MATHEMATICAL MODELING OF 2019 NOVEL CORONAVIRUS (2019 – NCOV) PANDEMIC IN NIGERIA

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Abstract. This study shows the mathematical modeling of 2019 novel coronavirus (2019 – nCoV) pandemic and reinfection in Nigeria using SEIAHQR model. We use both estimated and assumed parameters in our computations. The available statistical data regarding COVID-19 in Nigeria from its date of arrival till May 17, 2020 (22.00 WAT) was used to estimate some parameters, understand and predict the spread and reinfection of the virus. The disease free and endemic equilibrium was investigated using Jacobian transformation. The analysis carried out using the estimated parameters showed that the disease free-equilibrium point is stable. The basic reproduction number of the model was calculated and shown to be less than one. The numerical simulation shows that there is 94% chances of secondary reinfection when infected and asymptomatic individuals interact with the susceptible and exposed individuals through contact, hence the need for reinforced effort from the government, decision makers and stakeholders in compliance to all preventive measure as directed by World Health Organization (WHO) can effectively control the spread of this deadly virus in Nigeria.

Keywords: mathematical modeling; 2019 nCoV; pandemic; reinfection; SEIAHQR model

Introduction

The world is currently facing a devastating 2019 novel coronavirus (2019 – nCoV) pandemic, which started as an outbreak of pneumonia of unknown cause in the Wuhan City of China in December 2019. Within days and weeks, the COVID-19 pandemic has spread to over 210 countries. According to report as at May 15, 2020, COVID-19 has caused over 4.5 million confirmed cases and 306,000 fatalities globally.

As of Nigeria, the most populous country in Africa (with over 200 million citizens) through the Nigeria Centre for Disease Control (NCDC) reports the first

confirmed COVID-19 index case on February 27, 2020.[1)] The case was an Italian citizen who works in Nigeria and returned from Milan, Italy to Lagos, Nigeria on February 25, 2020. He was confirmed by the virology laboratory of the Lagos University Teaching Hospital, part of the Laboratory Network for the Nigeria Centre for Disease Control. As of May 17, 2020, data from the website of the NCDC shows that Nigeria has recorded 5959 confirmed cases and 182 deaths.[1)]

A number of modeling studies have already been performed for the coronavirus (COVID-19) pandemic. Wu et al. (2020) introduced a susceptible – exposed – infectious – recovered (SEIR) model to describe the transmission dynamics, based on reported data from December 31, 2019 to January 28, 2020. They also estimated that the basic reproductive number for COVID-19 was about 2.68. Yang & Wang (2020) proposed a mathematical model that investigates the current outbreak of the coronavirus disease 2019 (COVID-19), their model describes the multiple transmission pathways in the infection dynamics and emphasizes the role of the environmental reservoir in the transmission and spread of the disease using SEIRV model.

Qianying Lin et al. (2020) used the SEIR framework for a constant population to model the outbreak in Wuhan based on individual reaction and government action using some parameters of the 1918 influenza pandemic that occurred in London. Victor (2020), Nesteruk (2020) and Ming et al. (2020) focuses on the epidemic outbreak caused by COVID-19 coronavirus due to the global trend of the pandemic with its origin from mainland China. Also, Victor & Oduwole (2020) developed a new deterministic endemic model (Susceptible – Exposed – Infectious – Removed – Undetectable – Susceptible: SEIRUS) which was originally developed for the control of the prevalence of HIV/AIDS in Africa.

In this study, we present a new mathematical model for 2019 novel coronavirus (2019 – nCoV) that entail subdividing the total population at time t, denoted by $\boldsymbol{N(t)}$, into seven compartments of susceptible, exposed, symptomatically, infectious, asymptomatically-infectious, self-isolated or hospitalized, ICU patients and recovered individuals (SEIAHQR). A system of nonlinear differential equations is then derived for the rate of change of each of the seven stated variables of the model. Also, we analyze the temporal dynamics of the resulting model.

Table 1. Definition of parameters in SEIAHQR model

Variables/ Parameters	***Description***
$S(t)$	Number of Susceptible individuals at time t.
$E(t)$	Number of Exposed individuals at time t.
$I(t)$	Number of symptomatically-infectious individuals at time t.
$A(t)$	Number of asymptomatically-infectious individuals at time t.
$H(t)$	Number of self-isolated or hospitalized individuals at time t.
$Q(t)$	Number of ICU patients at time t.

