

A Mathematical Model of the Effects of Social Distancing and Community Lockdown on the Spread of Covid-19 Pandemic in Nigeria

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Abstract

The novel Coronavirus Disease 2019 (COVID-19) is a highly infectious disease caused by a new strain of severe acute respiratory syndrome of coronavirus 2 (SARS-CoV-2). The virus has spread from Wuhan city in China in December 2019 to no fewer than 200 countries as at June 2020 and still counting. Nigeria experienced a rapid spread of the virus amidst weak health system. In this study, we propose a mathematical model of COVID-19 which is designed and used to analyze the transmission dynamics and control of COVID-19 in Nigeria. The model incorporates the compartments and parameters regarding COVID-19 in Nigeria, and was analyzed and parameterized using COVID-19 data published by the Nigeria Centre for Disease Control (NCDC). This was adapted to assess the community-wide impact of two control and mitigation strategies adopted in Nigeria. Numerical simulations of the model showed that COVID-19 can be effectively controlled in Nigeria with moderate levels of social-distancing and community lockdown strategy in the entire nation. The model was able to analyze the stability of the disease-free equilibrium solution of the model and key parameters of the model were estimated. Sensitivity analysis was carried out to investigate the influence of the parameters in curtailing the disease. The model shows that COVID-19 can be effectively managed or eliminated in Nigeria if both control measures were systematically implemented to limit the basic reproduction number to less than unity.

Key Words: Community lockdown, Covid-19, Mathematical model, Social distancing, Infectious disease, Virus.

Introduction

A novel Coronavirus, christened COVID-19, caused by SARS-CoV-2, emerged out of

Wuhan City in China at the end of 2019.

The pandemic, which rapidly spread to many countries inflicted severe public health and socio-economic burden in many parts of the world, including in Nigeria. As at

September 30, 2020, there were over 28.8 million confirmed cases and about 921,000 deaths globally (World Health Organization, 2020). Coronavirus (COVID-19) is an infectious disease caused by severe acute respiratory syndrome (SARS-COVID-2). According to the World Health Organization (WHO), coronavirus (COVID-19) has caused monumental effects and has subjected the world to a health disaster, as no continent on the planet earth was free from the life-threatening and tragic pandemic.

In Africa, Nigeria recorded the first case of the coronavirus pandemic on February 27, 2020, from an Italian man who was diagnosed with the infectious disease in a laboratory in Lagos. Following the trend of the pandemic in other countries, the incidence triggered fear and reactions that the virus could be disastrous if proactive measures were not taken by the government to curb its spread. Feng et al (2020) revealed that the symptoms of COVID-19 include cough, fever, weakness and difficulty to breath. Coronaviruses could spread from person to person and can be extremely contagious. Transmission routes include direct and indirect transmission Indirect transmission relates to being air-borne of droplets from coughing and sneezing, and contacting some contaminated surfaces.

Mathematical models have historically, been used to provide realistic insight into the transmission dynamics and control of infectious diseases, dating back to the pioneering works of Kermack and McKendrick (1927). Different mathematical models exist in literature on infectious disease dynamics. However, for this work we are adopting the classical deterministic model for COVID-19 considering the quarantined individuals, confirmed cases, nonlinear forces of infection in the form of saturated incidence rates in humans and the impact of the direct transmission route from the virus in the environmental reservoir to humans. The study intends to describe the transmission from the exposed individuals to the susceptible individuals and from the infected individuals to the susceptible individuals. We shall therefore construct a deterministic 6-compartment model for COVID-19 incorporating the quarantined and the confirmed cases and we shall perform an analysis of the model to establish its biological relevance and establish by simulation, the impact of control measures.

The study therefore is intended to present a customized model of COVID-19 infection by identifying some appropriate compartments, representing the compartments as a system of non-linear

equations, testing the validity of the model and performing some numerical simulation of the model to determine the impact of control measures on the basic reproduction number. Some of the worst cases of COVID-19 according to World Health Organization (WHO) were recorded in the United States, Italy, Britain, Brazil, India and Russia, and in Africa, South Africa and Egypt had high numbers. Following the W.H.O declaration, Several Coronavirus Preparedness Groups were constituted at various levels in Nigeria. WHO had categorized Nigeria as one of the 13 high-risk African countries with respect to the spread of COVID-19. However, it has been established that behavioural moderation can help contain the spread of coronavirus. Some of the suggested measures to inhibit the spread of coronavirus pandemic include; improved individual habits such as personal hygiene, constant washing of hands with alcohol-based sanitizers, good respiratory attitude (closed coughing and sneezing), wearing of face mask, social distancing, avoiding touching of the face, and reducing contacts with people through self-isolation at home or avoiding nonessential travels or gatherings.

