TRANSMISSION DYNAMICS OF CORONAVIRUS PANDEMIC: MODELING AND STABILITY ANALYSIS

Abstract

Covid-19, as a pandemic disease around the world, has generated great threat to human society and caused enormous mortality with weak surveillance system. In this paper, we propose a mathematical model to describe the transmission of Covid-19. Moreover, basic reproduction number and the local and global dynamics of the dynamical model are obtained. Then we apply our model to characterize the transmission process of Covid-19 in Nigeria. It was found that, in order to avoid its outbreak in Nigeria, it may be better to adhere to government policy to curtail the spread through person-to-person transmission and make effort to improve personal hygiene as well as early detection and reporting. Our results may provide some new insights for elimination of Covid-19.

Keywords: Infectious disease, Coronavirus, Dynamical model, Stability

1. Introduction

A disease is infectious if the causative agent, whether a virus, bacterium, protozoa, or toxin, can be passed from one host to another through modes of transmission such as direct physical contact, airborne droplets, water or food, disease vectors, or mother to newborns. Infectious diseases have always been a major public health threat to human life and health. We face the challenge of the emergence of increasingly new infectious diseases, such as coronavirus disease (Covid-19). In late December, 2019, patients presenting with viral pneumonia due to an unidentified microbial agent were reported in Wuhan, China. A novel coronavirus was subsequently identified as the causative pathogen, provisionally named 2019 novel coronavirus (Covid-19) [6]. As of Jan 26, 2020, more than 2000 cases of Covid-19 infection have been confirmed, most of which involved people living in or visiting Wuhan, and human-to-human transmission has been established, such as through respiratory droplets [1], and there is also a suspicion of asymptomatic infection [2]. Although our phylogenetic analysis suggests that bats might be the original host of this virus, an animal sold at the seafood market in Wuhan might represent an intermediate host facilitating the emergence of the virus in humans [5].

The Covid-19 is believed to be zoonotic in origin, from bats to intermediate host to humans [7]; and its initiation is geographically associated, but with uncertainty, with the Huanan Seafood Market in Wuhan [1]. The disease has also been exported to other countries, including Nigeria. The World Health Organization [6] has declared the Covid-19 outbreak as a public health emergency of international concern, specifically to enhance the level of preparedness of countries that need additional support [1]. To prevent the global spread of the virus, many countries have imposed travel restrictions to and from China [2]. To describe and predict the dynamics of the disease, several preliminary mathematical models are formulated by various international study groups [5]. The model shows that the exposure time is a significant factor in spreading the disease. With a basic reproduction number equal to 2, and 14-day infectious period, an infected person staying more than 9 hours in the event could infect other people [7]. Assuming the exposure time is 18 hours, the model recommends that attendees of the social gathering should have a protection with more than 70 percent effectiveness [7].To the best of our knowledge, few studies developed mathematical models for Covid-19 transmission dynamics without providing in-depth information on its reproduction number as well as its stability has been published. The progress of an epidemic through the population is highly amenable to mathematical modeling. Mathematical modeling can provide an understanding of the underlying mechanisms of disease transmission and spread, help to pinpoint key factors in the disease transmission process, suggest effective control and preventive measures, and provide an

estimate for the severity and potential scale of the epidemic [4]. Mathematical modeling has proven to be an essential tool for the development of control strategies and in distinguishing driving factors in disease dynamics. Put it simply, mathematical modeling should become part of the toolbox of public health research and decision making [4]. Our goal in this paper is to develop a new mathematical model for the transmission of Covid-19 disease. We also show how to estimate the basic reproduction number as well as stability analysis of the model equilibrium in the absence or presence of the disease. However, Figure 1 shows the number of cases reported by NCDC each day. This suggests upward trend in the number of cases.

