ESTIMATION OF THE BASIC REPRODUCTION NUMBER OF COVID-19 IN NIGERIA

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ABSTRACT: *Corona virus disease is seen as a dreaded disease all over the world. This prompted many researchers into carrying out research on COVID-19. The essence of these is to provide solution for eradication of COVID-19. In this research work, we considered the basic reproduction number which is a determinant to the spread and control of any infectious diseases. We used the next generation matrix as a method of finding the basic reproduction number. Data for the analysis were obtained from literatures, World meters and from NCDC. Maple 2023 software was used for the analysis. The results show that $R_0 < 1$. This is an indication that COVID-19 is not spreading like wild fire as the case of other countries. This does not mean that Nigerians will relent and give room for re infection and spread of COVID-19 The information from this research work will enable the government, health care providers and general public in taking precautionary measures against COVID-19.*

KEYWORDS: COVID-19, Basic reproduction number, Disease, Estimation, Analysis.

INTRODUCTION

Corona virus disease (COVID -19) is a novel disease that has taken the life of many people, crippled economy, and placed restriction on social gathering all over the world. Corona virus disease (2019) is caused by a severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) (World Health Organization, 2019). SARS-COV2 is a highly virulent virus that has caused COVID-19 to be a fatal disease. Corona virus disease (COVID-19) outbreak was noticed in December 2019. The first outbreak started in Hubei province, Wuhan, China on 30 January, 2020). The World Health Organization (WHO) described the COVID-19 as a public health emergency and identified it as a pandemic on 11 March, 2020. COVID-19 is transmitted from human-to-human via direct contact with contaminated surfaces and through the inhalation of respiratory droplets from infected individuals (Bai, 2020). COVID-19 has presented itself as a mystery infection to the medical field, also requiring tremendous research and insights about the nature of the virus, and posing frequent challenges for a successful vaccine outcome (Umakanthan et al, 2020). Right from the time of the outbreak of this disease till now, the world has not been at ease. The whole world is battling with outbreaks of a corona virus disease.

The first case of COVID-19 in Africa was reported in Egypt on February 14, 2020 (Gibert et al (2020), Organization WH (2020)]. As of October 29, 2021, forty-seven (47) African countries have been affected by the disease, with over 6.07 million confirmed cases and over 150,000 confirmed deaths Health Organization WHO (2021)

The basic reproduction number is a threshold for stability of disease-free equilibrium and is related to the peak and final size of an epidemic. The epidemic interpretation of this threshold parameter is connected to the local and global stability of the disease-free equilibrium Driessche and Watmough(2008). This is defined as the average number of secondary cases that would be generated by a primary case in a totally susceptible population. It provides an overall measure of the potential for transmission of an infection within a population, and it is dependent not only on the transmission coefficient but also on the average duration of infectiousness.

The Basic reproduction number is the average number of secondary cases of the disease made by a typical infectious person (during his infectious period) in a wholly (or completely) susceptible population. Basic reproduction number is used to determine the ability of a disease to spread with a given population

Quite a great number of models have been developed to estimate the basic reproduction number of COVID-19 across the world [Park et al (2020), Kong et al (2021). In Kong et al's work, logistic growth curves were fitted to the daily reported cases of COVID-19 for 58 countries across the world. They estimated the basic reproduction number of COVID-19 for these countries and determined the social, economical, and environmental factors that influence the difference in this parameter across these countries. The exponential growth rate and basic reproduction number of COVID-19 for Africa were calculated in Musa et al's paper, using the method proposed by Ma (2020), together with the Poisson likelihood method for data fitting. They used the serial interval estimated from COVID-19 cases in Hong Kong, China. Zhao et al (2020) estimated the exponential growth rate of COVID-19 in Africa to be 0.22 per day (95% CI: 0.20–0.24) and the basic reproduction number as 2.37 (95% CI: 2.22–2.51).

Locatelli *et al* (2021) estimated the COVID-19 basic reproduction number for the 15 largest countries in Western Europe, using the exponential growth rate approach.

Xu *et al* (2020), used the maximum likelihood method and the sequential Bayesian method to calculate the COVID-19 basic reproduction number (R_0) and the time-varying estimate of the effective reproduction number (R_t), respectively, for the 12 countries that were most affect by COVID-19 in the early days of the pandemic.