The effort to understand the behavior of diseases through mathematical models has recently had a great resurgence,

especially regarding infectious diseases (Casals et al 2009). In 1760, Daniel Bernoulli proposed several mathematical models for some infectious diseases, especially smallpox, which at that time affected the English population (Bernoulli and Blower, 2004). In order to understand infectious diseases, mathematical models are employed to clearly reveal the dynamics of the disease and investigate the effects of control measures on the disease. Mathematical models analyses for infectious diseases tell the conditions to be satisfied for the disease to completely wipe out of a given population. Zeb et al (2020), Ming et al (2020) and Nesteruk (2022) developed mathematical models to study the dynamics of the covid-19 disease. Tsetimi and Ossaiugbo (2020) studied the Bifurcation Analysis of a Mathematical Model for the Covid-19 Infection among Pregnant and Non-Pregnant Women and revealed that amongst the more sensitive parameters of the basic reproduction number are the modification parameter accounting for increased susceptibility to covid-19 infection by pregnant women, the transmission coefficient of the hospitalised class, the rate of delivery of newborns, and the transmission coefficient of the infectious pregnant women. Incorporating isolation class, Zeb et al. (2020) developed a

mathematical model for the dynamical behavior of the coronavirus disease and used the nonstandard finite difference (NSFD) scheme and Runge-Kutta fourth order method for the numerical solution of the model. Todo et al (2022) studied the relationship between the number of deaths from Covid-19 and the number of infected cases using the Pearson's correlation coefficient and found that there exists a very strong relationship between them. Adegboye et al. (2020), used a log-linear Poisson regression model to estimate the early transmissibility of the novel coronavirus in Nigeria. Their 45-day estimates showed that, although COVID-19 cases in Nigeria have been remarkably lower than expected, more testing needs to be done to stop local transmission. Musa et. al. (2020), estimated the growth rate and basic reproduction number of the novel coronavirus to show the potential of the virus to spread, and to reveal the importance of sustaining stringent health measures to control the disease in Africa. Amzat et al (2020) said that the coronavirus disease of 2019 (COVID-19) pandemic gripped the world with a shock, thereby overwhelming the health system of most nations. Aghanenu et al (2022) developed a model which was analyzed to gain insight into the transmission dynamics of Covid-19. Their study explained the prospects of

controlling Covid-19 disease in Nigeria and shows that combining various intervention strategies such as face mask in publics, social distancing, contact tracing as well as the administration of an impactful vaccine will help in controlling the disease in the population. Daniel (2020) developed a mathematical model for COVID-19 transmission and the need for preventive measure in Nigeria. In her model, she was of the view that there may be underreporting of confirmed cases and death reported especially during the period of lockdown due to poor health system in Nigeria in terms of surveillance and level of testing. Ojarikre et al (2022) studied the simulation of infectious disease model and its effects to the Nigerian economy, they were of the opinion that COVID-19 been the deadliest communicable disease the world has seen so far has touched lives negatively in different magnitudes. They used different approaches in characterizing the likely situation resulting in infection of one or more individuals in a completely susceptible population. Iboi et al. (2020) developed a mathematical model to determine whether or not a hypothetical imperfect vaccine can lead to the elimination of COVID-19 in the United States. Their study showed that such elimination is feasible, using the hypothetical vaccine with assumed efficacy

of 80%, if the vaccine coverage is high enough to achieve herd immunity. In particular, the vaccine coverage needed to achieve herd immunity in US is 90%, while the computed herd threshold for the states of New York and the state of Florida are 84% and 85%, respectively. Kucharski et al. (2020) showed that a reduction in COVID-19 transmission can be achieved when travel restrictions are implemented. Li et al. (2020) showed that increasing influenza vaccine uptake would facilitate the management of outbreaks of respiratory pathogens circulating during the peak flu season.

The outbreak of COVID – 19 in Nigeria has had enormous negative impact on both human and material resources. This study seeks to provide an effective model for the impact of two key non-medical interventions (Social distancing and community lockdown) through simulation and thereby contribute to the global search for mitigations.