$R(t)$	Number of Recovered adults satisfying undetectable criteria at time *t*.
μ	Natural death rate of the population
α_0	Maximum date rate due to COVID-19 coronavirus ($\alpha \leq \alpha_0$)
α	Death rate of infected population due to COVID-19 coronavirus
γ	Disease induced death rate of infected but not asymptomatically infected, not hospitalized and not in ICU.
ζ	Disease induced death rate of Asymptomatically infected population at time *t*.
T	Maximum lifespan after infection (T ≥ 14days)
K	Efficacy of Quarantined ($0 \leq K \leq 1$)
ρ	Proportion of Asymptotically infected population in quarantine per unit time (treatment rate).
β	Rate of transmission
ε	Proportion of removed population still being observed and being moved to susceptible class.
$B(t)$	Incidence rate or force of infection in the population
π	Proportion of population from susceptible to exposed/latent class
σ	Proportion of infected population in quarantine per unit time (Treatment rate).
γ	Rate of recovery
t	Proportion of hospitalized population in quarantine per unit time.
Φ	Disease induced death rate of hospitalized population at time *t*
η	Disease induced death rate of ICU patient at time *t*

Model formulation and analysis

Model formulation

In this mathematical model, the total population at time tt, denoted by $N(t)$, was subdivided into the mutually-exclusive compartments of susceptible individuals $S(t)$; these are individuals who do not yet have the disease, but could get infected if they come in contact with someone who is already infected, exposed $E(t)$; these are individuals who are newly-infected but are not yet infectious, which means they are generally not sick, and not able to pass the disease to others, symptomatically-infectious $I(t)$; these are individuals with the clinical symptoms of COVID-19 asymptomatically infectious, $A(t)$; these are infectious individuals who show mild or no symptoms of the disease, self-isolated or hospitalized $H(t)$, ICU patients $Q(t)$ and recovered $R(t)$ individuals.

The following diagram below describes the dynamic of the model (Fig. 1)

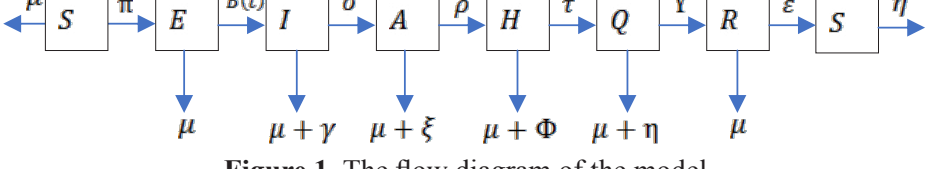

Figure 1. The flow diagram of the model

From the compartmental model, we obtained a seven-dimensional system of Ordinary Differential Equations that describes the transmission mechanisms of 2019 novel coronavirus (2019 – nCoV).

$$\frac{dS(t)}{dt} = \pi + \mu S \tag{1}$$

$$\frac{dE(t)}{dt} = S - (\pi + B)E \tag{2}$$

$$\frac{dI(t)}{dt} = BE - (\sigma + \mu + \gamma)I \tag{3}$$

$$\frac{dA(t)}{dt} = I\sigma - (\rho + \mu + \xi)A \tag{4}$$

$$\frac{dH}{dt} = \rho A - (\tau + \Phi + \mu)H \tag{5}$$

$$\frac{dQ}{dt} = \tau H - (\Upsilon + \mu + \eta)Q \tag{6}$$

$$\frac{dR}{dt} = \Upsilon Q - (\mu + \varepsilon)R \tag{7}$$

The total population $N(t)N(t)$ is given by the equation:

$$N(t) = S(t) + E(t) + I(t) + A(t) + H(t) + Q(t) + R(t) \tag{8}$$

The rate of infection at time tt denoted by $B(t)$ in the population is given as:

$$B(t) = \frac{\beta I + \sigma A + \rho H + \tau Q + \Upsilon R}{N} \tag{9}$$

The model equations in proportion according to Victor (2020) is as follows:

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dA(t)}{dt} + \frac{dH(t)}{dt} + \frac{dQ(t)}{dt} + \frac{dR(t)}{dt}$$

such that

$$\frac{dN(t)}{dt} = \pi + \mu S + S - \mu E - (\mu + \gamma)I - (\mu + \xi)A - (\mu + \Phi)H - (\Upsilon + \mu)Q - (\mu + \varepsilon)R \tag{10}$$

Using the following sets to perform the normalization:

$$s = \frac{S}{N}, \quad e = \frac{E}{N}, \quad i = \frac{I}{N}, \quad a = \frac{A}{N}, \quad h = \frac{H}{N}, \quad q = \frac{Q}{N}, \quad r = \frac{R}{N} \tag{11}$$

Then the normalized SEIAHQR model is changed as follows using Eq. (11):

$$\frac{ds}{dt} = \frac{1}{N}\left[\frac{dS(t)}{dt} - s\frac{dN(t)}{dt}\right]$$

Substituting Eq. (1) into Eq. (10) and using Eq. (11):

$$\frac{ds}{dt} = \frac{\pi(1-S)}{N} + \mu s + \mu s^2 + s^2 - sS^2 + \mu se + (\mu+\gamma)si + (\mu+\xi)sa + (\mu+\Phi)hs + (\Upsilon+\mu)qs + (\mu+\varepsilon)rs \quad (12)$$

$$\frac{de}{dt} = \frac{1}{N}\left[\frac{dE(t)}{dt} - e\frac{dN(t)}{dt}\right]$$

Substituting Eq. (2 into Eq. (10) and using Eq. (11):

