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MATHEMATICAL MODELLING ON THE DYNAMIC TRANSMISSION OF CORONAVIRUS (COVID-19) (A CASE STUDY OF NIGERIA)

Umar Yusuf Madaki*, Aliyu Ibrahim and Saudatu Baba Sambo

Department of Mathematics and Statistics, Yobe State University, Damaturu, Nigeria

ABSTRACT

This research work focused on "Mathematical Modelling on the Dynamic Transmission of Coronavirus" to reduce its prevalence to a level at which the disease will no longer constitute public health problems. In this work, we used to formulate a deterministic (SEIR susceptible, expose/latently infected, infectious and recovered) model incorporating the method of control adopted by epidemiologist and the process of computing the values in data obtained are done .The data was obtained and retrieved from the website of Nigeria center for disease control (NCDC). We established the disease free and the endemic equilibrium states and carried out the stability analysis of the disease Free and the equilibrium state. The negativity of all Eigen values that arosed from the stability analysis carried out in the research showed that there is high possibility of no return of the corona virus pandemic in Nigeria after eradication. We found out that the disease free equilibrium state is stable. Also, recommendations were made in the incidence of coronavirus which can greatly be minimized or possibly be eradicated in any population if effort is made to ensure that the endemic equilibrium of this model is never stable.

INTRODUCTION

Throughout history, infectious diseases have caused havoc among societies. Emerging and re-emerging infectious diseases are now occurring at unprecedented speed. According to the World Health Organization (WHO), the world has witnessed the emergence of several disease outbreaks and epidemics caused by more than 20 infectious agents over the past decade. Some of these epidemics were caused by novel infectious agents such as *hemagglutinin neuraminidases* (H1N1) and MERS. Over the past two decades, the emergence of coronavirus-associated diseases (SARS and MERS) inflicted global challenges to public health systems. SARS-CoV-2 (the causative agent for coronavirus disease COVID-19) is the latest addition to this growing list of unwelcomed novel agents. The WHO declared COVID-19 a public health emergency of international concern on 30 January and a pandemic on 11 March 2020.The size and reach of today's global travel network are unparalleled. In 2018 alone, more than 4 billion people

(approximately 60% of the world population) traveled globally using commercial flights. In today's global convergence, locally emerging pathogens have the capacity to spread rapidly and cross borders and become an imminent public health threat to the entire world. This is exemplified by the current COVID-19 pandemic where the appearance of a seemingly limited cluster of cases of pneumonia linked to a sea food market in Wuhan, China has become one of the worst pandemics in human history with a staggering number of more than 1.4 million infections in 177 countries and more than 85 000 deaths globally as of 9 April 2020. It is worth noting that only a few of the current 177 countries affected seem to have passed the peak of the epidemic while the majority of these countries are just beginning to see a surge in cases. As the COVID-19 pandemic continues to move at record speed, the speed and volume of the scientific knowledge on SARS-CoV-2 and COVID-19 are correspondingly fast and unprecedented. As of 9 April 2020, the WHO regularly updated bibliographic database of publications on COVID-19 astoundingly including more than 5300 publications of which about 1800 articles appeared in PubMed indexed journals.

BACKGROUND OF THE STUDY

On 31 December 2019, WHO was informed of cases of pneumonia of unknown cause in Wuhan City, China. A novel coronavirus was identified as the cause by Chinese authorities on 7 January 2020 and was temporarily named "2019-nCoV". The first known infections from SARS-CoV-2 were discovered in Wuhan, China. The original source of viral transmission to humans remains unclear, as does whether the virus became pathogenic before or after the spillover event. Nigeria Centre for Disease Control is Nigeria's leading national public health institute. The NCDC is a Nigerian federal government agency under the Federal Ministry of Health and its mandate was to coordinate, and control the activities in all states in Nigeria in order to significantly reduce the public burden of the coronavirus and all other diseases and pandemic in the country. The NCDC which is part of the ministry of health, control most of the activities and planning for the work on covid19 and other infectious diseases in Nigeria. The federal government of Nigeria has made a considerable effort in setting up the presidential task force PTF for covid19 control which is aimed to provide general information for the prevention and control measures, treatment and general protocol for the containment of the virus in line with the commitment of world health organization (WHO). However there are several difficulties affecting the progress of the plan in Nigeria especially due to large population, lack of access to hard-to-reach areas lack of awareness about the virus and lack of reporting cases of the infection. Also inadequate human resources and technical capacity are among the problem of the plan in Nigeria. Covid19 was first reported in Nigeria toward the end of 2019 and has now being declared as pandemic by the world health organization (WHO). Worldwide organizations are responding differently to the virus out break (khanna R.C 2020). Covid19 has many effect on developing countries like Nigeria, and its continued tragic impact on national and global health system.

STATEMENT OF THE PROBLEM

Despite numerous and existing management and control strategies of covid19 currently in place, coronavirus continue to cause great health effect worldwide (WHO, 2020). A number of studies have been conducted and shows that, coronavirus contributes too much illness including

respiratory illness and hence the mathematical model for the transmission of covid19 will be formulated.

AIM AND OBJECTIVES

The aim of this project work is to formulate a mathematical model on the transmission of covid19 infections.

The following objectives are to be achieved

i. Formulate and analyse a mathematical model on the dynamic and treatment of the covid19 infectious disease using SLIR model.
ii. To determine the stability analysis of the equilibrium points by using system of equations simultaneously.
iii. To obtain the basic reproduction number and determine equilibrium point by using Jacobian matrix.

SIGNIFICANCE OF THE STUDY

The significances of the study include the following

i. The model will help to understand the dynamic and treatment covid19.
ii. The study will also act as a base for further research on the coronavirus dynamic and treatment and other related diseases.
iii. The study intends to contribute on strategies of addressing covid19 and how to curtail it in the population.

The study will create awareness and inform people about the effect of covid19 dynamic and treatment.

SCOPE AND LIMITATION

This project work centered on the formulation of a mathematical model for coronavirus dynamics and its analysis by obtaining the equilibrium solution state and stability of such state. This study limited to only coronavirus, however, it can be extended to other epidemic with little modification.

RESEARCH QUESTIONS

i. Does mathematical modeling provide a unique approach to gain basic knowledge on coronavirus disease?
ii. What are the primary ways of contacting the virus?
iii. Does the virus threaten the lives of individual?
iv. What are the ways of getting the result in mathematical model?

2.0 LITERATURE REVIEW

Mathematical and computational models of infectious diseases are increasingly recognized as relevant quantitative support in epidemic preparedness and response. This chapter looks into various studies carried out by researches regarding a review of literatures on earlier works for coronavirus which will be discuss. Many studies have been proposed by researchers to investigate the transmission dynamic and control of the virus.

Jiang, S. Et-al. (2020), Described corona virus as an outbreak of unusual respiratory disease, initially dominated by pneumonia, in Wuhan, China, is caused by infection by a novel coronavirus. The new virus was initially named 2019-nCoV by W.H.O. On Feb 11, 2020, WHO renamed the disease as coronavirus disease 2019 (COVID-19).That same day, the Coronavirus Study Group (CSG) of the International Committee on Virus Taxonomy posted a manuscript on *bioRxiv* in which they suggested designating 2019-nCoV as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) on the basis of a phylogenetic analysis of related coronaviruses. The CSG claimed that they did not intend to make any reference to SARS when introducing yet another virus name derived from the term SARS; however, SARS is a disease name, and to name new virus SARS-CoV-2 actually implies that it causes SARS or similar, especially to scientists without much knowledge of virology and to citizens in the public domain. The new name is also not consistent with the disease name COVID-19. SARS-CoV-2, as a naturally occurring virus, is different from all other SARS-like or SARS-related coronaviruses, which are characterized mainly by their genome sequence.

