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# The Coronavirus Disease Pandemic and the Basic Reproduction Number $(R_0)$ in Nigeria: What Does the Data Reveal?

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### Abstract

Nigeria continues to record increasing number of persons infected with the coronavirus disease. Within the African region, Nigeria has the second-highest number of infected persons after South Africa, representing 9.95% of the region's total coronavirus disease cases as at June 1, 2020, despite its strict containment measures. With the fears of a second wave of the coronavirus (the COVID-19 Delta Virus), another lockdown might likely be. But can we establish a correlation between infected persons and those prone to infection (susceptible) as well as the correlation strength in Nigeria? Using both a descriptive and econometric technique, the study analyzed the reality of the transmission rate and the rising figures of the susceptible and that the basic reproduction number (R0) is less than 1 suggesting that the rate of transmission is low and the virus might not be endemic. The study, therefore, recommends that the containment measures of sanitizing/washing hands, physical distancing, and using face coverings are just enough to stem the tide. However, sustained lockdown measures will be too costly for the economy and a second lockdown will be highly unnecessary.

Keywords: Health, COVID-19, Basic Reproduction Number, Nigeria, JEL Classification: I1, I18

# Introduction

The terms lockdown, lock out, physical distancing, stay at home, stay safe, stay alert, wear nose mask and wash your hands with running water and soap have become very common since the outbreak of the coronavirus disease otherwise named COVID-19. All states in Nigeria were either in a partial or total lockdown, since the first of April 2020, as the country continues to record high cases of the coronavirus disease among its residents. From an index case that arrived the state of Lagos in the South Western part of the country on February 27<sup>th</sup>, 2020 the figure rose to 4,971 confirmed cases, in 27 states of the country, out of a tested sample of 29,

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408 persons as at 14<sup>th</sup> May, 2020, (NCDC COVID 19 Microsite, 2020).<sup>1</sup> Thus within a space of 90 days, the number of infected persons rose by more than 40,000,000%, an average of 63.73 persons being infected per day. Although more persons are recovering from the infection than they were dying, the social and economic effect of the coronavirus containment measures is taking a toll on the entire nation. Around the globe, countries that sustained lockdown as one of the containment measures experienced significant fall in economic growth and high rates of unemployment. This is evident in the developed countries of the USA and Spain which experienced a double-digit unemployment rate of 14.7% and 15.3% as at April 2020, against the unemployment rate of 3.6% and 13.9% respectively as at November 2019 prior to the outbreak (countryeconomy.com).<sup>2</sup> As the most populous black nation on earth with a population of 211,400,704 persons as of 2021 (The World Bank, 2021)3 and having the largest economic market in

Africa, a sustained or second lockdown will be counterproductive for Nigeria and Africa at large. Nigeria produces only 1/5 of its oil production requirement, earning just 1/5 of its expected oil revenue as observed by Olumide (2020).<sup>4</sup> Thus, an understanding of the relationship between the infected and the susceptible (those with the likelihood to be infected after exposure) is very critical in designing the containment strategy for Nigeria. Can a significant relationship between the number of susceptible (NSUS) and the number of infection (NINF) be established? What can be said about the relationship between the number of recovery (NREC) and the number of infection? How can the relationship between NSUS and NINF as well as NREC and NINF explain the COVD-19 containment design and strategy? This paper is divided into four sections:- a brief introductory section, a literature review on the epidemiology and pathology of the coronavirus, a descriptive and statistical analysis of the trend in the spread of the coronavirus and the implications on the containment strategy.

Viruses are predominantly the cause of widespread contagion (Vidyasagar 2016).<sup>5</sup> However, they cannot thrive or reproduce outside of a host cell. They are, therefore, incomplete cells that need another structure to survive. Thus, in order to survive, multiply and be able to cause a disease a virus must live in a host cell. According to Livescience.com (2020),<sup>6</sup> viruses are microscopic parasites that are generally smaller than bacteria, lack the capacity to thrive outside of a host body, and predominantly have a reputation for being the cause of contagion. Viruses have the capacity to reengineer or reorder the molecular machinery of their host cell, multiply themselves and cause a diseased condition for the host cell. The genetic material for most viruses is either the RNA (ribonucleic acid) or the DNA (deoxyribonucleic acid) needed to encode the required proteins for its cellular activities. Over the years different viruses have caused different diseases such as the Ebola virus, the HIV, the poliovirus, the H1N1/swine flu, hepatitis virus, and the novel coronavirus among others. Viruses are not the only microscopic parasites that invade a host cell to cause diseases or infections. There are also other microscopic parasites like bacteria, fungi and protozoa. In terms of comparison, viruses are much smaller than

bacteria and vary in sizes. For instance the measles virus (220nm in diameter) and the hepatitis virus (45nm in diameter) are smaller than the E.coli bacteria, 8 times and 40 times respectively. The polio virus (30nm in diameter) and the coronavirus (120nm in diameter) are all smaller in size than the E.coli bacteria.

