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Analysis of a Modified Covid-19 Model in Nigeria and Approximations Using Differential Transformation Method

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Abstract

Mathematical models has been useful over the years to understand the behavior and impacts of several infectious diseases such as Malaria, Ebola, Cholera, in human and non-human population. In this paper, a modified mathematical model of covid-19 virus in Nigeria is presented. The disease free equilibrium, endemic equilibrium state, threshold behavior R_0 and the bounded region where the model is mathematically and epidemiologically feasible is established. The global stability analysis for the disease-free and endemic equilibria are obtained using Carlos Chavez theorem and LaSalle's criterion. The results show that the virus will cause devastating impacts ($R_o > 1$) in Nigeria if the control and mitigation mechanisms are not adhered to. The numerical approximations of the model via differential transform method illustrate the impacts of the virus dynamical transmission in time/per week. The approximation's insight raises concern as more people will be susceptible and exposed to the virus, the number of infectious individuals will be on the increase for some time with more hospitalize-isolation individuals in Nigeria. The approximation also shows an increasing rate of recovery for infected individuals.

Keywords: COVID-19, Mathematical Model, Reproduction Number, Stability Analysis, Differential Transform Method.

INTRODUCTION

The novel corona virus SARS-COV-2 known as COVID-19 emerged from China in Wuhan city in the late 2019. The virus has since created global concerns in the health care and social-economic sector and have been declared pandemic by the world health organization on March 11th, 2020. The virus has rapidly spread to over 200 countries of the world and continues to inflict nations severely including Nigeria (Amoo *et al.,* 2020). Measures of intervention to control and mitigate the pandemic such as social-distance, society lock down, quarantine of suspected individuals, isolation, hand-washing, alcohol-base sanitizer and the uses of face mask have been proposed and adopted by world health organization and center for disease control in several countries to curtail the virus (Alshammari *et al.,* 2020), as the laboratory trials of effective vaccine are underway by different pharmaceutical industries. In Nigeria, the first incidence of covid-19 was recorded on February 27th, 2020 from an Italian citizen whose diagnoses showed upon coming to Nigeria from Milan, Italy (Anwar *et al.,* 2020). By 27th December, 2020 Nigeria had recorded confirmed number of

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covid-19 cases to be 84,414 and 1,254 deaths (Abayomi *et al.*, 2021).

Mathematical modeling has been extensively used to describe the transmission dynamics of infectious diseases over the years and has provided great insight to decision and policy makers in regards to mechanisms for controlling infectious diseases (Ayuba *et al.*, 2021). The authors (Okuonghae and Omame, 2020) developed a six compartmental mathematical model that examines the impacts of various non-pharmaceutical measures on the population dynamics of covid-19 in Lagos, Nigeria. The numerical simulation of control measures (social-distancing, face mask and case detection) revealed that if 55% of population adheres to the regulations for using face mask in public and social distancing, the disease will not cause devastating impacts in Lagos. Idris *et al.* (2021) developed a mathematical model with ordinary and fractional differential equations that includes asymptomatic and symptomatic classes for covid-19 disease and applied Dulac's criterion to establish the global stability analysis. The existence and uniqueness solution of the model were also obtained. The authors (Musibau *et al.*, 2021) formulated a deterministic model that governed the transmission dynamics of the novel corona virus involving seven system of ordinary differential equations and limited it to the analysis of the model by differential transform method. Anwar *et al.* (2020) developed an isolation-based mathematical model of novel corona virus (covid-19) and limited it to local stability analysis using the reproduction number. Jeffrey (2021) developed SIR (susceptible, infected, recovered) model and log-linear regression model to estimate the impacts of covid-19 virus in Italy and Spain. The predictive log-linear regression model was found to give better fit and simple daily estimates in both countries. Kayode *et al.* (2020) proposed a statistical curve estimator model for daily cumulative report of covid-19 in Nigeria using the NCDC data. The parameter estimators were confirmed cases, discharged cases and death cases in Nigeria. The mathematical model of Covid-19 in Nigeria by Enahoro *et al.* (2020) was limited to local stability analysis using the model reproduction number R_0 and Data fitting of parameter estimation. The authors also assumed non recruitment rate in susceptible population and ignored death rate of humans due to others factors.

METHODOLOGY

Covid-19 Model in Nigeria by Enahoro *et al.* (2020)

The model which has six compartments with the total human population $N(t)$ at time t is partitioned as follows: susceptible humans $S(t)$, exposed humans $E(t)$, symptomatically infected individuals $I_s(t)$, asymptomatically infected persons $I_a(t)$, hospitalized and isolated individuals $I_h(t)$ and recovered $R(t)$ individuals. Therefore, $N(t) = S(t) + E(t) + I_s(t) + I_a(t) + I_h(t) + R(t)$. The model equations, parameters and description are presented in Table 1 and equation (1) respectively.

$$\left.\begin{aligned}
\frac{dS}{dt} &= -\beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S - \beta_a(1-\epsilon_m-c_m)\frac{I_a}{N}S \\
\frac{dE}{dt} &= \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S + \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - \sigma E \\
\frac{dI_s}{dt} &= (1-r)\sigma E - (\phi_s+\gamma_s+\delta_s)I_s \\
\frac{dI_a}{dt} &= r\sigma E - \gamma_a I_a \\
\frac{dI_h}{dt} &= \phi_s I_s - (\gamma_h+\delta_h)I_h \\
\frac{dR}{dt} &= \gamma_s I_s + \gamma_a I_a + \gamma_h I_h
\end{aligned}\right\} \qquad (1)$$

Modified Model Theory

In Nigeria, federal government placed restriction of inter-state movement on May 4, 2020 as the burden of covid-19 virus increases concern in the health-care sector. Though, with the restriction, several people could make their way from one state to another thereby making other people more likely to contract the virus at all level of Nigeria society. Therefore, the modified model has the recruitment rate λ of humans into the susceptible sub-population and inclusion of death rate of humans μ due to other illness or factors aside covid-19, in each of the six compartments; susceptible, exposed, symptomatically infected, asymptomatically infected, hospitalized infected and recovered class. The flow diagram, fig. 1 depicting this interactions and the modified governing equations are shown in equation (2).