Jernigan, D.B. (2020), An outbreak of coronavirus disease 2019 (COVID-19) caused by the 2019 novel coronavirus (SARS-CoV-2) began in Wuhan, Hubei Province, China in December 2019, and has spread throughout China and to 31 other countries and territories, including the United States. As of February 23, 2020, there were 76,936 reported cases in mainland China and 1,875 cases in locations outside mainland China. There have been 2,462 associated deaths worldwide; no deaths have been reported in the United States. Fourteen cases have been diagnosed in the United States, and an additional 39 cases have occurred among repatriated persons from high-risk settings, for a current total of 53 cases within the United States.

Samui, p. et-al (2020),described the novel corona virus covid-19 as an infectious disease that has already exceed the earlier record of the two life threatening outbreaks, namely, severe acute respiratory syndrome corona virus (SARS-COV), and the middle east respiratory corona virus (MERS-COV), posing the major warning to the global public health and economy after 2nd world war. They further said, covid-19 are group of enveloped non-segmented with positive-sense, single-stranded RNA virus that belongs the order of nidovirales, family of corona viridae, sub family of arthrocoronavirinae, and are widely spread among mammals and humans.

Rothan, H. A., & Byrareddy, S. N. (2020), Coronavirus disease (COVID-19) is caused by SARS-COV2 and represents the causative agent of a potentially fatal disease that is of great global public health concern. Based on the large number of infected people that were exposed to the wet animal market in Wuhan City, China, it is suggested that this is likely the zoonotic origin of COVID-19. Person-to-person transmission of COVID-19 infection led to the isolation of patients that were subsequently administered a variety of treatments.

Zhang, L., & Liu, Y. (2020), Coronaviruses (CoVs) belong to the subfamily *Orthocoronavirinae* in the family of *Coronaviridae* in the order *Nidovirales*, and this subfamily including α-coronavirus, β-coronavirus, γ-coronavirus, and delta-coronavirus. Coronaviruses primarily cause enzootic infections in birds and mammals and, in the last decades, have shown to be capable of infecting humans as well. The outbreak of severe acute respiratory syndrome (SARS) in 2002 and Middle East respiratory syndrome (MERS) in 2012 has demonstrated the lethality of coronaviruses when they cross the species barrier and infect humans.

Lu, Q., & Shi, Y. (2020), SARS-CoV-2 is single-stranded RNA viruses, belongs to subgenus Sarbecovirus of the genus Betacoronavirus. SARS-CoV-2 particles contain spike and envelope; virions are spherical, oval, or pleomorphic with diameters of approximately 60 to 140 nm.

Erinsco, O.A,. Et-al, (2020), the clinical spectrum of SARS-CoV-2 infection is still evolving. Current evidence suggests that carriers of SARS-CoV-2 can present clinically with or without symptoms. Symptomatic patients usually present with one or more of the common symptoms: fever, dry cough, fatigue, and shortness of breath, anosmia, myalgia and other less common symptoms such as diarrhea, nausea and vomiting.

Adebayo, A. A., & Taiwo, E. A. (2020). the outbreak of corona virus disease (COVID-19) has been declared a global pandemic by the World Health Organisation. Many people have tested positive to the disease, others are dead with many economies shutting down. Many countries have also been placed on lock down so as to prevent the further spread of the disease. Given the vulnerability of inmates and personnel of correctional service or detention facilities to the outbreak COVID-19, there are legitimate concerns about their health and lives. Persons in correctional or detention facilities are particularly exposed considering the overcrowding and unhygienic conditions of such facilities in many countries.

Shrivastava, S. R., & Shrivastava, P. S. (2020), In Nigeria, since the detection of the first case on February 27, 2020, a total of 208 cases and four deaths has been reported. It is important to note that Nigeria remains one among the 3three nations who have not yet been certified for polio elimination and simultaneously is also fighting against the outbreak of Ebola virus disease in the recent past.

3.0 MATERIALS AND METHODS
3.1 MODEL FORMULATION

In this study we formulated a deterministic, compartment model to investigate the transmission dynamics between infected and susceptible individual in a population the progression of corona virus disease (covid19) within the total population can be simplified using four different equations representing four different groups of people namely, susceptible S(t),

Latently infected L(t), infectious I(t), and Recovered R(t), individuals. The flow Diagram of the model is as follow;

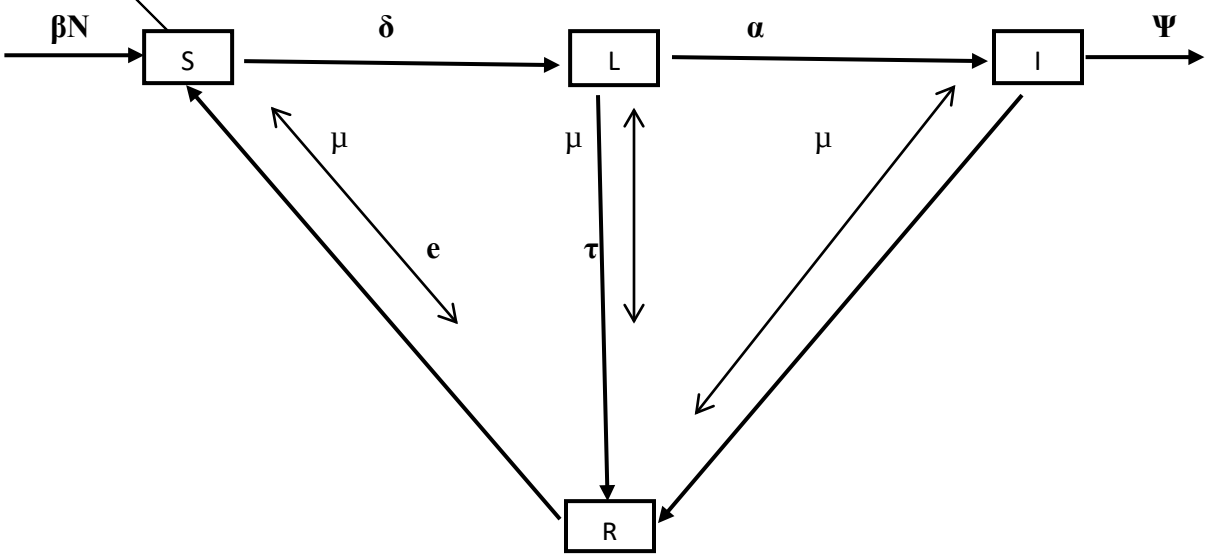


Figure 1.0: To showing deterministic

Presentation of the model above.

The susceptible population change due to the coming in of new susceptible into the population where the model parameters are at a constant rate βN (through contact or travelling), Natural death rate μ, coronavirus contraction rate α, Rate of

breakdown of latent covid19 into infectious δ, successful cure of infectious patients γ and Death cause as a result of chronic Infection at the rate ψ, Successful cure of infectious latent τ and e is rate which recovered individuals return to susceptible status due to loss immunity. Our study we assumed that there is homogeneous mixing of the population where all people are equally likely to be infected by infectious individuals in case of contact, we assumed equal natural death rate μ for each compartment. The model is represented by the following system of ordinary differential equation in developing the model which is as follow:

$$\frac{dS}{dt} = \beta N - \frac{\propto sI}{N} + eR - \mu S \quad (3.1)$$

$$\frac{dL}{dt} = \frac{\propto sI}{N} - (\delta + \tau + \mu)L \quad (3.2)$$

$$\frac{dI}{dt} = \delta L - (\gamma + \mu + \psi)I \quad (3.3)$$

$\frac{dR}{dt} = \gamma I + \tau L - (e + \mu)R$ (3.4)

Let $K_1 = \delta + \tau + \mu$

$K_2 = \gamma + \mu + \psi$

$K_3 = e + \mu$

Taking equation (3.1)

$\frac{dS}{dt} = \beta N - \frac{\alpha sI}{N} + eR - \mu s$

$\frac{dL}{dt} = \frac{\propto sI}{N} - k_1 L$ (3.5)

$\frac{dl}{dt} = \delta L - K_2 I$ (3.6)

$\frac{dR}{dt} = \gamma I + \tau L - K_3 R$ (3.7)

3.2 EXISTENCE OF DISEASE FREE - EQUILIBRIUM (DFE) STATE

The disease free equilibrium is a steady state solution of the coronavirus dynamic model with all infected population equal to zero. The stability of the disease free equilibrium state is extremely important because it help us to investigate the long term behavior of the system. It can determine whether or the viruses are capable of invading into a population. Now we recall the four equations: (3.1) to (3.4).

