MATHEMATICAL MODELING, PREDICTION AND PREVENTIVE MEASURES OF CORONAVIRUS DISEASE IN NIGERIA AS AN EPICENTRE IN AFRICA

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ABSTRACT

This paper examines the mathematical modelling and prediction of coronavirus in Nigeria.As a result, a lot of researchers have worked on the mechanisms for the spread, control and mitigation of coronavirus disease in almost all the communities. We therefore, propose a mathematical model which adopt SEIR framework to investigate the current outbreak of this pandemic in Nigeria. The disease free equilibrium was investigated using Jacobian transformation. We conducted a detailed analysis of this model using reported data of COVID-19 from NCDC website. We observed that despite the increase in infectious disease among population, cases of individuals that would recover from this infectious disease would continue to increase till the infectious disease vanish among human population. But, it is observed that mildly infectious individuals are more than the hospitalized individual and highly infectious are lesser than the hospitalized individuals, which could be alarming as time goes on, because of insufficient bed space in hospitals in Nigeria. With the prediction, it is observed that the COVID-19 curve will become flat if all the control measures are strictly adhered to. Hence, the need to practice social distancing, use of face mask to reduce cases of individuals that are mildly infected and highly infected. Reinforced effort from the government, decision makers and stakeholders in ensuring compliance to all preventive measure as directed by World Health Organization (WHO) can effectively control the spread of the virus in Nigeria.

Keywords: COVID-19 pandemic, mathematical model, SEIQAHR, social distancing, infectious disease.

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Introduction

Today, the whole world is grappling with coronavirus pandemic, the magnitude of which exceeds that of Ebola, MERS and SARS combined, originating from Wuhan city, ChinaRef. The virus that causes this pandemic has spread rapidly to the whole continent of the globe. The disease has overwhelmed countries with strong and resilient health systems and has had an enormous toll on human lives.

Early this year, the World Health Organization (WHO) declared the outbreak of this disease a public phenomenon that calls for international attention. As at April 11, 2020, all the continents had reported COVID-19 confirmed cases with many more countries across the globe reporting cases on a daily basis. Also, the organization has called for "aggressive preparedness" and improved efforts to contain the outbreak and protect health workers and citizens in all countries. This is particularly important for countries anticipated to be the most vulnerable; those with weak health systems and inadequate resources, further strained by large populations living in abysmal conditions and suffering from malnutrition and preventable illness.

Nigeria that has the largest population in Africa with estimate population of about 200 million is one of such vulnerable countries. The first case of this virus disease was in Nigeria on February 27, 2020, the country has experienced an unprecedented increase in the number of positive cases, with worrying evidence of community transmission. As at the time of writing this paper (July 1, 2020), data from Nigeria Centre for Disease Control (NCDC) website shows that Nigeria has recorded 26,484 confirmed cases, 10,152discharged cases and fatality cases of 603. This ravaging virus has changed the perspective of everyone in Nigeria regarding the outbreak of this disease as it is affecting and infecting human around in an exponential manner.

Different researchers have worked on the transmission dynamics, control and mitigation of coronavirus disease in almost all the communities. (Khan and Atangana2020) studied the mathematical modelling and transmission dynamics of a coronavirus (2019 – nCoV). They studied in details the interactions among the bats and unknown hosts, and also among the peoples with the infectious reservoir (seafood market), they assumed that the seafood market has enough source of infection that can be effective to infect people. (Igor 2020) analysed a statistics approach prediction of coronavirus disease spread in Mainland, China. Simple SIR mathematical model was used to predict the characteristics of the endemic in the area. The most reliable dependencies for victim numbers, infected and removed persons.

A mathematical model of the current novel COVID-19 under three compartments i.e. susceptible, infected and recovered was examined by (Ud Din *et al,* 2020) using nonstandard finite difference numerical method. (Kuniya2020) predicted the epidemic peak ofcoronavirus disease in Japan, taking into consideration the vagueness due to the incomplete identification of infective population. He used a statistical least square based method with Poisson noise on the SEIR compartmental model to predictthe future occurrence of this pandemic. (Iboi et al 2020) analysed the transmission dynamics and control of coronavirus in Nigeria as one of the epicentre of COVID-19 in Africa using Kermack-McKendrick-type compartmental epidemic model.

In this work, a mathematical model of transmission dynamics, prediction and control measures of this pandemic disease in Nigeriaas one of the main epicentres was developed using SEIQAHR model.

Model Formulation

We develop a model that adopts the SEIR framework with additional three compartments. Hence, we have 7 components for the model SEIQAHR namely: Susceptible

$$N(t)=S(t)+E(t)+I(t)+Q(t)+A(t)+H(t)+R(t)$$

The figure below shows the transmission dynamic of COVID-19 pandemic using SEIQAHR model.