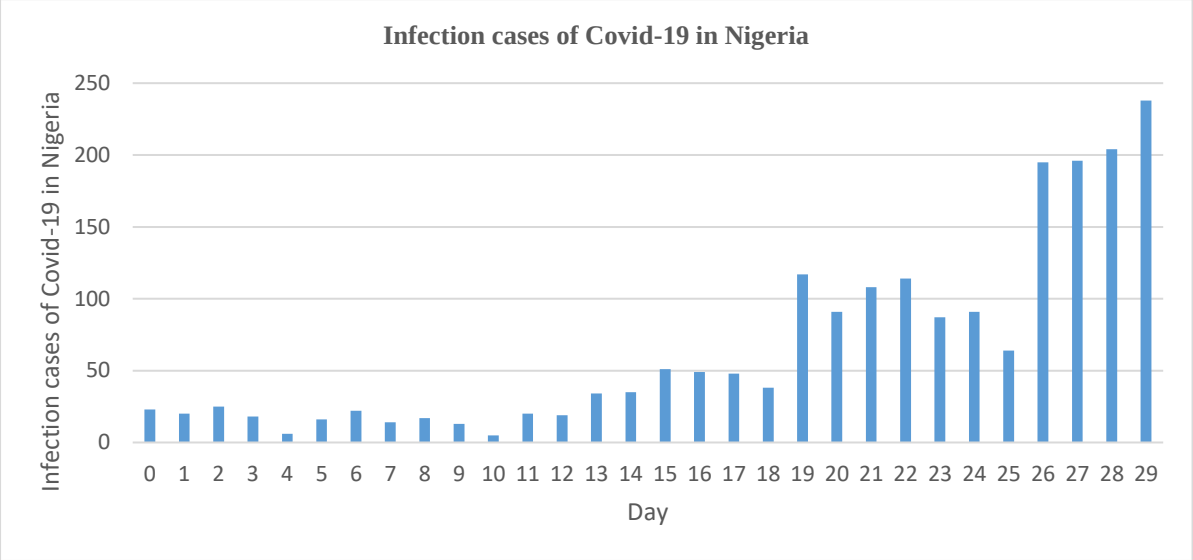
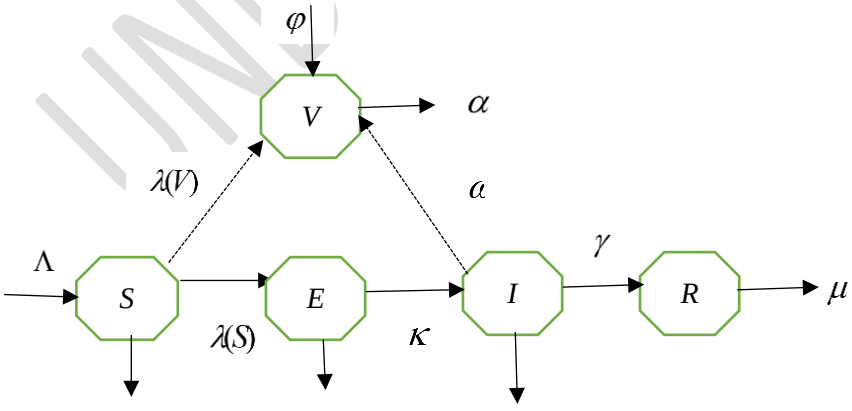


Fig. 1. The empirical infection cases of Covid-19 in Nigeria from April 2-May 1, 2020 [3]

2. A Dynamical Model of Covid-19 Transmission

In this section, we present our dynamic Covid-19 transmission model based on natural history of the disease. The human host population consists of four sub populations: namely susceptible ($S(t)$), asymptomatic ($E(t)$), symptomatic ($I(t)$), and recovered ($R(t)$). More so, coronavirus population ($V(t)$). We considered host due to the fact that Covid-19 is sufficiently divergent from *SARS-CoV* to be considered a new human-infecting beta coronavirus. The detailed descriptions see Table 1 and 2. The model diagram is given below.

Figure 1. The model flow diagram



Our Cov transmissio is given l llowing nonlinear system of differential equations:

$$\begin{cases} \dfrac{dS(t)}{dt} = \Lambda - \beta S\left(\dfrac{I+V+qE}{N}\right) - \mu S \\ \dfrac{dE(t)}{dt} = \beta S\left(\dfrac{I+V+qE}{N}\right) - (\kappa+\delta+\mu)E \\ \dfrac{dI(t)}{dt} = \kappa E - (\gamma+\delta+\mu)I \\ \dfrac{dR(t)}{dt} = \gamma I - \mu R \\ \dfrac{dV(t)}{dt} = \varphi V + \omega I - \alpha V \end{cases} \quad (1)$$

where $S(0), E(0), I(0), R(0), V(0)$ are given and the definitions of above model parameters are listed in Table 2.