$\frac{dS}{dt} = \beta N - \frac{\propto sI}{N} + eR - \mu S$ (3.1)

$\frac{dL}{dt} = \frac{\propto sI}{N} - k_1 L$ (3.2)

$\frac{dI}{dt} = \delta L - k_2 l$ (3.3)

$\frac{dR}{dt} = \gamma I + \tau L - k_3 R$ (3.4)

At equilibrium, the rate of change of variable is zero i.e

$\frac{dS}{dt} = \frac{dL}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$

(S, L, I, R) = (W, X, Y, Z)

Then the system of equations becomes,

From equations (3.1) to (3.4)

$\beta N - \frac{\propto WY}{N} + eZ - \mu W = 0$ (3.8)

$\frac{\propto WY}{N} - K_1 X = 0$ (3.9)

$\delta X - K_2 Y = 0$ (3.10)

$\gamma Y + \tau x - K_3 Z = 0$ (3.11)

From equation (3.10)),we now solve this system of equations simultaneously to obtain:

$\delta x - k_2 Y = 0$

$\delta x = k_2 Y$ (3.12)

$X = \frac{k_2 Y}{\delta}$ (3.13)

Substitute equation (3.13) in to equation (3.9)

$\frac{\propto WY}{N} - \frac{K_{1K_2Y}}{\delta} = 0$ (3.14)

$Y(\frac{\propto W}{N} - \frac{K_{1K_2}}{\delta}) = 0$

Either $Y = 0$ or $\frac{\propto W}{N} - \frac{K_{1K_2}}{\delta} = 0$

Substitute X = 0 into equation (3.13)

Y= 0

Substitute Y = X= 0 into equation (3.11)

W= 0

$subtitute$Y= X=W= 0 into equation (3.8)

$\beta N - \mu W = 0$ (3.15)

$W = \frac{\beta N}{\mu}$ (3.16)

$E = \begin{pmatrix} W \\ X \\ Y \\ z \end{pmatrix} = \begin{pmatrix} \frac{\beta N}{\mu} \\ 0 \\ 0 \\ 0 \end{pmatrix}$ (3.17)

As the disease free equilibrium state.

3.3 BASIC REPRODUCTION NUMBER

According to Diekmann et al. (2000) and Murray (2002), the basic reproduction number is denoted by R_0 is the expected number of secondary cases produced, in a completely susceptible population by a typical infected individual. it is one of the most useful threshold parameters, which characterized mathematical problems concerning infectious diseases if R_0 <1, this implies that, on average an infected individual produces less than one new infected individual during the infectious period and the infectious can be wiped out conversely, if R >1, then each infected individual produced can be wiped out new infection, and the disease is spread in the population.

Fi=$\left[\frac{dfi}{dxj}\right]$ **and** vi=$\left[\frac{dvi}{dxj}\right]$ (3.18)

$F = \begin{bmatrix} \frac{df1}{dL} & \frac{df1}{dI} \\ \frac{df2}{dL} & \frac{df2}{dI} \end{bmatrix}$ $V = \begin{bmatrix} \frac{dv1}{dL} & \frac{dv1}{dI} \\ \frac{dv2}{dL} & \frac{dv2}{dI} \end{bmatrix}$ (3.19)

Now we recall that the system of equations in this model at equilibrium state is

$\frac{dX}{dt} = \frac{\propto WY}{N} - K_1 X$

$\frac{dY}{dt} = \delta X - K_2 Y$

$\frac{dW}{dt} = \beta N - \frac{\propto WY}{N} + eZ - \mu W$

$\frac{dZ}{dt} = \gamma Y + \tau X - K_3 Z$

From (3.18) and (3.19)

$$F_{i=}\begin{bmatrix}\propto WY\\ \overline{N}\\ 0\end{bmatrix}$$

$$\mathbf{V}i=\begin{bmatrix}K_1X\\ K_2Y-\delta X\end{bmatrix}$$

$$\text{F}=\begin{bmatrix}0 & \frac{\propto W}{N}\\ 0 & 0\end{bmatrix} \quad \& \quad \text{V}=\begin{bmatrix}K_1 & 0\\ \delta & K_2\end{bmatrix} \tag{3.20}$$

Taking the inverse of (3.20)

$$V^{-1}=\frac{1}{K_1K_2}\begin{bmatrix}K_1 & 0\\ \delta & K_2\end{bmatrix} \tag{3.21}$$

$$V^{-1} \quad = \quad \begin{bmatrix}\frac{k_1}{k_{1k_2}} & 0\\ \frac{\delta}{k_ik_2} & \frac{k_2}{k_{1k_2}}\end{bmatrix}$$

$$V^{-1}=\begin{bmatrix}\frac{k_1}{k_{1k_2}} & 0\\ \frac{\delta}{k_ik_2} & \frac{k_2}{k_{1k_2}}\end{bmatrix} = \begin{bmatrix}\frac{1}{k_2} & 0\\ \frac{\delta}{k_{1\,k_2}} & \frac{1}{k_1}\end{bmatrix}$$

$$FV^{-1}\begin{bmatrix}0 & \frac{\propto W}{N}\\ 0 & 0\end{bmatrix}\begin{bmatrix}\frac{1}{k_2} & 0\\ \frac{\delta}{k_{1\,k_2}} & \frac{1}{k_1}\end{bmatrix}=\begin{bmatrix}\frac{\propto\delta W}{Nk_{1\,k_2}} & \frac{\propto W}{Nk_2}\\ 0 & 0\end{bmatrix} \tag{3.22}$$

$$(FV^{-1}\lambda \text{I})=0$$

$$\begin{bmatrix}\frac{\propto\delta W}{Nk_{1\,k_2}} & \frac{\propto W}{Nk_2}\\ 0 & 0\end{bmatrix}—\lambda\begin{bmatrix}1 & 0\\ 0 & 1\end{bmatrix}=0 \tag{3.23}$$

$$\begin{bmatrix}\frac{\propto\delta W}{Nk_{1\,k_2}} & \frac{\propto W}{Nk_1}\\ 0 & 0\end{bmatrix}—\begin{bmatrix}\lambda & 0\\ 0 & \lambda\end{bmatrix}=0 \tag{3.24}$$

$$=\begin{bmatrix}\frac{\propto\delta W}{Nk_{1\,k_2}}-\lambda & \frac{\propto W}{Nk_1}\\ 0 & -\lambda\end{bmatrix}=0 \tag{3.25}$$

$$(—\lambda)\left(\frac{\propto\delta W}{Nk_{1\,k_2}}\right) = 0 \tag{3.26}$$

Either $\lambda_1 = 0$ or $\frac{\propto\delta W}{Nk_{1\,k_2}}-\lambda=0$

$$\rightarrow\lambda_2=\frac{\propto\delta W}{Nk_{1\,k_2}}$$

$$R_{O=}\lambda_2=\frac{\propto\delta W}{Nk_{1\,k_2}} \tag{3.27}$$

Where $k_1=\delta+\tau+\mu$

$k_2=\gamma+\mu+\psi$

$$R_{O=}\frac{\propto\delta W}{N(\delta+\tau+\mu\ \ )(\gamma+\mu+\psi)} \tag{3.28}$$

3.4 LOCAL STABILITY OF DISEASE FREE EQUILIBRIUM

We now investigate the stability of the disease free equilibrium state. To do this we examine the behavior of the model population near the equilibrium state. The characteristic equation, now recall that the system of equation from (3.8) to (3.11) in this model at equilibrium state is

$$\beta N - \frac{\propto WY}{N} + eZ - \mu W = 0 \quad (3.8)$$

$$\frac{\propto WY}{N} - K_1 X = 0 \quad (3.9)$$

$$\delta X - K_2 Y = 0 \quad (3.10)$$

$$\gamma Y + \tau X - K_3 Z = 0 \quad (3.11)$$

The Jacobian matrix of this system of equations is given by:

$$J(E) = \begin{bmatrix} \frac{-\alpha Y}{N} - \mu & 0 & -\frac{\alpha W}{N} e \\ \frac{\alpha Y}{N} & -k_1 & \frac{\alpha W}{N} 0 \\ 0 & \delta & -k_2 \\ 0 & \tau\gamma - k_3 & -k_3 \end{bmatrix}$$

