



Stability of Covid-19 Dynamics: A Case Study of Nigeria

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Abstract:

In this paper, a SEIR epidemic model is considered; where individuals in the population are assigned to different compartments of SEIR defined with respect to epidemic status of Covid-19 in Nigeria. The article has demonstrated a simple mathematical model for the transmission of Covid-19 disease taking into account loss of human immunity with the aim that this model proves useful in controlling the possibility of a person contracting Covid-19 twice. When the basic reproduction number means that the Covid-19 free equilibrium solution is locally asymptotically stable. This suggests that the number of new cases of the disease will decrease over time and eventually will vanish as that which causes are established. The basic reproduction number and the model analysis (local stability of disease-free equilibrium and disease-endemic equilibrium) of the system were calculated and the stability of the SEIR model was checked.

Keywords:

SEIR model; basic reproduction number; covid-19 parameters; stability analysis.

I. Introduction

The globe has experienced Covid-19 (Corona virus disease 2019), the fifth pandemic since the 1918 flu pandemic [24]. This Viral Diseases (COVID-19) is an infectious disease with vertical transmission, the first case of which appeared towards the end of 2019 in Wuhan, China [24, 26]. This coronavirus has been linked to millions of infections worldwide and more than 2 million fatalities. The mortality rate differs from nation to nation [25]. There exist a wide variety of models that can be used to describe the evolution of an epidemic. Main standard is held by the so called compartmental models, i.e., the family of SIR based models (SIR, SEIR, SIRS, etc) [27, 28].

The dynamics of covid-19 in Nigeria is represented by the ordinary differential equations using mathematical modelling, which can be very useful in understanding the various disease spread factors and thereby formulating the best control practices [1]. The models are used to estimate numerous epidemiological parameters, including proliferative amount, and to forecast things including the way an infection transmits, overall amount of contaminated, the length of an epidemic, and many other things [2, 3]. The effective and basic reproduction number for COVID-19 dynamics in Nigeria between April 13, 2020, and May 7, 2020, was calculated by Adekunle et al. in [4] to be while Sunday et al in [5] compute in Nigeria between the February 27, 2020 to May 27, 2020. These COVID-19 symptoms and indicators may appear in people two days to two weeks after being exposed to the disease [12]. Also, it has been noted that asymptomatic people appear to make up 40% to 45% approximation of Covid-19 infestations, and this group of people can spread the virus for a protracted period of time [13]. As a result, we include this group of people in the exposed individuals. There are many different versions of the SEIR model, and with control strategies, for example, in [14],[15], [16] and [17], they computed the number of infected, recovered, and

dead individuals based on the number of contacts, probability of disease transmission, incubation period, recovery rate, and fatality rate. In this work, we are interested in the study of a continuous model of a vertically transmitted disease, a Susceptible, Exposed Infectious and Recovered (SEIR), spread model. In [21, 22, 23], the authors formulated and studied mathematical models giving the dynamics of the transmission of infectious diseases. They study the stability of steady states when the basic reproduction rate R_0 is less than one and greater than one. Also, they study the impact of quarantine on the dynamics of infectious disease transmission (this method is extensively applied to the outbreak of Corona Virus Diseases 2019 (COVID-19)).

The control techniques (hand sanitizer usage, COVID-19 patient treatment, and active screening with testing and prevention against recurrence and reinfection of persons who have recovered from COVID-19) must be carefully implemented if COVID-19 is to be successfully eradicated in Nigeria [18]. The incidence of reinfection and recurrence in persons who have recovered from COVID-19 will be determined in this investigation. An epidemiological model predicts that the Covid-19 virus's rates of transmission, recovery, and loss of immunity will change over time and depend on a variety of variables, including the seasonality of pneumonia, mobility, testing rates, capital weather [19], social behaviours, and strain-specific factors [20].

II. Reserach Methods

Following the previous models, the relevant compartments for the dynamics of Covid-19 in Nigeria are integrated into a general SEIR model. The population is divided into four compartments: susceptible (S), exposed (E), infectious (I) and cured (R). Transmission of the disease is thought to occur only when susceptible individuals come into contact with infectious individuals.

2.1 Properties of the Model

This work modifies the compartmental epidemiological Susceptible-Infectious-Removed (SIR) model [6] to Susceptible-Exposed-Infectious-Removed (SEIR) model that describes the spread of Covid-19 in Nigeria. The population under study is divided into Susceptible, S , Exposed, E , Infected, I , and Recovered, R , respectively, through a dynamical system. The name of these compartments represents the state variables or the number of people in each compartment at time t . Thus, $S(t)$, $E(t)$, $I(t)$ and $R(t)$ denote the susceptible, exposed, infectious and recovered population at time t . The four compartments make up the entire population of the country.