Table 1. Epidemiological classes definitions

Class	Definition
S	Susceptible individuals
E	Asymptomatic individuals who have been exposed to the virus but have not yet developed clinical symptoms of Covid-19 but infectious
I	Symptomatic individuals (infected, infectious and diagnosed)
R	Recovered individuals
V	The coronavirus free particles

Table 2. Parameter definitions

Parameter	Definition
Λ	Recruitment rate of humans due to immigration
β	Transmission rate per day for humans
q	Relative measure of infectiousness for the asymptomatic class *E*
κ	Rate of normal progression to the infectious state per day
γ	Natural recovery rate
ω	Contribution of infected individual to the population of coronavirus
δ	Covid-19-induced mortality per day
φ	Growth rate of the coronavirus population
μ	Death rate of humans
α	Death rate of coronavirus in the environment

We assume that a susceptible individual may be infected through contacts with an asymptomatic individual, an infected individual or through the environment.

2.1 Basic Properties of the Model

Since the model (1) monitors human population, all its associated parameters and state variables are assumed to be non-negative for all $t \geq 0$. Before analysing the model, it is instructive to show that the state variables of the model remain non-negative for all non-negative initial conditions. Thus, we claim the following result.

Theorem 1: Let the initial data be $S(0), E(0), I(0), R(0), V(0)$ be non-negative. Then, the solutions (S, E, I, R, V) of model (1) are positive and bounded for all $t > 0$, whenever they exists.

Proof:

Suppose $S(0) \geq 0$. The first equation of system (1) can be written as:

$$\frac{d}{dt}\left[S(t)\eta(t)\right] = \Lambda\eta(t),$$

where $\eta(t) = \exp\left(\int_0^t \left[(1-\sigma)\lambda(S) + \xi + \mu\right] dS\right) > 0$ is the integrating factor. Hence, integrating this last relation with respect to *t*, we have

$$S(t)\eta(t) - S(0) = \int_0^t \Lambda\eta(S) dS,$$

so that the division of both side by $\eta(t)$ yields

$$S(t) = \left[S(0) - \int_0^t \Lambda\eta(S) dS\right] \times \eta^{-1}(t) > 0.$$

The same arguments can be used to prove that $E(t), I(t), R(t), V(t) \geq 0$ for all $t > 0$.

Furthermore, let $N = S + E + I + R$. Then,

$$\dot{N}(t) = \dot{S} + \dot{E} + \dot{I} + \dot{R}$$
$$= \Lambda - \lambda S - \mu S + \lambda S - (\kappa + \delta + \mu)E + \kappa E - (\gamma + \delta + \mu)I + \gamma I - \mu R$$
$$\leq \Lambda - \mu N - \delta I, \ \delta = 0$$

This implies that as $t \to \infty, \sup N(t) \leq \frac{\Lambda}{\mu}$. Also from (1), we have that as: $t \to \infty, \sup S(t) \leq \frac{\Lambda}{\mu}$.

This completes the proof.

Combining Theorem 1 with the trivial existence and uniqueness of a local solution for the model (1), we have established the following theorem which ensures the mathematical and biological well-posedness of system (1).

Theorem 2: The dynamics of model (1) is a dynamical system in the biological feasible compact set

$$\Gamma := \left\{(S, E, I, R, V) \in \mathbb{R}^5_+ : 0 \leq S \leq \frac{\Lambda}{\mu}; N_h \leq \frac{\Lambda}{\mu}, N_v \leq \frac{\omega\Lambda}{\mu(\alpha - \varphi)}\right\} \qquad (2)$$

3. Basic Reproduction Number

It follows that the dynamics is completely determined by the reproduction number, R_0, given by:

$$R_0 = \frac{\beta\Lambda\left((\gamma + \delta + \mu)(\alpha - \varphi)q + (\alpha - \varphi)\kappa + \kappa\omega\right)}{\mu(\kappa + \delta + \mu)(\gamma + \delta + \mu)(\alpha - \varphi)} \qquad (3)$$