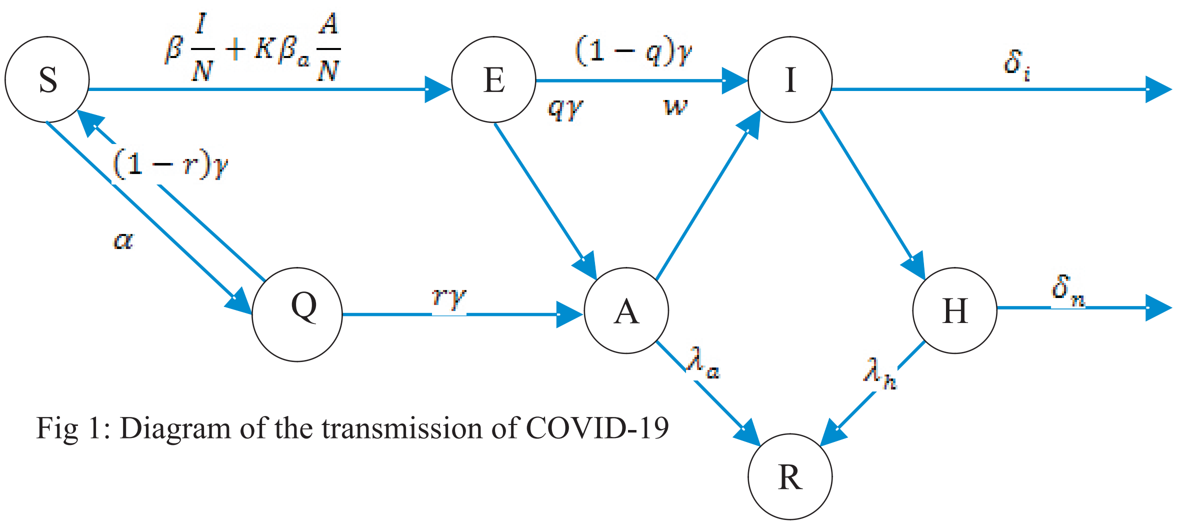

Fig 1: Diagram of the transmission of COVID-19

A seven-dimensional system of non-linear ordinary differential equations are obtained from Figure 1 describing the transmission dynamic of the disease which are:

$$
\begin{cases}
\frac{dS}{dt} = -\beta_i \frac{I}{N} S - k\beta_a \frac{A}{N} S + (1-r)\gamma Q - \alpha s \\
\frac{dE}{dt} = \beta_i \frac{I}{N} S + k\beta_a \frac{A}{N} S - (q\gamma)E \\
\frac{dI}{dt} = (1-q)\gamma E + wA - (\phi + \delta_i)I \\
\frac{dQ}{dt} = \alpha S - r\gamma Q \\
\frac{dA}{dt} = r\gamma Q + q\gamma E - (\lambda a + w)A \\
\frac{dH}{dt} = \phi I - (\lambda_n + \delta_n)H \\
\frac{dR}{dt} = \lambda_a A + \lambda_n H
\end{cases}
$$

The variables and parameters used in this model are defined in the tables below

Table 1: Definition of stated variables

Variable	Definition
S	Individuals that are susceptible to the infection
E	Individuals exposed
I	Individuals that are highly infectious
Q	Individuals that are quarantined
A	Individuals showing mild symptoms of the disease
H	Individuals hospitalized
R	Recovered individuals

Table 2: Definition of the parameters

Parameter	Definition
q	Proportion of exposed individual showing mild infection after incubation period.
$1-r$	Population of non-infected individuals.
$\beta_i(\beta a)$	Contact rate from the infected (mild infectious) individual to susceptible individuals
$\frac{1}{\gamma}$	Incubation period between the infectious and the onset of symptoms
$\delta_i(\delta_n)$	Disease-induced rate of hospitalized individuals
ϕ	Rate of hospitalized individuals

Parameter	Definition
$\lambda_a(\lambda_n)$	Recovery rate for mild infectious (hospitalized) individuals
α	Rate at which susceptible are quarantine
$1-q$	Proportion of exposed individuals that are highly infectious after incubation period
k	Multiple of transmissibility of asymptomatically infectious to that of symptomatically infectious to that of highly infectious individuals
w	Infectious rate for mild infectious individuals

Existence of Disease Free Equilibrium Point (DFE)

Finding DFE point for the model equation (1), we let

$$E\_0=(S_*,E_*,I_*,Q_*,A_*,H_*,R_*)$$

Thus at DFE point E_0, $E_*,I_*,Q_*,A_*,H_*,R_*=0$. So that the resulting DFE point is given by

$$E\_0=(S(0),0,0,0,0,0,0)$$

Where S(0) is the initial size of susceptible individuals (N(0)=S(0))

Basic Reproduction Number

To compute the basic reproduction number of equation (1), we adopt the next generation matrix technique (Diekmanet al, 1990). The infection matrix F and the transition matrix V are respectively:

$$F=\begin{bmatrix}0 & \beta_i & \beta_a & 0\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\end{bmatrix}$$

$$V=\begin{bmatrix}q\gamma & 0 & 0 & 0\\ -(1-q)\gamma & (\phi+\delta_i) & -w & 0\\ -q\gamma & 0 & (\lambda_a+w) & 0\\ 0 & -\phi & 0 & (\lambda_n+\delta_n)\end{bmatrix}$$

The reproduction number for the model equation (1) is:

$$R_0=\rho(FV^{-1})=+\frac{\beta_i(wq+(\lambda_a+w)(1-q))}{q(\phi+\delta_i)(\lambda_a+w)}+\frac{\beta_a}{\lambda_a+w} \qquad (2)$$

Where ρ is the spectral radius

The reproduction number of the model equation (1) measures the overall infection risk from highly infectious compartment and the mild infectious compartment such that:

$$R_0=R_I+R_A \qquad (3)$$

The constituent reproduction number R_I measures the product of the contact rate of susceptible individuals from highly infected individuals near the DFE β_i the proportion of exposed individuals and mildly infected individuals that moved to the highly infected compartment $\left(w+\frac{(\lambda_a+w)(1-q)}{q}\right)$ over the average time in the highly infectious and the a symptomatically infectious compartment $\left(\frac{1}{(\phi+\delta_i)(\lambda_a+w)}\right)$

Similarly, the constituent reproduction number R_A easures the contact rate of susceptible individual from mildly infected individuals near the DFE β_a over the average duration in the mild infected class $\dfrac{1}{\lambda_a+w}$

The Disease Free Equilibrium Point

Theorem 1: The DFE point E_0 is asymptotically stable if $J(E_0)$ is negative and unstable if $J(E_0)$ is positive.