Generally, the coronavirus is any virus that belongs to the family coronaviridae, having an enveloped virions (virus particles) with spiky glycoproteins. In 2002, a similar virus known to be a member of the Beta-coronavirus subgroup, SARS-CoV, that causes Severe Acute Respiratory Syndrome (SARS) emanated from Guangdong, China (Hu, B et. al. 2015).<sup>7</sup> Infected persons manifested pneumonia symptoms with a diffused alveolar injury which leads to acute respiratory distress syndrome (ARDS). SARS-CoV infected more than 8,096 persons and killed about 9.6% (774) around the globe (WHO, 2004).<sup>8</sup> Some 10 years later, by 2012, another virus the Middle East Respiratory Syndrome Coronavirus (MERS-Cov) was detected in Saudi Arabia, infecting more than 2,428 persons and causing 838 deaths (CDC, 2014).<sup>9</sup> In 2019, less than a decade after the MERS-Cov, another virus, a member of the Beta-coronavirus subgroup named COVID-19, emanated from Wuhan, China. It is a disease that affects the respiratory system causing upper respiratory infections. As at May 15, 2020, just about 6 months since its appearance the Betacoronavirus subgroup, COVID-19 has infected more than 4.6million persons in 188 countries, killing over 310,000 persons (John Hopkins Coronavirus Resource Centre, 2020).<sup>10</sup> It is observed that 175,306,598 have been infected with about 3,792,777 deaths as at June 13, 2021 (WHO coronavirus [COVID-19] Dashboard, 2021).<sup>11</sup> It noted that the coronavirus disease (COVID-19) is an infectious disease caused by a newly discovered coronavirus (SARS CoV2) causing mild to moderate respiratory illness for which most persons can recover without requiring special treatment but for which older people and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease, and cancer are more likely to develop serious illness even die. It is not so clear whether COVID-19 is airborne and for how long it could remain in the air, however, the WHO observed that the novel coronavirus is believed to be transmitted via contact with infected

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persons. These contacts might include handshakes, hugs, or touching things touched by infected persons and using same hands on the nose, eyes or mouth. The coronavirus is thought to be contained in the saliva and sneeze discharges; thus, the virus is said to spread primarily through saliva droplets and nose discharge as an infected person coughs or sneezes. Initially, COVID- 19 was thought to emanate from the seafood market, where live animals were sold in Wuhan China and to be transmitted from animals but when those who did not visit the market were known to exhibit symptoms of the COVID-19 disease, it became obvious that the virus had a human to human transmission capability. The US Centre for Disease Control and Prevention posits that the coronavirus disease is transmitted from person to person when infected persons breath out droplets or particles containing the virus and this is inhaled or it lands on the nose, eyes or mouth of the person close to them (CDC, 2021).<sup>12</sup> In its July 2020 report, the European Centre for Disease Prevention and Control  $(ECDC)^{13}$  observed that the coronavirus is mainly transmitted when the respiratory droplets, are inhaled or deposited on mucosal surfaces during person to person interaction. It noted that there is no documented evidence of the coronavirus transmission via contact with contaminated surfaces or fomites even though it is presumed possible. This argument might sound true since viruses do not survive outside a host cell. Hence even when there are droplets of the virus on fomites, such fomites cannot act as vectors when sufficient times have elapsed after the droplet. The WHO  $(2021)^{11}$  noted that all viruses do not retain the same characteristics but do change over time and this includes the virus that causes COVID-19, SARS-CoV-2. These changes do not often affect their physical properties but do affect their transmission rate, mechanism, severity and in most cases the efficacy of vaccines, current diagnostic tools and processes as well as safety measures put in place.

This underscores the fact that for a novel virus like the SARS-COV-2 or coronavirus, the study of its transmission rate, mechanism and containment remains an ongoing exercise.