Formulation of the Proposed Model

This research adopts the SEIR model framework with total human population of size U with two additional classes (Quarantined and Confirmed cases), giving a deterministic 6-compartments-model. The assumptions upon which the model is built, and the schematic diagram showing the

dynamical flow of infections shall be clearly presented. Some of the parameter estimates used for simulation in this work were drawn from literature. Others were estimated from the available COVID-19 data (confirmed cases, recovered cases, deaths, and samples tested) published by the NCDC to stimulate the unknown parameters. Population and birth rate data were collected from Countrymeters (2020) Nigeria Population 2020. The initial data correspond to the epidemic data officially released on 29th of February, 2020. The corresponding estimated parameters are obtained by fitting an optimization method (Maximum Likelihood Estimation (MLE)) based on the reported data and the epidemic occurrence is predicted for the future. This was analyzed using Python 3.6.0 by generating a curve fitting model using `scipy.stats` library with `optimize` option and passing some initial guesses for the parameters, which are fitted with `numpy`. We fit the cumulative number of confirmed cases generated from the model (1.1) to the NCDC reported data of cumulative number of confirmed cases, which are in agreement with the reported data from February 29, 2020 to May 14, 2020.

To study the transmission and the spread of COVID-19 in Nigeria, we partitioned the total human population at time t , denoted by $U(t)$, into six (6) mutually-exclusive compartments. They are the Susceptible population denoted by M , the Exposed population denoted by N , the Infected population denoted by O , the Quarantined population denoted by P , the Confirmed cases denoted by Q , and the Recovered population denoted by R . The susceptible population consists of individuals who may be infected with the virus, the exposed population are individuals who have been infected but they are without symptoms usually at the early stage or incubation period of the virus. The infected population are those that are fully showing

the disease symptoms usually the latent period of the virus and are capable of infecting others. The exposed population and the infected population contain asymptomatic infected and symptomatic infected individuals respectively. The quarantined population are individuals who are quarantined for some time, if they start showing symptoms of the infectious disease and are tested to determine whether the diagnosis is confirmed. If tested positive to the virus, they are isolated to receive treatment. After a period of treatment and have satisfied all observatory requirement, they moved to the recovered population.

Therefore, the proposed model is simply presented as

$$U(t) = M(t) + N(t) + O(t) + P(t) + Q(t) + R(t),$$

where $U(t)$ is the total number of individuals at a given time t , $M(t)$ is the number of susceptible individuals at a given time t , $N(t)$ is the number of individuals infected but no symptoms shown yet at a given time t , $O(t)$ is the number of individuals infected but not yet isolated at a given time t , $P(t)$ is the

number of quarantined individuals at time t , $Q(t)$ is the number of confirmed infected individuals that are isolated and expecting recovery at a given time t , and $R(t)$ is the number of recovered individuals at a given time t

Table 1: Description of the parameters of the model

Parameter	Description
U	Total population
$1/\varphi$	Incubation period
∇	Birth rate of individuals
α	Death rate
a_{cr}	Recovery rate
β	COVID-19 death rate
a_{mp}	Rate of susceptible being quarantined
a_{pm}	Rate of quarantined going back to the susceptible class
a_{np}	Rate of exposed been quarantined
a_{pq}	Rate of quarantined individuals being confirmed
a_{oq}	Rate of infectious individuals being confirmed
γ_N	Rate of transition from the exposed to the susceptible
γ_O	Rate of transition from the infected to the susceptible
γ_V	Rate of transition from the environment to the susceptible
γ_w	Rate of removal of the virus from the environmental reservoir
k_1	Rate at which the exposed contributes the disease to the environmental reservoir
k_2	Rate at which the infected contributes the disease to the environmental reservoir
v	Coefficient providing adjustment to the transmission rate