The reproduction number, R_0, is defined as the number of secondary infections that one infectious person would produce in a fully susceptible population through the entire duration of the infectious period. The result below follows from theorem 2 in [9]. Based on the available information (which may not be realistic), we estimated the basic reproduction number $R_0 \approx 2.8$ for Covid-19 in Nigeria. This indicates that Covid-19 can get worst when people violate government policy to curtail the spread of Covid-19 (especially through person-to-person transmission route). With the current prevention measures (such as proper personal hygiene, social distancing, staying at home as well as early detection and reporting) in Nigeria, basic reproduction number can be reduced thereby minimizing the spread of Covid-19 in the country.

4. Stability Analysis of DFE and EEP

By stability we mean the condition of being stable or in equilibrium. That is, the tendency to recover from perturbations. Here, we analyze the stability of the model equilibrium in the absence and presence of Covid-19.

Lemma 1: The DFE (ξ_0) of the model (1) is locally asymptomatically stable (LAS) if $R_0 < 1,$ and unstable if $R_0 > 1.$

Epidemiologically, this implies that Covid-19 will be eliminated from the population whenever $R_0 < 1,$ if the initial size of the sub-populations are in the basin of attraction of the DFE i.e. a small influx of Covid-19 infectious individuals into the community will not generate a large Covid-19 outbreak and the disease dies out in time.

4.1 Global Stability of the Disease-free Equilibrium (DFE)

Lemma 2: If $R_0 < 1,$ the disease-free equilibrium of the model system (1) is globally asymptotically stable and unstable if $R_0 > 1.$

By the comparison theorem, the rate of change of the variables representing the infected components of model system (1) can be re-written as:

$$\begin{bmatrix} E'(t) \\ I'(t) \\ V'(t) \end{bmatrix} = (F - V)\begin{bmatrix} E(t) \\ I(t) \\ V(t) \end{bmatrix} - \left(1 - \frac{S}{N}\right)\begin{bmatrix} E(t) \\ I(t) \\ V(t) \end{bmatrix} \qquad (4)$$

where the matrices F and V are defined by the expressions. Since $S \le \Lambda/\mu$ for all $t > 0$ in Γ, it follows that

$$\begin{bmatrix} E'(t) \\ I'(t) \\ V'(t) \end{bmatrix} \le (F - V)\begin{bmatrix} E(t) \\ I(t) \\ V(t) \end{bmatrix} \qquad (5)$$

Using the fact that the eigenvalues of the matrix $(F - V)$ all have negative real parts, it follows that the linearized differential inequality system (5), is stable whenever $R_0 < 1$. Consequently, using the equations (2), (3) and (5), $(E, I, V) \to (0, 0, 0)$ as $t \to \infty$. Thus by a comparison theorem according to [4], $(E, I, V) \to (0, 0, 0)$ as, and evaluating system (1) at $E = I = V = 0$ gives $S \to \Lambda/\mu$, for $R_0 < 1$. Hence, the disease-free equilibrium is globally asymptotically stable for $R_0 < 1$.

4.2 Existence of Endemic Equilibrium Point

Next conditions for the existence of endemic equilibria for the model (1) is explored. Let

$$\xi_1 = \left(S^{**}, E^{**}, I^{**}, R^{**}, V^{**}\right), \qquad (6)$$

be the arbitrary endemic equilibrium of model (1), in which at least one of the infected components of the model is non-zero. Let

$$\lambda^{**} = \beta\left(\frac{I + V + qE}{N}\right) = \tilde{\beta}(I + V + qE), \tilde{\beta} = \frac{1}{N} \qquad (7)$$

be the force of infection. Setting the right-hand sides of the equations in (1) to zero gives the following expressions (force of infection)

$$
\begin{aligned}
S^{**} &= \frac{\Lambda}{\lambda^{**}+\mu},\\
E^{**} &= \frac{\lambda^{**}\Lambda}{(\kappa+\delta+\mu)(\lambda^{**}+\mu)},\\
I^{**} &= \frac{\lambda^{**}\Lambda\kappa}{(\kappa+\delta+\mu)(\gamma+\delta+\mu)(\lambda^{**}+\mu)},\\
R^{**} &= \frac{\lambda^{**}\Lambda\kappa\gamma}{\mu(\kappa+\delta+\mu)(\gamma+\delta+\mu)(\lambda^{**}+\mu)},\\
V^{**} &= \frac{\lambda^{**}\Lambda\kappa\omega}{(\kappa+\delta+\mu)(\gamma+\delta+\mu)(\alpha-\varphi)(\lambda^{**}+\mu)}
\end{aligned}
\qquad (8)
$$