### Materials and method

This research employed two methods to analyse the relationship between the infected and susceptible in Nigeria, to determine the reality of the rate of infection of COVID-19 in Nigeria. The first method is the econometric approach involving the use of multiple regression techniques while the second method is descriptive involving charts, percentages and ratios. The study basically used 3 variables, the number of persons infected with COVID-19, the number of persons tested for COVID-19 and the lagged values of the number of those infected with COVID-19. The variables were obtained from the Nigerian Centre for Disease Control (NCDC) composite data microsite found at www.ncdc.gov.ng. The variables and their notations are explained in table 1.1.

The econometric approach begins with the adoption of a mathematical epidemiologic model often used in epidemiological studies as proposed by Kermack and Mckendrick (1927). It is a deterministic model often called the compartmental model or the SIR model. The model is often used to explain the following: whether or not an infection can spread within a population over time, the estimated number of infected persons over time, to evaluate the impact of different containment strategies, and to determine optimal vaccination strategies among others. The model is based on the assumption that the population is fixed and there are no external infiltrations into the system. Keeping the population fixed makes it easier to establish a constant infection rate. The SIR model divides the population into three compartments or groups. The first compartment is the susceptible, often denoted with 'S', representing the fraction of the population that will be infected over time, usually a larger

<b>Table 1.1:</b>	Variable	notation	and	definition
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Variables	Definition	Type of Variable			
INFC	Natural log of Number of infected persons	Dependent			
TESTED	Natural log of Number of susceptible*	Independent			
LINFC	Natural log of Lagged values of the number of infected	Independent			
Source: Author's Initiative. *Note that susceptible and tested is used interchangeably.					

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proportion of the population. The second compartment is the infected or infective often denoted with 'I', representing the fraction of the population that is infected and can infect the susceptible, those in the first compartment. The third compartment is the recovery or removed group, often denoted with 'R', which is the fraction of the population that recovered from the infection to live a normal life. Note that the recovered is also known as the removed and include those who either die or have developed some immunity and so cannot get infected again. The SIR model is often expressed or illustrated as follows:

$$S \to I \to R$$
 (1)

From model (1), the arrows indicate that individuals in the first compartment (S) can move to the next compartment (I) and eventually to the third compartment (R). The model assumes a one-way directional movement without reversal. The movement from the first compartment occurs when the susceptible comes in contact with the infected and the contact transmits the infection such that the susceptible is now infected. As more of the susceptible get infected, the size of the susceptible diminishes while the size of the infected grows over time due to the transmitting contacts between the two compartments. Also, there is the possibility of people moving from the second compartment (I), the infected, to the third compartment (R), either when they recover from the infection to continue living healthy lives or they die.

Two questions become critical at this point (i) what is the rate at which a susceptible gets infected? (ii) what is the rate at which an infected recovers from the infection? The answers to these questions will stem from the strength of the correlation between the susceptibles and the infected as well as between the infected and the recovered. Answering these questions will also help to determine how many persons can be infected with the disease during a given period and what appropriate preventive or containment measures need to be taken. Equation (1) can be restated as a mathematical relationship from which further inferences can be made as follows.

S + I + R = N....(2)

From equation (2) it can be seen that the sum of the susceptible, the infected and the recovered equals the entire population. Four assumptions are critical here: (i) that the epidemic will not last so long and so the population is constant, (ii) that the degree of infection is proportional to the rate of contact between the susceptible and the infected at some constant rate, (iii) that there is a constant rate of recovery, and (iv) that all contacts have a high probability of being contagious. These assumptions will give rise to a system of the equation relating the three components in equation (2). These are expressed below:

$$\frac{\partial S}{\partial t} = -\beta S_t I_t .....(3)$$

$$\frac{\partial I}{\partial t} = \beta S_t I_t - \alpha I_t .....(4)$$

$$\frac{\partial R}{\partial t} = \alpha I_t .....(5)$$

The system of equations denoted by equations 3, 4 & 5 indicates that there exists a relationship between the susceptible, the infected and the recovered. Equation (3), shows that changes occur in the susceptible compartment by some negative constant  $(\beta)$  through the interactive contact between the susceptible and the infected. The negativity is because the susceptible is reducing in number since individuals who get infected move out of the susceptible compartment to the infected compartment and there are no external entrants. The constant ( $\beta$ ) is the rate of infection which depends largely on the size of the infected but more significantly on the number of contacts between the susceptible and the infected and the probability that the contact will lead to a transmission of the infection. Equation (4), indicates that changes in the number of infected persons will occur due to interactive contacts between the susceptible and the infected via a positive constant ( $\beta$ ) but will also be negatively affected by the number of those who recover, via a negative constant ( $\alpha$ ), and move out of the infected group. Equation (5) indicates that the recovery depends on the rate of recovery and the number of infected persons. Having explained the relationship exiting between the compartments in the model we can estimate or state the number of persons who can be infected by the disease at any

given period. We restate equation (2) in the mathematical form again but with time essence as follows.