2.2 Mathematical Formulation of the Model

In this model the total population size, N , is considered closed as birth and death (death induced by the virus) rates are assumed equal. The total population is divided into four classes as shown below with Susceptible (S), Exposed (E), Infected (I) and Recovered (R) compartments. The incidence rate $\frac{\alpha_1 SI}{N}$, where $\alpha_1 I$ measures the infecting force of Covid-19 infection. The model diagram is shown below.

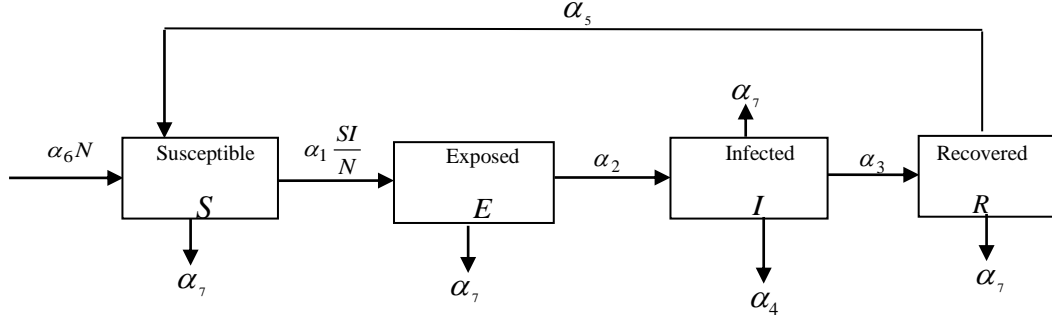


Figure 1. Model diagram for the five compartments

The susceptible people (S) will move to the exposed compartment (E) updating the number of exposed person to $a_1 SI$. Out of this exposed ones, $a_2 E$ individuals will move from E compartment to the infectious compartment (I). From the infectious compartment, $a_3 I$ persons move to the recovery group while $a_4 I$ persons die of the disease.

Table 1. Summary of Parameters and meaning

Parameters	Meaning
α_1	Disease transmission rate
α_2	Progression rate
α_3	Recovery rate
α_4	Disease induced death rate
α_5	Immunity rate
α_6	Birth rate
α_7	Natural death rate

The total number of fixed people in the population at time t is given by $N = S(t) + E(t) + I(t) + R(t)$. The initial values of $S(t)$, $E(t)$, $I(t)$ and $R(t)$ are denoted by S_0 , E_0 , I_0 and R_0 respectively.

2.3 Covid-19 SEIR Model equations

Using the model diagram, we derived the following system of ordinary differential equations.

$$\begin{aligned}\frac{dS}{dt} &= \alpha_6 N - \alpha_1 \frac{SI}{N} + \alpha_5 R - \alpha_7 S, \\ \frac{dE}{dt} &= \alpha_1 \frac{SI}{N} - (\alpha_2 + \alpha_7) E, \\ \frac{dI}{dt} &= \alpha_2 E - (\alpha_3 + \alpha_4 + \alpha_7) I, \\ \frac{dR}{dt} &= \alpha_3 I - (\alpha_5 + \alpha_7) R.\end{aligned}$$

The dead people per unit time is given by $\frac{dD}{dt} = -\frac{dN(t)}{dt} = \alpha_4 I$; $D(0) \geq 0$ using the assumption that $\alpha_6 = \alpha_7$.

Considering the varying population, $N(t)$, and the proportions of each compartment of individuals in the population namely $s = S/N$, $e = E/N$, $i = I/N$, and $r = R/N$

We obtain the state variables s, e, i , and r . These variables satisfy the following system of differential equations.

$$\frac{ds}{dt} = \alpha_6 - \alpha_1 si + \alpha_5 r - \alpha_7 s,$$

1

$$\frac{de}{dt} = \alpha_1 si - (\alpha_2 + \alpha_7) e,$$

2

$$\frac{di}{dt} = \alpha_2 e - (\alpha_3 + \alpha_4 + \alpha_7) i,$$

3

$$\frac{dr}{dt} = \alpha_3 i - (\alpha_5 + \alpha_7) r.$$

4

Here, $N(t) = s(t) + e(t) + i(t) + r(t) = 1$ for all $t \in [0, T]$ and T is the total time of investigation. It follows that $\frac{ds}{dt} + \frac{de}{dt} + \frac{di}{dt} + \frac{dr}{dt} = \alpha_6 - \alpha_7(s + e + i + r) = \alpha_6 - \alpha_7 N(t)$.

It follows that the death induced by covi-19 is given as:

$$\frac{dd}{dt} = \alpha_3 I$$

Table 2. Fractions of the population

Compartment	Description
s	Fraction of population that are susceptible
e	Fraction of population that are exposed
i	Fraction of population that are infectious
r	Fraction of population that recovered

It is assumed that all the state variables and parameters are positive and no pre-existing immunity.

2.4 Covid-19 SEIR Model Analysis

To find the feasible region of the model (1 – 4), the following theorem is adopted in the study.