Substituting the above into (8), gives $a_0\lambda^{**}+b_0=0$, where

$$
\begin{aligned}
a_0 &= (\kappa+\delta+\mu)(\gamma+\delta+\mu)(\alpha-\varphi),\\
b_0 &= \mu(\kappa+\delta+\mu)(\gamma+\delta+\mu)(\alpha-\varphi)-\tilde{\beta}\left(\kappa\Lambda(\alpha-\varphi)+\omega\kappa\Lambda+q\Lambda(\gamma+\delta+\mu)(\alpha-\varphi)\right)\\
&= \mu(\kappa+\delta+\mu)(\gamma+\delta+\mu)(\alpha-\varphi)\left[1-\frac{\tilde{\beta}\left(\kappa\Lambda(\alpha-\varphi)+\omega\kappa\Lambda+q\Lambda(\gamma+\delta+\mu)(\alpha-\varphi)\right)}{\mu(\kappa+\delta+\mu)(\gamma+\delta+\mu)(\alpha-\varphi)}\right]\\
&= \mu(\kappa+\delta+\mu)(\gamma+\delta+\mu)(\alpha-\varphi)(1-R_0)
\end{aligned}
$$

The coefficient a_0 is always positive, the coefficient b_0 is positive (negative) if R_0 is less than (greater than) unity. Furthermore, there is no positive endemic equilibrium if $b_0 \geq 0$. If $b_0 < 0$, then there is a unique endemic equilibrium (given by $\lambda = {}^{b_0}\!/_{a_0}$). This result is summarized below.

Lemma 3. The model (1) has a unique positive endemic equilibrium whenever $R_0 > 1$, and no positive endemic equilibrium otherwise.

4.3 Global Stability of the Endemic Equilibrium

Lemma 4. The unique endemic equilibrium, ξ_1, of the model (1) is GAS in Γ whenever $R_0 > 1$.

Proof:

Let $F = S - S^{**} - S^{**}In\frac{S}{S^{**}} + \left(E - E^{**} - E^{**}In\frac{E}{E^{**}}\right) + A\left(I - I^{**} - I^{**}In\frac{I}{I^{**}}\right) + B\left(V - V^{**} - V^{**}In\frac{V}{V^{**}}\right)$ (9)

be the Lyaponuv function of the Goh-Voltera type

$$
\begin{aligned}
\dot{F} &= \dot{S} - \frac{S^{**}}{S}\dot{S} + \left(\dot{E} - \frac{E^{**}}{E}\dot{E}\right) + A\left(\dot{I} - \frac{I^{**}}{I}\dot{I}\right) + B\left(\dot{V} - \frac{V^{**}}{V}\dot{V}\right)\\
\dot{F} &= \Lambda - \tilde{\beta}S(I+V+qE) - \mu S - \frac{S^{**}}{S}\left(\Lambda - \tilde{\beta}S(I+V+qE) - \mu S\right)\\
&+\tilde{\beta}S(I+V+qE) - (\kappa+\delta+\mu)E - \frac{E^{**}}{E}\left(\tilde{\beta}S(I+V+qE) - (\kappa+\delta+\mu)E\right)\\
&+A\left(\kappa E - (\gamma+\delta+\mu)I - \frac{I^{**}}{I}\left(\kappa E - (\gamma+\delta+\mu)I\right)\right) + B\left((\alpha-\varphi)V + \omega I - \frac{V^{**}}{V}\left((\alpha-\varphi)V + \omega I\right)\right)
\end{aligned}
$$