Dharmaratne et al (2020), estimated R_0 for Sri Lanka using three different approaches: a SIR compartmental model, exponential growth rate method, and the maximum likelihood method. For the SIR model, they obtained R_0 = 1.02 with confidence interval (CI) of 0.75–1.29; 0.93 (CI: 0.77–1.10) from the exponential growth rate method; and 1.23 (CI: 0.94–1.57) using the maximum likelihood method. The variation in the value of R0 they obtained using these three methods ranges from 0.69 to 2.20.

Adekunle *et al* (20200, estimated the basic reproduction of COVID-19 in Nigeria by fitting an SEIR-type model to the cumulative reported cases and death data.

Iyaniwura *et al* (2022) also carried out a research work titled 'The basic reproduction number of COVID-19 across Africa' in their work, they used SEIR model and a Bayesian inference framework to estimate the basic reproduction number of COVID-19 across Africa

MATERIALS AND METHOD

We use the ten (10) compartmental models below to estimate the basic reproduction number.

The essence of finding the basic reproduction number is to find out if the spread of the disease is actually reducing or not. In our model, we assume that recovered individual can loss immunity and then go back to the susceptible class.

The Model Equations

$$\frac{dS}{dt} = \pi - (1 - P_1)(\beta_2 I_A + S\beta_3 I_S)S - (1 - P_2)S\beta_1 V + ZV_c + nQ +$$

$$R\varpi_1 - (\Gamma + \mu_1)S \tag{1}$$

$$\frac{dE}{dt} = (1 - p_1)(\beta_{DA} I_A + \beta_{DS} I_S)S + (1 - p_2)S\beta_1 V - (\delta + \varpi_2 + \mu_1)E \tag{2}$$

$$\frac{dI_A}{dt} = (1 - r)\delta E - (\rho_A + \gamma_A + \omega_1 + \mu_1)I_A \tag{3}$$

$$\frac{d I_S}{dt} = r\delta E - (\rho_s + \mu_s + \gamma_s + \omega_2 + \mu_1)I_s \tag{4}$$

$$\frac{d I_H}{dt} = \alpha_A \gamma_A I_A + \alpha_s \gamma_s I_s + \nu I_W - (\rho_H + \mu_H + \mu_1)I_H \tag{5}$$

$$\frac{d I_W}{dt} = (1-\alpha_A)\gamma_A I_A + (1-\alpha_s)\gamma_s I_s + mQ - (\nu + \rho_W + \mu_W + \mu_1)I_W \tag{6}$$

$$\frac{dR}{dt} = \rho_A I_A + \rho_s I_s + \rho_H I_H + \rho_W I_W - (\varpi_1 + \mu_1)R \tag{7}$$

$$\frac{dV}{dt} = \omega_1 I_A + \omega_2 I_s - (\varphi + \mu_1)V \tag{8}$$

$$\frac{dQ}{dt} = \varpi_2 E - (n + m + \mu_1)Q \tag{9}$$

$$\frac{d V_C}{dt} = \Gamma S - (Z + \mu_1)V_C \tag{10}$$

In our model, there are 6 infected compartments E, I_A, I_s, I_H, I_W, V it follows that we are going to have 6×6 matrices.

Recall

DFE is $E^* = I_A^*, = I_S^* = I_H^* = I_W^* = V = 0$ and $S^* = V_C^* \neq 0$

Following the notations of Vanden Driesseche and Watmough (2002), we have the following

$$f = \begin{pmatrix} (1-p_1)(\beta_{DA}I_A + \beta_{DS}I_A) + (1-P_2)S\beta_1 V \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{11}$$

This is the inflow of disease into the infected compartment

$$F = \begin{pmatrix} 0 & (1-P_1)S\beta_{DA} & (1-P_1)S\beta_{DS} & 0 & 0 & (1-P_2)S\beta_1 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$(12)$$

This is obtained by partially differentiating the inflow with respect to each of the infected compartments.