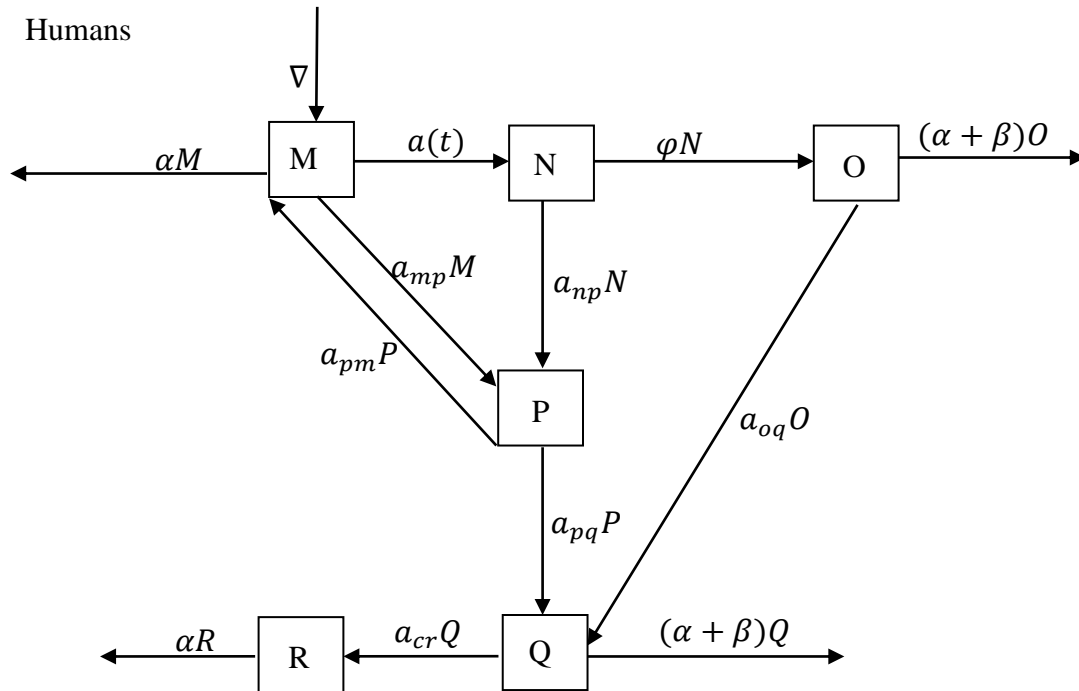


Figure 1: The model of compartmental transmission of COVID-19 among individuals

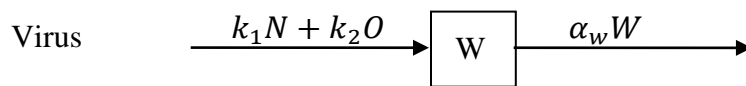


Figure 2: Compartmental concentration of COVID-19 virus on the environmental reservoir

From the compartmental model, we obtain a seven-dimensional system of ordinary differential equation which describes the dynamic transmission mechanism of the infectious disease as:

$$\frac{dM}{dt} = \nabla - a(t) + a_{pm}P - (a_{mp} + \alpha)M$$

$$\frac{dN}{dt} = a(t) - (\varphi + a_{np} + \alpha)N$$

$$\frac{dO}{dt} = \varphi N - (\alpha + \beta + a_{oq})O$$

$$\frac{dP}{dt} = a_{mp}M + a_{np}N - (a_{pm} + a_{pq} + \alpha)P \tag{1.1}$$

$$\frac{dQ}{dt} = a_{pq}P + a_{oq}O - (a_{cr} + \beta + \alpha)Q$$

$$\frac{dR}{dt} = a_{cr}Q - \alpha R$$

$$\frac{dW}{dt} = k_1N + k_2O - \alpha_w W$$

Together with the initial conditions

$$M(0) = M_o, N(0) = N_o, O(0) = O_o, P(0) = P_o, Q(0) = Q_o, R(0) = R_o, W(0) = W_o \tag{1.2}$$

Where W is the concentration of the virus in the environmental reservoir. The parameter ∇ represents the population influx, α is the natural death in human, β is the disease-induced fatality rate, φ^{-1} is the incubation period between the infected and the onset of symptoms, a_{cr} is the rate of recovery from the infectious disease. a_{oq} is the rate at which those that are fully showing the disease symptoms are diagnosed to be positive to the disease. We assume that not all individuals showing the disease symptoms are infected with COVID-19 because Influenza is also a respiratory disease with related symptoms as COVID-19 which can also be transmitted by contacts droplet and fomites (World Health Organization, 2020 Q&A:

