MODELING ANALYSIS OF CORONAVIRUS EPIDEMIC IN NIGERIA USING LYAPUNOV FUNCTIONS

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Abstract: In this work, a mathematical modelling of coronavirus epidemic using Lyapunov function is analyzed. The basic Kermack-McKendric- type of mathematical model is used to divide the total human population into four compartments, SEIR model. The basic reproduction number R_0 is computed using Lyapunov functions; likewise the global stability was also established. The numerical solution showed that $R_0 < 1\ (i.e. R_0 = -0.0019)$ indicating that there is 99.99% chances of re-infection when infected individuals and exposed individuals interact with the susceptible individuals through contact. The numerical simulation indicate that, the rate of infection will continue to increase, but will be superseded by the rate of recovery after 21 days.

Keywords: Coronavirus, epidemic, lyapunov function, global stability, mathematical model, SEIR

Introduction

Coronaviruses are a large family of viruses which may cause illness in humans and animals. In humans, several coronaviruses are known to cause respiratory infections ranging from the common cold to more several diseases such as Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS). The recently discovered coronavirus causes coronavirus disease (COVID-19) which is now a pandemic affecting many countries globally has great negative impacts on the economy of the whole world.

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, which is the most populous country in Africa with estimate population of 200 million is one of such vulnerable countries. The first case of this virus disease was discovered 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 (August 29, 2020), data from Nigeria Centre for Disease Control (NCDC) website shows that Nigeria has recorded 58,865 confirmed cases, 41,513 discharged cases and fatality cases of 1,013. 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 Atangana (2020) 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. (Kuniya, 2020) predicted the epidemic peak of coronavirus 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 predict the future occurrence of this pandemic.

Shuai and Driessche (2020) presented two systematic methods to guide the construction of Lyapunov functions for general infectious disease models and are applicable to establish their global dynamics. A matrix-theoretic method using the Perron eigenvector is applied to prove the global stability of the disease – free equilibrium, while a graph-theoretic method based on Kirchhoff's matrix tree theorems and two new combinational identities are used to prove the global stability of the endemic equilibrium.

Iboi *et al.* (2020) developed a mathematical model for understanding the transmission of dynamics and control of covid-19 in Nigeria as one of the main epicentres in Africa. The analysis of the Kermach-McKendrick type compartmental epidemic model was developed which take the form of a deterministic system of nonlinear differential equations, revealed that the model has a continuum of disease-free equilibria which is local asymptotically stable.

Onitilo *et al.* (2020) studied the mathematical modelling of 2019 novel coronavirus (2019 – nCov) pandemic in Nigeria using SEIAHQR model. In their work, the basic reproduction number of the model shows to be less than 1.

Bernoussi *et al.* (2014) proposed the global dynamic of an SIRI epidemic model with latency and a general nonlinear incidence function. Their model was based on the susceptible, infective and recovered (SIR) compartmental structure with relapse (SIRI). Also the global stability of equilibria was obtained using Lyapunov-LaSalle theorem.

Recently, attentions has been paid to compartmental models using Kermack-McKendrick-type of mathematical model, but in this work Lyapunov function has been introduced to obtain the global stability of equilibria and reproduction number.

Model Formulation and Analysis

Model formulation

In this work, a basic Kermack-McKendrick type of mathematical model is used to divide the total human population at time t, denoted by $N(t)$into four compartments;

the susceptible class (denoted by S), the exposed class (denoted by E), the infected class (denoted by I), and the recovered class (denoted by R). Individuals in the susceptible class $S(t)$are individuals who do not yet have the disease but could get infected if they come in contact with the individuals in the infected class. Individuals in the infected class$I(t)$ are those with the symptoms of the virus disease. Individuals in the exposed class are those that are confirmed to have the virus and can transmit the disease/virus but under quarantine. Individuals in the recovered class R(t) are those that has been tested negative of the virus.