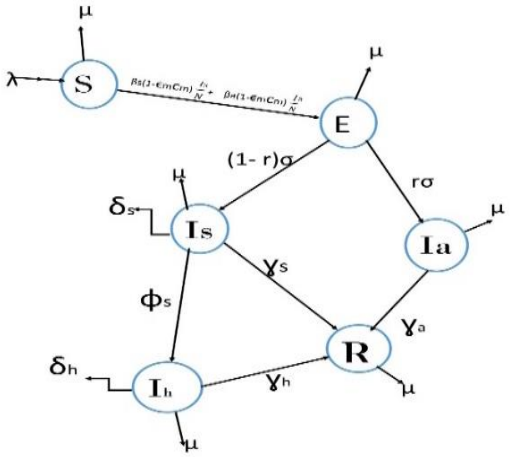


Figure 1: Flow diagram of the modified model

$$\left.\begin{aligned}
\frac{dS}{dt} &= \lambda - \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S - \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - \mu S \\
\frac{dE}{dt} &= \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S + \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - (\sigma+\mu)E \\
\frac{dI_s}{dt} &= (1-r)\sigma E - (\phi_s + \gamma_s + \delta_s + \mu)I_s \\
\frac{dI_a}{dt} &= r\sigma E - (\gamma_a + \mu)I_a \\
\frac{dI_h}{dt} &= \phi_s I_s - (\gamma_h + \delta_h + \mu)I_h \\
\frac{dR}{dt} &= \gamma_s I_s + \gamma_a I_a + \gamma_h I_h - \mu R
\end{aligned}\right\} \quad (2)$$

RESULTS AND DISCUSSION

Positive Invariant Region

In this section, the bounded region of solution for the covid-19 model equations (2) is derived. Let the feasible region Θ be defined by

Θ={S(t),E(t),$I_s(t)$,$I_a(t)$,$I_h(t)$,R(t)$\in \Re_+^6$:$N(0) \leq N(t) \leq \frac{\lambda}{\mu}$}

with initial conditions $S(0) \geq 0$, $E(0) \geq 0$, $I_s(0) \geq 0$, $I_a(0) \geq 0$, $I_h(0) \geq 0$, R(0)$\geq$ 0 as positive invariant for the dynamical system of equations (2)

Proof: The total human population is given by

$N(t) = S(t) + E(t) + I_s(t) + I_a(t) + I_h(t) + R(t)$. (4)

Differentiate equation (4) with respect to t

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI_s}{dt} + \frac{dI_a}{dt} + \frac{dI_h}{dt} + \frac{dR}{dt} \quad (5)$$

Substitute model (2) equations into (5), we obtain

$\frac{dN}{dt} = -\mu S - \mu E - \delta_s I_s - \mu I_s - \mu I_a - \mu I_h - \mu R$

$\frac{dN}{dt} \leq \lambda - \mu(S + E + I_s + I_a + I_h + R)$

$\frac{dN}{dt} \leq \lambda - \mu N$. Solving for N at $t \to \infty$, we obtain $N \leq \frac{\lambda}{\mu}$

Thus, Θ is a positivity invariant set under the model described by equation (2)

The Equilibrium State

Disease free Equilibrium State

To achieve the free equilibrium point, we set the left-hand-side derivative of the ODEs in equation (2) to zero and solve for the values of S, E I_s, I_a, I_h and R at time t=0. This follows

$$\left.\begin{array}{c} \lambda - \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S - \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - \mu S = 0 \\ \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S + \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - (\sigma+\mu)E = 0 \\ (1-r)\sigma E - (\phi_s + \gamma_s + \delta_s + \mu)I_s = 0 \\ r\sigma E - (\gamma_a + \mu)I_a = 0 \\ \phi_s I_s - (\gamma_h + \delta_h + \mu)I_h = 0 \\ \gamma_s I_s + \gamma_a I_a + \gamma_h I_h - \mu R = 0 \end{array}\right\} \quad (6)$$

Since at t=0, $I_s = I_a = I_h = 0$, then $(1-r)\sigma E = (\phi_s + \gamma_s + \delta_s + \mu)I_s$. For $E = 0$, and $\gamma_s I_s + \gamma_a I_a + \gamma_h I_h = \mu R$, R=0. Also $\lambda = \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S - \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - \mu S$ substituting of E, I_s, I_a, I_h into above equation, we have $\lambda - \mu S = 0 \Rightarrow S = \frac{\lambda}{\mu}$. Thus, the disease free equilibrium point is given by $U_0(S, E, I_s, I_a, I_h, R) = \left(\frac{\lambda}{\mu}, 0,0,0,0,0\right)$

At the disease free equilibrium point, it is assumed that there is no case infection in the population.

Endemic Equilibrium State

To obtain the endemic point of model equations (2), the left-hand-side derivatives are set to zero, and we obtain the endemic points $S^*, E^*, I_s^*, I_a^*, I_h^*$ and R^* as shown.

$$S^* = \frac{(\sigma+\mu)(\gamma_a+\mu)(\phi_s+\gamma_s+\delta_s+\mu)}{\sigma(1-\epsilon_M c_M)[\beta_s(1-r)(\gamma_a+\mu) + \beta_a(\phi_s+\gamma_s+\delta_s+\mu)r]}$$

$$E^* = \frac{\lambda\sigma(1-\epsilon_M c_M)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r] - \mu(\sigma+\mu)(\gamma_a+\mu)(\phi_s+\gamma_s+\delta_s+\mu)}{\sigma(1-\epsilon_M c_M)(\sigma+\mu)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r]}$$

$$I_s^* = (1-r)\frac{\{\lambda\sigma(1-\epsilon_M c_M)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r] - \mu(\sigma+\mu)(\gamma_a+\mu)(\phi_s+\gamma_s+\delta_s+\mu)\}}{(1-\epsilon_M c_M)(\gamma_a+\mu)(\sigma+\mu)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r]}$$

$$I_a^* = r\frac{\{\lambda\sigma(1-\epsilon_M c_M)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r] - \mu(\sigma+\mu)(\gamma_a+\mu)(\phi_s+\gamma_s+\delta_s+\mu)\}}{(1-\epsilon_M c_M)(\sigma+\mu)(\phi_s+\gamma_s+\delta_s+\mu)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r]}$$