Proof: We start by finding the Jacobian matrix of the model equation (1) at the DFE point which can be obtained as

$$\begin{bmatrix} -\alpha & 0 & \beta_i & (1-r)\gamma & \beta_a & 0 & 0 \\ 0 & -q\gamma & 0 & 0 & 0 & 0 & 0 \\ 0 & (1-q)\gamma & -(\phi+\delta_i) & 0 & w & 0 & 0 \\ \alpha & 0 & 0 & -r\gamma & 0 & 0 & 0 \\ 0 & q\gamma & 0 & r\gamma & -(\lambda_a+w) & 0 & 0 \\ 0 & 0 & \phi & 0 & 0 & -(\delta_a+\delta_n) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -(\lambda_n+\lambda_n) \end{bmatrix}$$

The corresponding eigenvalues are:

$$-(\delta_a+\delta_n)\ , \qquad -(\lambda_n+\lambda_n), \qquad -q\gamma$$

The remaining eigenvalues are obtained from the submatrix

$$\begin{bmatrix} -\alpha & \beta & (1-r)\gamma & \beta_a \\ 0 & -(\phi+\delta_i) & 0 & w \\ \alpha & 0 & -r\gamma & 0 \\ 0 & 0 & r\gamma & -(\lambda_n+w) \end{bmatrix}$$

Which is deduce from the following characteristic equation

$$\begin{aligned} \lambda^4 + \lambda^3(\alpha+\phi+\delta_i+r\gamma+\lambda_a+w) + \lambda^2\big((\alpha+\lambda_a+w)(\phi+\delta_i)+(\alpha+r\gamma)(\lambda_a+w)+r\alpha\gamma\big) \\ + \lambda\big(2\alpha r\gamma(\phi+\delta_i+\lambda_a+w)+(\alpha+r\gamma)(\phi+\delta_i)(\lambda_a+w) \\ - \alpha\gamma(r\beta_a+\lambda_a+w+\phi+\delta_i)\big) + \alpha\gamma(\phi+\delta_i)\big(1-r(1+\beta_a)\big) \\ + \alpha\lambda_a r\gamma(\phi+\delta_i) + w\alpha\phi r\gamma + wr\gamma(\delta_i-\beta_i) = 0 \end{aligned} \tag{4}$$

Equation (4) can be written as:

$$A_4\lambda^4 + A_3\lambda^3 + A_2\lambda^2 + A_1\lambda + A_0 = 0 \tag{5}$$

Where

$$A_4 = 1$$

$$A_3 = \alpha + \phi + \delta_i + r\gamma + \lambda_a + w$$
$$A_2 = (\alpha + \lambda_a + w)(\phi + \delta_i) + (\alpha + r\gamma)(\lambda_a + w) + r\alpha\gamma$$
$$A_1 = 2\alpha r\gamma(\phi + \delta_i + \lambda_a + w) + (\alpha + r\gamma)(\phi + \delta_i)(\lambda_a + w) - \alpha\gamma(r\beta_a + \lambda_a + w + \phi + \delta_i)$$
$$A_0 = \alpha\gamma(\phi + \delta_i)(1 - r(1 + \beta_a)) + \alpha\lambda_a r\gamma(\phi + \delta_i) + w\alpha\phi r\gamma + wr\gamma(\delta_i - \beta_i)$$

Using Rooth-Hurwitz criterion (Murray, 2007), from (5), we have that $A_4, A_3, A_2 > 0$ and $A_1 > 0$ if $\beta_a < 1$ and $A_0 > 0$ if $\delta_i > \beta_i$

Also the Hurwitz matrix for the polynomial (5) are positive

$$H_1 = A_3 > 0, \qquad H_2 = \begin{vmatrix} A_3 & A_4 \\ A_0 & A_1 \end{vmatrix} > 0, \qquad H_3 = \begin{vmatrix} A_3 & A_4 & 0 \\ A_1 & A_2 & A_3 \\ 0 & A_0 & A_1 \end{vmatrix} > 0,$$

$$H_4 = \begin{vmatrix} A_3 & A_4 & 0 & 0 \\ A_1 & A_2 & A_3 & A_4 \\ 0 & A_0 & A_1 & A_2 \\ 0 & 0 & 0 & A_0 \end{vmatrix} > 0$$

Therefore, the eigenvalues of the Jacobian matrix have negative real part when $\beta_a < 1$ and $\delta_i > \beta_i$ and the disease free equilibrium point is asymptotically stable. However, when $\beta_a > 1$ and $\delta_i < \beta_i$, the DFE point is unstable.

Existence of the Endemic State

Following the proof of Arino et al (2007), we derive the final size of coronavirus pandemic using our model. Using the notation in (Arino et al, 2007), we use $x \in \mathbb{R}_+^4, y \in \mathbb{R}_+^2$ ar $z = \mathbb{R}_+$ to represent the sets of infected, susceptible, quarantine and recovered compartment of the model. Consequently, we have:

$$x(t) = \big(E(t), I(t), A(t), H(t)\big)^T, \quad y(t) = \big(S(t), Q(t)\big) \text{ and } Z(t) = R(t)$$

Let $m \times n$ diagonal matrix whose diagonal entries are represented by $E_i(i = 1,2,3,\dots,m)$ are the relative susceptibilities of the corresponding susceptive individual class. Define ϕ as the $m \times n$ matrix with the property (i,j) representing the proportion of the j^{th} susceptible that goes into the i^{th} infection component when infected with the intectious disease. Let d be an n- dimensional row of vectors of relative horizon transmission.