The following equation model will describe the transmission dynamics of the coronavirus epidemic using SEIR.

$$\frac{dS}{dt} = \pi + \eta s$$
$$\frac{dE}{dt} = S - PE - \eta E$$
$$\frac{dI}{dt} = PE - \alpha I - (\eta + \gamma)I \quad (1)$$
$$\frac{dR}{dt} = \alpha I - \eta R - \xi R$$

Where: P- incidence rate of the population; η- natural death rate; α- recovery rate; γ- disease induced death rate for infectious individuals; ξ– rate of removed individuals; π– rate of susceptible to exposed individuals.

$dIdt = PE - \alpha I - \eta + \gamma I$ (1) is:

$$\Gamma\left\{(S,E,I,R) \in \mathbb{R}_+^4 \mid S + E + I + R \leq \frac{\pi}{\eta}\right\}$$

Since $S + E + I + R = 1$ satisfy the conservation law, then we can reduce the number of equations in the model equation $dIdt = PE - \alpha I - \eta + \gamma I$ (1). In fact, $dIdt = PE - \alpha I - \eta + \gamma I$ (1) is a three dimensional system. To satisfy our analysis, we can ignore the equation involving $R(t)$ since the first three equation in (1) do not contain $R(t)$. Once the behaviour of $S(t), E(t), I(t)$ are known, $R(t)$ can be easily obtained from:

$$S + E + I + R = 1$$

Then $R = 1 - S - E - I$. Therefore, we can consider the following equivalent system of equations;

$$\frac{dS}{dt} = \pi + \eta s$$
$$\frac{dE}{dt} = S - (P + \eta)E \quad (2)$$
$$\frac{dI}{dt} = PE - (\alpha + \eta + \gamma)I$$

In a 3-dimensional feasible region;

$\Gamma\{(S,E,I,R \in \mathbb{R}_+^3) \mid 0 \leq S + E + I \leq 1\}$

Disease free and endemic equilibrium

$$\frac{dS}{dt} = \pi + \eta s$$
$$\frac{dE}{dt} = S - (P + \eta)E \quad (3)$$
$$\frac{dI}{dt} = PE - (\eta + \gamma + \alpha)I$$

Since $S + E + I \leq 1$, then $\frac{dN(t)}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt}$

$\frac{dN}{dt} = \pi + \eta s + S - \eta E - \eta I - \alpha I - \gamma I$ (4)

$\frac{ds}{dt} = \frac{\pi(1-s)}{N} - s - \eta e + \eta i + \alpha i + \gamma I + s\eta + s^2\eta - ss^2$ (5)

$\frac{de}{dt} = s - \eta e - Pe - \frac{e\pi}{N} - \eta se - es + e^2\eta + e^2\eta i + e\gamma i + e\alpha i$ (6)

$\frac{di}{dt} = Pe - \eta i - \gamma i - \alpha i - \frac{\pi i}{N} - \eta si - si + \eta e + \eta i + \gamma i + \alpha i$ (7)

Equations (5), (6) and (7) was arrived at as a result of non dimensionalization.

Solving (5), (6) and (7), we set each of the equations to zero. Hence,

$$\frac{\pi(1-s)}{N} - s - \eta e + \eta i + \alpha i + \gamma I + s\eta + s^2\eta = 0$$

$$s - \eta e - Pe - \frac{e\pi}{N} - \eta se - es + e^2\eta + e^2\eta i + e\gamma i + e\alpha i = 0$$

$$Pe - \eta i - \gamma i - \alpha i - \frac{\pi i}{N} - \eta si - si + \eta e + \eta i + \gamma i + \alpha i = 0$$

Setting the disease component s, e, i to zero, we have

$$\frac{\pi}{N} = 0 \quad (8)$$

Hence $s = 0$ (9)