$$S_{(t)} + I_{(t)} + R_{(t)} = N$$
.....(6)

Equation (6) shows that a change in any of the components S,I and R will lead to a change in the same direction in N, which is constant since the population is constant. But more importantly, the equation is deterministic, and every variable is determined within the model. Thus, to determine the number of persons to be infected over time we focus on I, the infected variable. Therefore, from equation (6) the number of persons infected by a given virus or ailment s defined as follows:

$$I_{(t)} = N - (S_{(t)} + R_{(t)})....(7)$$

Equation (7) indicates the number of infected persons at a given time. However, to determine the number of persons to be infected over time, that is to predict the number of infections given an outbreak, it is appropriate to know the rate of infection, that is, by how many people get infected over time. This is defined by a given constant as shown in equation (8).

From equation (8), the total number of persons to be infected at any one period, say  $_{t+1}$ , is equal to the sum of the infected persons in the current period (,) plus the fraction of the susceptible that will get infected

in period<sub>t+1</sub>. In equation (8) the term  $\frac{(S_{t+1})}{N}(I_t)$ 

indicates that the fraction of the susceptible that gets infected must have interacted with the infected at some constant ratio since not all contacts bring about an infection. It is obvious, therefore, that the number of infected persons at any point is determined by the size of the susceptible, the size of the previously infected and the rate of contact, given that each contact has a high potential of transmission. This relationship can be expressed in a functional form as follows:

$$I_{t} = f(S_{t}, I_{t-1})....(9)$$

Equation (9) simply states that the number of infected persons is a function of the size of the susceptible and the number or size of those previously infected, that is to say, the number of

infected at any current period is given by the sum of the number of susceptible that will be infected in the current period and the number of infected persons in the previous period. This relationship is further expressed in the mathematical and econometric form in equations (10) and (11) as follows:

$$I_{t} = S_{t} + I_{t-1}....(10)$$
  
$$I_{t} = \alpha_{0} + \alpha_{1}S_{t} + \alpha_{2}I_{t-1}....(11)$$

Equation (9) is the functional form of equation (8)and states that the number of infected persons in a given population and at a given period, is a function of the number of newly infected persons and the number of previously infected persons. We assume that the new infections are a result of contagious contacts within the population. Thus, equation (9) is expressed in the deterministic (non-stochastic) econometric form in equation (11). Equation (11) is expressed to imply that the number of infected persons at a point (t) is explained or determined by the sum of the number of newly infected and the previously infected. However, equation (11) is a deterministic model, implying that St and It-1 alone determine the number of infections in the period (t). This does not fully explain relationships in economics since there are a host of other variables that explain a given economic condition that are not readily known or even captured in a given model. In relation to the novel coronavirus, a lot is yet to be known about its mode of transmission, whether it is person to person, airborne, age or health-related, geographically inclined etc. It suffices, therefore, to assume an indeterministic model, which captures the unknown variables in the transmission mechanism. This is appropriate to allow for a realistic estimation of the parameters of the variables S and I and to be able to state a quantifiable rate of infection given a defined relationship between the infected and the susceptible. It is known that if a person with an infectious disease comes in contact with a population there is every likelihood of the infection spreading within the population. But the question is, what is the probability that every contact will lead to a transmission? This can be explained by the correlation coefficient or the parameter coefficient of the explanatory variables (St and It-1). Thus, equation (11) is expressed in the stochastic econometric form as follows:

$$S_{(t)} + I_{(t)} + R_{(t)} = N.....(6)$$

Equation (12) is now the model to be estimated to determine the number of infected at any point in time and the strength of the relationship between the number of infected in the current period and the explanatory variables (susceptible and previously infected). Since we have introduced lagged values, the model to be estimated will be stated in the autoregressive form as follows:

$$\Delta I_t = \alpha_0 + \varphi I_{t-1} + \alpha_1 S_t + \sum_{i=1}^{p-1} \pi_i \Delta I_{t-i} + u_t \dots \dots (13)$$

#### Results

The result of this study is presented in two approaches, an econometric estimation and a descriptive analysis. The econometric approach estimates the result based on the multiple regression techniques using STATA version 15. Below is the multiple regression result as estimated with the STATA application using data on COVID-19 as contained on the Nigerian Centre for Disease Control (NCDC) composite data microsite.