Theorem 1: let $s_0 > 0$, $e_0 \geq 0$, $i_0 \geq 0$, $r_0 \geq 0$. Then the solutions $s(t)$, $e(t)$, $i(t)$, $r(t)$ of the model will remain non-negative for all time $t > 0$.

Proof Since the equation on the right-hand side of the model (1) – (4) is a continuous smooth function on $R^4 = \{s(t), i(t), e(t), r(t) : s(0) > 0, e(0) \geq 0, i(t) \geq 0, r(t) \geq 0\}$, for $t \geq 0$.

It can be seen from equation (1) that.

$$\frac{ds}{dt} = \alpha_6 - (\alpha_1 i + \alpha_7) s + \alpha_5 r, \quad \frac{ds}{s(t)} = \left(\frac{\alpha_6 + \alpha_5 r}{s(t)} - (\alpha_1 i(t) + \alpha_7) \right) dt$$

$$s(t) = s(0) + e^{\int_0^t \left(\frac{1}{s(x)} (\alpha_6 - \alpha_5 r(x)) - (\alpha_1 i(x) + \alpha_7) \right) dx} > 0$$

$$e(t) = e(0) + e^{\int_0^t \left(\frac{\alpha_1 s(x) i(x)}{e(x)} - (\alpha_3 + \alpha_4 + \alpha_7) \right) dx} \geq 0 \quad 5$$

$$i(t) = i(0) + e^{\int_0^t \left(\frac{\alpha_2 e(x)}{i(x)} - (\alpha_3 + \alpha_4 + \alpha_7) \right) dx} \geq 0 \quad 7$$

$$r(t) = r(0) + e^{\int_0^t \left(\frac{\alpha_3 i(x)}{r(x)} - (\alpha_5 + \alpha_7) \right) dx} \geq 0 \quad 8$$

Therefore, the solution $s(0) > 0$, $e(0) \geq 0$, $i(t) \geq 0$, and $r(t) \geq 0$, for $t \geq 0$

Theorem 2. The model (1) – (4) of the initial condition in R_+^4 is positively invariant in

$$\phi = \{s, e, i, r\} \in R_+^4 : 0 \leq s(t) + e(t) + i(t) + r(t) \leq \frac{\alpha_6}{\alpha_7}\}$$

9

Proof

Add equations (1) – (4), yields $dN = \frac{d(s, e, i, r)}{dt} = \alpha_6 - \alpha_7 N$ then $\frac{dN}{dt} = \alpha_6 - \alpha_7 N$

It can easily be deduced that the solution of the equation by applying comparison principle is

$$N(t) = \frac{\alpha_6}{\alpha_7} + N(0)e^{(-\alpha_7 t)}, \text{ When } t \rightarrow \infty \text{ then}$$

$$N(t) \leq \frac{\alpha_6}{\alpha_7}.$$

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2.5 Determination of the Basic Reproduction Number

The basic reproduction number, R_0 , of the model is determined by employing the results of the next-generation matrix [9] and the first four differential equations. Let $x = (s, e, i, r)$, $f(x)$ be the rate of appearance of new infection and $v(x)$ be the rate of transfer of individuals from all other sources into the compartment and transfer of individuals out of the compartment. The infected compartments are only e and i then F and V are the Jacobian matrices of order 2×2 as defined as defined in Mathematical Tools for understanding Disease Dynamics [10] and the values of F and V for the new infection terms and the transmission terms are given respectively as

$$F = \begin{pmatrix} 0 & \alpha_1 \\ 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} \alpha_2 + \alpha_7 & 0 \\ -\alpha_2 & \alpha_3 + \alpha_4 + \alpha_7 \end{pmatrix}.$$

$$|V| = (\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7)$$

$$K = FV^{-1} = \begin{pmatrix} \frac{\alpha_1 \alpha_2}{(\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7)} & \frac{\alpha_1}{\alpha_7(\alpha_3)} \\ 0 & 0 \end{pmatrix}$$

Hence, the basic reproduction number R_0 for the COVID-19 model (1 – 4) is obtained by calculating the spectral radius of the matrix FV^{-1} as:

$$R_0 = \frac{\alpha_1 \alpha_2}{(\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7)}.$$

2.6 Stability Analysis of the Covid-19 Model

We note that at endemic equilibrium point,

$$s^* = \frac{(\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7)}{\alpha_1 \alpha_2} = \frac{1}{R_0} \text{ and}$$

$$i^* = \frac{\alpha_7(\alpha_2 + \alpha_7)(\alpha_1 \alpha_2 - (\alpha_2 + \alpha_7)(\phi))}{\alpha_1(\alpha_2 \alpha_4(\alpha_5 + \alpha_7) + \alpha_7(\phi)(\alpha_5 + \alpha_7) + \alpha_2 \alpha_7(\phi))} > 0;$$

$$i^* = \frac{\alpha_7(\alpha_2 + \alpha_7)(\{R_0 - 1\}(\alpha_2 + \alpha_7)(\phi))}{\alpha_1(\alpha_2 \alpha_4(\alpha_5 + \alpha_7) + \alpha_7(\phi)(\alpha_5 + \alpha_7) + \alpha_2 \alpha_7(\phi))} > 0.$$

Where $(\alpha_3 + \alpha_4 + \alpha_7) = \phi$.