$\mu = \beta(x,y,z)$ Define the $m -$ dimentional vector

$$\pi = [\pi_1, \pi_2, \pi_3, \dots, \pi_m] = \beta d V^{-1} \phi D$$

From the model equation (1), it follows that

$$d = [0,1,1,0] \;\; \pi = R_0, D = 1, \qquad \phi = \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

With regards to the above changes, variables and definition, the model equation (1)reduces to:

$$\dot{x} = \phi D y \beta(x,y,z) dx - Vx$$
$$\dot{y} = -D y \beta(x,y,z) dx \qquad (6)$$
$$\dot{z} = Wx$$

Where V is the transition matrix in section (2.2), W is a $k \times n$ matrix with the property that the (i, j) entry signifies the rate of transition from the j^{th} (column) infected compartment into the recovered i^{th} (row) compartment upon recovery.

Theorem 2: Endemic size of the epidemic model equation (1) (or equivalently 6) is given by:

$$\ln\left(\frac{S(0)}{S(\infty)}\right) \geq R_0 \frac{S(0)-S(\infty)}{S(0)} + \frac{\beta_i \gamma\big(wq + (\lambda_a + w)(1-q)\big)I(0)}{q(\phi+\delta_i)(\lambda_a + w)S(0)} + \frac{\beta_a A(0)}{(\lambda_a + w)S(0)} \qquad (7)$$

By setting $A_a(0) = 0$ with $S(0) > 0$ and $I(0) >$, the endemic state is given by the inequality (7) reduces to

$$\ln\left(\frac{S(0)}{S(\infty)}\right) \geq R_0 \frac{S(0)-S(\infty)}{S(0)} + \frac{\beta_i \gamma\big(wq + (\lambda_a + w)(1-q)\big)I(0)}{q(\phi+\delta_i)(\lambda_a + w)S(0)}$$

Table 3: Nigeria reported laboratory-confirmed, recoveries and death cases as at 1st July, 2020

STATES	CONFIRMED CASES		DISCHARGED CASES		DEATHS		TOTAL ACTIVE CASES	DAYS SINCE LAST REPORTED CASE
	CUMULATIVE	NEW	CUMULATIVE	NEW	CUMULATIVE	NEW		
Lagos	10,630	120	1,610	7	129	1	8,891	0
FCT	1,935	65	588	18	34	1	1,313	0
Oyo	1,391	11	703	7	12	0	676	0
Kano	1,257	41	958	27	52	0	247	0
Edo	1,165	60	418	130	40	1	707	0
Delta	1,131	166	190	0	23	0	918	0
Rivers	1,088	32	648	26	38	0	402	0
Ogun	869	43	609	38	19	0	241	0
Kaduna	805	39	552	20	12	0	241	0
Katsina	578	21	285	0	23	0	270	0
Gombe	507	4	363	11	19	0	125	0
Bauchi	505	2	461	12	12	0	32	0
Borno	493	0	432	10	32	0	29	1
Ebonyi	438	0	357	0	3	0	78	2
Plateau	382	0	197	0	10	0	175	1
Imo	352	20	50	10	6	0	296	0

Enugu	**327**	**66**	**126**	**53**	**9**	**3**	**192**	**0**
Ondo	325	33	110	8	19	0	196	0
Abia	320	10	207	0	3	0	110	0
Jigawa	318	0	308	1	9	3	1	1
Kwara	235	18	135	4	9	3	91	0
Bayelsa	234	29	105	5	15	1	114	0
Nasarawa	213	0	113	0	8	0	92	2
Sokoto	151	0	119	0	15	0	17	4
Osun	127	0	48	0	5	0	74	1
Niger	116	0	45	8	7	0	64	1
AkwaIbom	86	0	54	0	2	0	30	3
Adamawa	84	0	47	0	6	0	31	3
Kebbi	81	2	58	0	7	0	16	0
Zamfara	76	0	71	0	5	0	0	44
Anambra	73	0	57	0	9	0	7	2
Benue	65	6	30	0	1	0	34	0
Yobe	61	2	48	0	8	0	5	0
Ekiti	43	0	40	11	2	0	1	4
Taraba	19	0	10	0	0	0	9	6
Kogi	4	0	0	0	0	0	4	3
Total	26,484	790	10,152	406	603	13	15,729	