$$\frac{de}{dt} = s - \mu e - Be - \frac{e\pi}{N} - \mu se + (\mu+\gamma)ei + (\mu+\xi)ea + (\mu+\Phi)he + (\Upsilon+\mu)qe + (\mu+\varepsilon)re \quad (13)$$

$$\frac{di}{dt} = \frac{1}{N}\left[\frac{dI(t)}{dt} - i\frac{dN(t)}{dt}\right]$$

Substituting Eq. (3) into Eq. (10) and using Eq. (11):

$$\frac{di}{dt} = Be - (\sigma+\mu+\gamma)i - \frac{\pi i}{N} - \mu si - is + \mu ei + (\mu+\gamma)i^2 + (\mu+\xi)ai + (\mu+\Phi)hi + (\Upsilon+\mu)qi + (\mu+\varepsilon)ri \quad (14)$$

$$\frac{da}{dt} = \frac{1}{N}\left[\frac{dA(t)}{dt} - a\frac{dN(t)}{dt}\right]$$

Substituting Eq. (4) into Eq. (10) and using Eq. (11):

$$\frac{da}{dt} = \sigma i - (\rho+\mu+\xi)a - \frac{\pi a}{N} - \mu sa - sa + \mu ae + (\mu+\gamma)ai + (\mu+\xi)a^2 + (\mu+\Phi)ha + (\Upsilon+\mu)qa + (\mu+\varepsilon)ra \quad (15)$$

$$\frac{dh}{dt} = \frac{1}{N}\left[\frac{dH(t)}{dt} - h\frac{dN(t)}{dt}\right]$$

Substituting Eq. (5) into Eq. (10) and using Eq. (11):

$$\frac{dh}{dt} = \rho a - (\tau+\Phi+\mu)h - \frac{\pi h}{N} - \mu sh - sh + \mu he + (\mu+\gamma)hi + (\mu+\xi)ha + (\mu+\Phi)h^2 + (\Upsilon+\mu)qh + (\mu+\varepsilon)rh \quad (16)$$

$$\frac{dq}{dt} = \frac{1}{N}\left[\frac{dQ(t)}{dt} - q\frac{dN(t)}{dt}\right]$$

Substituting Eq. (6) into Eq. (10) and using Eq. (11):

$$\frac{dq}{dt} = \tau h - (\Upsilon + \mu + \eta)q - \frac{q\pi}{N} - \mu qs - qs + q\mu e + (\mu + \gamma)qi + (\mu + \xi)qa + (\mu + \Phi)qh + (\Upsilon + \mu)q^2 + (\mu + \varepsilon)qr \quad (17)$$

$$\frac{dr}{dt} = \frac{1}{N}\left[\frac{dR(t)}{dt} - r\frac{dN(t)}{dt}\right]$$

Substituting Eq. (7) into Eq. (10) and using Eq. (11):

$$\frac{dr}{dt} = \Upsilon q - (\mu + \xi)r - \frac{\pi r}{N} - \mu sr - sr + \mu re + (\mu + \gamma)ir + (\mu + \xi)ra + (\mu + \Phi)rh + (\Upsilon + \mu)qr + (\mu + \varepsilon)r^2 \quad (18)$$

Therefore,

$$s + e + i + a + h + q + r = 1 \quad (19)$$

Eqs. (12) to (18) are the normalized model equations.

Equilibrium analysis of disease free equilibrium point $(E_0)(E_0)$ *of the SEIAHQRS model*

The disease-free equilibrium (DFE) state of the SEIAHQRS model is obtained by setting the left hand sides of equations (12) to (18) to zero while setting the disease component

$$e = i = a = h = q = r = 0$$

We have Eqs. (20) and (21):

$$0 = \frac{\pi(1 - S)}{N} + \mu s - \mu s^2 - sS^2 \quad (20)$$

$$0 = s \quad (21)$$

Substituting Eq. (21) into Eq. (20), we have:

$$0 = \frac{\pi}{N} \quad (22)$$

Eq. (21) when $s = 0s = 0$ becomes:

$$0 = \mu - \mu s - s^2 \quad (23)$$

Hence

$$-s^2 - \mu s + \mu = 0$$

$$s^2 + \mu s - \mu = 0 s^2 + \mu s - \mu = 0$$

Using quadratic formula where

$$S^* = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$$

$$a = 1, \qquad b = \mu, \qquad c = -\mu$$

$$S^* = \frac{-\mu \pm \sqrt{\mu^2 - 4(1)(-\mu)}}{2(1)}$$

$$S^* = \frac{-\mu \pm \sqrt{\mu^2 + 4\mu}}{2}$$

$$S^* = \frac{-\mu + \sqrt{\mu^2 + 4\mu}}{2}, \qquad \frac{-\mu - \sqrt{\mu^2 + 4\mu}}{2}$$