$$I_h^* = \phi_s(1-r)\frac{\{\lambda\sigma(1-\epsilon_M c_M)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r] - \mu(\sigma+\mu)(\gamma_a+\mu)(\phi_s+\gamma_s+\delta_s+\mu)\}}{(1-\epsilon_M c_M)(\sigma+\mu)(\phi_s+\gamma_s+\delta_s+\mu)(\gamma_h+\delta_h+\mu)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r]}$$

$$R^* = \frac{\{\gamma_s(1-r)(\gamma_a+\mu)(\gamma_h+\delta_h+\mu)+\gamma_a(\phi_s+\gamma_s+\delta_s+\mu)(\gamma_h+\delta_h+\mu)r+\phi_s\gamma_h(1-r)(\gamma_a+\mu)\}}{(1-\epsilon_M c_M)(\sigma+\mu)(\phi_s+\gamma_s+\delta_s+\mu)(\gamma_a+\mu)(\gamma_h+\delta_h+\mu)}$$
$$\frac{\{\lambda\sigma(1-\epsilon_M c_M)[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r]-\mu(\sigma+\mu)(\gamma_a+\mu)(\phi_s+\gamma_s+\delta_s+\mu)\}}{[\beta_s(1-r)(\gamma_a+\mu)+\beta_a(\phi_s+\gamma_s+\delta_s+\mu)r]}$$

Reproduction Number

A very important concern about any infectious disease is its ability to invade a population (Van den & Watmough, 2002). The threshold condition known as the basic reproduction number (usually written as R_0) is used in determining whether the disease will persist or dies out in the population with respect to time. If $R_0 \leq 1$, then the disease free equilibrium (DFE) will be globally asymptotically stable and the disease cannot invade the population while when $R_0 > 1$, then the DFE is unstable and invasion is possible which could leads to an endemic equilibrium state (Van den & Watmough, 2002). To obtain the basic reproduction number, we applied the next generation matrix operator as used by several authors (Ayuba *et* al., 2021; Idris *et al*., 2021; Van den & Watmough, 2002). We obtained the reproduction number $R_c = AB^{-1}$. Where A is the matrix of appearance for new infection and B is the matrix for transfer of infected individuals from the compartments (E,I_s, I_a). Considering the model equations (2), we then obtain

$$a = \begin{bmatrix} \beta_s(1-\epsilon_M c_M)\frac{I_s}{N}S + \beta_a(1-\epsilon_M c_M)\frac{I_a}{N}S \\ 0 \\ 0 \end{bmatrix}$$
$$b = \begin{bmatrix} (\sigma+\mu) \\ -(1-r)\sigma E + (\phi_s+\gamma_s+\delta_s+\mu)I_s \\ -r\sigma + (\gamma_a+\mu)I_a \end{bmatrix}$$

Differentiate partially a and b with respect to E, I_s, I_a compartments at disease free state, we obtain

$$A = \begin{bmatrix} 0 & \beta_s(1-\epsilon_M c_M) & \beta_a(1-\epsilon_M c_M) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix},$$
$$B = \begin{bmatrix} (\sigma+\mu) & 0 & 0 \\ -(1-r)\sigma & (\phi_s+\gamma_s+\delta_s+\mu) & 0 \\ -r\sigma & 0 & (\gamma_a+\mu) \end{bmatrix}$$
$$B^{-1} = \begin{bmatrix} \frac{1}{(\sigma+\mu)} & 0 & 0 \\ \frac{(1-r)\sigma}{(\sigma+\mu)(\phi_s+\gamma_s+\delta_s+\mu)} & \frac{1}{(\phi_s+\gamma_s+\delta_s+\mu)} & 0 \\ \frac{r\sigma}{(\sigma+\mu)(\gamma_a+\mu)} & 0 & \frac{1}{(\gamma_a+\mu)} \end{bmatrix}$$
$$AB^{-1} = \begin{bmatrix} \frac{\sigma(1-r)(1-\epsilon_M c_M)\beta_s}{(\sigma+\mu)(\phi_s+\gamma_s+\delta_s+\mu)} + \frac{r\sigma(1-\epsilon_M c_M)\beta_a}{(\sigma+\mu)(\gamma_a+\mu)} & \frac{\beta_s(1-\epsilon_M c_M)}{(\phi_s+\gamma_s+\delta_s+\mu)} & \frac{\beta_a(1-\epsilon_M c_M)}{(\gamma_a+\mu)} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

The reproduction number of the modified covid-19 model R_c is obtain by $p(AB^{-1}) = \frac{\sigma(1-r)(1-\epsilon_M c_M)\beta_s}{(\sigma+\mu)(\phi_s+\gamma_s+\delta_s+\mu)} \frac{r\sigma(1-\epsilon_M c_M)\beta_a}{(\sigma+\mu)(\gamma_a+\mu)}$, which follows that $R_c = RI_I + RI_a$, then

$$R_c = \frac{\sigma(1-r)(1-\epsilon_M c_M)\beta_s}{(\sigma+\mu)(\phi_s+\gamma_s+\delta_s+\mu)} + \frac{r\sigma(1-\epsilon_M c_M)\beta_a}{(\sigma+\mu)(\gamma_a+\mu)}$$

Global Stability Analysis

In this section, we obtain the global stability of disease free equilibrium and endemic state of the model (2).

Global Stability for the free Equilibrium State

The Carlos Chavez theorem is applied to prove the global stability of the disease free equilibrium state. The disease free equilibrium point is obtained as $E_0(S, E, I_s, I_a, I_h, R) = (\frac{\lambda}{\mu}, 0,0,0,0,0)$.