We need the aid of Routh-Hurwitz stability criterion in this section: Routh-Hurwitz Stability Criterion [7]

The Routh-Hurwitz stability criterion states that for a system having a characteristic equation

$a_0 s^n + a_1 s^{n-1} + \dots + a_{n-1} s + a_n = 0$ to be asymptotically stable, all the principal minors of the matrix

$$H_n = \begin{pmatrix} a_1 & a_3 & a_5 & \dots & \dots & 0 \\ a_0 & a_2 & a_4 & \dots & \dots & 0 \\ 0 & a_1 & a_3 & a_5 & \dots & 0 \\ 0 & a_0 & a_2 & a_4 & \dots & 0 \\ 0 & 0 & a_1 & a_3 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & \dots & \dots & \dots \end{pmatrix}$$

must be positive and nonzero.

Theorem 3: When $R_0 < 1$, the Covid-19 free equilibrium ε_0 of the dynamical COVID-19 model (1 – 4) is locally asymptotically stable.

Proof: By evaluating the Jacobian matrix of the first four equations at the Covi9-19 free equilibrium point, we obtained the simplified Jacobian matrix given by

$$J(s^*, e^*, i^*, r^*) = \begin{pmatrix} -\alpha_1 i^* - \alpha_7 & 0 & -\alpha_1 s^* & \alpha_5 \\ \alpha_1 i^* & -(\alpha_2 + \alpha_7) & \alpha_1 s^* & 0 \\ 0 & \alpha_2 & -(\alpha_3 + \alpha_4 + \alpha_7) & 0 \\ 0 & 0 & \alpha_3 & -(\alpha_5 + \alpha_7) \end{pmatrix}$$

Using $i^* = 0$ and $s^* = 1$, we evaluate the characteristics equation as shown below.

$$\begin{vmatrix} -\alpha_7 - \lambda & 0 & -\alpha_1 & \alpha_5 \\ 0 & -(\alpha_2 + \alpha_7) - \lambda & \alpha_1 & 0 \\ 0 & \alpha_2 & -(\alpha_3 + \alpha_4 + \alpha_7) - \lambda & 0 \\ 0 & 0 & \alpha_3 & -\alpha_5 - \alpha_7 - \lambda \end{vmatrix} = 0$$

$$(\lambda + \alpha_7)(\lambda + \alpha_5 + \alpha_7)(\lambda^2 + \alpha_2\lambda + \alpha_3\lambda + \alpha_4\lambda + 2\alpha_7\lambda + \alpha_2\alpha_3 + \alpha_2\alpha_4 + \alpha_2\alpha_7 + \alpha_7\alpha_3 + \alpha_7\alpha_4 + \alpha_7^2 - \alpha_1\alpha_2) = 0$$

The first two roots are negative:

$$\lambda = -\alpha_7 \text{ and } \lambda = -(\alpha_5 + \alpha_7).$$

$$\lambda^2 + (\alpha_2 + \alpha_3 + \alpha_4 + 2\alpha_7)\lambda + \alpha_2\alpha_3 + \alpha_2\alpha_4 + \alpha_2\alpha_7 + \alpha_7\alpha_3 + \alpha_7\alpha_4 + \alpha_7^2 - \alpha_1\alpha_2 = 0$$

Let

$$w_0 = 1; \quad w_1 = \alpha_2 + \alpha_3 + \alpha_4 + 2\alpha_7; \\ w_2 = \alpha_2\alpha_3 + \alpha_2\alpha_4 + \alpha_2\alpha_7 + \alpha_7\alpha_3 + \alpha_7\alpha_4 + \alpha_7^2 - \alpha_1\alpha_2$$

Then, the characteristics equation at disease free equilibrium becomes

$$w_0\lambda^2 + w_1\lambda + w_2 = 0.$$

By Routh-Hurwitz criterion, we need to show that $w_1 > 0$ and $w_1w_2 > 0$. We note that $w_1 > 0$ since all the parameters are positive. $w_1w_2 > 0$ implies that $w_2 > 0$. Thus,

$$w_2 = (\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7) - \alpha_1\alpha_2 > 0 \\ (\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7) > \alpha_1\alpha_2. \\ 1 > \frac{\alpha_1\alpha_2}{(\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7)} = R_0.$$

Hence, $w_2 > 0$ whenever $R_0 < 1$.