Influenza and COVID-19-similarities and differences). a_{mp} is the rate at which individual are quarantined being traced to have had contact with those confirmed to be positive. If they do not show symptoms, they are removed back to the susceptible population at the rate of a_{pm} . a_{np} is the rate at which individuals from the exposed population are quarantined, a_{pq} is the rate at which quarantined individuals are diagnosed to be positive to the disease. k_1 and k_2 are the rates of the exposed and infected human contributing the infectious disease to the environmental reservoir and α_w is the removal of the virus from the environment due to some control measure. $a(t)$ is the infection degree of the infectious disease

in the susceptible population, the mathematical expression is as follows:

$$A(t) = \gamma_{MN}(N)MN + \gamma_{MO}(O)MO + \gamma_{MW}(W)MW$$

The function $\gamma_{MN}(N)$ and $\gamma_{MO}(O)$ and the infected population respectively denotes the direct (human-to-human) transmission rate between susceptible population and the exposed population and between susceptible population and the infected population respectively. $\gamma_{MW}(W)$ denotes the indirect (environment to human) transmission rate. $A(N, O, W)$ is further defined as:

$$a(N, O) = \frac{\gamma_N}{1 + vN}MN + \frac{\gamma_O}{1 + vO}MO + \frac{\gamma_W}{1 + vW}MW$$

Where γ_N , γ_O and γ_W are positive constants representing the maximum values of these transmission rates and v is a positive coefficient (otherwise constant) providing adjustment to the transmission rate.

Validation of the Proposed Model

Boundedness of the solution

The following provides the result which guarantees the dynamic transmission governed by the system (1.1) is epidemiologically and mathematically well-posed in a feasible region D

$$\text{given by } D_h = \left\{ (M, N, O, P, Q, R) \in \mathcal{R}_+^6 : N \leq \frac{V}{\alpha} \right\} \text{ and } D_w = \left\{ W \in \mathcal{R}_+ : W \leq \frac{(k_1 + k_2)V}{\alpha\alpha_w} \right\}$$

$$\text{Since, } U(t) = M(t) + N(t) + O(t) + P(t) + Q(t) + R(t)$$

Theorem:

There exist a domain D in which the set (M, N, O, P, Q, R) is contained and bounded

Proof:

Given the solution set (M, N, O, P, Q, R) with positive initial conditions (1.2), we let

$$V_a(M, N, O, P, Q, R) = M(t) + N(t) + O(t) + P(t) + Q(t) + R(t)$$

$$\text{And } V_b(W) = W(t)$$

Then the derivatives V'_a and V'_b along solutions of the system (1.1) are obtained by

$$V'_a = \frac{\partial V_a}{\partial M} \frac{\partial M}{\partial t} + \frac{\partial V_a}{\partial N} \frac{\partial N}{\partial t} + \frac{\partial V_a}{\partial O} \frac{\partial O}{\partial t} + \frac{\partial V_a}{\partial P} \frac{\partial P}{\partial t} + \frac{\partial V_a}{\partial Q} \frac{\partial Q}{\partial t} + \frac{\partial V_a}{\partial R} \frac{\partial R}{\partial t}$$

And $V'_b = \frac{\partial V_b}{\partial W} \frac{\partial W}{\partial t}$

It follows that $V'_a \leq \nabla - \alpha V_a$ and $V'_b \leq (k_1 + k_2)\nabla - \alpha\alpha_w$ (1.3)

Solving the differential equations (1.3) we get

$$V_a \leq \frac{\nabla}{\alpha} (1 - \exp(-\alpha t)) + V_a(M_0, N_0, O_0, V_b, Q, R_0) \exp(-\alpha t)$$

And $V_b \leq \frac{(k_1+k_2)\nabla}{\alpha\alpha_w} (1 - \exp(-\alpha\alpha_w t)) + V_b(W_0) \exp(-\alpha\alpha_w t)$

Consequently, taking the limits as $t \rightarrow \infty$ yields

$$V_a \leq \frac{\nabla}{\alpha} \text{ and } V_b \leq \frac{(k_1 + k_2)\nabla}{\alpha\alpha_w}$$

Thus, all solutions of the population are confined in the feasible region D , showing that the feasible region for the formulated model in the equation (1.1) exist and is defined by

$$D = \left\{ (M, N, O, P, Q, R, W) \in \mathbb{R}_+^7 : N \leq \frac{\nabla}{\alpha}, W \leq \frac{(k_1 + k_2)\nabla}{\alpha\alpha_w} \right\}$$

Equilibrium point

Here, we state the result of the disease-free and endemic equilibrium of the model. The point at which the differential equation of the system (1.1) equals to zero is the equilibrium point. It should be noted that as long the growth term ∇ is

not equal to zero, there will be no trivial equilibrium point. Consequently, $(M, N, O, P, Q, R, W) \neq (0,0,0,0,0,0,0)$ and the population will not vanish.