By Carlos Chavez theorem, we derived the following from the model equations (2)

$$F(X,Z) = \begin{bmatrix} \lambda - \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S - \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - \mu S \\ \phi_s I_s - (\gamma_h + \delta_h + \mu)I_h \\ \gamma_s I_s + \gamma_a I_a + \gamma_h I_h - \mu R \end{bmatrix}$$

$$G(X,Z) = \begin{bmatrix} \beta_s(1-\epsilon_m c_m)\frac{I_s}{N}S + \beta_a(1-\epsilon_m c_m)\frac{I_a}{N}S - (\sigma+\mu)E \\ (1-r)\sigma E - (\phi_s + \gamma_s + \delta_s + \mu)I_s \\ r\sigma E - (\gamma_a + \mu)I_a \end{bmatrix}$$

Substituting the disease free equilibrium point into $F(X,Z)$ we obtained

$$F(X^*,0) = \begin{bmatrix} \lambda - \mu S \\ 0 \\ 0 \end{bmatrix}$$

For $\frac{dX}{dt} = F(X^*,0), X^*$ is globally asymptotically stable by (H_1). The second condition(H_2) implies $G(X,Z) = AZ - \hat{G}(X,Z); \hat{G}(X,Z) \geq 0$, where $A = D_z G(X^*,0)$. For $A = D_z(X,Z)$,

$$D_z(X,Z) = \begin{bmatrix} -(\sigma+\mu) & \beta_s(1-\epsilon_M c_M)S & \beta_a(1-\epsilon_M c_M)S \\ (1-r)\sigma & -(\phi_s+\gamma_s+\delta_s+\mu) & 0 \\ r\sigma & 0 & -(\gamma_a+\mu) \end{bmatrix}$$

At disease free equilibrium point, $S = \frac{\lambda}{\mu}$

$$D_z(X,Z) = \begin{bmatrix} -(\sigma+\mu) & \beta_s(1-\epsilon_M c_M)\frac{\lambda}{\mu} & \beta_a(1-\epsilon_M c_M)\frac{\lambda}{\mu} \\ (1-r)\sigma & -(\phi_s+\gamma_s+\delta_s+\mu) & 0 \\ r\sigma & 0 & -(\gamma_a+\mu) \end{bmatrix}$$

$G(X,Z) = AZ - \hat{G}(X,Z) =$

$$\begin{bmatrix} -(\sigma+\mu) & \beta_s(1-\epsilon_M c_M)\frac{\lambda}{\mu} & \beta_a(1-\epsilon_M c_M)\frac{\lambda}{\mu} \\ (1-r)\sigma & -(\phi_s+\gamma_s+\delta_s+\mu) & 0 \\ r\sigma & 0 & -(\gamma_a+\mu) \end{bmatrix} \begin{bmatrix} E \\ I_s \\ I_a \end{bmatrix}$$

$$- \begin{bmatrix} (1-\epsilon_M c_M)(\beta_s I_s + \beta_a I_a)(\frac{\lambda}{\mu} - \frac{S}{N}) \\ 0 \\ 0 \end{bmatrix}$$

$$\hat{G}(X,Z) = \begin{bmatrix} (1-\epsilon_M c_M)(\beta_s I_s + \beta_a I_a)(\frac{\lambda}{\mu} - \frac{S}{N}) \\ 0 \\ 0 \end{bmatrix}$$

Since $S < N$ and $\mu < \lambda$ then $\frac{S}{N} < \frac{\lambda}{\mu}$. Thus, the conditions (H_1) and (H_2) are satisfied. By theorem (1) in section 2, the disease free equilibrium E_0 of the model (2) is globally

asymptotically stable provided $R_0 < 1$. The epidemiological implication of the above result is that the disease can be eliminated from the country if the threshold quantity R_0 can be brought to (and maintained at) a value less than unity.

Global Stability of Endemic State

In this section we investigate the global stability of the endemic equilibrium point using Lyapunov function and LaSalle's criterion.

Theorem 3: The unique endemic equilibrium E_e of the the model (2) is globally asymptotically stable if $R_0 > 1$ and $\dot{L} \leq 0$.

Proof. From equation (2), let $\beta_s' I_s S = \beta_s(1 - \epsilon_M c_M)\frac{I_s}{N}S$ and $\beta_a' I_a S = \beta_a(1 - \epsilon_M c_M)\frac{I_a}{N}S$ then modified model (2) becomes

$$\begin{aligned}
\frac{dS}{dt} &= \lambda - \beta_s' I_s S - \beta_a' I_a S - \mu S \\
\frac{dE}{dt} &= \beta_s' I_s S + \beta_a' I_a S - (\sigma + \mu)E \\
\frac{dI_s}{dt} &= (1-r)\sigma E - (\phi_s + \gamma_s + \delta_s + \mu)I_s \\
\frac{dI_a}{dt} &= r\sigma E - (\gamma_a + \mu)I_a \\
\frac{dI_h}{dt} &= \phi_s I_s - (\gamma_h + \delta_h + \mu)I_h \\
\frac{dR}{dt} &= \gamma_s I_s + \gamma_a I_a + \gamma_h I_h - \mu R
\end{aligned} \tag{7}$$

Let $E_1 = (S^{**}, E^{**}, I_s^{**}, I_a^{**}, I_h^{**}, R^{**})$ represents any arbitrary endemic (positive) equilibrium of the modified model (2). Let $R_0 > 1$ so that a unique endemic equilibrium exists and consider the following non-linear Lyapunov function of Goh-Volterra type (Sangotola & Onifade, 2019) which in our case is defined by

$$\begin{aligned}
L = (S - S^{**} - S^{**} log\frac{S}{S^{**}}) + (E - E^{**} - E^{**} log\frac{E}{E^{**}}) + P(I_s - I_s^{**} - I_s^{**} log\frac{I_s}{I_s^{**}}) \\
+Q(I_a - I_a^{**} - I_a^{**} log\frac{I_a}{I_a^{**}}) + T(I_h - I_h^{**} - I_h^{**} log\frac{I_h}{I_h^{**}})
\end{aligned} \tag{8}$$

Where L is Lyapunov function, P, Q and T are the constants to be determined. Differentiating (8),

$$\dot{L} = (1 - \frac{S^{**}}{S})\dot{S} + (1 - \frac{E^{**}}{E})\dot{E} + P(1 - \frac{I_s^{**}}{I_s})\dot{I}_s + Q(1 - \frac{I_a^{**}}{I_a})\dot{I}_a + T(1 - \frac{I_h^{**}}{I_h})\dot{I}_h \tag{9}$$