By Routh-Hurwitz criterion, we conclude that the SEIR model is locally asymptotically stable if $R_0 < 1$.

2.7 Global Stability of Covid-19 free Equilibrium

To obtain the conditions for the global stability for ε_0 , we employed the approach presented in [8], which states that the SEIR system model can be written as

$$\frac{dX}{dt} = F(X, Z) \\ \frac{dZ}{dt} = G(X, Z), G(X, 0) = 0$$

Where $X \in R^n$ represent the uninfected individuals and $Z \in R^m$ describes the infected individuals. According to this notation, the Covid-19-free equilibrium is given by $Q_0 = (X_0, 0)$. Now, the following two conditions guarantee the global stability of the Covid-19 free equilibrium.

$P_1 : \frac{dX}{dt} F(X, 0), X_0$ is globally asymptotically stable

$P_1 : G(X, Z) = BZ - \hat{G}(X, Z)$, where $\hat{G}(X, Z) \geq 0$ for $X, Z \in \Omega$

Lemma 1: The equilibrium point $Q_0 = (X_0, 0)$ is globally asymptotically stable when $R_0 \leq 1$ and assumptions P_1 and P_2 are satisfied

Theorem 4: The DFE point ε_0 is globally asymptotically stable provided $R_0 \leq 1$. Proof

$$F(X,0) = \begin{bmatrix} \alpha_6 - \alpha_7 s + \alpha_5 r \\ -(\alpha_5 + \alpha_7)r \end{bmatrix}$$

$$|J_{F(X,0)} - I\lambda| = \begin{bmatrix} -\alpha_7 & \alpha_5 \\ 0 & -(\alpha_5 + \alpha_7) \end{bmatrix}$$

The characteristic polynomial of $J_{F(X,0)}$ is:

$$(-\alpha_7 - \lambda)(-\alpha_5 + \alpha_7) - \lambda = 0$$

$$\lambda_1 = -\alpha_7, \text{ and } \lambda_2 = -(\alpha_5 + \alpha_7)$$

Therefore, $X = X_0$ is globally asymptotically stable

Then,

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

We have

$$G(X,Z) = \begin{bmatrix} -(\alpha_2 + \alpha_7) & \alpha_1 s \\ \alpha_2 & -(\alpha_3 + \alpha_4 + \alpha_7) \end{bmatrix} \begin{bmatrix} e \\ i \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

Hence, it can be seen that B satisfies all conditions explained in P_2 .

Theorem 4. The endemic equilibrium point of the COVID-19 model (1 - 4) is locally asymptotically stable when $R_0 > 1$.

Proof: The Jacobian matrix evaluated at $\varepsilon_* = (s^*, e^*, i^*, r^*)$ is denoted by

$$J(s^*, e^*, i^*, r^*) = \begin{pmatrix} -\alpha_1 i^* - \alpha_7 & 0 & -\alpha_1 s^* & \alpha_5 \\ \alpha_1 i^* & -(\alpha_2 + \alpha_7) & \alpha_1 s^* & 0 \\ 0 & \alpha_2 & -(\alpha_3 + \alpha_4 + \alpha_7) & 0 \\ 0 & 0 & \alpha_3 & -(\alpha_5 + \alpha_7) \end{pmatrix}$$

Then, we solve

$$\begin{vmatrix} -\alpha_1 i^* - \alpha_7 - \lambda & 0 & -\alpha_1 s^* & \alpha_5 \\ \alpha_1 i^* & -(\alpha_2 + \alpha_7) - \lambda & \alpha_1 s^* & 0 \\ 0 & \alpha_2 & -(\alpha_3 + \alpha_4 + \alpha_7) - \lambda & 0 \\ 0 & 0 & \alpha_3 & -\alpha_5 - \alpha_7 - \lambda \end{vmatrix} = 0$$

Then, the characteristics equation at endemic equilibrium point becomes

$$w_0 \lambda^4 + w_1 \lambda^3 + w_2 \lambda^2 + w_3 \lambda + w_4 = 0.$$

Routh-Hurwitz criterion wants us to show that $\delta_1 > 0$, $\delta_2 > 0$, $\delta_3 > 0$ and $\delta_4 > 0$ using

$$H_4 = \begin{pmatrix} w_1 & w_3 & 0 & 0 \\ w_0 & w_2 & w_4 & 0 \\ 0 & w_1 & w_3 & 0 \\ 0 & w_0 & w_2 & w_4 \end{pmatrix}; \quad \delta_1 = w_1; \quad \delta_2 = \begin{vmatrix} w_1 & w_3 \\ w_0 & w_2 \end{vmatrix}, \quad \delta_3 = \begin{vmatrix} w_1 & w_3 & 0 \\ w_0 & w_2 & w_4 \\ 0 & w_1 & w_3 \end{vmatrix} \text{ and}$$

$$\delta_4 = \begin{vmatrix} w_1 & w_3 & 0 & 0 \\ w_0 & w_2 & w_4 & 0 \\ 0 & w_1 & w_3 & 0 \\ 0 & w_0 & w_2 & w_4 \end{vmatrix} = w_4 \delta_3,$$