$$v = \begin{pmatrix} (\delta + \mu_1 + \varpi_2)E \\ -(1-r)\delta E + (\rho_A + \gamma_A + \omega_1 + \mu_1)I_A \\ -r\delta E + (\rho_S + \mu_S + \gamma_A + \omega_1 + \mu_1)I_S \\ -\alpha_A\gamma_A I_A - \alpha_S\gamma_S I_S - vI_W + (\rho_H + \mu_H + \mu_1)I_H \\ -(1-\alpha_A)\gamma_A I_A - (1-\alpha_S)\gamma_S I_S - mQ + (v + \rho_W + \mu_W + \mu_1)I_W \\ -\omega_1 I_A - \omega_2 I_S - (\varphi + \mu_1)V \end{pmatrix}$$

$$(13)$$

Similarly, the partial derivatives of v with respect to the infected compartments at disease-free equilibrium E_0 gives

$$V = \begin{pmatrix} k_2 & 0 & 0 & 0 & 0 & 0 \\ -b_1 & k_3 & 0 & 0 & 0 & 0 \\ -b_2 & 0 & k_4 & 0 & 0 & 0 \\ 0 & -c_1 & -c_2 & k_5 & -v & 0 \\ 0 & -d_1 & -d_2 & 0 & k_6 & 0 \\ 0 & -\omega_1 & -\omega_2 & 0 & 0 & k_8 \end{pmatrix}$$

$$(14)$$

$$FV^{-1} = \begin{bmatrix} A & B & C & 0 & 0 & D \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$(\hat{}15)$$

Where;

$$A = \frac{(1-p_1)\beta_2 S_0 b_1}{k_2 k_3} + \frac{(1-p_1)\beta_3 S_0 b_2}{k_2 k_4} + \frac{(1-p_2)\beta_1 S_0 (b_2 \omega_2 k_3 + k_4 b_1 \omega_1}{k_2 k_3 k_4 k_8}$$

$$B = \frac{(1-p_1)\beta_2 S_0}{k_3} + \frac{(1-p_2)\beta_1 S_0 \omega_1}{k_3 k_8}$$

$$C = \frac{(1-p_1)\beta_3 S_0}{k_4} + \frac{(1-p_2)\beta_1 S_0}{k_4 k_8}$$

$$D = \frac{(1-p_2)\beta_1 S_0}{k_8}$$

Therefore, it follows that R_0 is the spectral radius of FV^{-1} and it is given as;

$$R_0 = A = R_{oA} + R_{0S} + R_{0V}$$

$$\boldsymbol{R_0} = \rho\left(FV^{-1}\right) = \frac{(1-p_1)\beta_2 S_0 b_1}{k_2 k_3} + \frac{(1-p_1)\beta_3 S_0 b_2}{k_2 k_4} + \frac{(1-p_2)\beta_1 S_0 (b_2 \omega_2 k_3 + k_4 b_1 \omega_1}{k_2 k_3 k_4 k_8}$$

$$(16)$$

Where;

$$R_0 A = \frac{(1-p_1)\beta_{DA} S_0 b_1}{k_2 k_3}$$

$$R_0 S = \frac{(1-p_1)\beta_{DS} S_0 b_1}{k_2 k_4}$$

$$R_0 V = \frac{(1-p_2)\beta_1 S_0 (b_2 \omega_2 k_3 + b_1 \omega_1 k_4)}{k_2 k_3 k_4 k_8}$$

Note

$$\beta_2 = \beta_{DA}$$
$$\beta_3 = \beta_{DS}$$

$$\Rightarrow A = \frac{(1-p_1)\beta_2 S_0 b_1}{k_2 k_3} + \frac{(1-p_1)\beta_3 S_0 b_2}{k_2 k_4} + \frac{(1-p_2)\beta_1 S_0 (b_2 \omega_2 k_3 + k_4 b_1 \omega_1}{k_2 k_3 k_4 k_8}$$

$$A = \frac{(1-p_1)\beta_2 S_0 b_1}{k_2 k_3} + \frac{(1-p_1)\beta_3 S_0 b_2}{k_2 k_4} + \frac{(1-p_2)\beta_1 S_0 (b_2 \omega_2 k_3 + k_4 b_1 \omega_1}{k_2 k_3 k_4 k_8}$$

$$B = \frac{(1-p_1)\beta_2 S_0}{k_3} + \frac{(1-p_2)\beta_1 S_0 \omega_1}{k_3 k_8}$$