Substituting (7) into (9)

$$\begin{aligned}
\dot{L} &= \lambda - \beta_s' I_s S - \beta_a' I_a S - \mu S - \frac{S^{**}}{S}[\lambda - \beta_s' I_s S - \beta_a' I_a S - \mu S] \\
&+\beta_s' I_s S + \beta_a' I_a S - (\sigma + \mu)E - \frac{E^{**}}{E}[\beta_s' I_s S + \beta_a' I_a S - (\sigma + \mu)E] \\
&+P[(1-r)\sigma E - (\phi_s + \gamma_s + \delta_s + \mu)I_s - \frac{I_s^{**}}{I_s}((1-r)\sigma E - (\phi_s + \gamma_s + \delta_s + \mu)I_s)] \\
&+Q[r\sigma E - (\gamma_a + \mu)I_a - \frac{I_a^{**}}{I_a}(r\sigma E - (\gamma_a + \mu)I_a)] + T[\phi_s I_s - (\gamma_h + \delta_h + \mu)I_h - \\
&\frac{I_h^{**}}{I_h}(\phi_s I_s - (\gamma_h + \delta_h + \mu)I_h)]
\end{aligned} \tag{10}$$

Where P=$\frac{(\sigma+\mu)}{(1-r)\sigma}$, Q=$\frac{(\sigma+\mu)}{r\sigma}$, and T=$\frac{(\phi_s+\gamma_s+\delta_s+\mu)}{\phi_s}$. Substituting the above parameters into (10) yields

$$\dot{L} = \lambda - \beta_s' I_s S - \beta_a' I_a S - \mu S - \lambda\frac{S^{**}}{S} + \beta_s' I_s S^{**} + \beta_a' I_a S^{**} + \mu S^{**}$$
$$+\beta_s' I_s S + \beta_a' I_a S - (\sigma+\mu)E - \frac{\beta_s' I_s S E^{**}}{E} - \frac{\beta_a' I_a S E^{**}}{E} + (\sigma+\mu)E^{**}$$
$$+\frac{(\sigma+\mu)}{(1-r)\sigma}[(1-r)\sigma E - (\phi_s+\gamma_s+\delta_s+\mu)I_s - \frac{(1-r)\sigma E I_s^{**}}{I_s} + \quad (11)$$
$$(\phi_s+\gamma_s+\delta_s+\mu)I_s^{**}] + \frac{(\sigma+\mu)}{r\sigma}[r\sigma E - (\gamma_a+\mu)I_a - \frac{r\sigma E I_a^{**}}{I_a} + (\gamma_a+\mu)I_a^{**}]$$
$$+\frac{(\phi_s+\gamma_s+\delta_s+\mu)}{\phi_s}[\phi_s I_s - (\gamma_h+\delta_h+\mu)I_h - \frac{\phi_s I_s I_h^{**}}{I_h} + (\gamma_h+\delta_h+\mu)I_h^{**}]$$

Collecting the infected compartments with (**), we obtained

$$\dot{L} = \lambda - \lambda\frac{S^{**}}{S} + \mu S^{**} - \mu S - \frac{\beta_s' I_s S E^{**}}{E} - \frac{\beta_a' I_a S E^{**}}{E} + (\sigma+\mu)E^{**}$$
$$-\frac{(\sigma+\mu)E I_s^{**}}{I_s} + \frac{(\sigma+\mu)}{(1-r)\sigma}(\phi_s+\gamma_s+\delta_s+\mu)I_s^{**} - \frac{(\sigma+\mu)E I_a^{**}}{I_a} + \quad (12)$$
$$\frac{(\gamma_a+\mu)(\sigma+\mu)}{r\sigma}I_a^{**} - (\phi_s+\gamma_s+\delta_s+\mu)\frac{I_s I_h^{**}}{I_h}$$
$$+\frac{(\phi_s+\gamma_s+\delta_s+\mu)}{\phi_s}(\gamma_h+\delta_h+\mu)I_h^{**}$$

At the endemic equilibrium, it can be seen from (7) that

$$\left.\begin{aligned}
\lambda &= \beta_s' I_s^{**} S^{**} + \beta_a' I_a^{**} S^{**} + \mu S^{**} \\
(\phi_s+\gamma_s+\delta_s+\mu) &= \frac{(1-r)\sigma E^{**}}{I_s^{**}} \\
(\sigma+\mu) &= \frac{S^{**}(\beta_s' I_s^{**} + \beta_a' I_a^{**})}{E^{**}} \\
(\gamma_a+\mu) &= \frac{r\sigma E^{**}}{I^{**}} \\
(\gamma_h+\delta_h+\mu) &= \frac{\phi_s I_s^{**}}{I_a^{**}}
\end{aligned}\right\} \quad (13)$$

Substitute (13) into (12)

$$\dot{L} = \beta_s' I_s^{**} S^{**} + \beta_a' I_a^{**} S^{**} + 2\mu S^{**} - \mu S - \frac{\beta_s' I_s^{**}(S^{**})^2}{S} - \frac{\beta_a' I_a^{**}(S^{**})^2}{S}$$
$$-\mu\frac{(S^{**})^2}{S} - \frac{\beta_s I_s S E^{**}}{E} - \frac{\beta_a I_a S E^{**}}{E} + \beta_s' I_s^{**} S^{**} + \beta_a' I_a^{**} S^{**} - \frac{\beta_s (I_s^{**})^2 S^{**} E}{I_s E^{**}}$$
$$-\frac{\beta_a I_s^{**} I_a^{**} S^{**} E}{I_s E^{**}} + \beta_s' I_s^{**} S^{**} + \beta_a' I_a^{**} S^{**} + \frac{\beta_s' I_s^{**} S^{**}}{E^{**}} + \frac{\beta_a' I_a^{**} S^{**}}{E^{**}} - \frac{\beta_s I_s^{**} I_a^{**} S^{**} E}{I_a E^{**}} \quad (14)$$
$$-\frac{\beta_s (I_a^{**})^2 S^{**} E}{I_a E^{**}} + \left[-\frac{(1-r)\sigma E^{**} I_s I_h^{**}}{I_a^{**}} I_h + \frac{(1-r)\sigma E^{**} I_h^{**}}{I_a^{**}}\right]$$