Therefore, the solution to the simultaneous Eq. (23) is given by

$$(S_1^*, S_2^*) = \left\{(0,0), \qquad \left(\frac{-\mu + \sqrt{\mu^2 + 4\mu}}{2}, \frac{-\mu - \sqrt{\mu^2 + 4\mu}}{2}\right)\right\} \tag{24}$$

Stability of the free disease equilibrium point (E_0) *recovered population*

In order to study the behavior of the system Eqs. (12) – (18) around the disease free equilibrium state $E_0 = [0,0,0,0,0]$, we resort to the linearized stability appro ach from Victor (2020) gives us a Jacobian $J(E_0)$ transformation of the form.

$$F(s,e,i,a,h,q,r) = \frac{\pi(1-S)}{N} + \mu s + \mu s^2 + s^2 - sS^2 + \mu se +$$
$$(\mu + \gamma)si + (\mu + \xi)sa + (\mu + \Phi)hs + (\Upsilon + \mu)qs + (\mu + \varepsilon)rs$$

$$F(s,e,i,a,h,q,r) = \frac{\pi(1-S)}{N} + \mu s + \mu s^2 + s^2 - sS^2 + \mu se +$$
$$(\mu + \gamma)si + (\mu + \xi)sa + (\mu + \Phi)hs + (\Upsilon + \mu)qs + (\mu + \varepsilon)rs$$

$$G(s,e,i,a,h,q,r) = s - \mu e - Be - \frac{e\pi}{N} - \mu se + (\mu + \gamma)ei +$$
$$(\mu + \xi)ea + (\mu + \Phi)he + (\Upsilon + \mu)qe + (\mu + \varepsilon)re$$

$$G(s,e,i,a,h,q,r) = s - \mu e - Be - \frac{e\pi}{N} - \mu se + (\mu + \gamma)ei +$$
$$(\mu + \xi)ea + (\mu + \Phi)he + (\Upsilon + \mu)qe + (\mu + \varepsilon)re$$

$$H(s,e,i,a,h,q,r) = Be - (\sigma + \mu + \gamma)i - \frac{\pi i}{N} - \mu si - is + \mu ei +$$
$$(\mu + \gamma)i^2 + (\mu + \xi)ai + (\mu + \Phi)hi + (\Upsilon + \mu)qi + (\mu + \varepsilon)ri$$

$$H(s,e,i,a,h,q,r) = Be - (\sigma + \mu + \gamma)i - \frac{\pi i}{N} - \mu si - is + \mu ei +$$
$$(\mu + \gamma)i^2 + (\mu + \xi)ai + (\mu + \Phi)hi + (\Upsilon + \mu)qi + (\mu + \varepsilon)ri$$

$$I(s,e,i,a,h,q,r) = \sigma i - (\rho + \mu + \xi)a - \frac{\pi a}{N} - \mu sa - sa + \mu ae +$$
$$(\mu + \gamma)ai + (\mu + \xi)a^2 + (\mu + \Phi)ha + (\Upsilon + \mu)qa + (\mu + \varepsilon)ra$$

$$I(s,e,i,a,h,q,r) = \sigma i - (\rho + \mu + \xi)a - \frac{\pi a}{N} - \mu sa - sa + \mu ae +$$
$$(\mu + \gamma)ai + (\mu + \xi)a^2 + (\mu + \Phi)ha + (\Upsilon + \mu)qa + (\mu + \varepsilon)ra$$

$$J(s,e,i,a,h,q,r) = \rho a - (\tau + \Phi + \mu)h - \frac{\pi h}{N} - \mu sh - sh + \mu he +$$
$$(\mu + \gamma)hi + (\mu + \xi)ha + (\mu + \Phi)h^2 + (\Upsilon + \mu)qh + (\mu + \varepsilon)rh$$

$$J(s,e,i,a,h,q,r) = \rho a - (\tau + \Phi + \mu)h - \frac{\pi h}{N} - \mu sh - sh + \mu he +$$
$$(\mu + \gamma)hi + (\mu + \xi)ha + (\mu + \Phi)h^2 + (\Upsilon + \mu)qh + (\mu + \varepsilon)rh$$

$$K(s,e,i,a,h,q,r) = \tau h - (\Upsilon + \mu + \eta)q - \frac{q\pi}{N} - \mu qs - qs + q\mu e +$$
$$(\mu + \gamma)qi + (\mu + \xi)qa + (\mu + \Phi)qh + (\Upsilon + \mu)q^2 + (\mu + \varepsilon)qr$$

$$K(s,e,i,a,h,q,r) = \tau h - (\Upsilon + \mu + \eta)q - \frac{q\pi}{N} - \mu qs - qs + q\mu e +$$
$$(\mu + \gamma)qi + (\mu + \xi)qa + (\mu + \Phi)qh + (\Upsilon + \mu)q^2 + (\mu + \varepsilon)qr$$