On the other hand, the descriptive approach involved the use of charts, graphs, percentages and ratios from which inferences were made about the reality of the infection rate of the coronavirus disease in Nigeria. Expectedly, the results of both the econometric and descriptive statistics was not significantly different to draw a reliable and robust conclusion.

The data used for the descriptive analysis of the coronavirus infection is obtained from the official website of the Nigerian Centre for Disease Control (NCDC). The data cover the period from April 16, 2020, to June 15, 2020 and is given in table 1.3. The analysis includes the number of persons infected during the period, the number of persons tested (the susceptibles), and the number of persons that died or recovered. The data was not transformed in any form and was also used to plot a graphical relationship between those infected by the coronavirus and those who are susceptible to the coronavirus, indicated in figure 1.1 and 1.2.

 Table 1.2: Regression INFEC on SUSCEPTIBLE (TESTED), LINFEC

Variables	Coefficient	Std. Error	T-value	P> t-value	95% con int.
CONSTANT	-1.3010	.4627	-2.81	0.009	-2.2503 -0.3517
TESTED	0.2145	0.0988	2.17	0.039	0.0117 0.4173
LINFEC	0.8878	0.0652	13.61	0.000	0.7539 1.0217
Num. of Obs.	= 30				
F(2 27)	= 12086.51				
Prob > F	= 0.0000				
R-squared	= 0.9989				
Adj R-squared	= 0.9988				
Root MSE	= 0.0274				
Durbin Watson	= 2.0827				

Source: Author's initiative

Table 1.3: Variable data, dates and statistics

Period	Variables						
DATES	*INFC	*TESTED	*DIED	*REC	**INFC/TES	** INFC/DIED	**INFC/REC
16/4/2020	442	6649	13	152	1:0.06	34.0:1	2.9
30/4/2020	1932	15759	58	319	1:0.12	33.3:1	6.0
15/5/2020	5445	32942	171	1320	1:0.16	31.8:1	4.1
31/5/2020	10162	63882	287	3007	1:0.16	35.4:1	3.4
15/6/2020	16658	96402	424	5349	1:0.17	39.3:1	3.1

Data Source: \* Nigerian Centre for Disease Control (NCDC). \*\* Author Initiative. \*\*\* Tested and susceptible are similar and used interchangeably.

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The graphical illustration of the interrelationship among those infected by the coronavirus, lagged values of the infected and the susceptible is presented by chats as shown in figure 1.1 and 1.2. The vertical axis indicates the number of those infected or susceptible to the infection while the horizontal axis indicates the period covered measured in days.

### Fig 1.1



# Fig 1.2



### Discussion

The discussion of results begins with the econometric result of the infection rate from the Nigerian data as indicated in equations 14. The relationship expressed in equation 14 was obtained from the econometric estimation indicated in table 1.2. (The complete results including relevant preliminary test results are contained in appendix A):

$$INFC_t = -1.3010 + 0.2145TESTED_t + 0.8878LINFC_{t-1} + u_t$$
.....(14)

From equation 14, it can be observed that the coefficients of the dependent variables are both positive which is expected. The coefficient of the tested (susceptible) shows a positive but weak correlation between the susceptible and the infected. Thus, a 1% change in the number of susceptible (tested) leads to a 0.21% (table 1.2) change in the number of infected in the same direction. This change could result from an increase in the number of the tested (susceptible), or some sort of interaction between the infected and the susceptible that alters the infection status of the susceptible. Thus, the rate at which people will move from one compartment (the susceptible) to another compartment (the infected) per day is 0.21%, assuming that there is a chance of daily contact. This means that for every interaction between an infected and a susceptible, the probability of the susceptible being infected is 0.21. It could be said as well that if one infected person interacts with a susceptible there is just 0.21%chance that such an interaction could be contagious leading to infection transmission. Again, the lagged values of the infected have a positive correlation with the current values of the infected. This suggests that infected persons who do not receive treatment early enough to suppress the effect of the disease in their system have a higher probability of infecting the susceptible and in this case, persons with underlying health problems are more at risk. As noted, a 1% change in the past level of infected leads to a change in the current level of infected by 0.88%. But even more significant from the result is the value of the constant (-1.3010) which is negative. This negative value of -1.3010 gives the value of the current level of coronavirus infection given that there are no infected person is in the population or given that the infected persons are quarantined and do not have contact with the population. It indicates that if the spread of the disease is controlled and transmission is completely prevented, then the disease will reduce to nothing. Besides, negative quantities are meaningless in economics and imply no possibility of infection transmission.