Factorizing (14), we obtained

$$\dot{L} = \mu S^{**}\left[2 - \frac{S^{**}}{S} - \frac{S}{S^{**}}\right]$$
$$+\beta_s' I_s^{**} S^{**}\left[3 - \frac{S^{**}}{S} + \frac{1}{E^{**}} - \frac{I_s^{**} E}{I_s E^{**}} - \frac{I_a^{**} E}{I_a E^{**}} - \frac{I_s S E^{**}}{I_s^{**} S^{**} E}\right] \quad (15)$$
$$+\beta_a' I_a^{**} S^{**}\left[3 - \frac{S^{**}}{S} + \frac{1}{E^{**}} - \frac{I_s^{**} E}{I_s E^{**}} - \frac{I_a^{**} E}{I_a E^{**}} - \frac{I_a S E^{**}}{I_a^{**} S^{**} E}\right]$$
$$+(1-r)\sigma I_h^{**} E^{**}\left[\frac{1}{I_h^{**}} - \frac{I_s}{I_s^{**} I_h}\right]$$

Finally, since the arithmetic>geometric mean, then the following inequality holds;

$$\left(2 - \frac{S^{**}}{S} - \frac{S}{S^{**}}\right) \leq 0$$
$$\left[3 - \frac{S^{**}}{S} + \frac{1}{E^{**}} - \frac{I_s^{**} E}{I_s E^{**}} - \frac{I_a^{**} E}{I_a E^{**}} - \frac{I_s S E^{**}}{I_s^{**} S^{**} E}\right] \leq 0$$
$$\left[3 - \frac{S^{**}}{S} + \frac{1}{E^{**}} - \frac{I_s^{**} E}{I_s E^{**}} - \frac{I_a^{**} E}{I_a E^{**}} - \frac{I_a S E^{**}}{I_a^{**} S^{**} E}\right] \leq 0$$

$$\left[\frac{1}{I_h^{**}} - \frac{I_s}{I_s^{**} I_h}\right] \leq 0$$

Therefore, $\dot{L} \leq 0$ for $R_o > 1$. Hence, L is a Lyapunov function θ and it follows by LaSalle's Invariance that every solution of model (2) approaches a unique endemic equilibrium of the model as $t \to \infty$ for $R_0 > 1$.
Hence, the endemic state is globally asymptotically stable.

Numerical Approximation
In this section, we discussed the approximation results for dynamical model equations (2). The differential transform method (DTM) is used to convert the modified model equations governing the novel corona virus in Nigeria to approximate form. The parameter values in table (2) are used to obtain the approximation results of the model compartments using *Maple 17 software*. The total population N is estimated to be 1, 0000000 with initial conditions for the state variables as: $\mathrm{S}(0) = 1500,\ \mathrm{E}(0) = 1000,\ I_s(0) = 500, I_a(0) = 400,\ I_h(0) = 350,\ \mathrm{R}(0) = 330.$

Table 2: Parameters Estimation/Value (Enahoro *et al.*, 2020)

Parameter	Value
λ	200
μ	0.2
σ	0.1961
r	0.5
ϕ_s	0.003
β_s	0.401
β_a	0.3
ϵ_M	0.5
c_M	0.1
γ_s	0.1429
γ_a	0.1429
γ_h	0.0714
δ_s	0.011
δ_h	0.01

Model Approximation by Differential Transform Method
The differential transform method (DTM) for a function $f(t)$ is defined by

$$F(t) = \frac{1}{k!}\left(\frac{d^k}{dt^k} f(t)\right)|_{t=t_0} \qquad (16)$$

The inverse transform is obtained as

$$f(t) = \sum_{k=0}^{\infty} F(k)(t - t_0)^k \qquad (17)$$

Combining equation (16) and (17), we obtained

$$f(t) = \sum_{k=0}^{\infty} F(k)(t - t_0)^k \frac{1}{k!}\left(\frac{d^k}{dt^k} f(t)\right)|_{t=t_0} \qquad (18)$$

In practical sense, the approximation of $f(t)$ is given by

$$\sum_{k=0}^{n} F(k)(t - t_0)^k \qquad (19)$$

And the error term is

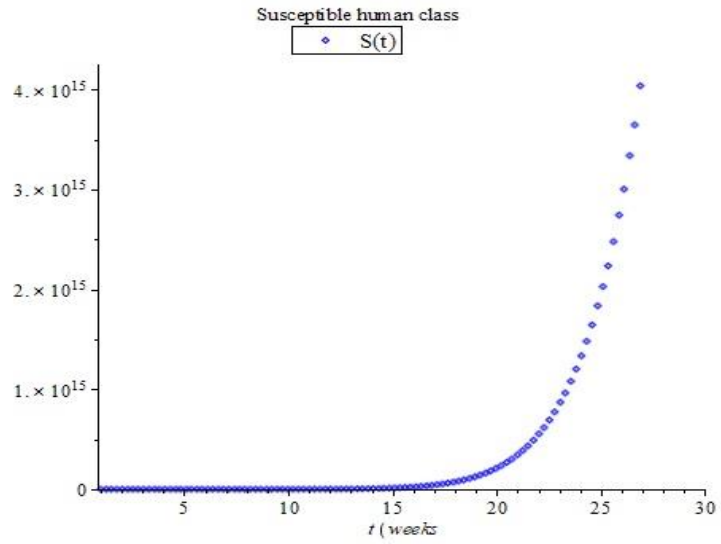
$$\sum_{k=n+1}^{\infty} F(k)(t-t_0)^k F(k) \qquad (20)$$