Substitute $s = 0$ in equation (5), we obtained

$$\frac{\pi}{N} - \frac{\pi s}{N} + \eta s - \eta s^2 - ss^2 = 0$$
$$\eta s - \eta s^2 - ss^2 = 0$$
$$s(\eta - \eta s - s^2) = 0$$
$$\eta - \eta s - \eta^2 = 0$$
$$\therefore \ \eta^2 + \eta s - \eta = 0$$
$$Using \ x = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$$
$$s^* = \frac{-\eta \pm \sqrt{\eta^2 + 4\eta}}{2}$$
$$(s_1^*, s_2^*) = \left\{(0,0)\left(\frac{-\eta + \sqrt{\eta^2 + 4\eta}}{2}, \frac{-\eta - \sqrt{\eta^2 + 4\eta}}{2}\right)\right\}$$

Local stability of Covid-19 free equilibrium state analysis

In this section, we discuss the local/global stability of a disease-free equilibrium state $E_0 = \left[\frac{\pi}{\eta}, 0, 0\right]$. This linearized stability approach gives us a Jacobian matrix JE_0 transformation of the form:

$$JE_0 = \begin{bmatrix} -\frac{\pi}{N} + \eta & 0 & 0 \\ 1 & -\left(\eta + \frac{\pi}{N}\right) & 0 \\ 0 & \rho & -(\eta + \gamma + \alpha) - \frac{\pi}{N} \end{bmatrix} \quad (10)$$

Therefore, the determinant of the Jacobian Matrix JE_0 is given by the recursive of a 3×3 matrix defined as:

$$Det(JE_0) = a_{11}\det(JE_{0_{11}}) - a_{12}\det(JE_{0_{12}}) + a_{13}\det(JE_{0_{13}})$$

From (10) $Det(JE_0) > 0$

Hence, we find the trace of the Jacobian matrix in equation (10)

$$Trace(JE_0) = -\frac{\pi}{N} + \eta + \left(-\eta - \frac{\pi}{N}\right) - (\eta + \gamma + \alpha) - \frac{\pi}{N} = -\frac{3\pi}{N} - \eta - \gamma - \alpha < 0$$

Since $Det(JE_0) > 0$ and $Trace(JE_0) < 0$that satisfies the prescribe threshold criteria based on the disease free equilibrium (E_0) for COVID-19 coronavirus then the criteria for local stability is satisfied.

Reproduction number (R_0) of the model

To compute the reproduction number (R_0) of the model, next generation matrix techniques should be adopted. R_0 is the basic reproductive number of infectious that one infectious individual would be adopted.

To complete the basic reproductive number (R_0) the next generation matrix is applied.

$$F_i = \begin{pmatrix} \eta i \\ 0 \end{pmatrix} \qquad (11)$$

while

$$V_i = \begin{bmatrix} \frac{\pi(1-s)}{N} - s - \eta e + \eta i + \gamma i + \alpha i + s\eta - s^2\eta - ss^2 \\ s - \eta e - pe - \frac{e\pi}{N} - \pi se - es + e^2\eta + e^2\eta i + e\gamma i + e\alpha i \\ pe - \eta i - \gamma i - \alpha i - \frac{\pi i}{N} - \eta si - si + \eta e + \eta i + \gamma i + \alpha i \end{bmatrix} \quad (12)$$

Where F_i and V_i are the rate of appearance of new infections in compartment i and the transfer of individuals into and out of compartment i by all means, respectively.

Using the linearization method, the associated matrices at disease free equilibrium (E_0) and after taking partial derivatives as defined by:

$$DF_i(E_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix} \; and \; DV_i(E_0) = \begin{pmatrix} V & 0 \\ J_1 & J_2 \end{pmatrix}$$

Where F and V are $m \times m$ matrices defined by:

$$F = \left[\frac{\partial F_i}{\partial x_i}(E_0)\right] \quad and \quad V = \left[\frac{\partial V_i}{\partial x_i}E_0\right] \qquad (13)$$