$$C = \frac{(1-p_1)\beta_3 S_0}{k_4} + \frac{(1-p_2)\beta_1 S_0}{k_4 k_8}$$

$$D = \frac{(1-p_2)\beta_1 S_0}{k_8}$$

Therefore, it follows that R_0 is the spectral radius of FV^{-1} and it is given as;

$$R_0 = A = R_{oA} + R_{0S} + R_{0V}$$

$$\boldsymbol{R_0} = \rho\left(FV^{-1}\right) = \frac{(1-p_1)\beta_2 S_0 b_1}{k_2 k_3} + \frac{(1-p_1)\beta_3 S_0 b_2}{k_2 k_4} + \frac{(1-p_2)\beta_1 S_0 (b_2 \omega_2 k_3 + k_4 b_1 \omega_1}{k_2 k_3 k_4 k_8}$$

DATA

The data for this work were obtained from existing literatures, from World meters and for NCDC. It is represented in the Table 1

Table 1: Table of Parameters values

S/N	Parameters	Values	Source
1	π	0.01888	World Bank Birth rate(2018)
2	P1	0.0351	Rabajante(2020)
3	β_{DA}	0.000000622	Jummy et al, 2021
4	β_{DS}	0.0000004306	Jummy et al, 2021
5	P_2	0.01255	Rabajante(2020)
6	β_1	0.00000016462	Jummy et al, 2021
7	Γ	0.138	World meters,2023
8	ϖ_1	0.01	Assumed
9	ϖ_2	0.1259	Sanchez and Blower2020)
10	Z	0.0003	World meters,2023
11	n	0.001	Assumed
12	μ_1	0.00712	WorldBank Death rate(2018)
13	δ	0.025	Shaikh et al (2020)
14	r	0.05	Jummy et al,2021

15	ρ_A	0.007	Jummy et al,2021
16	γ_A	0.029389	Jummy et al,2021
17	ω_2	0.0356	Jummy et al,2021
18	ρ_S	0.24701	Jummy et al,2021
19	γ_S	0.12072	Jummy et al,2021
20	ω_2	0.025193	Jummy et al, 2021
21	α_A	0.74087	Jummy et al, 2021
22	α_S	0.82189	Jummy et al, 2021
23	ρ_H	0.0357	Jummy et al, 2021
24	μ_H	$\dfrac{1}{10}$	Jummy et al, 2021
25	ν	0.012277	Jummy et al, 2021
26	ρ_W	0.0001	Jummy et al, 2021
27	μ_W	$\dfrac{1}{15}$	Jummy et al, 2021
28	μ_S	0.034632	Jummy et al,2021
29	m	0.002	Assumed

RESULTS AND DISCUSSION

We used the data we got from world meter and literatures to estimate the basic reproduction number of COVID-19 in Nigeria. This is represented in table 1 above. We then substituted the values of the parameters in equation (16), which is our basic reproduction number and obtained 0.2335400100 .We also got the basic reproduction number for asymptomatic, symptomatic and virus shed as, $5.601895189 \times 10^{-6}$, $8.595314992 \times 10^{-7}$, 0.2335335486. These are represented with the graphs below;
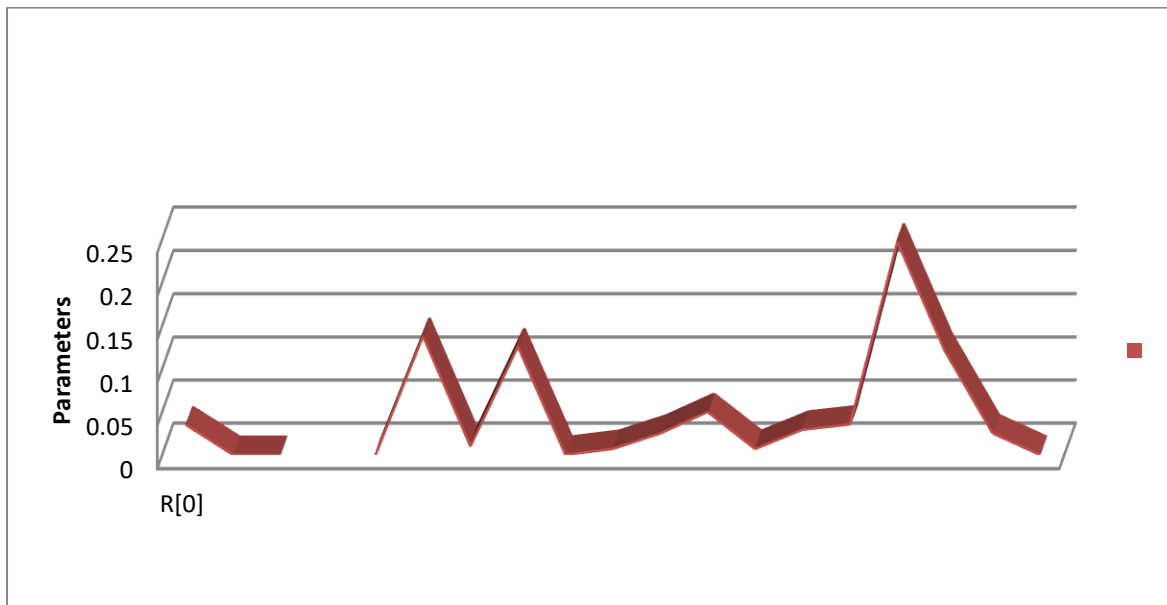