Source: Nigeria Centre for Disease Control, (NCDC)1st July,2020

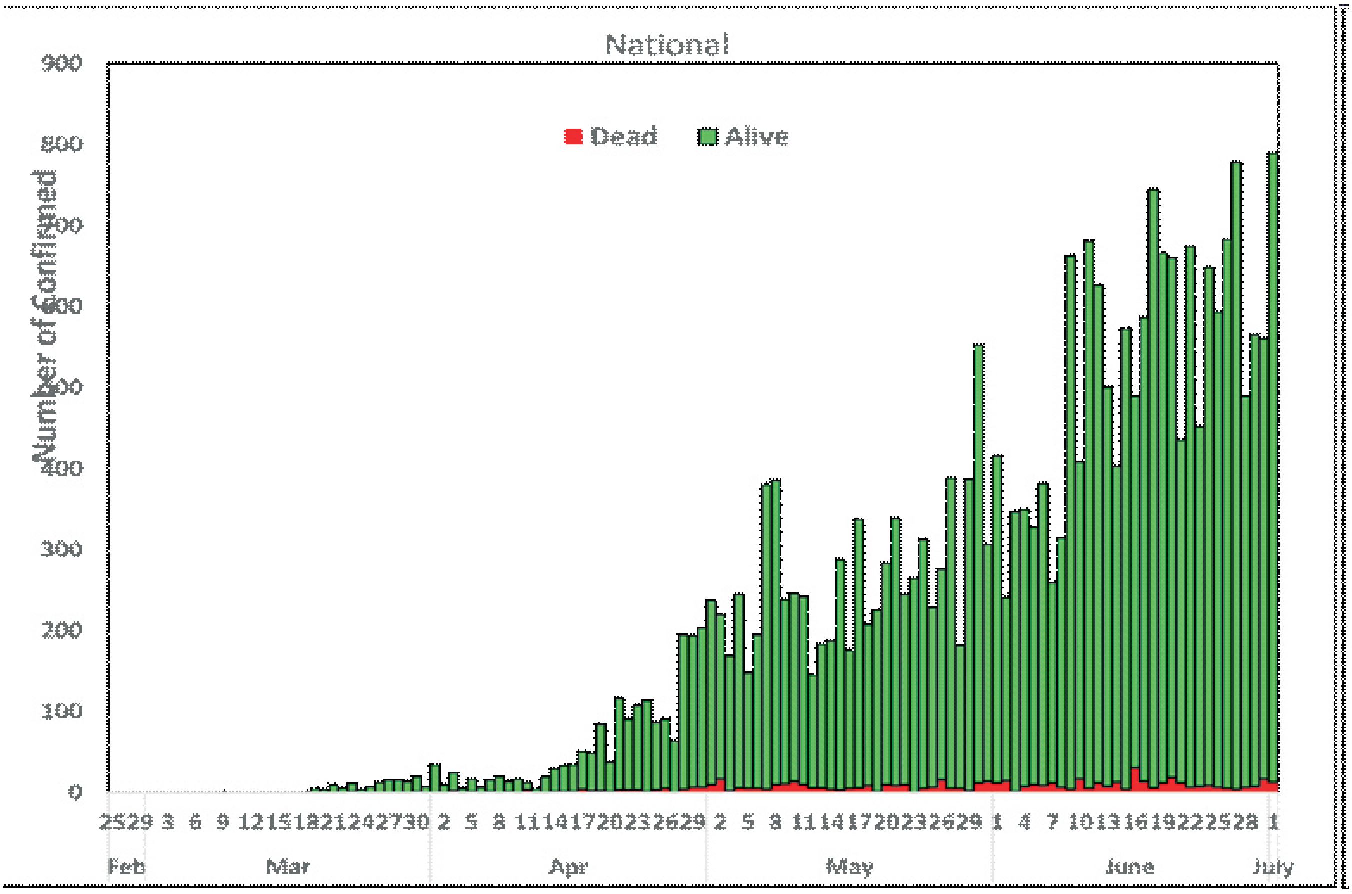

Figure 2:Curve of Daily Confirmed Cases as at 1st July, 2020. (Source NCDC)

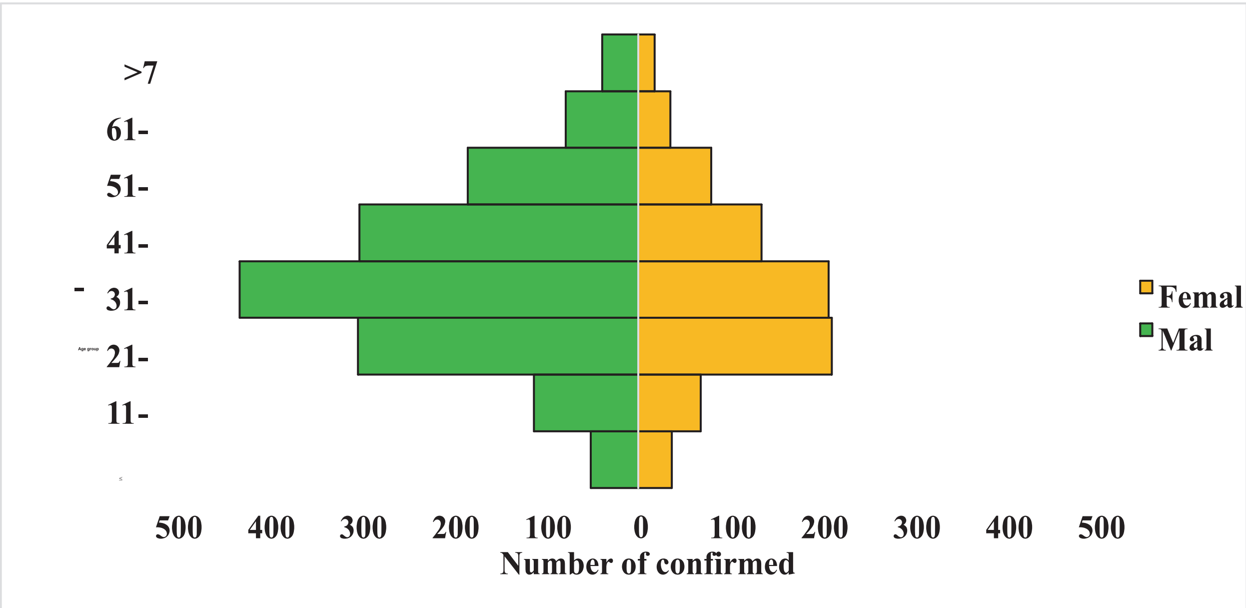

Figure 3:Age-Sex Distribution of Confirmed Cases in Nigeria as at 1st July, 2020 (Source NCDC)