Where $1 < i$ and $j \leq m$ is the number of infected cases, we have

$$F = \begin{pmatrix} p & \eta \\ 0 & p \end{pmatrix} \; and \; V = \begin{pmatrix} -(\alpha+\gamma) & 0 \\ 0 & -(\alpha+\gamma) \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} -\frac{p}{\alpha+\gamma} & -\frac{\eta}{\alpha+\gamma} \\ 0 & -\frac{p}{\alpha+\gamma} \end{pmatrix}$$

We find the eigen values of FV^{-1} by getting the determinant $|FV^{-1} - \lambda I| = 0$

Hence,

$$|FV^{-1} - \lambda I| = \begin{vmatrix} -\frac{p}{\alpha+\gamma} - \lambda & -\frac{\eta}{\alpha+\gamma} \\ 0 & -\frac{p}{\alpha+\gamma} - \lambda \end{vmatrix}$$

Therefore, the characteristic polynomial

$$\rho(\lambda) = \lambda^2 - \left(\frac{2p}{\alpha+\gamma}\right)\lambda + \left(\frac{p}{\alpha+\gamma}\right)^2 = 0 \qquad (14)$$

Equation (14) gives

$$\lambda = -\frac{p}{\alpha+\gamma}$$

$$\lambda < 1$$

Hence $R_0 < 1$

$$R_0 = \rho(FV^{-1}) = -\frac{p}{\alpha+\gamma} \qquad (15)$$

Establishing the global stability using Lyapunov function

The general compartments disease transmission model can be written as:

$$x' = F(x,y) - V(x,y) \qquad (16)$$

$$y' = g(x,y)$$

Where $g = (g_1, \dots, g_m)^T$. Here ' denotes differentiation with respect to time; $x = (x_1, \dots, x_n) \in \mathbb{R}^n$ and $y = (y_1, \dots, y_m)^T \in \mathbb{R}^m$ represent the population in disease compartments and non disease compartments respectively; $F = (F_1, \dots, F_n)^T$ and $V = (V_1, \dots, V_n)^T$, where F_i represents the rate of new infection in ith disease compartment; and V_i represents the transition terms, for example, death and recovery in the ith disease compartment.

Let $f(x,y) = (F-V)x - F(x,y) + V(x,y) \qquad (17)$

Then (16) for the disease compartments can be written as:

$$x' = (F-V)x - f(x,y) \qquad (18)$$

Note that $f(0,y) = 0$. Let $w^T \geq 0$ be the left eigen-vector of the non negative matrix $V^{-1}F$ corresponding to the eigen value $\rho(V^{-1}F) = \rho(FV^{-1}) = R_0$. The following result provides a general method to construct a Lyapunov function for (16);

Theorem 1: Let F, V and $f(x,y)$ be defined as in (13) and (17), respectively. If $f(x,y) \geq 0$ in $\Gamma \subset \mathbb{R}_+^{n+m}, F \geq 0, V^{-1} \geq 0$ and $R_0 \leq 1$, then the function $Q = w^T V^{-1} x$ is a Lyapunov function for model (26) on Γ.

Proof:

Differentiating Q along solution of (16) gives

$Q' = Q' = w^T V^{-1}(F-V)x - w^T V^{-1} f(x,y)$

$= (R_0 - 1)w^T x - w^T V^{-1} f(x,y)$

Since $w^T \geq 0, V^{-1} \geq 0$ and $f(x,y) \geq 0$ in Γ, the last term is non-positive. If $R_0 \leq 1$, then $Q' \leq 0$in Γ, and thus Q is a Lyapunov function of system.

Theorem 2: Let R_0 be as defined in (15), then the sharp threshold property holds for (1.1)

Proof:

Since matrix $V^{-1}F$ is reducible, the Lyapunov function constructed in theorem 1 can be used to establish the global asymptotic stability of S_0. Let $x = (S, E, I)^T$, then $x' = (F-V)x - f(x,s)$ with $f(x,s) \coloneqq (s_0 - s)$in Γ.