Existence of disease-free equilibrium point

Disease-free equilibrium points are steady-state solutions or equilibrium point where there's no infection of COVID-19. Thus, at the disease-free

equilibrium point E_0 , we have that $N_*, O_*, P_*, Q_*, R_*, W_* = 0$. Hence, the resulting disease-free equilibrium point obtained solving (1.1)

$$E_0 = \left(\frac{\nabla}{\alpha + a_{mp}}, 0, 0, 0, 0, 0, 0 \right)$$

Table 2: Parameter values

Parameter	Description	Value	Source
U	Total population	200×10^6	Countrysmeters (2020), Nigeria Population 2020
$1/\varphi$	Incubation period	0.0142	Yang C & Wang J.A (2020)
∇	Birth rate of individuals	22.657	Countrysmeters (2020), Nigeria Population
α	Death rate	0.0185	Estimated
a_{cr}	Recovery rate	0.0677	Yang C & Wang J.A (2020)
β	COVID-19 death rate	0.021	Estimated
a_{mp}	Rate of susceptible being quarantined	1.5×10^{-5}	Estimated
a_{pm}	Rate of quarantined going back to the susceptible class	0.8667	Estimated
a_{np}	Rate of exposed being quarantined	4.103×10^{-5}	Estimated
a_{pq}	Rate of quarantined individuals being confirmed	0.1333	Estimated
a_{oq}	Rate of infectious individuals being confirmed	0.6260	Estimated
γ_N	Rate of transmission from the exposed to the susceptible	3.366×10^{-7}	Estimated
γ_O	Rate of transmission from the infected to the susceptible	6.396×10^{-8}	Estimated
γ_V	Rate of transmission from the environment to the susceptible	1.886×10^{-7}	Estimated
γ_w	Rate of removal of the virus from the environmental reservoir	1.0	Yang C & Wang J.A (2020)
k_1	Rate at which the exposed contributes the disease to the environmental reservoir	2.010	Estimated
k_2	Rate at which the infected contributes the disease to the environmental reservoir	0.2350	Estimated
v	Coefficient providing adjustment to the transmission rate	0.0066	Estimated

Discussion of Results

Simulation of the Proposed Model

The model (1.1) is now simulated, using the baseline parameter values tabulated in Tables 3, to assess the community-wide impact of the various intervention strategies incorporated into the model for the entire Nigerian nation. For simulation convenience (and for computational tractability), we re-scaled the total Nigerian population to 1.5 million and simulated the pandemic starting with one index case in the symptomatically-infectious class, while initially fixing all other state variables for the infected and recovered classes of the model to zero.

Impact of social distancing

This involves reducing the transmission rate from the exposed to susceptible, highly infectious to susceptible and environment to human. The effect of social distancing can be monitored by simulating the model using the estimated parameters in Table 3 with the following effective measure of social distancing: Slight level of effectiveness of social distancing: This requires reducing the

transmission rates $(\gamma_N, \gamma_O, \gamma_W)$ by 15% such that we have $\gamma_N = 2.861e^{-7}$ and $\gamma_O = 5.437e^{-8}$. Average level effectiveness of social distancing: This requires reducing the transmission rates $(\gamma_N, \gamma_O, \gamma_W)$ by 50% such that we have $\gamma_N = 1.683e^{-7}$ and $\gamma_O = 3.198e^{-8}$. Strict level effectiveness of social distancing: This requires reducing the transmission rates $(\gamma_N, \gamma_O, \gamma_W)$ by 75% such that we have $\gamma_N = 8.415e^{-7}$ and $\gamma_O = 1.599e^{-8}$.

Figure 4 shows the simulation for various effectiveness of social-distancing control measures in the absence of hygienic culture and face mask. For no social-distancing measured as the base line value estimated in Table 2, while, slight social distancing, average social distancing and strict social distancing measured as 15%, 50% and 75% reduction of their baseline value respectively. In comparison with no social distancing, result shows that: adopting a strict social distancing will reduce the cumulative number of confirmed cases by 54%-58%; adopting

average social distancing will reduce the cumulative number of confirmed cases by 41%-45% while adopting slight social distancing will the cumulative number of confirmed cases by 23%-27%. Increasing

social-distancing control measure would results in reduction in the number of individuals that would be confirmed with COVID-19.