Simplify to give

$$\dot{F} = \Lambda - \tilde{\beta}S\left(I+V+qE\right) - \mu S - \frac{S^{**}}{S}\Lambda + \tilde{\beta}S^{**}\left(I+V+qE\right) + \mu S^{**} +$$

$$\tilde{\beta}S\left(I+V+qE\right) - \left(\kappa+\delta+\mu\right)E - \frac{E^{**}}{E}\tilde{\beta}S\left(I+V+qE\right) + \left(\kappa+\delta+\mu\right)E^{**}$$

$$+A\kappa E - A\left(\gamma+\delta+\mu\right)I - \frac{I^{**}}{I}A\kappa E - A\left(\gamma+\delta+\mu\right)I^{**} + B\omega I - B\left(\alpha-\varphi\right)V - \frac{V^{**}}{V}B\left(\alpha-\varphi\right)V^{**} - B\omega I^{**}$$

At the steady state, we observe

$$\Lambda = \tilde{\beta}S^{**}\left(I^{**}+V^{**}+qE^{**}\right) + \mu S^{**}$$

Substituting, we have

$$\dot{F} = \tilde{\beta}S^{**}\left(I^{**}+V^{**}+qE^{**}\right) + \mu S^{**} - \tilde{\beta}S\left(I+V+qE\right) - \mu S - \frac{S^{**^2}}{S}\tilde{\beta}S^{**}\left(I^{**}+V^{**}+qE^{**}\right)$$

$$+\mu\frac{S^{**^2}}{S} + \tilde{\beta}S^{**}\left(I+V+qE\right) + \mu S^{**} + \tilde{\beta}S\left(I+V+qE\right) - \left(\kappa+\delta+\mu\right)E - \frac{E^{**}}{E}\tilde{\beta}S\left(I+V+qE\right) + \left(\kappa+\delta+\mu\right)E^{**}$$

$$+A\kappa E - A\left(\gamma+\delta+\mu\right)I - \frac{I^{**}}{I}A\kappa E - A\left(\gamma+\delta+\mu\right)I^{**} + B\omega I - B\left(\alpha-\varphi\right)V - \frac{V^{**}}{V}B\left(\alpha-\varphi\right)V^{**} - B\omega I^{**}$$

Now, equating coefficients to zero and solving, we get

$$A = \frac{\left(\kappa+\delta+\mu\right)}{\kappa}, B = \frac{\left(\kappa+\delta+\mu\right)\left(\gamma+\delta+\mu\right)}{\kappa\omega}$$

Substituting for *A* and *B*, we get

$$\dot{F} = \tilde{\beta}S^{**}\left(I^{**}+V^{**}+qE^{**}\right) + \mu S^{**} - \mu S - \frac{\tilde{\beta}S^{**^2}}{S} - \frac{E^{**}}{E}\tilde{\beta}S\left(I+V+qE\right) + \left(\kappa+\delta+\mu\right)E^{**}$$

$$+\frac{\left(\kappa+\delta+\mu\right)}{\kappa}\frac{I^{**}}{I}\kappa E - \frac{\left(\kappa+\delta+\mu\right)}{\kappa}\left(\gamma+\delta+\mu\right)I^{**} + \frac{\left(\kappa+\delta+\mu\right)\left(\gamma+\delta+\mu\right)}{\kappa\omega}\frac{V^{**}}{V}\left(\alpha-\varphi\right)V^{**} - \frac{\left(\kappa+\delta+\mu\right)\left(\gamma+\delta+\mu\right)}{\kappa\omega}\omega I^{**}$$

Note, at steady state, we have

$$\left(\kappa+\delta+\mu\right) = \frac{\tilde{\beta}S^{**}\left(I^{**}+V^{**}+qE^{**}\right)}{E^{**}}, \kappa = \frac{\left(\gamma+\delta+\mu\right)I^{**}}{E^{**}}, \left(\alpha-\varphi\right) = \frac{\omega I^{**}}{V^{**}}$$

Substituting, we get

$$\dot{F} = \mu S^{**}\left(1-\frac{S}{S^{**}}\right) + \tilde{\beta}S^{**}\left(3\left(I^{**}+V^{**}+qE^{**}\right) - \frac{S^{**}}{S} - \frac{\left(I+V+qE\right)E^{**}}{E} - \frac{\left(I^{**}+V^{**}+qE^{**}\right)I^{**}E}{E^{**}I}\right)$$