Figure 1: Graph of the basic Reproduction number

From the graph, the values at the y-axis are the parameter values for the parameters that show up in the R_0 . Looking at this graph, it shows that the basic reproduction number is less than 1.
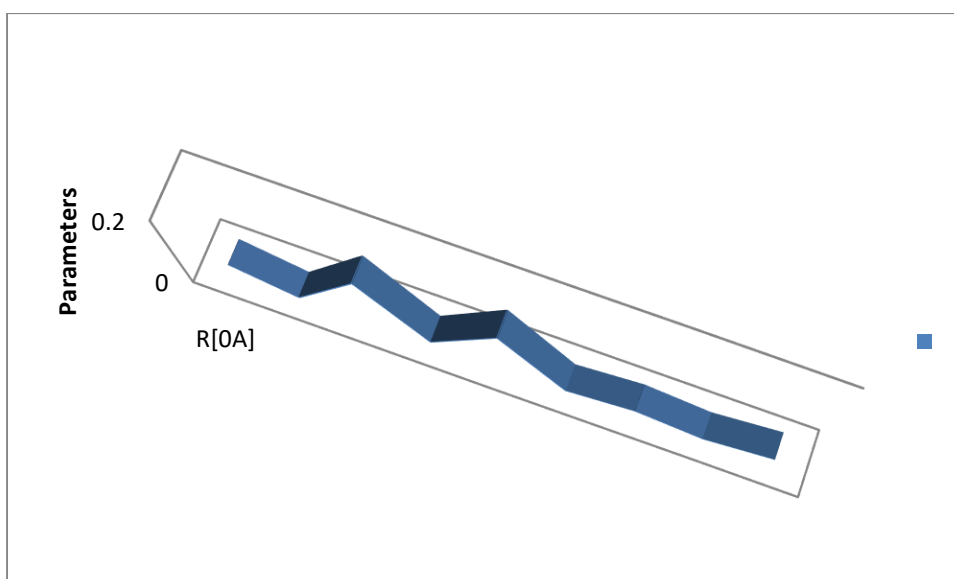

Figure 2: Graph of the basic reproduction number for the asymptomatic individuals