The characteristic equation is obtained from Jacobian determinant with the Eigen values λ

det [J- λ I] = 0 becomes

$$\begin{bmatrix} \frac{-\alpha Y}{N} - \mu & 0 & -\frac{\alpha W}{N} e \\ \frac{\alpha Y}{N} & -k_1 & \frac{\alpha W}{N} 0 \\ 0 & \delta & -k_2 \\ 0 & \tau\gamma - k_3 & -k_3 \end{bmatrix} - \lambda \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} = 0$$

$$\begin{bmatrix} \frac{-\alpha Y}{N} - \mu & 0 & -\frac{\alpha W}{N} e \\ \frac{\alpha Y}{N} & -k_1 & \frac{\alpha W}{N} 0 \\ 0 & \delta & -k_2 \\ 0 & \tau\gamma - k_3 & -k_3 \end{bmatrix} - \begin{bmatrix} \lambda & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{bmatrix} = 0$$

$$\begin{bmatrix} -\mu - \lambda & 0 & \frac{-\alpha W}{N} & e \\ 0 & -k_1 - \lambda & \frac{\alpha W}{N} & 0 \\ 0 & \delta & -k_{2-\lambda} & 0 \\ 0 & \tau & \gamma - k_3 & -k_{3-\lambda} \end{bmatrix} = 0$$

$$-\mu - \lambda \begin{bmatrix} -k_1 - \lambda & \frac{\alpha W}{N} & 0 \\ \delta & -k_{2-\lambda} & 0 \\ \tau & \gamma - k_3 & -k_{3-\lambda} \end{bmatrix} + \left(\frac{\propto W}{N}\right) \begin{bmatrix} 0 & -k_1 - \lambda & 0 \\ 0 & \delta & 0 \\ 0 & \tau & -k_{3-\lambda} \end{bmatrix} -$$

$$e \begin{bmatrix} 0 & -k_1 - \lambda & \frac{\alpha W}{N} \\ 0 & \delta & -k_{2-\lambda} \\ 0 & \tau & \gamma - k_3 \end{bmatrix} = 0$$

$$(-\mu - \lambda)(-k_1 - \lambda) \begin{bmatrix} -k_{2-\lambda} & 0 \\ \gamma - k_3 & -k_{3-\lambda} \end{bmatrix} + (-\mu - \lambda) \left(\frac{-\propto W}{N}\right) \begin{vmatrix} \delta & 0 \\ \tau & k_3 - \lambda \end{vmatrix}$$

$+ (k_{1+}\lambda)\left(\frac{-\propto W}{N}\right)\begin{vmatrix}0 & 0\\ 0 & -k_3-\lambda\end{vmatrix} - (k_{1+}\lambda)\mathrm{e}\begin{vmatrix}0 & -k_2-\lambda\\ 0 & \gamma - k_3\end{vmatrix} - \mathrm{e}\left(\frac{-\alpha W}{N}\right)\begin{bmatrix}0 & \delta\\ 0 & \tau\end{bmatrix} = 0$

$=(-\mu-\lambda)(-k_1-\lambda)(-k_2-\lambda)(-k_3-\lambda)+(-\mu-\lambda)\left(\frac{-\alpha W}{N}\right)(\delta) - k_{3-}\lambda) = 0$

$(-\mu-\lambda)(-k_3-\lambda)\left[k_1k_2 + k_1\lambda + k_2\lambda + \lambda^{2-\frac{\alpha\delta W}{N}}\right] = 0$

Either $-\mu-\lambda = 0$

$-k_3-\lambda = 0$

OR

$\lambda^2 + (k_{1+}k_2)\lambda + k_1k_2 - \frac{\propto\delta W}{N} = 0$

$\rightarrow\lambda_1 = -\mu$

$\lambda_2 = -k_3$

This is quadratic equation

$\lambda^2 + (k_{1+}k_2)\lambda + k_1k_2 - \frac{\propto\delta W}{N} = 0$

Using the general quadratic equation

Where:

a=1

b= $k_{1+}k_2$

c = $k_1k_2 - \frac{\propto\delta W}{N}$

Substitute the values into the general quadratic equation.

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

$\lambda = \frac{-(k_{1+}k_2)\pm\sqrt{(k_{1+}k_2)^{\ 2}-4(k_{1k_2}-\frac{\alpha\delta W}{N})}}{2}$

$$\frac{-(k_1+k_2)\pm\sqrt{(k_{1+}k_2)^{\ 2}-4k_{1k_2}\left(1-\frac{\propto\delta W}{Nk_{1k_2}}\right)}}{2}$$

Where $\frac{\propto\delta W}{Nk_{1k_2}} = R_0$

$\frac{\lambda_{3\_}(k_{1+}k_2)\pm\sqrt{(k_{1+}k_{2)^2-4}k_{1k_2}(1-R_0\ )}}{2}$

$\lambda_4 = \frac{-(k_{1+}k_2)\pm\sqrt{(k_{1+}k_{2)^2-4}k_{1k_2}(1-R_0\ )}}{2} < 0$

$if\sqrt{(k_1+k_2)^2-4k_1k_2}(1-R_0) < (k_1+k_2)$

Taking the square of both sides

$(k_1+k_2)^2 - 4k_1k_2(1-R_0) < (k_1+k_2)^2$

$-4k_1k_2(1-R_0) < 0$

$1-R_0 < 0$

$1 > R_0$

$R_0 < 1$

The Jacobean stability technique requires that all Eigen values be negative for stability to hold. The above shows $\lambda_1, \lambda_2, \lambda_3$ are negative while λ_4 is negative if $R_0 < 1$. Therefore the disease free equilibrium (DFE) is locally asymptotically stable if $R_0 < 1$.

3.5 ENDEMIC EQUILIBRIUM STATE

We now state where the disease cannot be totally eradicated but remain in the population. For the disease to persist in the population, the susceptible class, the latently infected, the infectious class and the recovered class must not be zero at equilibrium state.

From equation (3.14)

$$\frac{\alpha W}{N} - \frac{k_1 k_2}{\delta} = 0$$

Multiply $\frac{N}{\alpha}$ to both sides

$$\frac{N}{\alpha} \cdot \frac{\alpha W}{N} - \frac{k_1 k_2}{\delta} \cdot \frac{N}{\alpha} = 0$$

$$W - N\frac{k_1 k_2}{\alpha\delta} = 0, W = N\frac{k_1 k_2}{\alpha\delta} \quad (3.29)$$

From equations (3.10)

$$\delta X - K_2 Y = 0$$

dividing both sides by δ

$$\frac{\delta X}{\delta} = \frac{K_2 Y}{\delta}$$

$$X = \frac{K_2 Y}{\delta} \quad (3.30)$$

Substitute $X = \frac{K_2 Y}{\delta}$ into (3.11)

$$\gamma Y + \frac{\tau K_2 Y}{\delta} - K_3 Z = 0$$

$$Z = \frac{1}{K_3}(\gamma Y + \frac{\tau K_2 Y}{\delta}) \quad (3.31)$$

Substitute equation (3.31) in to (3.8)

$$BN - \frac{\alpha W Y}{N} + \frac{e}{k_3}(\gamma Y + \frac{\tau K_2 Y}{\delta}) - \mu W = 0$$

$$\frac{-\alpha W Y}{N} + \frac{e}{K_3}\left(\gamma Y + \frac{\tau k_{2Y}}{\delta}\right) = -\beta N + \mu W \quad (3.32)$$

$$Y\left(\frac{e}{k_3} + \left(\gamma + \frac{\tau k_2}{\delta}\right) - \frac{\alpha W}{N}\right) = \mu W + \beta N$$

$$Y\left(\frac{\gamma e + \tau K_2 - \alpha W}{k_3 \delta N}\right) = \mu W + \beta N \quad (3.33)$$

Dividing through by the co-efficient of Y

$$Y = \frac{\mu W + \beta N}{\frac{\gamma e + \tau K_2 - \alpha W}{k_3 \delta N}} \quad (3.34)$$

$$Y = \frac{K_3 \delta N(\mu W + \beta N)}{\gamma e + \tau K_2 - \alpha W} \quad (3.35)$$

Now the values of W, X, Y,Z, became this.

$$\begin{pmatrix} W \\ X \\ Y \\ Z \end{pmatrix} = \begin{bmatrix} \frac{N K_1 K_2}{\alpha\delta} \\ \frac{K_2 Y}{\delta} \\ \frac{K_3 \delta N(\mu W + \beta N)}{\gamma e + \tau K_2 - \alpha W} \\ \frac{1}{k_3}(\gamma Y + \frac{\tau K_2 Y}{\delta}) \end{bmatrix} \quad (3.36)$$

As the endemic equilibrium state.