On the other hand, table 1.2, shows the data used for the descriptive analysis. The first 4 columns of the variables were obtained from the NCDC COVID-19 data update site while the last 3 columns were the author's initiatives. The data on the first 4 columns covered the number of infected with COVID-19 (INFC), number of those tested for COVID-19 (TESTED), number of those who recovered from COVID-19 (REC) after treatment and number of those who died from COVID-19 (DIED). The data covered a period of 60days (16/04/2021 to

15/06/2021) which gives enough period to analyse the spread of variables like the SARS-COV-2 within a population on a daily basis. Table 1.2 also shows figures in ratios to give a bird's eye view and inferential diagnosis of the spread of the coronavirus infection in Nigeria from April 16, 2020, to June 15, 2020. From the table, the ratio of the susceptible to the infected was not constant but averaged 1:0.13 during the period. As at 16<sup>th</sup> April, 2020 the ratio of the infected to the susceptible was 1:0.06 suggesting that if one infected person interacts with another person the probability of the interaction becoming contagious is 0.06. If the infected interacts with 10 or more persons the probability of transmission is 0.6 i.e (0.06 x 10). By the 15<sup>th</sup> of May, the ratio of infected to the susceptible had increased by 62.5% from 1:0.06 to 1:0.16. Thus the probability of infection has increased by a reasonable margin from 0.06 per contact to 0.16. It means that if there is a 1% level of interaction between an infected and the susceptible, there is about a 0.16 % level of infection transmission. If we take the number of the susceptible as of 15<sup>th</sup> May, 2020 for instance, and given the infection transmission probability of 0.16, it follows that the number of persons likely to be infected after contacts or interaction with an infected person is less than one [32,942/5445 = $6.0449 \div 6.0499 (0.16) = 0.95$ ]. Thus less than or at most one person will be infected with the disease. Also, as at 15<sup>th</sup> June, 2020 the ratio of the infected to the susceptible remained virtually the same increasing only by 0.01. If we take the number of the susceptible as at 15<sup>th</sup> June, 2020 as a population sample and give the infection transmission probability of 0.17, it follows that the number of persons likely to be infected after contacts or interaction with an infected person is less than one  $[96,402/16,658 = 5.7871 \div 5.7871 (0.17) = 0.98].$ Again less than or at most one person will be infected with the disease during the period. (Note that the figures in parenthesis were obtained from table 1.3).

To further corroborate the result of the econometric and descriptive approaches, the rate of infection can also be measured by the basic reproduction number  $(R_0)$  which is an epidemiologic metric used to indicate how far and fast an infectious disease could spread or decline within a community.  $R_0$  measures

the transmission potential of disease beginning with the index case. It is defined as the average number of secondary infections produced by an index infection case in a population where everyone is susceptible. In reality, though not everyone is susceptible due to several factors such as natural immunity, life-long or conferred immunity, and immunization. R<sub>0</sub> is often calculated using complex mathematical equations that involve a variety of data obtained at the onset of the outbreak of the disease often impractical to obtain. Such data includes the disease's characteristics and transmissibility, human behavior, frequency of contacts, location of the community, age, etc. Due to the difficulty of obtaining these data, the basic reproduction number  $(R_0)$  is often estimated retrospectively using seroepidemiologic data. In most cases, the basic reproduction number  $(R_0)$  obtained based on mathematical models is conditioned by subjective factors of the modeler (Delamater et. al. 2019).<sup>14</sup> However, one rule of the thumb approach used to calculate the basic reproduction number by epidemiologists is by collating the contact tracing data obtained at the outbreak of the epidemic. Thus, a person's contacts are traced and tested and if his diagnosis is positive the  $R_0$  is computed by obtaining the average number of secondary cases caused by the diagnosed individuals (Breban et. al. 2007).<sup>15</sup> Therefore, the basic reproduction number can be obtained by dividing the total number of infected persons by the number of contacts traced.