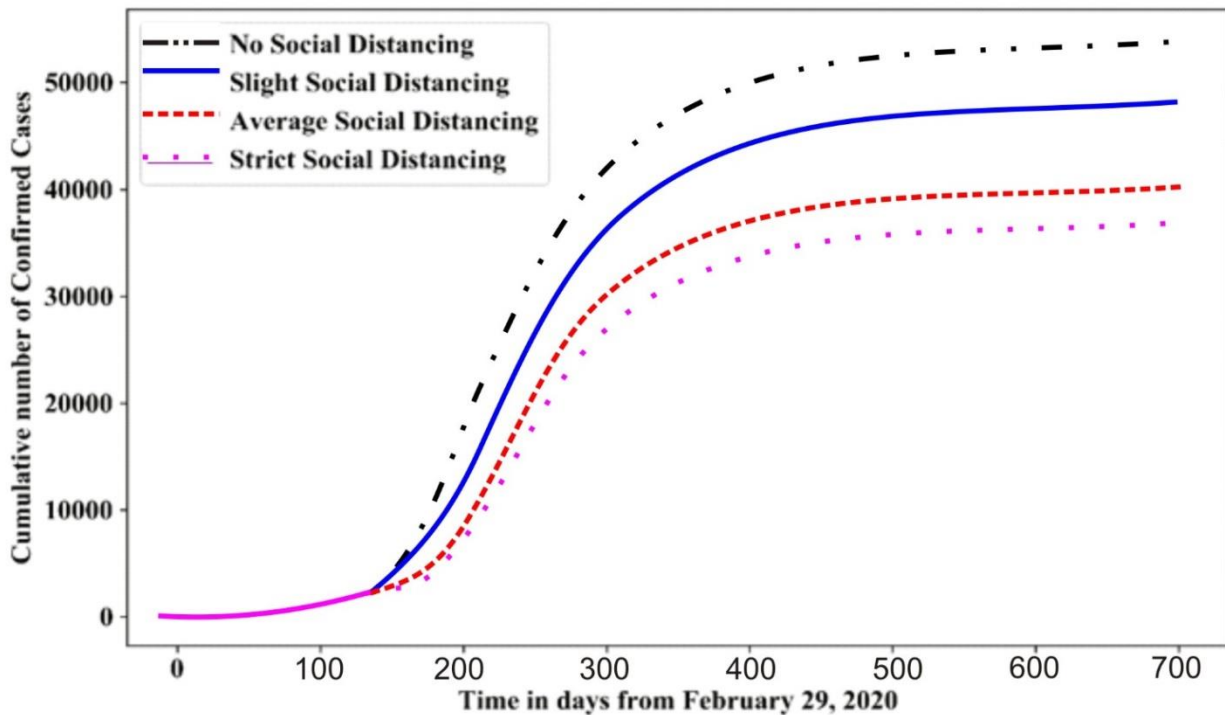


Figure 4: Simulation of model (1.1) for various effectiveness of social-distancing control measures in the absence of hygienic culture and face mask.

Impact of relaxation of lockdown

This involves increasing the transmission rate/contact rate from the exposed to susceptible, highly infectious to susceptible and environment to human. The effect of relaxation of lockdown can

be monitored by simulating the model using the estimated parameters in Table 2 with the following effective measure of social distancing: Slight relaxation of lockdown measures: This requires reducing the transmission rates $(\gamma_N, \gamma_O, \gamma_W)$ by 15% such that we have $\gamma_N = 3.871e^{-7}$ and $\gamma_O = 7.355e^{-8}$.

Average relaxation of lockdown measures: This requires reducing the transmission rates ($\gamma_N, \gamma_O, \gamma_W$) by 50% such that we have $\gamma_N = 5.049e^{-7}$ and $\gamma_O = 9.594e^{-8}$. Full relaxation of lockdown measures: This requires reducing the transmission rates ($\gamma_N, \gamma_O, \gamma_W$) by 75% such that we have $\gamma_N = 5.891e^{-7}$ and $\gamma_O = 1.119e^{-8}$

value in Table 2, while, slight relaxation of lockdown, average social relaxation of lockdown and strict relaxation of lockdown measured as 15%, 50% and 75% increase of their baseline value respectively. In comparison with no relaxation of lockdown, result shows that: full relaxation of lockdown increases the cumulative number of confirmed cases by 66%-68%; average relaxation of lockdown increases the cumulative number of confirmed cases by 33%-35%; slight relaxation of lockdown increases the cumulative number of confirmed cases by 11%-13%.