RESULT AND DISCUSSION

VARIABLES AND PARAMETER VALUES

In this chapter, we present the numerical simulation of the model equations from (3.1) to (3.4) using the defined parameters which are presented in the table (1.0) and table (1.1) shows the values of some parameters collected from Nigeria center for disease control (NCDC), in April 15, 2021 2021. We will vary the key parameters to investigate the impact of vaccination on the transmission dynamics of coronavirus using pictorial representation (Graphs obtained from the tables).

TABLE 1.0: SHOWING THE VALUES OF PARAMETERS WHICH ARE PRESENTED BELOW

S/N	parameter	meaning	Values	Source(s)
1	β	Rate of infection	1.55	Ndairou et al (2020)
2	α	Rate of contraction	1.66	Ndairou et al (2020)
3	δ	Latent to infectious rate	0.25	Ndairou et al (2020)
4	μ	Removed rate	0.27	Ndairou et al (2020)
5	γ	Isolated patient's rate	0.5	Ndairou et al (2020)
6	e	Removed to infected	0.58	Ndairou et al (2020)
7	τ	Successful recovery	0.27	Ndairou et al (2020)
8	Ψ	rate of death contraction	0.26	Ndairou et al (2020)
9	N	Estimated No of pop,	5000	Asssumed

The chapter also present the data retrieved the Nigeria center for the disease control (NCDC) , for a period of ten weeks. Starting from the day an index case was recorded in Nigeria to 2nd may 2020.

TABLE 1.1: TO SHOWS THE DATA FOR THE SUSCEPTIBLE, LATENTLY INFECTED, INFECTIOUS, REMOVED (death/ recovered) PEOPLE AND TIME PERIOD FOR CORONAVIRUS (COVID19).

Time/week	1	2	3	4	5	6	7	8	9	10
Susceptible	5	219	48	133	97	214	238	542	918	918
Latent	19	28	15	97	24	17	13	49	7	34

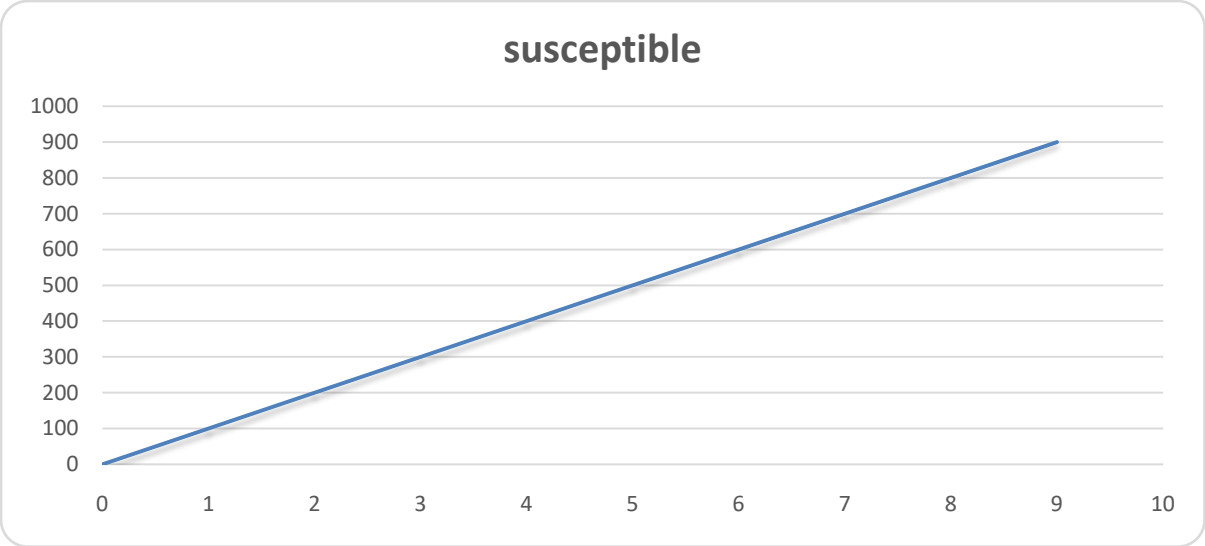
Infectious	1	23	46	25	93	185	318	357	357	220
removed	0	0	6	23	3	25	70	166	166	385

From table 1.1 data were analyzed each with varying figures depending on the time and its correspondent from either the susceptible, latently infected, infectious or the removed population.

TABLE 1.2: SHOWS THE TABLE OF SUSCEPTIBLE AGAINST TIME.

Time/week	1	2	3	4	5	6	7	8	9	10
Susceptible	5	219	48	133	97	214	238	542	981	918

FIGURE 1.1: SHOWS THE GRAPH OF SUSCEPTIBLE AGAINST TIME.



Time (weeks)

However, the table 1.2 and the above figure 1.1 the susceptible population against time with infection rate, shows that the susceptible population increases with time due to the fact that virus does not confer permanent recovery and recovered individuals may likely be re-infected. And also shows the effect of varying infection rate on the population of susceptible. The figure shows the little change in the number of susceptible over time.

From the model 3.1, we now solve for the susceptible individuals for the period of ten weeks to get another results.
From equation (3.1)
$\frac{dS}{dt} = \beta N - \frac{\alpha SI}{N} + eR - \mu S$
By Separation of Variables
$dS = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) dt$
Now we integrate both sides

$$\int dS = \int \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) dt$$

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right)$ (4.1)

When t = 1

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

$S(1) = \left(2.55 - \frac{1.96\times5\times1}{5000} + 0.580 \times 0 - 0.27 \times 1\right) 1$

= (2.55+0.00196+0.58 – 0.27 +) 1

= 2.9

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

When t=2

$S(2) = \left(2.55 - \frac{1.96\times219\times23}{5000} + 0.580 \times 0 - 0.27 \times 219\right) 2$

= (2.55-1.97+0.580×0-0.27×219) 2

= (2.55 – 1.97 + 0 – 58.55)2

= (0.58 – 58.55)2

= -115.94

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

When t = 3

$S(3) = \left(2.55 - \frac{1.96\times48\times46}{5000} + 0.580 \times 6 - 0.27 \times 48\right) 3$

= (2.55-0.87+3.48-12.96)3

=(1.68-9.48)3

= -7.8×3

= -23.4

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

When t =4

$S(3) = \left(2.55 - \frac{1.96\times133\times25}{5000} + 0.580 \times 23 - 0.27 \times 133\right)4$

=(2.55 – 1.3 + 13.4 – 35.9)4

=(1.3 - 22.5)4

= - 0.21.2×4

= - 84.8

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

When t =5

$S(5) = \left(2.55 - \frac{1.96\times93\times97}{5000} + 0.580 \times 3 - 0.27 \times 97\right) 5$

=(2.55 – 5.04 – 26.2)5

=(- 2.5-26.2)5

= - 28.69×5

= - 143.45

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

when t =6

$S(6) = \left(2.55 - \frac{1.96\times214\times185}{5000} + 0.580 \times 25 - 0.27 \times 214\right) 6$