The transformation of the modified model equations (2) by DTM is obtained as

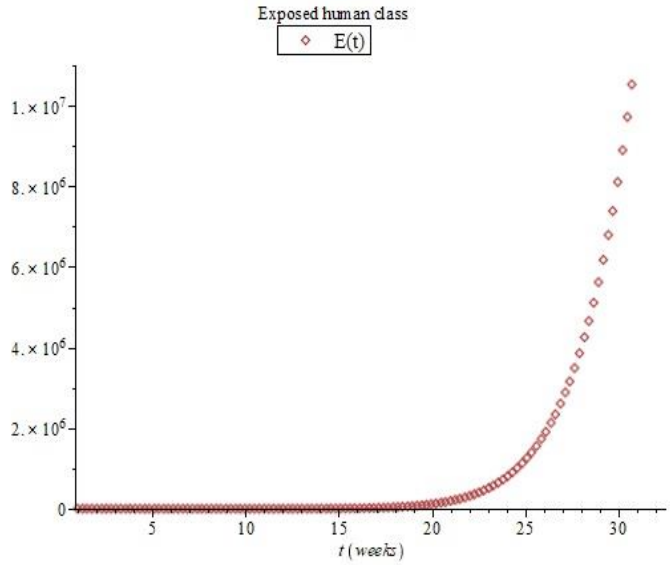
$$\left.\begin{aligned}
S(k+1) &= \frac{1}{k+1}\left[\lambda - \beta_s(1-\epsilon_m c_m)\frac{1}{N}\sum_{i=0}^{k} S(k-i)I_s(k) - \beta_a(1-\epsilon_m c_m)\frac{1}{N}\sum_{i=0}^{k} S(k-i)I_a(k) - \mu S(k)\right] \\
E(k+1) &= \frac{1}{k+1}\left[\beta_s(1-\epsilon_m c_m)\frac{1}{N}\sum_{i=0}^{k} S(k-i)I_s(k) + \beta_a(1-\epsilon_m c_m)\frac{1}{N}\sum_{i=0}^{k} S(k-i)I_a(k) - (\sigma+\mu)E(k)\right] \\
I_s(k+1) &= \frac{1}{k+1}[(1-r)\sigma E(k) - (\phi_s + \gamma_s + \delta_s + \mu)I_s(k)] \\
I_a(k+1) &= \frac{1}{k+1}[r\sigma E(k) - (\gamma_a + \mu)I_a(k)] \\
I_h(k+1) &= \frac{1}{k+1}[\phi_s I_s(k) - (\gamma_h + \delta_h + \mu)I_h(k)] \\
R(k+1) &= \frac{1}{k+1}[\gamma_s I_s(k) + \gamma_a I_a(k) + \gamma_h I_h(k) - \mu R(k)]
\end{aligned}\right\} \qquad (21)$$

Using the initial estimation and the parameters value in table (2), and for k=0, 1, 2,…, 10, the semi-analytical approximation of equations (21) for time t in weeks is obtained by

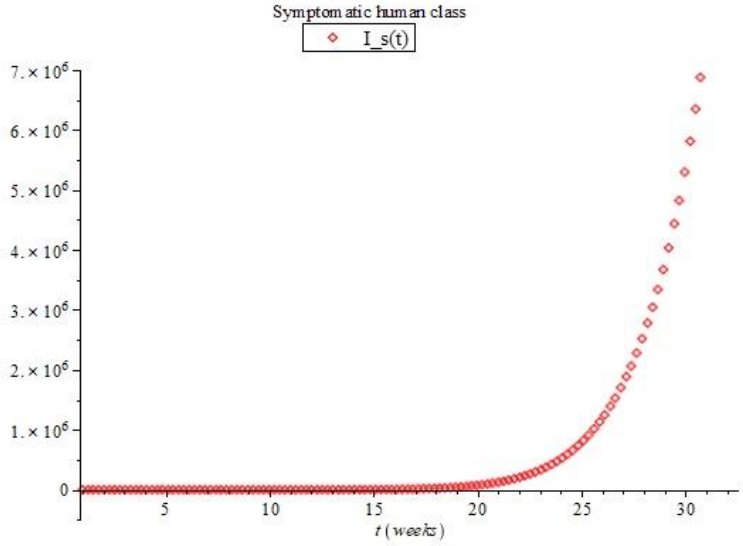
$$S[t] = \sum_{i=0}^{k} S(i)t^i = 1500 - 99.9894288 * t + 109.9928615 * t^2 + 59.33498403 * t^3 + 47.03310238 * t^4 + 38.11868996 * t^5 + 32.06270928 * t^6 + 27.65535121 * t^7 + 24.30861622 * t^8 + 21.68203076 * t^9 + 19.56635938 * t^{10}$$



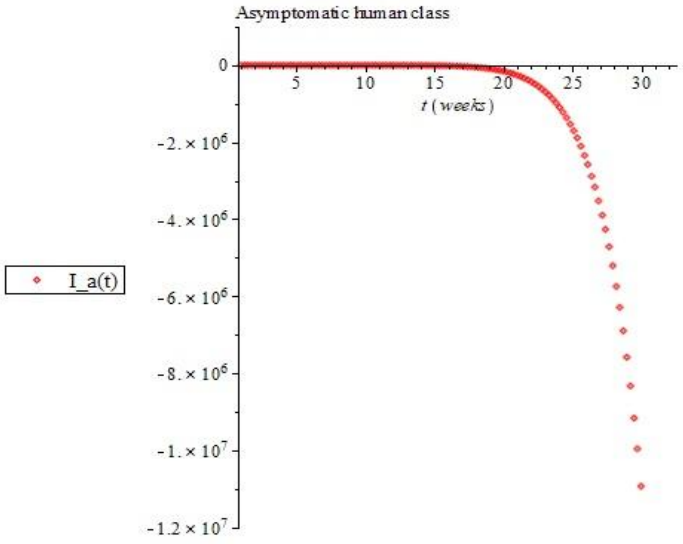
$$E[t] = \sum_{i=0}^{k} E(i)t^i = 1000 - 396.0543288 * t + 78.43087685 * t^2 - 10.35468958 * t^3 + 1.025316900 * t^4 - 0.8122286334e-1 * t^5 + 0.5361985473e-2 * t^6 - 0.3034127174e-3 * t^7 + 0.1502300440e-4 * t^8 - 6.612007908 * 10^(-7) * t^9 + 2.619134769 * 10^(-8) * t^{10}$$