By theorem 1, $Q = w^T V^{-1} x$ is a Lyapunov function where $w^T = (0,1,0)$ is the left eigenvector of matrix $V^{-1}F$ straight forward calculation gives.

$Q = \frac{R_0}{s_0}(S + \alpha + \gamma I + \alpha + \gamma R)$ and $Q' = (R_0 - 1)I - \frac{R_0}{s_0} I(s_0 - s) \leq 0$ provided $R_0 < 1$.

Results and Discussion

In this study, we developed SEIR model, which considered the susceptible individuals, the exposed individuals, the infected individuals and the recovered individuals. For the numerical result, we considered the prevalence of Covid-19 in Nigeria. The result from the numerical simulation showed that R_0 is -0.0019<1 which implies that there is a 99.99% chances of secondary infection when infected individuals and exposed individuals interact with susceptible through contact. We set the initial data of this analysis to 29th of August, 2020

Table 1: States with reported laboratory-confirmed COVID-19 cases, recoveries, deaths and days since last reported case

States	Confirmed cases		Discharged cases		Deaths		Total active cases	Days since last reported case
	Total	New	Total	New	Total	New		
Lagos	18,119	15	15,228	0	202	0	2,689	0
FCT	5,156	7	1,531	7	50	0	3,575	0
Oyo	3,118	11	1,952	0	37	0	1,129	0
Edo	2,578	1	2,300	0	100	0	178	0
Plateau	2,498	55	1,374	46	29	0	1,095	0
Rivers	2,141	7	1,969	9	57	0	115	0
Kaduna	2,120	6	1,977	27	12	0	131	0
Delta	1,744	0	1,540	0	47	0	157	1
Kano	1,725	0	1,537	0	54	0	134	2
Ogun	1,646	0	1,489	1	26	0	131	1
Ondo	1,539	5	1,380	20	31	0	128	0
Enugu	1,155	0	907	0	21	0	227	1
Ebonyi	984	11	931	0	27	0	26	0
Kwara	961	3	773	0	25	0	163	0
Katsina	789	0	457	0	24	0	308	2
Osun	779	0	732	3	17	1	30	1
Abia	771	8	697	28	8	1	66	0
Borno	740	0	667	0	36	0	37	7
Gombe	723	0	636	0	23	0	64	1
Bauchi	667	1	581	31	14	0	72	0
Imo	527	0	193	0	11	0	323	1
Benue	452	1	216	0	9	0	227	0
Nasarawa	434	0	298	0	12	0	124	1
Bayelsa	391	0	345	0	21	0	25	1
Jigawa	322	0	308	0	11	0	3	45
Akwa Ibom	278	0	229	0	8	0	41	3
Ekiti	262	0	203	18	4	0	55	1
Niger	241	0	214	0	12	0	15	3
Adamawa	221	0	180	0	15	0	26	1
Anambra	214	7	168	9	18	0	28	0
Sokoto	158	0	138	0	16	0	4	7
Kebbi	93	0	82	0	8	0	3	2
Taraba	87	0	73	0	5	0	9	5
Cross River	82	0	73	0	8	0	1	6
Zamfara	78	0	73	0	5	0	0	10
Yobe	67	0	59	0	8	0	0	31
Kogi	5	0	3	0	2	0	0	58
Total	53,865	138	41,513	199	1,013	2	11,339	

States, including FCT, are arranged in descending order by number of total confirmed cases and then alphabetical order (Source: NCDC)