= (2.55 – 15.5 +1 4.5 –5 7.8)6

=(2.55 –30 -57.8)6
= 2.55-87.8×6
= - 85.25×6
-511.5

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

when t =7

$S(7) = \left(2.55 - \frac{1.96\times238\times318}{5000} + 0.580 \times 70 - 0.27 \times 238\right) 7$

= (2.55 – 29.7 + 40.6 –64.3)7
=(2.55 -70.3– 64.3)7
= 2.55-134.6×7
= - 132.05×7
=-924.35

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

when t =8

$S(8) = \left(2.55 - \frac{1.96\times542\times357}{5000} + 0.580 \times 166 - 0.27 \times 542\right) 8$

= (0.045 – 0.23 + 4.725 – 9.8)8
=(2.55 -75.8 +96.3-146 .3)8
=2.55 -318×8
= - 315.75×8
=-2526

when t =9

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

$S(9) = \left(2.55 - \frac{1.96\times542\times357}{5000} + 0.580 \times 166 - 0.27 \times 542\right) 9$

= (0.045 – 0.23 + 4.725 – 9.8)9
=(2.55 -75.8 +96.3-146 .3)9
=2.55 -318×9
= - 315.75×9
= -2841.75

when t =10

$S(t) = \left(\beta N - \frac{\alpha SI}{N} + eR - \mu S\right) t$

$S(10) = \left(2.55 - \frac{1.96\times918\times220}{5000} + 0.580 \times 385 - 0.27 \times 918\right) 10$

= (2.55 – 79.2 + 223. – 247.8)10
=(2.55 -302.5 -247.8)10
=-547.75×10
= - 5477.5
= -5477.5

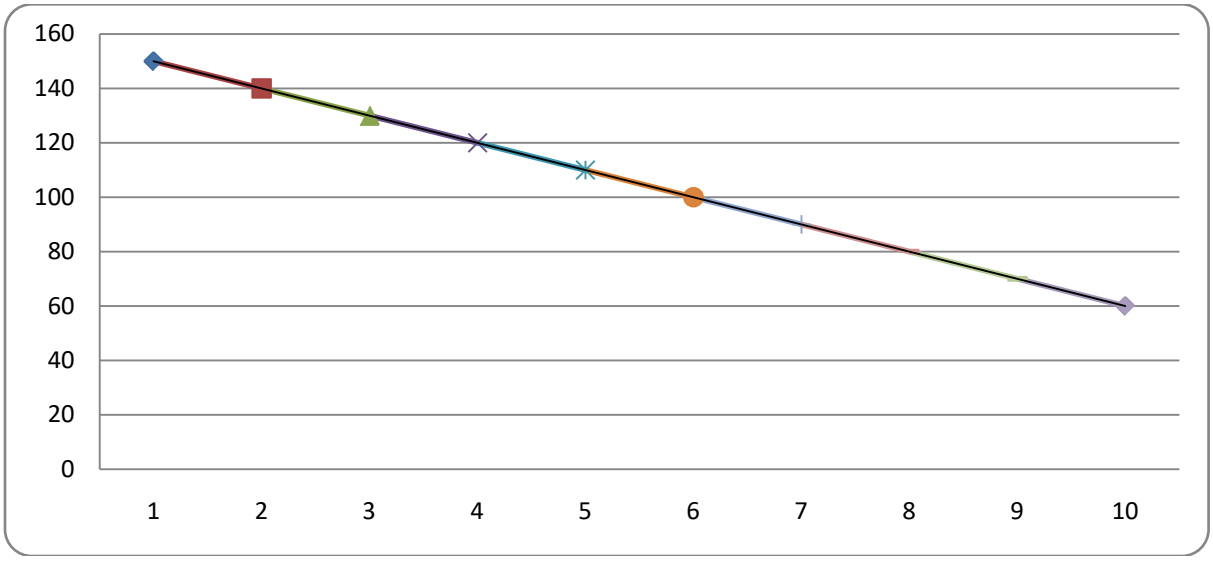
This shows that, ≈ - 5478 people will be susceptible to the virus in the period of ten weeks.
Also based on the values we got from the above solution, we can see that at the initial week of infection of the virus in Nigeria, that is week (1) the values is positive value showing that, people have only comply with the government directives for the containment the virus. Thus, susceptible individuals are stable. And also after one week that is from (2,3, 4,...) is negative

values, is also to shows that the susceptible individuals are mingling in the community, resulting that the containment of the virus is not at a stable state.

TABLE 1.3: SHOWS THE TABLE OF LATENTLY INFECTED AGAINST TIME.

Time/week	1	2	3	4	5	6	7	8	9	10
Latent	19	2	5	4	7	5	13	49	7	34

FIGURE 1.2: SHOWS THE GRAPH OF LATENTLY INFECTED AGAINST TIME.



Time (weeks)

From table 1.3, based on figure 1.2, the population of latently infected against time with infection rate to shows that the population of latently infected decreases with time due to progression to infected compartment. Then shows the effect of varying infection rate on the population of the latently infected due to treatment.

From the model 3.2, we now solve for the latently infected individuals for the period of ten weeks to get the results.

From equation (3.2)

$$\frac{dL}{dt} = \frac{\alpha SI}{N} - (\delta + \tau + \mu)L$$

$$dL = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right) dt$$

We now integrate both sides

$$\int dL = \int \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right) dt$$

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$ (4.2)