Figure 5 shows the simulation for various level of relaxation of lockdown control measures in the absence of hygienic culture and face mask. For no relaxation of lockdown measured as the baseline

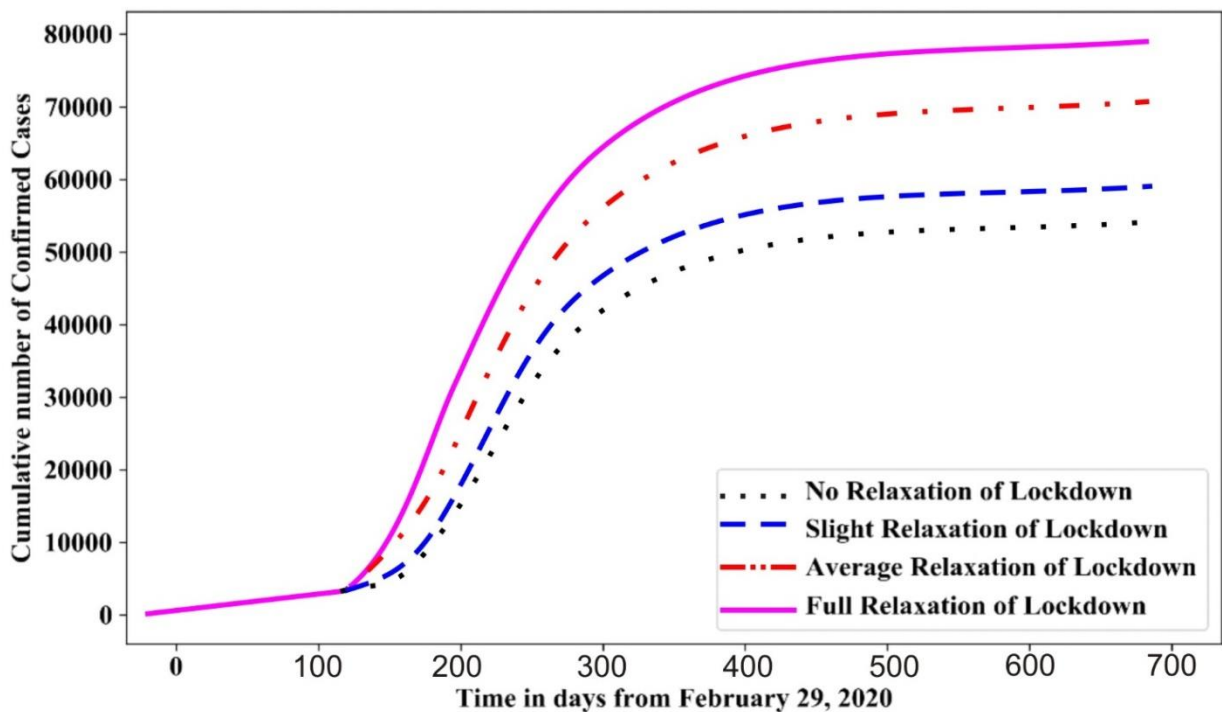


Figure 5: Simulation of model (1.1) for various level of relaxation of lockdown control measures in the absence of hygienic culture and face mask

Recommendations

The modified COVID-19 infection model should be employed in the management and eradication of COVID-19 infections within any human population. Also, the initial population

sizes of the different categories of individuals in the modified infection model should be kept

by all possible means within the basin of attraction of the disease-free equilibrium in order to

ensure that the stability of disease-free equilibrium is guaranteed.

Conclusion

Unless effective public health interventions are implemented, and sustained for a significant period of time (as was done, and is being done, in New York state), Nigeria would undoubtedly continue to record catastrophic burden of the pandemic (even if the ensuing case and mortality numbers are not realistically recorded by the Nigeria's public health authorities). However, our study emphasize the fact that the COVID-19 pandemic is controllable in Nigeria using basic non-pharmaceutical interventions, such as social (physical)-distancing, community lockdown, the use of face masks in public, the use of personal protection equipment (PPE) by frontline healthcare workers, widespread diagnostic testing and contact

tracing, personal hygiene and hand washing, rapid isolation of confirmed cases and the quarantine of people suspected of being exposed to the pandemic (provided these interventions are implemented at moderate levels of effectiveness and coverage).

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