$$L(s,e,i,a,h,q,r) = \Upsilon q - (\mu + \xi)r - \frac{\pi r}{N} - \mu sr - sr + \mu re +$$
$$(\mu + \gamma)ir + (\mu + \xi)ra + (\mu + \Phi)rh + (\Upsilon + \mu)qr + (\mu + \varepsilon)r^2$$

$$L(s,e,i,a,h,q,r) = \Upsilon q - (\mu + \xi)r - \frac{\pi r}{N} - \mu sr - sr + \mu re +$$
$$(\mu + \gamma)ir + (\mu + \xi)ra + (\mu + \Phi)rh + (\Upsilon + \mu)qr + (\mu + \varepsilon)r^2$$

$$J(E_0) = \begin{bmatrix} \frac{\partial F}{\partial s} & \frac{\partial F}{\partial e} & \frac{\partial F}{\partial i} & \frac{\partial F}{\partial a} & \frac{\partial F}{\partial h} & \frac{\partial F}{\partial q} & \frac{\partial F}{\partial r} \\ \frac{\partial G}{\partial s} & \frac{\partial G}{\partial e} & \frac{\partial G}{\partial i} & \frac{\partial G}{\partial a} & \frac{\partial G}{\partial h} & \frac{\partial G}{\partial q} & \frac{\partial G}{\partial r} \\ \frac{\partial H}{\partial s} & \frac{\partial H}{\partial e} & \frac{\partial H}{\partial i} & \frac{\partial H}{\partial a} & \frac{\partial H}{\partial h} & \frac{\partial H}{\partial q} & \frac{\partial H}{\partial r} \\ \frac{\partial I}{\partial s} & \frac{\partial I}{\partial e} & \frac{\partial I}{\partial i} & \frac{\partial I}{\partial a} & \frac{\partial I}{\partial h} & \frac{\partial I}{\partial q} & \frac{\partial I}{\partial r} \\ \frac{\partial J}{\partial s} & \frac{\partial J}{\partial e} & \frac{\partial J}{\partial i} & \frac{\partial J}{\partial a} & \frac{\partial J}{\partial h} & \frac{\partial J}{\partial q} & \frac{\partial J}{\partial r} \\ \frac{\partial K}{\partial s} & \frac{\partial K}{\partial e} & \frac{\partial K}{\partial i} & \frac{\partial K}{\partial a} & \frac{\partial K}{\partial h} & \frac{\partial K}{\partial q} & \frac{\partial K}{\partial r} \\ \frac{\partial L}{\partial s} & \frac{\partial L}{\partial e} & \frac{\partial L}{\partial i} & \frac{\partial L}{\partial a} & \frac{\partial L}{\partial h} & \frac{\partial L}{\partial q} & \frac{\partial L}{\partial r} \end{bmatrix}$$

$$J(E_0) = \begin{bmatrix} -\frac{\pi}{N}+\mu & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & -\left(\mu+\frac{\pi}{N}\right) & 0 & 0 & 0 & 0 & 0 \\ 0 & B & -(\sigma+\mu+\gamma)-\frac{\pi}{N} & 0 & 0 & 0 & 0 \\ 0 & 0 & \sigma & -(\rho+\mu+\xi)-\frac{\pi}{N} & 0 & 0 & 0 \\ 0 & 0 & 0 & \rho & -(\tau+\Phi+\mu)-\frac{\pi}{N} & 0 & 0 \\ 0 & 0 & 0 & 0 & \tau & -(\Upsilon+\mu+\eta)-\frac{\pi}{N} & 0 \\ 0 & 0 & 0 & 0 & 0 & \Upsilon & -(\mu+\xi)-\frac{\pi}{N} \end{bmatrix} \quad (25)$$

Hence, the determinant of the Jacobian matrix $J(E_0)$ is given as:

$$Det[J(E_0)] = a_{11}\det(JE_{011}) - a_{12}\det(JE_{012}) + a_{13}\det(JE_{013}) - a_{14}\det(JE_{014}) + a_{15}\det(JE_{015}) - a_{16}\det(JE_{016}) + a_{17}\det(JE_{017})$$

And from Eq. (25)

$Det(JE_0) > 0$

Hence, the trace of Eq .(25) is:

$$Trace(JE_0) = -\frac{\pi}{N}+\mu-\left(\mu+\frac{\pi}{N}\right)-(\sigma+\mu+\gamma)-\frac{\pi}{N}-(\rho+\mu+\xi)-\frac{\pi}{N}-(\tau+\Phi+\mu) -\frac{\pi}{N}-(\Upsilon+\mu+\eta)-\frac{\pi}{N}-(\mu+\xi)$$

$$Trace(JE_0) = -\frac{7\pi}{N} - (\rho + \mu + \xi) - (\tau + \Phi + \mu) - (\Upsilon + \mu + \eta) - (\mu + \xi) - (\sigma + \mu + \gamma)$$

$$Trace(JE_0) = -\frac{7\pi}{N} - 5\mu - (\rho + \xi) - (\tau + \Phi) - (\Upsilon + \mu) - \xi - (\sigma + \gamma) < 0$$

Hence

$$Trace(JE_0) < 0$$

Since $Det(JE_0) > 0$ and $Trace(JE_0) < 0$, this satisfies that the disease free equilibrium (E_0) for 2019 novel coronavirus (2019 – nCov) satisfy the criteria for a locally or globally asymptotic stability for the recorded population.