Result and Discussions

In this work, SEIQAHR model was developed to consider the susceptible individuals, the exposed individuals, quarantined individuals, the highly infected individuals, the mildly infected individuals, the hospitalized individuals and the recovered individuals. The model (1.0) is now simulated using parameters in the table below. We set the initial data of this analysis to first of July, 2020. The numerical simulation results showed that the reproduction number R_o is 2.26 showing the contribution from the highly infectious individuals and the mildly infectious individuals.

Table 1: Estimation values of parameters used in the numerical simulation.

N=200e6,	
E(0)=1000,	Assumed
I(0)=11110,	Estimation
Q(0)=144833,	Assumed
R(0)=10804,	NCDC (2020)
A(0)=1600,	Estimation
H(0)=8000,	Estimation
??$_{??}$= 0.487	Iboi et al. (2020)
??$_{??}$ = 0.380	Iboi et al. (2020)
??= 0.25	Assumed
??= 0.5872	Estimation
??= 0.85	Assumed
?? = 0.35	Assumed
??$_{??}$= 0.043	Iboi et al. (2020)
?$_h$ = 0.103	Iboi et al. (2020)
?? = 0.11	Assumed
??= 1/5.1	Lauer *et al.* (2020), Li *et al*. (2020)
??= 0.0000724	Estimation
??$_{??}$ = 1/7	Zhou *et al.* (2020), Tang *et al*. (2020)
?$_h$ = 1/14	Tang *et al*. (2020), Zhou *et al.* (2020)
??= 350days	

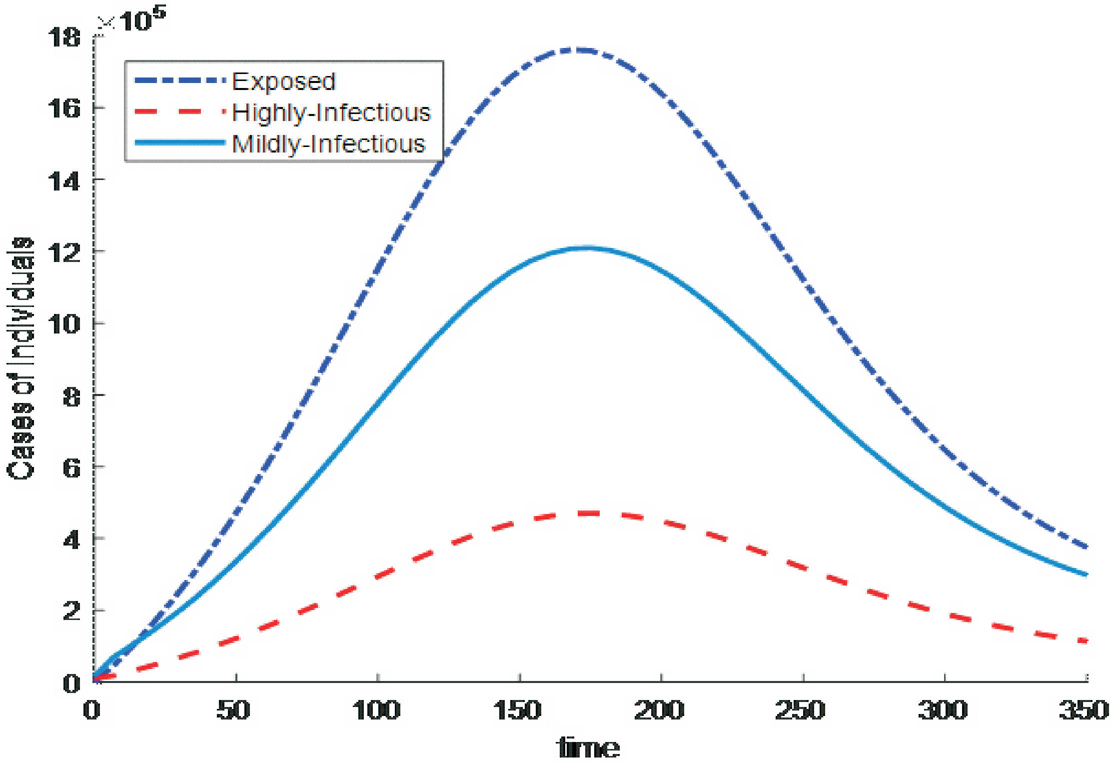

Figure 4: A simulation showing cases of exposed, highly-infectious and mildly infectious individuals