When t = 1

$= \left(\frac{1.96\times5\times1}{5000} - (0.25 + 0.27 + 0.27)19\right)1$

$=0.00196 - 15.01 \times 1$

$= -15.002$

When t= 2

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$

At t = 2

$= \left(\frac{1.96\times219\times23}{5000} - (0.25 + 0.27 + 0.27)2\right)2$

$=1.97 - 1.58 \times 2$

$= 0.78$

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$

When t = 3

$= (\frac{1.96\times48\times46}{5000} - (0.25 + 0.27 + 0.27)2)3$

$=(0.87 - 2.37) \times3$

$=-4.5$

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$

When t = 4

$= \left(\frac{1.96\times133\times25}{5000} - (0.25 + 0.27 + 0.27)5\right)4$

$= 1.3 - 3.95. \times4$

$=-10.6$

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$

When t = 5

$= \left(\frac{1.96\times97\times93}{5000} - (0.25 + 0.27 + 0.27)7\right)5$

$= 3.5 - 5.53 \times5$

$=10.15$

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$

When t = 6

$= \left(\frac{1.96\times214\times185}{5000} - (0.25 + 0.27 + 0.27)5\right)6$

$= 15.5 - 3.9 \times6$

$=69.6$

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$

When t = 7

$= \left(\frac{1.96\times238\times318}{5000} - (0.25 + 0.27 + 0.27)13\right)7$

$= 29.7 - 10.3 \times7$

$=135.1$

$L(t) = \left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)t$

When t = 8

$= \left(\frac{1.96\times542\times357}{5000} - (0.25 + 0.27 + 0.27)49\right)8$

=75 .8 – 38.7 ×8

=328.8

L(t) = $\left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)$t

When t = 9

$= \left(\frac{1.96\times542\times357}{5000} - (0.25 + 0.27 + 0.27)7\right)9$

=75.8 – 5.5 ×9

=632.7

L(t) = $\left(\frac{\alpha SI}{N} - (\delta + \tau + \mu)L\right)$t

When t = 10

$= \left(\frac{1.96\times918\times220}{5000} - (0.25 + 0.27 + 0.27)34\right)10$

= 79.2 – 26.8 ×10

= 524

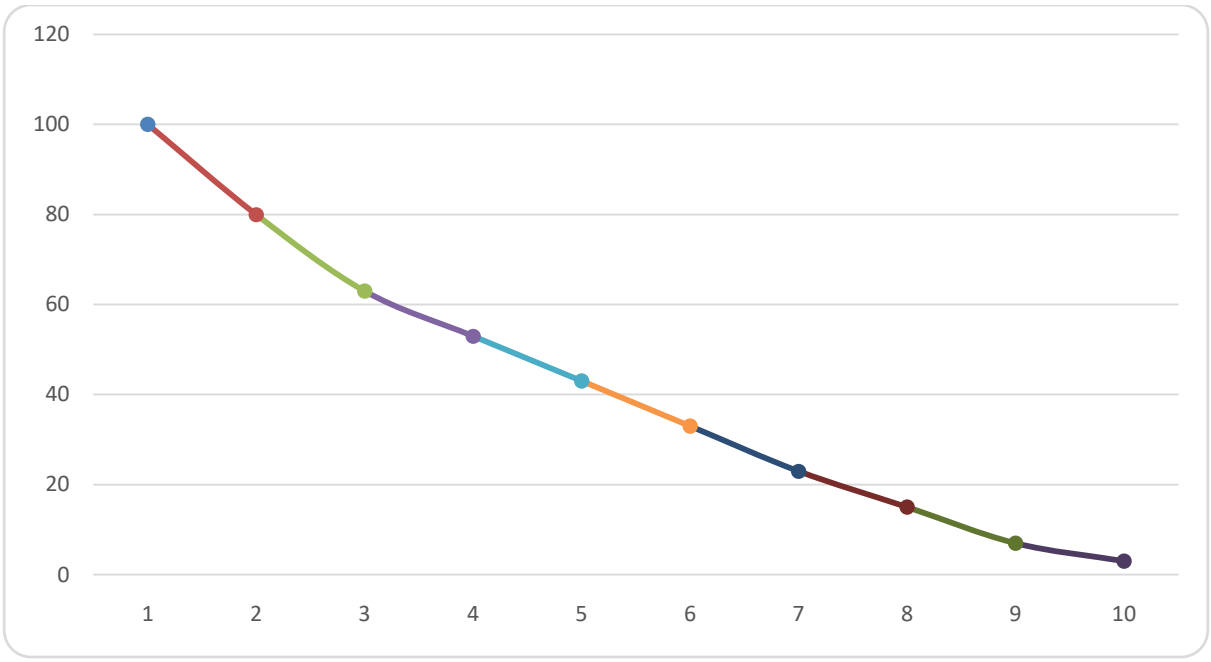
This shows that, ≈ 524 people will be infected with the virus, but will not show any symptoms for the period of ten weeks.

The results we obtained from the latently infected has a special character which increases from some weeks, but later starts to decrease with the time due to some non-pharmaceutical measures put in place before the finding of vaccine.

TABLE 1.4: SHOWS THE TABLE OF INFECTIOUS AGANIST TIME.

Time/week	1	2	3	4	5	6	7	8	9	10
Infectious	1	23	46	25	93	185	318	357	357	220

FIGURE 1.3: THE GRAPH OF INFECTIOUS AGAINST TIME.



Time (week)

Hence from figure 1.3, graph infectious to undergoing treatment against time with infection rate, that shows the population of infected individual's increases due to increase in the reproduction number of the virus, lack of vaccination and adhering to the non-pharmaceutical intervention(which include; social and physical distancing, wearing of face mask, regular washing of hands with soap and water etc.). And progression to recovered compartment. And also shows the effect of varying treatment rate on the population of infected individuals. The figure show that infected population started to decreases toward zero because of effective reproduction number being less than 1 and since infected individual's progress in the class of those that undergoing treatment

From the model 3.3, we now solve for the infectious individuals for the period of ten weeks to get the results.
From equation (3.3)

$$\frac{dI}{dt} = \delta L - (\gamma + \mu + \Psi)I$$

$dI = (\delta L - (\gamma + \mu + \Psi)I)dt$

$$\int dI = \int (\delta L - (\gamma + \mu + \Psi)I)\, dt$$

$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$ (4.3)

At t =1

$I(1) = (0.25 \times 19 - (0.5 + 0.27 + 1.0)1)1$

$= 0.25 \times 19 - (0.5 + 0.27 + 1.0)\ 1$

$= 4.75 - 0.135 \times 1$

$= 1.254 \times 1$

$= 4.62$

$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$

At t =2

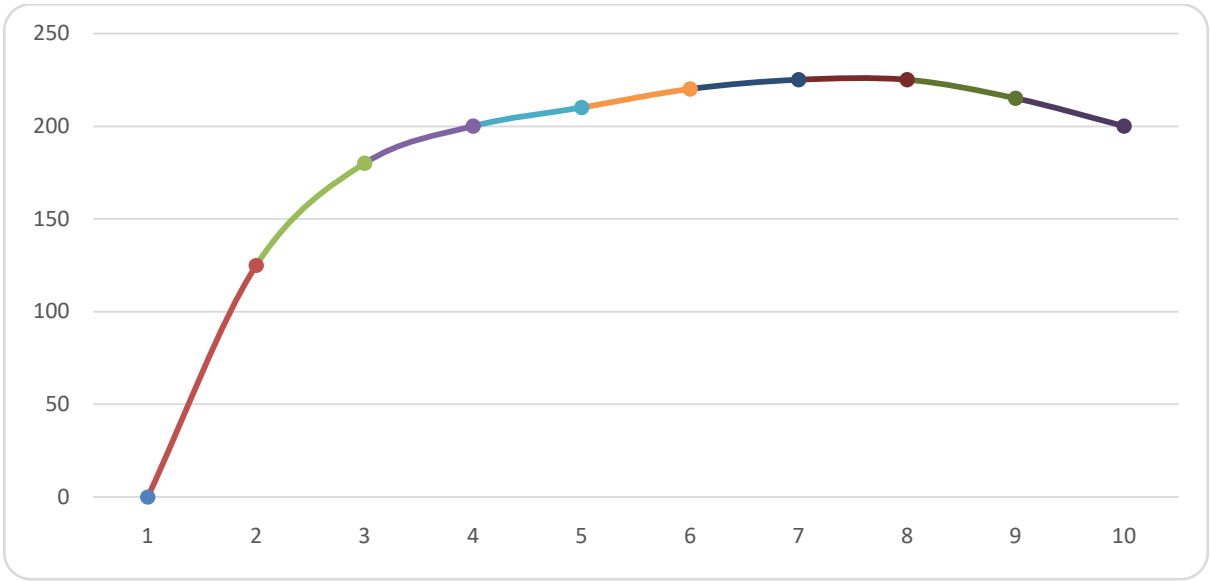
$I(2) = (0.25 \times 2 - (0.5 + 0.27 + 1.0)23)2$
$= (0.25 \times 2 - (0.23 + 0.014 + 0.002)23)2$
$= 0.5 - 3.105 \times 2$
$= 2.605 \times 2$
$= 5.21$
$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$
At t =3
$I(3) = (0.25 \times 5 - (0.5 + 0.27 + 1.0)46)3$
$= 0.25 \times 5 - (0.5 + 0.27 + 1.0)46)3$
$= 1.3 - 6.21 \times 3$
$= -4.91 \times 3$
$= -14.73$
$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$
At t =4
$I(4) = (0.25 \times 24 - (0.5 + 0.27 + 1.0)25)4$
$= 0.25 \times 24 - (0.25 + 0.27 + 1.0)25)4$
$= 6.0 - 3.375 \times 4$
$= 3.625 \times 4$
$= 10.5$
$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$
At t =5
$I(5) = (0.25 \times 7 - (0.5 + 0.27 + 1.0)93)5$
$= 0.25 \times 7 - (0.25 + 0.27 + 1.0)93)5$
$= 1.74 - 12.56 \times 5$
$= -10.8 \times 5$
$= -54.05$
$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$
At t =6
$I(6) = (0.25 \times 5 - (0.5 + 0.27 + 1.0)185)6$
$= 0.25 \times 5 - (0.25 + 0.27 + 1.0)185)6$
$= 1.25 - 24.97 \times 6$
$= -23.72 \times 6$
$= -142.32$
$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$
At t =7
$I(7) = (0.25 \times 13 - (0.5 + 0.27 + 1.0)318)7$
$= 0.25 \times 13 - (0.25 + 0.27 + 1.0)318)7$
$= 3.25 - 42.93 \times 7$
$= -39.68 \times 7$
$= -277.76$
$I(t) = (\delta L - (\gamma + \mu + \Psi)I)t$
At t =8
$I(8) = (0.25 \times 49 - (0.5 + 0.27 + 1.0)357)8$
$= 0.25 \times 49 - (0.25 + 0.27 + 1.0)357)8$
$= 12.25 - 48.2 \times 8$
$= -35.95 \times 8$