Basic reproduction number

To obtain the reproduction number denoted by $(R_0)(R_0)$ for the model in equations (12) – (18), we use the next generation matrix technique (Hefferman et al., 2005) as:

$$F_i = \begin{pmatrix} BE + \mu i \\ Be \end{pmatrix} \tag{26}$$

$$V_i = \begin{bmatrix} \frac{\pi(1-S)}{N} + \mu s + \mu s^2 + s^2 - sS^2 + \mu s e + (\mu + \gamma) si + (\mu + \xi) sa + (\mu + \Phi) hs + (\Upsilon + \mu) qs + (\mu + \varepsilon) rs \\ s - \mu e - Be - \frac{e\pi}{N} - \mu s e + (\mu + \gamma) ei + (\mu + \xi) ea + (\mu + \Phi) he + (\Upsilon + \mu) qe + (\mu + \varepsilon) re \\ Be - (\sigma + \mu + \gamma) i - \frac{\pi i}{N} - \mu s i - is + \mu e i + (\mu + \gamma) i^2 + (\mu + \xi) ai + (\mu + \Phi) hi + (\Upsilon + \mu) qi + (\mu + \varepsilon) ri \\ \sigma i - (\rho + \mu + \xi) a - \frac{\pi a}{N} - \mu s a - sa + \mu a e + (\mu + \gamma) ai + (\mu + \xi) a^2 + (\mu + \Phi) ha + (\Upsilon + \mu) qa + (\mu + \varepsilon) ra \\ \rho a - (\tau + \Phi + \mu) h - \frac{\pi h}{N} - \mu s h - sh + \mu h e + (\mu + \gamma) hi + (\mu + \xi) ha + (\mu + \Phi) h^2 + (\Upsilon + \mu) qh + (\mu + \varepsilon) rh \\ \tau h - (\Upsilon + \mu + \eta) q - \frac{q\pi}{N} - \mu q s - qs + q\mu e + (\mu + \gamma) qi + (\mu + \xi) qa + (\mu + \Phi) qh + (\Upsilon + \mu) q^2 + (\mu + \varepsilon) qr \\ \Upsilon q - (\mu + \xi) r - \frac{\pi r}{N} - \mu s r - sr + \mu r e + (\mu + \gamma) ir + (\mu + \xi) ra + (\mu + \Phi) rh + (\Upsilon + \mu) qr + (\mu + \varepsilon) r^2 \end{bmatrix} \tag{27}$$

where the matrices F_i and V_i are the rate of the appearance of new infections in compartment i and the transfer of individuals into and out of compartment ii by all means respectively. Using the linearization method, the associated matrices at disease free equilibrium (E_0) and after taking partial derivative as defined by:

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

where F is a non-negative and V is a non-singular matrix, in which both are $m \times m$ $m \times m$ matrices defined by:

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

with $1 \leq i,\ j \leq m1 \leq i,\ j \leq m$ and mm is the number of infected cases.

In particular $m = 2$, we have

$$F = \begin{pmatrix} B & \mu \\ 0 & B \end{pmatrix}$$

and

$$V = \begin{pmatrix} -(\sigma+\gamma) & 0 \\ 0 & -(\sigma+\gamma) \end{pmatrix}$$

$$V^{-1} = \begin{bmatrix} -\frac{1}{\sigma+\gamma} & 0 \\ 0 & -\frac{1}{\sigma+\gamma} \end{bmatrix}$$

Then the next matrix denoted by FV^{-1} is given as:

$$FV^{-1} = \begin{bmatrix} -\frac{B}{\sigma+\gamma} & 0 \\ 0 & -\frac{B}{\sigma+\gamma} \end{bmatrix}$$

We find the eigenvalues of FV^{-1} by setting the determinant $|FV^{-1} - \lambda I| = 0$ $|FV^{-1} - \lambda I|$ been a characteristics equation given as characteristics polynomial.

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

$$P(\lambda) = \lambda^2 + \left(\frac{2B}{\sigma+\gamma}\right)\lambda + \left(\frac{B}{\sigma+\gamma}\right)^2 = 0$$

Using the general formula method to solve the quadratic equation above, we have

$$\lambda = \frac{-\frac{2B}{\sigma+\gamma} \pm \sqrt{\left(\frac{2B}{\sigma+\gamma}\right)^2 - 4(1)\left(\frac{B}{\sigma+\gamma}\right)^2}}{2}$$

$$\lambda = \frac{-\frac{2B}{\sigma+\gamma} \pm \frac{2B}{\sigma+\gamma} - 2\left(\frac{B}{\sigma+\gamma}\right)}{2}$$

$$\lambda_1 = -\frac{2B}{\sigma+\gamma}$$

$$\lambda_2 = -\frac{6B}{\sigma+\gamma}$$

Hence $R_0 < 1$ which satisfies the threshold.