Where $|\cdot|$ denotes determinant.

$$\begin{aligned}\delta_1 &= w_1 = \alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + 4\alpha_7 + \alpha_1 i^* \\ &= \alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + 4\alpha_7 + \alpha_1 i^* \\ \alpha_1 &\left[\frac{\alpha_7(\alpha_2 + \alpha_7)(\{R_0 - 1\}(\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7))}{\alpha_1(\alpha_2\alpha_4(\alpha_5 + \alpha_7) + \alpha_7(\alpha_3 + \alpha_4 + \alpha_7)(\alpha_5 + \alpha_7) + \alpha_2\alpha_7(\alpha_3 + \alpha_5 + \alpha_7))} \right]\end{aligned}$$

Hence, $\delta_1 > 0$ whenever $R_0 > 1$. Obviously, $\delta_1 > 0$ since all the parameters are positive, and the state variables are also positive. It follows that $\delta_2 > 0$, $\delta_3 > 0$ and $\delta_4 > 0$ whenever $R_0 > 1$ and

$$i^* = \frac{\alpha_7(\alpha_2 + \alpha_7)(R_0 - 1)(\alpha_2 + \alpha_7)(\alpha_3 + \alpha_4 + \alpha_7)}{\alpha_1(\alpha_2\alpha_4(\alpha_2 + \alpha_7) + \alpha_7(\alpha_3 + \alpha_4 + \alpha_7)(\alpha_5 + \alpha_7) + \alpha_2\alpha_7(\alpha_3 + \alpha_4 + \alpha_7))}.$$

By Routh-Hurwitz criterion, the disease endemic equilibrium point is locally asymptotically stable.

III. Results and Discussion

3.1 Parameters Values

The table below represents the values of the model parameters.

Table 3. Summary of Parameter values		
Parameters	Value	Reference
α_1	0.70746202	[5]
α_2	0.18764358	[5]
α_3	0.31817251	[5, 11]
α_4	0.002942	[5, 11]
α_5	0.00000049243	[5]
α_6	0.0001	[5]
α_7	0.0001	[5, 11]

3.2 Verification of the Stability Condition

In confirmation that the disease free equilibrium of the SEIR model is locally asymptotically stable when $R_0 < 1$, the numerical result of disease free equilibrium of the SEIR model shows that $w_1 = 0.508958 > 0$ and $w_1 * w_2 = 0.0598478 > 0$. The value of the parameters are

$$s^* = 0.4542, e^* = 0.00029, i^* = 0.00017063, r^* = 0.540238 \text{ and } d^* = 0.00501994.$$

Also, the disease endemic equilibrium of the SEIR model is locally asymptotically stable when $R_0 > 1$, so the numerical result of disease endemic equilibrium of the SEIR model shows that

$$\begin{aligned}\partial_1 &= 0.509279 > 0, & \partial_2 &= 7.596295 \times 10^{-5} > 0, & \partial_3 &= 3.650295 \times 10^{-10} > 0 & \text{and} \\ \partial_4 &= 2.657467 \times 10^{-19} > 0\end{aligned}$$

3.3 Covid-19 model with control

On introducing a control $u(t)$ which stands for the control measure, i.e, the prescribed social distancing order in Nigeria, to the system (1 – 4) as given below:

$$\begin{aligned}\frac{ds}{dt} &= \alpha_6 - (1-u)\alpha_1 si + \alpha_5 r - \alpha_7 s, \\ \frac{de}{dt} &= (1-u)\alpha_1 si - (\alpha_2 + \alpha_7)e, \\ \frac{di}{dt} &= \alpha_2 e - (\alpha_3 + \alpha_4 + \alpha_7)i, \\ \frac{dr}{dt} &= \alpha_3 i - (\alpha_5 + \alpha_7)r.\end{aligned}$$

3.4 Linearized form of the Covid-19 model

Set $x_1 = s - s^*$, $x_2 = e - e^*$, $x_3 = i - i^*$, $x_4 = r - r^*$ and $f_1 = \dot{s}$, $f_2 = \dot{e}$, $f_3 = \dot{i}$, $f_4 = \dot{r}$,