Often, a distinction is made between the basic reproduction number  $(R_0)$  and the effective reproductive ratio (R) which is the average number of secondary cases per infectious case in a population made up of both susceptible and nonsusceptible hosts (Dharmaratne et.al. 2020).<sup>16</sup> As a rule, if the  $R_0 > 1$ , then the infection will spread fast among the susceptible population in which case the infection rate is high. But if the  $R_0 < 1$ , the infection will spread slowly within a limited number of the population and shrink or eventually disappear in which case the infection rate is low. If the  $R_0 = 1$ , the infection is endemic, affecting a specific area over time. The basic reproduction number is often determined by the rate of contacts within the host population, the probability of contact being contagious, and the duration of infectiousness. From table 1.3 we can obtain the basic reproduction number for the five selected period given by the ratio of the infected to the tested as rule of thumb. The ratios and the respective periods in brackets are stated accordingly as follows:

0.06(16/04/2020); 0.12(30/04/2020);0.16(15/05/2020); 0.16(31/05/2020) and 0.17(15/06/2020).

For all the five periods, the  $R_0$  are all less than 1 and the average  $R_0$  for the five-period given by the sum of the ratios divided by the periods is also less than 1 (0.13). This shows that the transmission rate of the coronavirus or the probability of a contact being contagious for Nigeria is low, in which case the disease will not be endemic but will spread slowly and eventually shrink. The study is neither asserting nor suggesting that the coronavirus does not pose a threat or that it does not transmit from one person to another. For a country like Italy, the basic reproduction number ranged between 2.43 to 3.10 indicating that the rate of transmission is high (D'Arienzo & Coniglio, 2020).<sup>17</sup> Thus the basic reproduction number for Nigeria casts doubt on the rate of transmission or spread as claimed.

In addition to table 1.3, figure 1.1 shows the relationship among the susceptible, infected and lagged values of infected individuals with the coronavirus disease. It shows the level or rate of growth among the infected, lagged values of infected and the susceptible. The number of the susceptible for each day is coloured blue and exceeds the number of infected and lagged values of infected for the period, coloured orange and gray respectively. These are the number of those tested for COVID 19 per day and are considered susceptible. There is a close relationship between the number of infected and lagged values of infected as indicated in the chart. In particular the number of infected and the lagged value of infected did not depart significantly from each other but showed a slow but steady rise. When placed horizontally in figure 1.2, the three variables all move in the same direction with the infected and lagged values of infected falling below the susceptible. The charts (fig. 1.1 & 1.2), indicate an upward trend in the number of infected and its lagged values but the statistical significance of such upward trend is not readily verifiable.

#### Conclusion

From the result obtained using the econometric and descriptive statistics, the infection rate for the coronavirus in Nigeria is low. The econometric results showed that the probability of a susceptible to move from its compartment to the infected compartment or the probability of getting infected is 0.21% which is less than 1%. Also, from the descriptive analysis, the basic reproductive number at the onset of the epidemic (as at16/04/2020) is 0.06 and the average basic reproductive number for the selected period (April  $16^{th}$  – June  $15^{th}$ , 2020) is 0.13 which are both less than 1. This implies that the coronavirus disease will not spread as fast as proposed but will shrink and may not be endemic. This contradicts the rumor that the coronavirus is spreading very rapidly in Nigeria and will kill hundreds of thousands in the near future if necessary actions are not taken. Nevertheless, all measures to reduce the spread that will not negatively impact on production can be adopted as documented evidence on the destructive impact of the coronavirus exists in some parts of the world. The study, therefore, recommends the following:

I. That the coronavirus containment measure of physical distancing, hand washing/sanitization, and face or nose coverings are enough and should be sustained.

II. That a second lockdown will be highly unnecessary and will negatively impact the already ailing economy with consequences on the socioeconomic livelihood of the people.

III. That the methods of collating the coronavirus data in Nigeria need to be reviewed so that accurate data is obtained that will inform appropriate policy and actions.

IV. That additional testing and treatment facilities are required to ensure that more persons are tested since the disease is still a novel disease.

V. That the Basic Reproduction Number  $(R_0)$ remains the appropriate yardstick for measuring the rate of infection rather than the nominal figures.

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