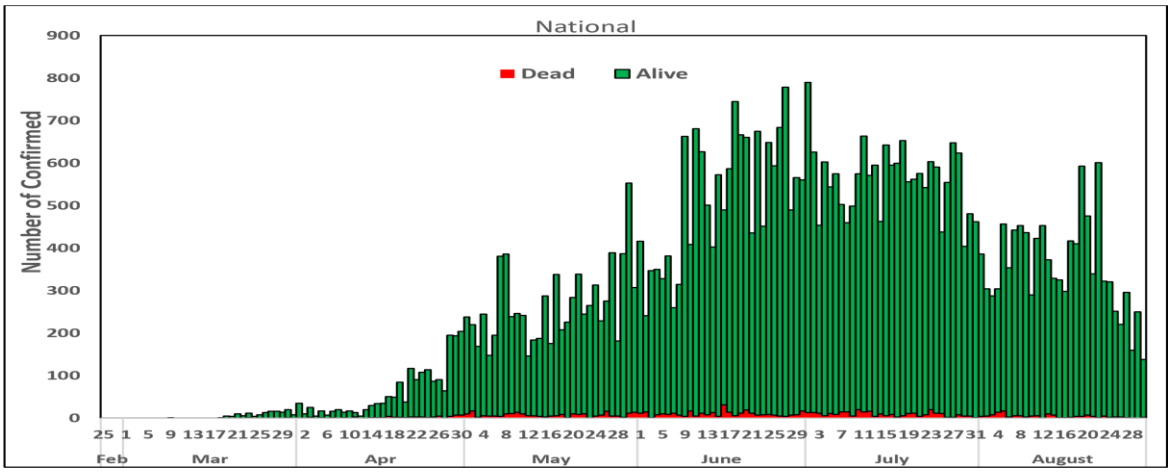

Fig. 1: Daily epidemic curve of confirmed cases (Source: NCDC)

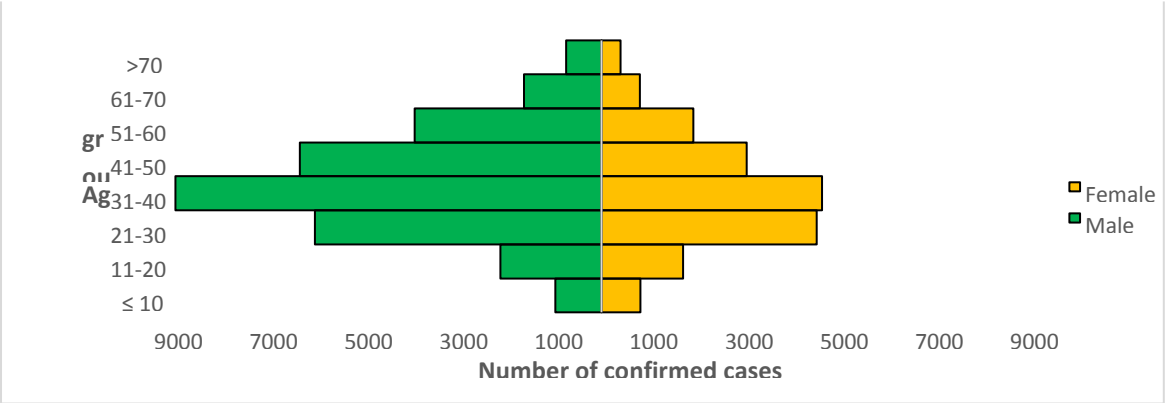

Fig. 2: Age-sex distribution of confirmed cases (Source: NCDC)

Figure 1 shows the daily epidemic curve of confirmed cased from Feb 29, 2020 to August 29, 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. This shows that the covid-19 curve is getting flattened. Fig. 2 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 25% of the total confirmed cases. Fig. 3 shows the rate of infection in 30 days from 29th of August, 2020. It is observed that the rate of infection keeps increasing. Fig. 4 shows that the rate of recovery. It is found out that the rate at which individuals recovers would keep increasing over time.