We have

$$\dot{x}_1 = x_1 \frac{\partial f_1}{\partial s} + x_2 \frac{\partial f_1}{\partial e} + x_3 \frac{\partial f_1}{\partial i} + x_4 \frac{\partial f_1}{\partial r}$$

$$\dot{x}_2 = x_1 \frac{\partial f_2}{\partial s} + x_2 \frac{\partial f_2}{\partial e} + x_3 \frac{\partial f_2}{\partial i} + x_4 \frac{\partial f_2}{\partial r}$$

$$\dot{x}_3 = x_1 \frac{\partial f_3}{\partial s} + x_2 \frac{\partial f_3}{\partial e} + x_3 \frac{\partial f_3}{\partial i} + x_4 \frac{\partial f_3}{\partial r}$$

$$\dot{x}_4 = x_1 \frac{\partial f_4}{\partial s} + x_2 \frac{\partial f_4}{\partial e} + x_3 \frac{\partial f_4}{\partial i} + x_4 \frac{\partial f_4}{\partial r}$$

$$\dot{x}_1 = \alpha_1 x_1 i^* - \alpha_7 x_1 - \alpha_1 x_3 s^* + \alpha_5 x_4 + \alpha_1 u s i$$

$$\dot{x}_2 = \alpha_1 x_1 i^* - (\alpha_2 + \alpha_7) x_2 + \alpha_1 x_3 s^* - \alpha_1 u s i$$

$$\dot{x}_3 = \alpha_2 x_2 - (\alpha_2 + \alpha_4 + \alpha_7) x_3$$

$$\dot{x}_4 = \alpha_3 x_3 - (\alpha_5 + \alpha_7) x_4$$

$$\begin{pmatrix} \dot{x}_1 \\ \dot{x}_2 \\ \dot{x}_3 \\ \dot{x}_4 \end{pmatrix} = \begin{pmatrix} -\alpha_1 i^* - \alpha_7 & 0 & -\alpha_1 s^* & \alpha_5 \\ \alpha_1 i^* & -(\alpha_2 + \alpha_7) & \alpha_1 s^* & 0 \\ 0 & \alpha_2 & -(\alpha_3 + \alpha_4 + \alpha_7) & 0 \\ 0 & 0 & \alpha_3 & -(\alpha_5 + \alpha_7) \end{pmatrix} \begin{pmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \end{pmatrix} + \begin{pmatrix} \alpha_1 s^* i^* \\ -\alpha_1 s^* i^* \\ 0 \\ 0 \end{pmatrix} u$$

The state space model for the system is given as

$$\dot{x} = Ax + Bu;$$

We want to compute the concept of controllability and observability.

$$A = \begin{pmatrix} -\alpha_1 i^* - \alpha_7 & 0 & -\alpha_1 s^* & \alpha_5 \\ \alpha_1 i^* & -(\alpha_2 + \alpha_7) & \alpha_1 s^* & 0 \\ 0 & \alpha_2 & -(\alpha_3 + \alpha_4 + \alpha_7) & 0 \\ 0 & 0 & \alpha_3 & -(\alpha_5 + \alpha_7) \end{pmatrix}, B = \begin{pmatrix} \alpha_1 s^* i^* \\ -\alpha_1 s^* i^* \\ 0 \\ 0 \end{pmatrix}$$

Substituting the parameter values, we have

$$A = \begin{pmatrix} -0.000220714 & 0 & -0.321386 & 0.0000004924 \\ 0.000120714 & -0.187744 & 0.321385 & 0 \\ 0 & 0.187644 & -0.321215 & 0 \\ 0 & 0 & 0.3181725 & -0.0001005 \end{pmatrix}, B = \begin{pmatrix} 0.00005484 \\ -0.00005484 \\ 0 \\ 0 \end{pmatrix}$$

Test for Controllability

$M_c = [B \ AB \ A^2 B \ A^{n-1} B]$ is controllable if the rank of $M_c = n$ where $n = 4$ then

$$M_c = [B \ AB \ A^2 B \ A^3 B]$$

Controllable matrix is

$$M_c = \begin{pmatrix} 0.00000548 & -0.0000000012 & 0.0000003307 & -0.000000168 \\ -0.000005484 & 0.0000010303 & -0.000000524 & 0.0000002668 \\ 0 & -0.000001029 & 0.0000005239 & -0.000000267 \\ 0 & 0 & -0.000003274 & 0.000001667 \end{pmatrix}$$

$$|M_c| = 7.39 \times 10^{-33}$$

Since the determinant of M_c is non-zero, therefore $M_c = n = 4$. Hence, the system is completely controllable.

Test for Observability

$Q_b = [C^T \ A^T C^T \ (A^T)^2 C^T \ \dots (A^T)^{n-1} C^T]$ is observable if the rank of $Q_b = n$ where $n = 4$ then

$$Q_b = [C^T \ A^T C^T \ (A^T)^2 C^T \ (A^T)^3 C^T]$$

$$Q_b = \begin{pmatrix} 0 & 0 & 1 & 0 \\ 0 & 0.1876 & -0.3212 & 0 \\ 0.00002265 & -0.0955 & 0.1635 & 0 \\ -0.0000115 & 0.0486 & -0.0832 & 0.000000000011 \end{pmatrix}$$

$$|Q_b| = -4.47 \times 10^{17}$$

Since the determinant of Q_b is non-zero, therefore $Q_b = n = 4$. Hence, the system is completely observable.

