowledgements

Emmanuel Agunloye is grateful to the Nigerian Academy of Engineering for their encouragement.