The y-axis contains the parameter values for the parameters that show up in the R_0. This graph shows that the basic reproduction number for the asymptomatic individuals is less than one
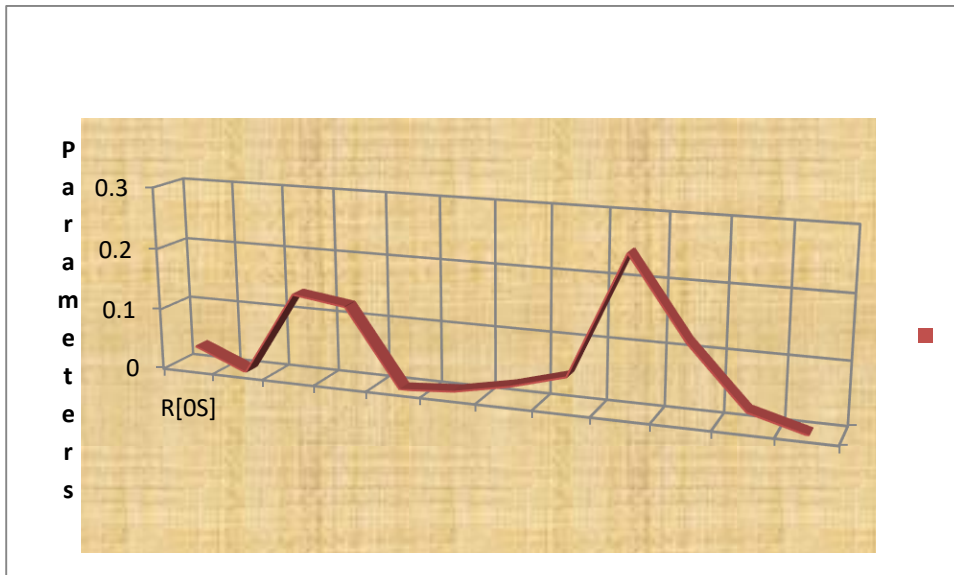

Figure 3: Graph of the basic reproduction number for the symptomatic individuals

This results show that the basic reproduction number for Nigeria is less than 1 ($R_0 < 1$), meaning that COVID-19 is no longer spreading beyond control.

Figure 4: Graph of the basic reproduction number for the virus shed.

This also indicates that the basic reproduction number is less than one.

These results show that the basic reproduction number for Nigeria is less than 1 ($R_0 < 1$), meaning that COVID-19 is no longer spreading beyond control.
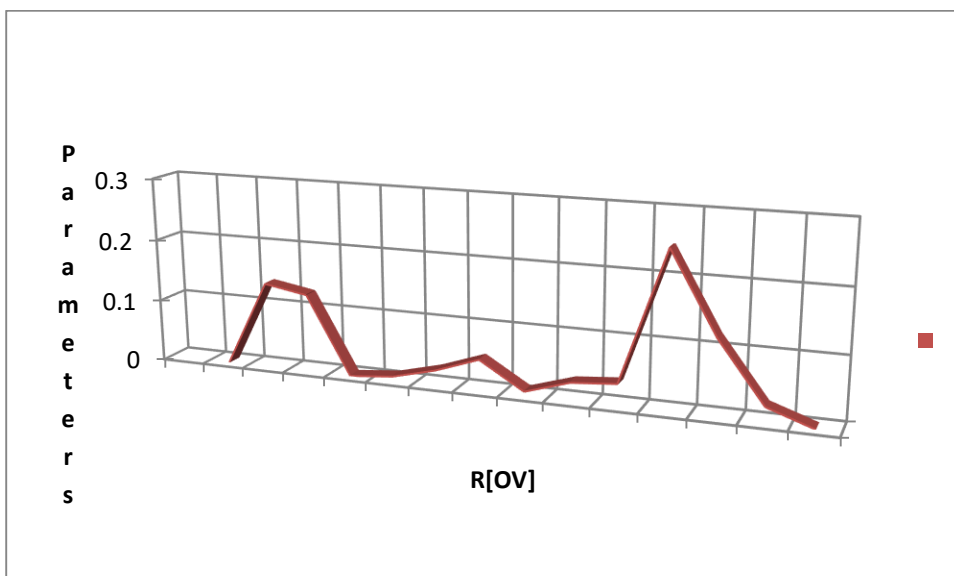
CONCLUSION

COVID-19 is no longer spreading as before in Nigeria. This is attributed to effective control measures that are put in place. It should be noted that that does not mean that COVID-19 is eradicated. However, individuals and public health service providers should not relax in emphasizing the control measures so as to avoid wide spread of the disease. This is because the result from this study will help the government, health care providers and the general public in finding and mapping out strategies on how to get rid of COVID-19 in Nigeria completely.

AUTHOR CONTRIBUTIONS

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Validation: Okorie Charity Ebelechukwu

Visualization: Okorie Charity Ebelechukwu

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Writing – review & editing: Okorie Charity Ebelechukwu, Haruna Yusuf, Bala Ma'aji Abdulhamid, Hina Aliyu Danladi

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