= 287.6
I(t) = $(\delta L - (\gamma + \mu + \Psi)I)t$
At t =9
I(9) = $(0.25 \times 7 - (0.5 + 0.27 + 1.0)357)9$
= 0.25× 7 – (0.25+ 0.27 + 1.0)357)9
= 1.75 – 48.2 × 9
= -46.5×9
= -418.05
I(t) = $(\delta L - (\gamma + \mu + \Psi)I)t$
At t =10
I(10) = $(0.25 \times 34 - (0.5 + 0.27 + 1.0)220)10$
= 0.25× 34– (0.25+ 0.27 + 1.0)220)10
= 8.5 – 29.7 × 10
=-21.2×10
=-212
This shows that, ≈ 200 people will be infected with the virus, and they will show visible symptoms of the virus within the period of ten weeks.
From the above model we use the values we obtain to show the effect of varying treatment rate on the population infected individuals and their progression to recovered compartment. The infected individuals are isolated in a safer area (isolation centers) to prevent further transmission of the virus.

TABLE 1.5: SHOWS THE TABLE OF RECOVERED AGAINST TIME.

Time/week	1	2	3	4	5	6	7	8	9	10
Removed	0	0	6	23	30	25	70	166	166	385

FIGURE 1.4: THE GRAPH OF RECOVERED AGAINST TIME.



Time (weeks)

However, from table 1.5, based on Figure 1.4, graph of recovered individuals against time with infection rate, shows an increase in the population of recovered individuals after a while and then a decrease due to progression to the susceptible compartment. And also shows the effect of varying treatment rate on the population of infected individuals. The population of infected individuals increases for a while and then decrease after some time since the effective reproduction number is less than 1 and since individuals undergoing treatment progress later to susceptible class.

From the model 3.4, we now solve for the recovered individuals for the period of ten weeks to get the results.

From equation (3.4)

$\frac{dR}{dt} = \gamma I + \tau L - (e + \mu) R$

$dR = (\gamma I + \tau L - (e + \mu)R)dt$

Net, we integrate both sides

$$\int dR = \int (\gamma I + \tau L - (e + \mu)R)dt$$

$R(t) = (\gamma I + \tau L - (e + \mu)R)t$ (4.4)

When t = 1

$R(1) = R(t) = (\gamma I + \tau L - (e + \mu)R)t\ 1$

= (0.5+5.13 – (0.1665)0)1

= 5.61

$R(t) = (\gamma I + \tau L - (e + \mu)R)t$

When t= 2

$R(2) = (0.5 \times 23 + 0.27 \times 2 - (0.580 + 0.27)0)2$

= (11.5+0.54 – 0)2

= (11.54)2

=23.08

$R(t) = (\gamma I + \tau L - (e + \mu)R)t$

When t= 3

$R(3) = (0.5 \times 46 + 0.27 \times 5 - (0.580 + 0.27)46)3$

=(23+1.35-39.1)3

=(24.35-39.1)3

= (-14.75)3

= -44.25

$R(t) = (\gamma I + \tau L - (e + \mu)R)t$

When t= 4

$R(4) = (0.5 \times 25 + 0.27 \times 24 - (0.580 + 0.27)23)5$

=(12.5+6.48-19.55)4

=(-0.57)4

=-2.28

$R(t) = (\gamma I + \tau L - (e + \mu)R)t$

When t= 5

$R(5) = (0.5 \times 93 + 0.27 \times 7 - (0.580 + 0.27)3)5$

= (46.5+1.89-2.55)5

= (48.39-2.55)5

= (45.84)5
=229.2
R (t) = $(\gamma I + \tau L - (e + \mu)R)t$
When t= 6
R (6) = $(0.5 \times 185 + 0.27 \times 5 - (0.580 + 0.27)25)6$
=(92.5+1.35-21.25)6
= (93.85-21.25)6
= (72.6)6
=435.6
R (t) = $(\gamma I + \tau L - (e + \mu)R)t$
When t= 7
R (7) = $(0.5 \times 318 + 0.27 \times 13 - (0.580 + 0.27)70)7$
=(159+3.51-59.5)7
= (162.51-21.25)7
= (141.26)7
= 988.8
R (t) = $(\gamma I + \tau L - (e + \mu)R)t$
When t= 8
R (8) = $(0.5 \times 357 + 0.27 \times 49 - (0.580 + 0.27)166)8$
=(178.5+13.23-141.1)8
= (191.73-141.1)8
= (50.6)8
= 505.04
R (t) = $(\gamma I + \tau L - (e + \mu)R)t$
When t= 9
R (9) = $(0.5 \times 357 + 0.27 \times 7 - (0.580 + 0.27)166)9$
=(92.5+1.89-21.25)9
= (94.39-21.25)9
= (73.14)9
= 658.26
R (t) = $(\gamma I + \tau L - (e + \mu)R)t$
When t= 10
R (10) = $(0.5 \times 220 + 0.27 \times 34 - (0.580 + 0.27)385)10$
=(110+9.18-327.25)10
= (119.18-327.25)10
= (-208.07)10
= -2080.7
This shows that, ≈ 2080 people will recover from the virus if undergone treatment while adhering to all the non-pharmaceutical measures for the period of 10 weeks.
According to the values obtained in this model we can see that the population of infected individuals increases for almost ten weeks under consideration. This is due the high contraction of the virus and lack of approved vaccine.

SUMMARY, CONCLUSION AND RECOMMENDATION

SUMMARY

In this study, we modeled the effect of varying infection rate and treatment on the transmission dynamics of coronavirus disease (covid19). The disease free equilibrium state and the endemic equilibrium state of the model were obtained, the basic reproduction number, (R_0) was derived and the analysis showed that covid19 can effectively be curtailed or even be contained if effort is made to ensure that latently infected individuals are detected, and ensuring proper isolation of infected individuals appropriately. In the absence of vaccine following the non-pharmaceutical measure is of tremendous important in curtailing the virus. This includes hand washing regularly, wearing of face mask, observing social and physical distancing among others.

CONCLUSION

The existence of the disease free equilibrium state implies that there is possibility of complete total eradication of coronavirus (covid19) from Nigeria. The negativity of all the eigenvalues arising from the stability analysis carried out in chapter three shows that there will be no return of the coronavirus 9covid190 pandemic after eradication from Nigeria. The existence of the endemic equilibrium state in chapter three signifies the possibility of Nigeria to continue recording cases of the virus and if vaccine is not approved, it will be an epicenter in the region or an endemic nation.

RECOMMENDATION

The incidence of coronavirus in 2020 and beyond, can greatly be minimized or possibly be eradicated in Nigeria or any population if effort is made to ensure that the endemic equilibrium of this model is never stable. That is if $R_0<1$, this can be achieved if the following recommendations are considered.

1. There should be more enlightenment campaign on the dangers of coronavirus and on its symptoms to the public.
2. More effort should be made to encourage people to voluntarily go for civid19 tests by discouraging stigmatization of people infected by the virus.
3. Covid19 tests and treatment should continue to be free of charge to enable poor people assess them and in all public and private health centers.
4. People should be educated on the mode of transmission of the virus, and on home care strategies for people infected by the virus before going to hospital.
5. The conditions that promote rapid spread of covid19 should be discouraged. Such conditions include: overcrowded accommodation, high level of illiteracy, lack or inadequate medical facilities, vanning of traveling to the highly infected countries.
6. There should be provision of more trained personnel and more covid19 test centers in the country.
7. Non-pharmaceutical measures (hand washing regularly with soap and water, using alcohol based sanitizers, observing social and physical distancing etc.) Should also be practice and ensure adequate compliance to them.

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