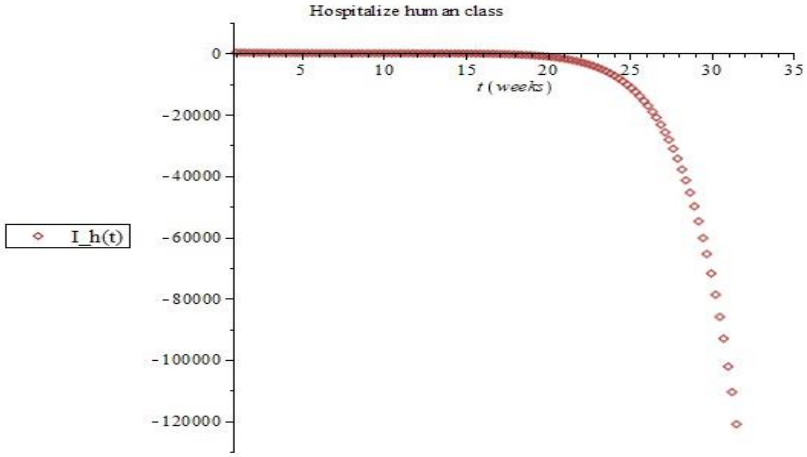
$$I_s[t] = \sum_{i=0}^{k} I_s\,(i)t^i = 500 - 258.85000 * t + 51.25933150 * t^2 - 6.767277493 * t^3 + .6700778495 * t^4 - 0.5308065592e - 1 * t^5 + 0.3504089697e - 2 * t^6 - 0.1982785627e - 3 * t^7 + 0.9817297732e - 5 * t^8 - 4.320782988 * 10^(-7) * t^9 + 1.711518247 * 10^(-8) * t^{10}$$



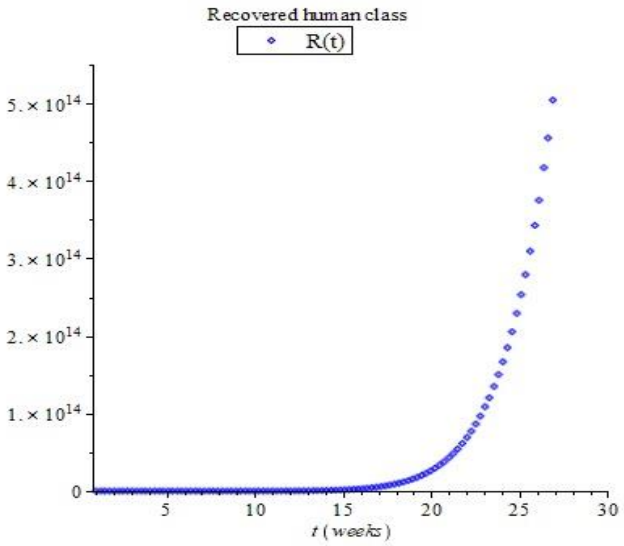
$$I_a[t] = \sum_{i=0}^{k} I_a\,(i)t^i = 400 - 39.11000 * t - 12.71115397 * t^2 + 4.016267390 * t^3 - .5981138502 * t^4 + 0.6112511224e - 1 * t^5 - 0.4820617123e - 2 * t^6 + 0.3112474696e - 3 * t^7 - 0.1705954678e - 4 * t^8 + 8.136360191 * 10^(-7) * t^9 - 3.438265284 * 10^(-8) * t^{10}$$



$$I_h[t] = \sum_{i=0}^{k} I_h\,(i)t^i = 350 - 93.4900 * t + 12.29831800 * t^2 - 1.061328503 * t^3 + 0.6693568080e - 1 * t^4 - 0.3231222044e - 2 * t^5 + 0.1196186158e - 3 * t^6 - 0.3136031891e - 5 * t^7 + 3.203542089 * 10^(-8) * t^8 + 2.306386663 * 10^(-9) * t^9 - 1.922188236 * 10^(-10) * t^{10}$$



$$R[t] = \sum_{i=0}^{k} R\,(i)t^i = 330 + 87.6000 * t - 17.55424200 * t^2 + 11.33646099 * t^3 + 5.582397115 * t^4 + 4.776760846 * t^5 + 4.005966230 * t^6 + 3.455516944 * t^7 + 3.037364095 * t^8 + 2.709169571 * t^9 + 2.444816615 * t^{10}$$



DISCUSSION

In this study, the covid-19 model in Nigeria by Enahoro *et al.* (2020) is modified. The modified model assume that, there is recruitment rate (migration) of people between the Nigeria states thereby making the other people at risk of the virus. The model also assumed that the mortality rate of people is not only due to covid-19 virus but other factors too. The global stability analysis for both disease free and endemic equilibrium state shows that: (i) The disease free equilibrium of the modified model (2) is globally-asymptotically stable whenever the associated reproduction number R_c is less than 1. (ii) The modified model has a unique endemic equilibrium, whenever the reproduction number R_c is greater than one and it is globally-asymptotically stable. The modified model equations were transformed into differential transform method (DTM). *Maple 17* software is used to approximate the transformed equations by DTM at time t/weeks with conservative estimates and data from Enahoro *et al.* (2020) to analyzed the dynamical feature of the model. The approximation results raises concern as more people will be susceptible and exposed to the virus, the number of infectious individuals will be on the increase for some time with more hospitalize-isolation individuals in Nigeria. The approximation also shows an increasing rate of recovery for infected individuals. Thus, control and mitigating mechanisms such as the use of effective face mask and efficacy, social distancing, restriction in movement and hospitalization/isolation of infected individuals is highly recommendable to curtail the virus projected impacts.

CONCLUSION

This paper demonstrated the impacts of novel coronavirus in Nigeria using mathematical modeling, a non-pharmaceutical approach and approximation. The parameters measured for social-distancing and effectiveness $\beta_a\beta_s$, face mask compliance and efficacy c_m, ϵ_m, plays an important role in curtailing the virus. The recruitment rate λ, progression rate σ from being expose to the virus and become symptomatic, the rate ϕ_s of infected individuals being hospitalized or isolated showed a great influence in the interactions and impacts of the virus in Nigeria state as seen in the approximation figures $S(t), E(t)$ and $I_s(t)$. The decreasing rate in hospitalized/isolated class $I_h(t)$ is influenced by large number of infected-infectious individuals recovery from the virus γ_h thereby increasing the number of recovery individuals ($\gamma_a, \gamma_h, \gamma_s$) for $R(t)$ from the virus as seen in $R(t)$ approximation graph.

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