Numerical results and discussion

In this study, we developed SEIAHQR model, which considered the susceptible individuals, the exposed individuals, the infected individuals, the asymptomatic individuals, the hospitalized individuals, the quarantined individuals and the recovered individuals. We considered the prevalence of COVID-19 in Nigeria. The numerical simulation results showed that the $\mathcal{R}_0$ is -0.0593<1 which implies that there is a 94% chances of secondary infection when infected individuals and asymptomatic individuals interact with susceptible and exposed individuals through contact.

The initial data of this analysis is set to 18th of May, 2020

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

N=200exp6,	
e(0)=1,	Victor & Oduwole (2020)
i(0)=0.0003,	Estimation
q(0)=0.0001,	Assumed
r(0)=0.0001,	Victor & Oduwole (2020)
a(0)=0.0001,	Assumed
h(0)=0.0001,	Assumed
s(0)=1,	Estimation
n(0)=6175,	NCDC[1)]
π =0.00567,	Victor & Oduwole (2020)
μ =0.000001,	
σ =0.36404,	
T=100days	
ρ =0.2262,	
δ=0.000005,	
γ =0.2619,	NCDC[1)]
ξ =0.0000007,	
ε =0.00000095,	
B(t)=0.0027,	Victor & Pduwole (2020)
τ =0.2361,	
Φ =0.000003,	
η =0.000008,	Assumed

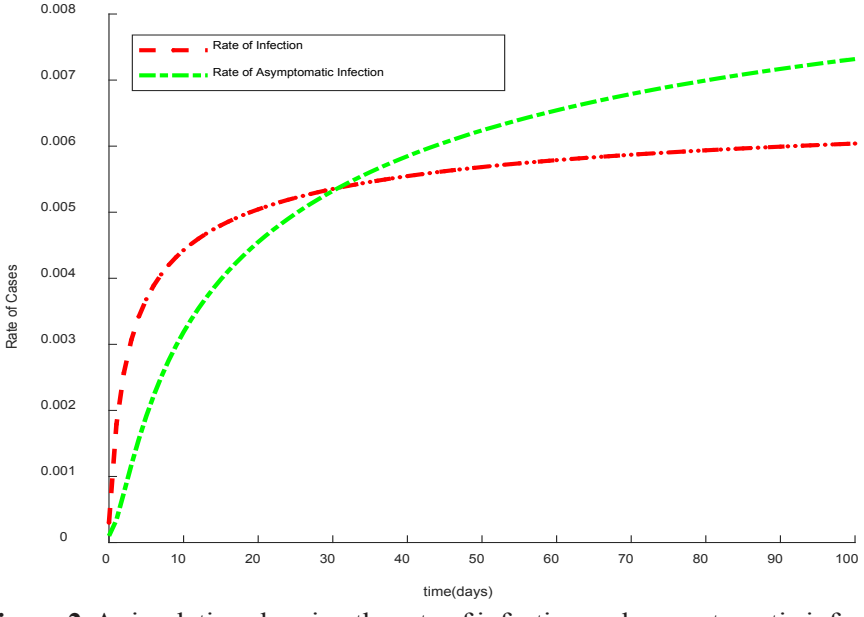

Figure 2. A simulation showing the rate of infection and asymptomatic infection

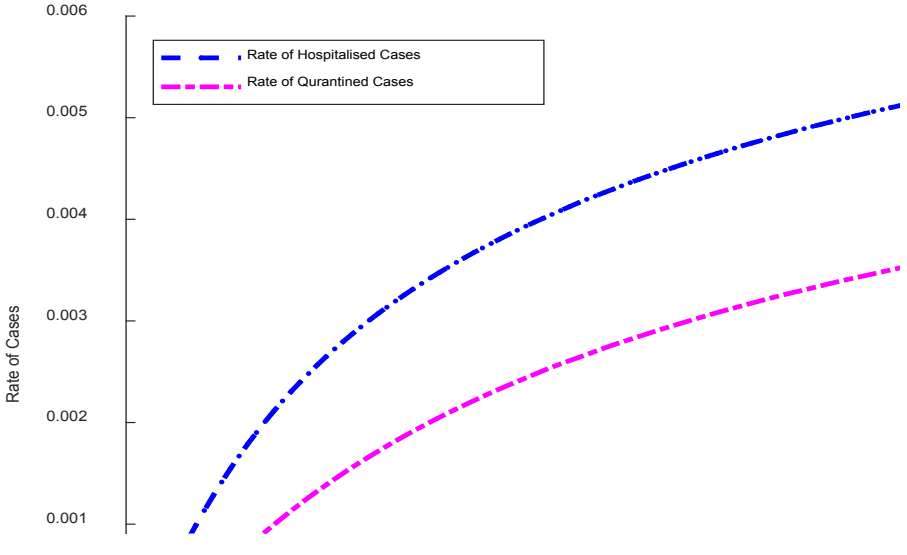

Figure 3. A simulation showing the rate of hospitalized cases and Quarantined cases