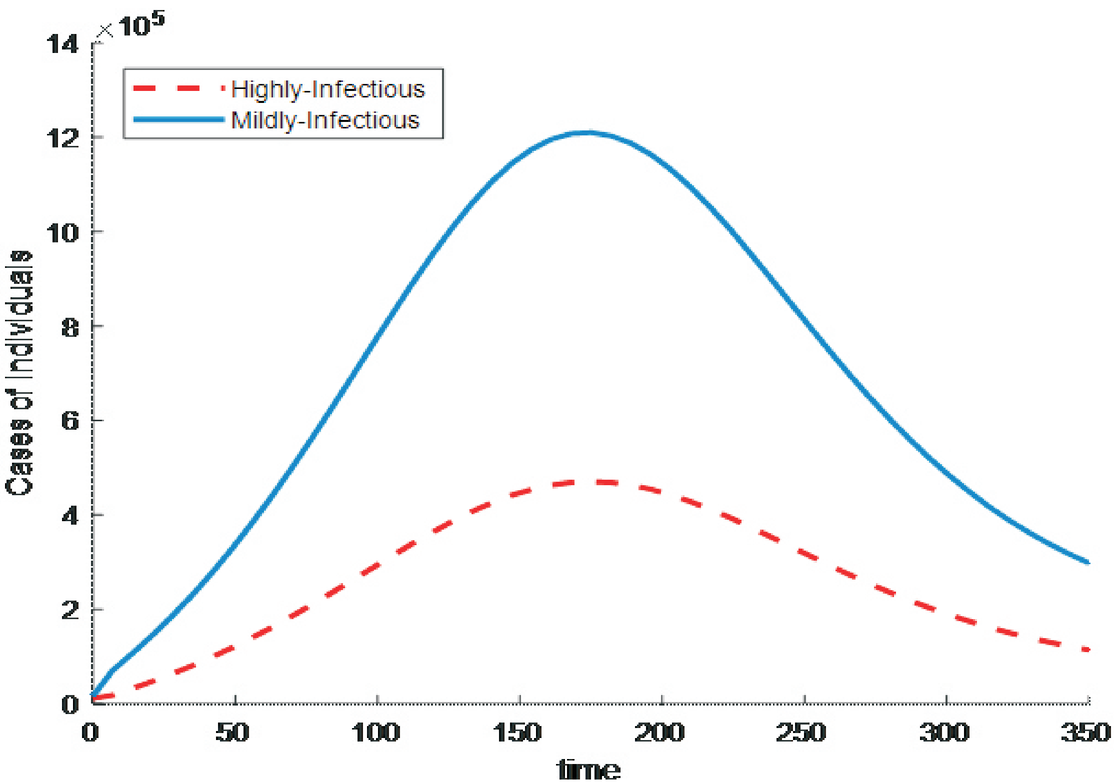

Figure 5: A simulation showing cases of mildly infectious and highly infectious individuals

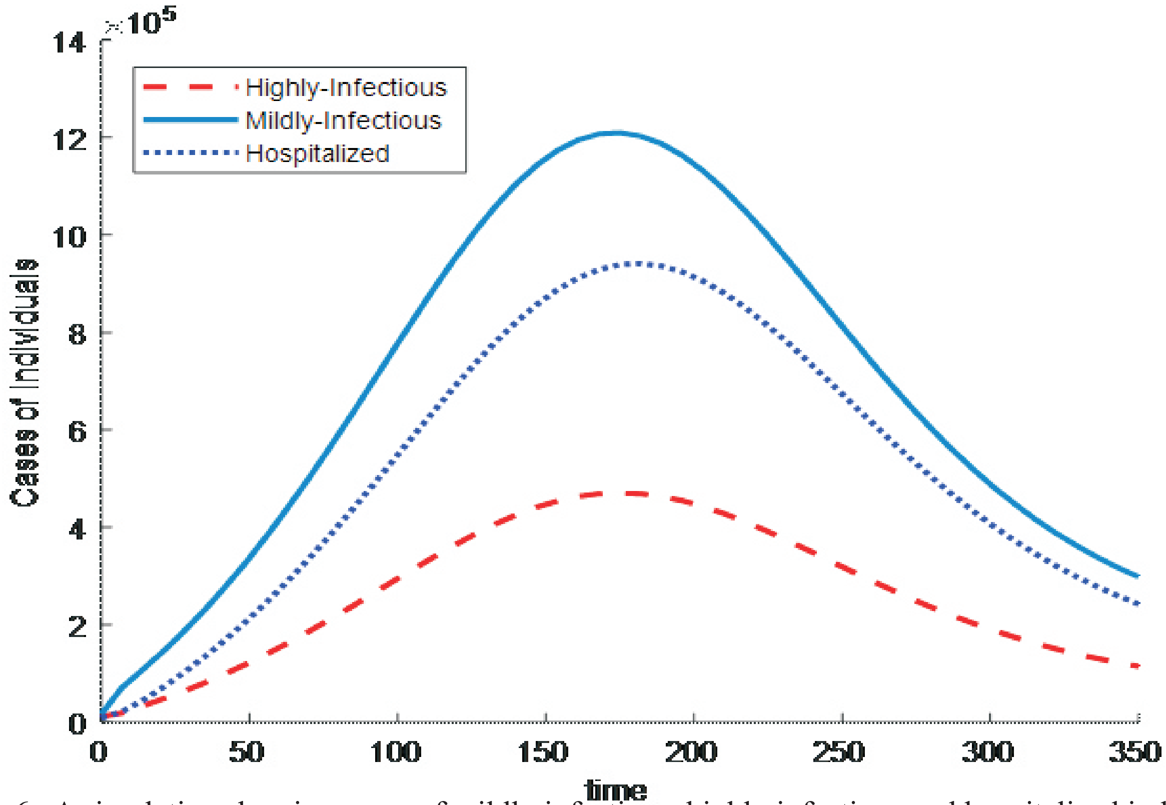

Figure 6: A simulation showing cases of mildly infectious, highly infectious and hospitalized individuals