Table 2: Estimation values of parameters used in the numerical simulation

N=200e6,	
e0=1,	Victor (2020)
i0=0.0003,	Estimation
r0=0.0001,	Victor (2020)
s0=1,	Estimation
π =0.00567,	Victor (2020)
γ=0.0005,	Assumed
T=30days	
η=0.0001,	
ξ=0.0007,	Assumed
α =0.12,	NCDC (2020)
P=0.0027,	Victor (2020)

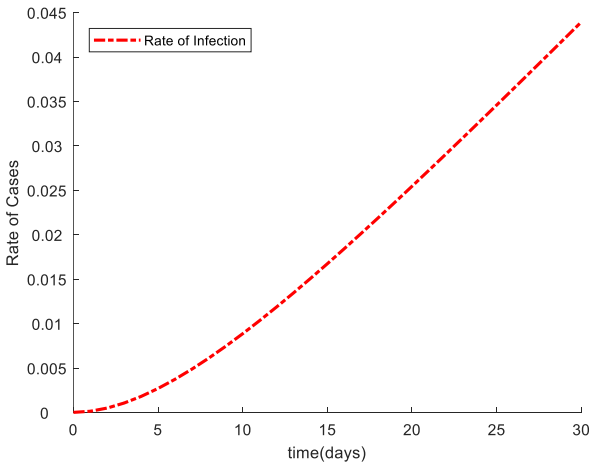

Fig. 3: Simulation showing rate of infection

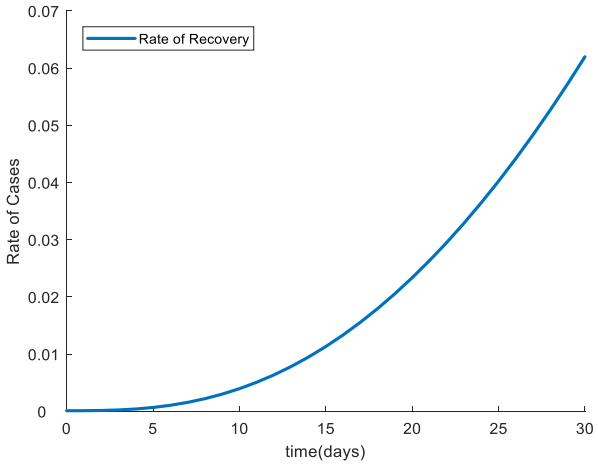

Fig. 4: Simulation showing rate of recovery

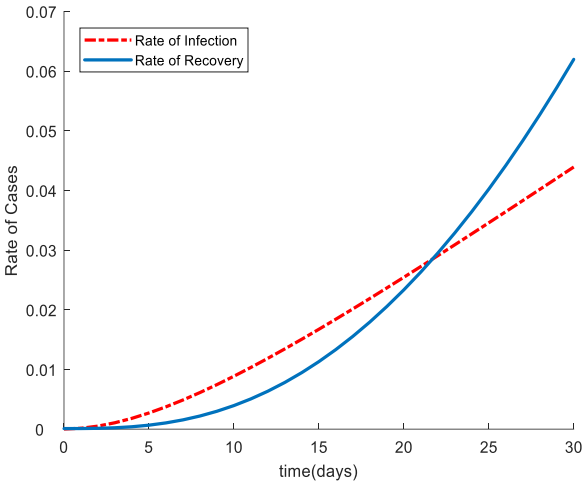

Fig. 5: Simulation showing rate of infection and recovery

Figure 5 shows that the rate of infection will continue to increase but will be superseded by the rate of recovery after 21 days. Hence, there is continual need for social distancing, constant use of face mask to reduce infection curve. We have from Fig. 3 that the rate of recovery will continue to increase,

despite the increase in the rate of infection. Consequently, Nigeria would hardly be free of COVID-19; hence, the need for reinforced effort from the government, stakeholders and decision makers in ensuring compliance to all preventive measure as directed by NCDC and WHO. Also, government should ensure all facilities/equipment are on ground/provided before the opening of schools and tertiary institutions in Nigeria.

Conclusion

It is clear 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 30 days 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, and the government should not relent in their efforts to contain this coronavirus disease, 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.

Conflict of Interest

The authors declare that there is no conflict of interest related to this work.

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