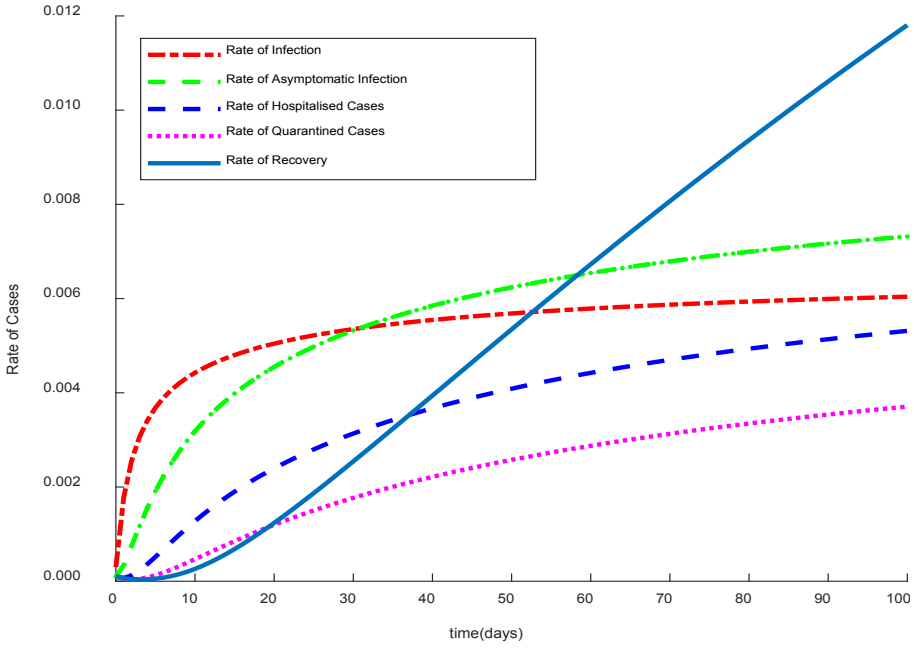

Figure 4. A simulation showing the rate of infection, asymptomatic

Fig. 2 shows the rate of infection and the rate of asymptomatic infection in 100 days. It is observed that the rate of infection was higher than the rate of asymptomatic infection initially but after 30days, it shows that rate of asymptomatic infection is higher than the rate of infection.

Fig. 3 shows that the rate of hospitalized cases and the quarantined case. It is found out that the rate at which individuals are hospitalized would be greater than the rate at which individuals are quarantined. Which would be alarming because of insufficient bed space in hospitals in Nigeria.

Fig. 4 shows that the rate of infection, asymptomatic infection, hospitalized cases will continue to increase before normalizing at a point where future occurrence will be halted. Hence, the need to practice social distance, using of face mask to reduce asymptomatic infection and infection. We also hope that vaccine would be made available very soon. Also, Fig. 3 shows that the rate of recovery will continue to increase, with increase in the rate of infection, asymptomatic infection, hospitalized cases, and quarantined cases. Consequently, Nigeria would hardly be free of COVID-19 hence, the need for reinforced effort from the government, decision makers and stakeholders in ensuring compliance to all preventive measure as directed by WHO.

In the absence of a safe and effective vaccine or antiviral, to prevent secondary reinfection in Nigeria, we have no choice but to focus on implementing the tried-and-tested non-pharmaceutical interventions such as social-distancing, community lockdown, quarantine, isolation, contact tracing, widescale random testing etc. If we do this successfully, we indeed can minimize and mitigate the burden of the pandemic in Nigeria.

Conclusions

The model equation exhibits that the disease-free equilibrium $(E_0)(E_0)$ state for 2019 novel coronavirus (2019 – nCoV) exists and hence satisfies the criteria for a locally or globally asymptotic stability when the reproductive number is less than 1 $(R_0 < 1)$. It was declared by WHO (2020) that the COVID-19 coronavirus does not have curative vaccine for use in humans (although some promising candidate vaccines are undergoing various accelerated stages of clinical trials in humans). There are also no safe and approved antiviral drugs for use to treat COVID-19 patients, hence, efforts aimed at controlling and mitigating the burden of COVID-19 are focused on the implementation of non-pharmaceutical interventions such as social-distancing, community lockdown / stay-at-home orders, using of face-masks in public, quarantine of suspected cases, isolation and hospitalization of confirmed cases and contact-tracing of confirmed cases introduced by federal government of Nigeria must be seriously followed to the letters in order to curtail the spread of this deadly virus.

NOTES

1. https://ncdc.gov.ng/

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