Since the arithmetic mean exceeds the geometric mean, it means that

$$\mu S^{**}\left(1-\frac{S}{S^{**}}\right) \le 0,\ \tilde{\beta}S^{**}\left(I^{**}+V^{**}+qE^{**}\right)\left(3-\frac{S^{**}}{S}-\frac{I^{**}E}{E^{**}I}\right) \le 0,\ \frac{-\tilde{\beta}S^{**}\left(I+V+qE\right)E^{**}}{E} \le 0.$$

This implies that $\dot{F} \le 0$. One can see that the largest invariant subset, whenever $\dot{F} = 0$, is ξ_1. By LaSalle's Invariance Principle [8], ξ_1 is globally asymptotically stable when $R_0 > 1$.

5. Concluding Remarks

In this paper, we presented a coronavirus (Covid-19) model using a deterministic system of differential equations and established that the model is locally and globally asymptotically stable when the associated reproduction number is less (or greater) than unity. Though the basic reproduction number of Covid-19 in Nigeria is about 2.8, the situation is still not optimistic due to limited environment protection and poor medical condition. While for the control of Covid-19, it is instructive to increase personal hygiene, social distancing, staying at home as well as early detection and reporting. As mentioned in the review [3], the total number of Covid-19 cases reported by NCDC is less than realistic infected cases. Therefore, we may also underestimate the empirical situation in Nigeria based on the reported data from April 02 to May 01, 2020. Meanwhile, the data of Covid-19 in Nigeria in our

paper is not enough and precise. To obtain the data with more useful information, we may need more economic investment and sophisticated statistical methods, which indicates that the revealing of Covid-19 transmission rule requires collaborative efforts from different disciplines. It should be noted that total lockdown is not an option. This is because Nigeria cannot afford lockdown. Thus, pandemic history can be of help in this regard. However, this paper focused on the theoretical assessment of Covid-19 transmission dynamics due to the fact that we lack realistic data to further consider numerical simulation. Hence, numerical simulation analysis will be consider in our next paper.

References

[1] Cohen J. (2020). *Mining coronavirus genomes for clues to the outbreak's origins. Science, 31 January 2020 (news)*. Retrieved 08 February 2020 from https://www.sciencemag.org

[2] Kupferschmidt K. (2020). *Study claiming new coronavirus can be transmitted by people without symptoms was flawed. Science.* Retrieved 08 February 2020 from https://www.sciencemag.org/news/2020/02/paper

[3] Nigerian Centre for Disease Control. (2020). *Disease background of 2019-nCoV*. NCDC. Retrieved 08 February 2020 from https://www.ncdc.org /2019-ncov-background.

[4] Obasi, C. & Mbah, G.C.E. (2019). On the basic reproduction number of Lassa fever epidemics and its relationship with inter-epidemic period. *Journal of the Nigerian Society for Mathematical Biology*, 2 (1), 69-79.

[5] Riou J. & Althaus C.L. (2020). Pattern of early human-to-human transmission of Wuhan 2019- nCoV. *bioRxiv* (preprint), https://doi.org/10.1101/2020.01.23.917351.

[6] World Health Organization. (2020). *Novel Coronavirus (2019-nCoV) advice for the public: Basic protective measures against the new coronavirus*. World Health Organization. Retrieved 08 February 2020 from https://www.who.int/emergencies/diseases

[7] Zhou T., Liu Q., Yang Z., Liao J., Yang K., Bai W., Lu X. & Zhang, W. (2020*). Preliminary prediction of the basic reproduction number of the Wuhan novel coronavirus 2019-nCoV*. arXiv (preprint), arXiv:2001.10530.

[8] Lasalle J.P. (1977). *Stability theory for difference equations. Studies in ordinary differential equations*. Washington DC: Mathematical Association of America. Hale JK, editor.

[9] Keeling M.J. & Rohani P. (2008). *Modeling infectious diseases in humans and animals*. Princeton: Princeton University Press.