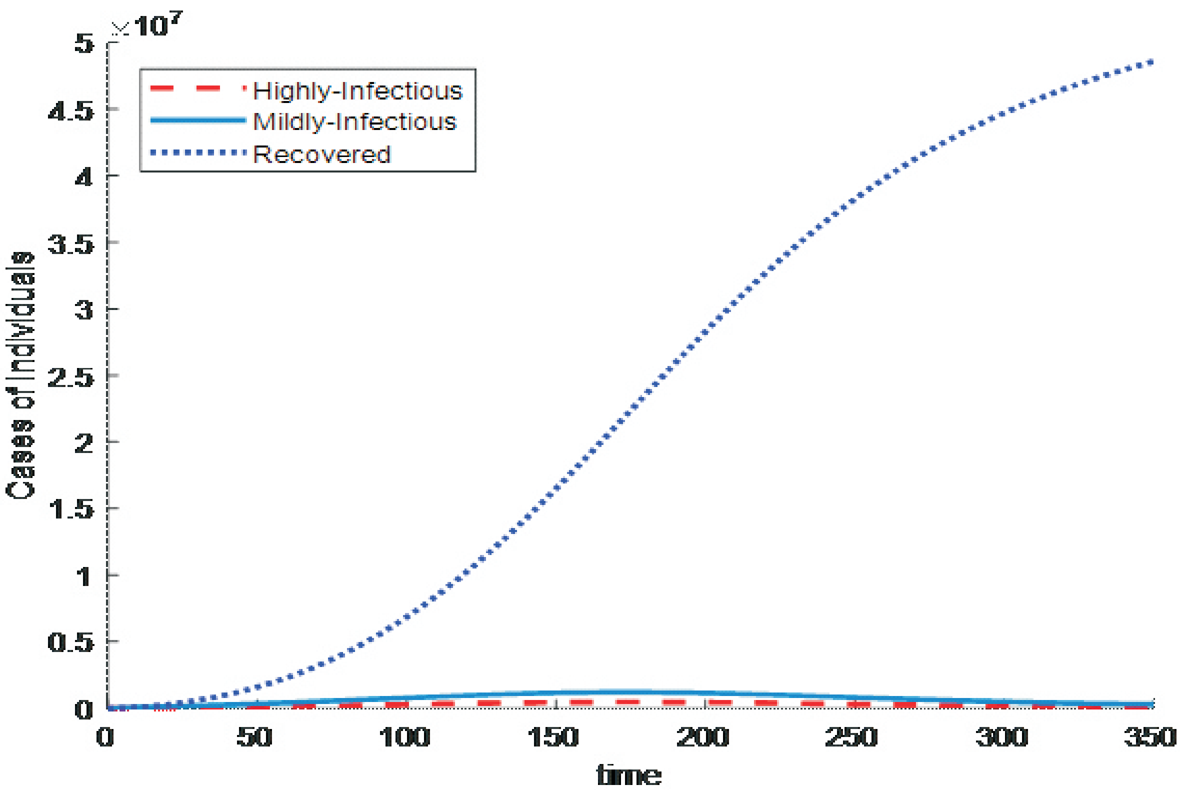

Figure 7: A simulation showing cases of highly infectious, mildly infectious and recovered individuals

Figure 2 shows the daily epidemic curve of confirmed cases from Feb 29, 2020 to July 1, 2020. It shows that the number of confirmed cases fluctuate, it increases and decreases on daily basis. But cumulatively, the number of confirmed cases increases likewise the fatality cases.

Figure 3 shows the Age-Sex distribution of confirmed cases. This shows that the most affected age group for both male and female is 31-40 years of age which is about 24% of the total confirmed cases. The figure also indicates that male individuals are more infected with this virus than female individuals. The demographics shows that there ae 17,549 infected male individuals which is 66% and 8,935 infected female individuals which gives 34%.

Figure 4 shows the cases of exposed, mildly infectious and highly infectious individuals from 1st of July, 2020. It is observed that individuals exposed would continue to be on the increase and mildly infectious are greater than those that are highly infectious.

Figure 5 shows the cases of mildly infectious and highly infectious individuals from 1st of July, 2020. We observed that individuals that are mildly infectious would be greater than the highly infectious.

Figure 6 shows the cases of mildly infectious, highly infectious and hospitalized individuals. It is observed that the mildly infectious individuals are more than the hospitalized individual. It is also seen that the highly infectious are lesser than the hospitalized individuals. Which would be alarming as times goes on, because of insufficient bed spaces in hospitals in Nigeria.

Figure 7 shows the cases of mildly infectious, highly infectious and the recovered individuals. It is observed that despite the increase in infectious disease among population, cases of individuals that would recover from this infectious disease would continue to increases till the infectious disease vanish among human population. Hence, the need to practice social distance, using of face mask to reduce cases of individuals that are mildly infected and highly infected, reinforced effort from the government, decision makers and stakeholders in ensuring compliance to all preventive measure as directed by WHO.

Conclusion

It is no more a news that the coronavirus pandemic is ravaging the whole world. In this research work, with the prediction made, it shows that with the stipulated time of 350days from the time of this work, the COVID-19 curve will flatten if the government can enforce all the guidelines given by the Nigeria Centre for Disease Control (NCDC), Presidential Task Force (PTF) on coronavirus disease and World Health Organisation (WHO) to letters, despite the non-availability of anti-virus vaccine, we will see its end.

It is important to take responsibility for the most vulnerable including the elderly and those with pre-existing medical problems because they are at a considerably high risk of having complications from the disease. It is important that people with underlying health immune-compromised conditions take extra precautions to protect themselves, due to their weakened immune system which put them at a higher risk of infection.

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