IV. Conclusion

In this paper, the mathematical model for transmission of covid-19 disease can be useful in understanding the dynamical behaviour of covid-19 in Nigeria, his suggested that the number of new cases of the disease will decline over time as the strategies that cause are established. The system was shown to be completely controllable and observable. The basic reproduction number and examined the stability analysis (local stability of both disease free equilibrium and disease endemic equilibrium) of the system were computed and the stability of the SEIR model verified.

References

- Abioye I. A., Peter J. O., Ogunseye A. H., Oguntolu A. F., Oshinubi K., Ibrahim A. A., Khan I. (2021). Mathematical model of COVID-19 in Nigeria with optimal control. National Library of Medicine. doi:10.1016/j.rinp.2021.104598
- Adekunle A. I., Adegboye O. A., Gayawan E., McBryde E. S. (2020). Is Nigeria really on top of COVID-19? Message from effective reproduction number. Epidemiology and infection. doi:10.1101/2020.05.16.20104471
- Brauer, F. (2017). Mathematical epidemiology: past, present, and future. Infectious Disease Modeling, 2, 113 - 127. Retrieved from <http://doi.org/10.1016/j.idm.2017.02.001>
- Castillo-Chavez, C., and B. Song. (2004). Dynamical models of tuberculosis and their applications. Math Biosci Eng, 1(2):361
- Diekmann , O., Heesterbeek , H., Britton , T. (2013). Mathematical Tools for understanding Disease Dynamics. Princeton: Princeton University Press. <https://doi.org/10.1515/9781400845620>
- Diekmann, O., Heesterbeek, H., Britton, T. (2013). Mathematical Tools for understanding Disease Dynamics. Princeton Series in Thoretical and Computaion Biology (1st ed.). Princeton University Press. <https://press.princeton.edu/books>
- Drisessche, P. V., and Watmough, J. (2002). Reproduction number and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences, 180:29-48..
- Emmanuel N, Sunday NA, Louis O, Michael U. (2023). Optimal Control of COVID-19: Examining the Incidence of Contamination and Its Recurrence in Nigeria. American Journal of Applied Mathematics, 11: 23-31. doi: 10.11648/j.ajam.20231102.12
- Guirao, A., Ouedraogo, D., Ouedraogo, H. (2018). Stability Analysis for a Discrete SIR Epidemic Model with Delay and General Nonlinear Incidence Function, Applied Mathematics pp. 1039–1054.
- Hethcote, H. (2000). The mathematics of infectious diseases. SIAM Rev. doi:10.1137/S0036144500371907
- IHME COVID-19 Forecasting Team. (2021). Modeling COVID-19 scenarios for the United States. Nature medicine, 27(1), 94-105. <https://doi.org/10.1038/s41591-020-1132-9>
- Ivorra, B., Ngom, D., and Ramos, A. M. Be-CoDis: (2015). A Mathematical Model to Predict the Risk of Human Diseases Spread Between Countries Validation and Application to the 2014-2015 Ebola Virus Disease Epidemic, Bulletin of Mathematical Biology, 17, 9 pp.1668–1704.
- Kermack, W. O. and McKendrick, A. G. (1927). A Contribution to the Mathematical Theory of Epidemics. Proceeding of the Royal Society of London. Series A, Mathematical and Physical Character, 115 (772), 700-721. <https://www.jstor.org/stable/94815>
- Kiran, R., Roy, M., Abbas, S. and Taraphder A. (2021). Effect of population migration and punctuated lockdown on the spread of infectious diseases, arXiv:2006.15010v2.

- Lauer, S.A., Grantz, K.H. and Bi, Q., (2020). The Incubation Period of Coronavirus Disease 2019 (COVID-19) From Publicly Reported Confirmed Cases: Estimation and Application. *Ann Intern Med.* doi: 10.7326/M20-0504.
- Mummert, A., and Otunuga, O. M. (2019). Parameter identification for a stochastic SEIRS epidemic model: case study influenza. *Mathematical Biology.*;79(2). doi:10.1007/s00285-019-01374-z.
- Oran, D.P. and, Topol, E.J. (2021). Prevalence of Asymptomatic SARS-CoV-2 infections: doi:10.7326/M20-6976.
- Reiner, R.C., Perkins, T.A., Barker, C.M., Niu, T., Chaves, L.F., Ellis, A.M., George, D. A., Le Menach, A., Pullian, J. R., Bisanzio, D., Bckee, C., Chiyaka, C., Cummings, D. A., Gattton, M. L., Gething, P. W., Hartley, D. M., Johnston, G., Klein, E. Y., Michael, E., Smith, D.L. 2013. A systematic review of mathematical models of mosquito-borne pathogen transmission: 1970-2010. *Journal of the Royal Society, Interface*, 10(81), 20120921. doi:10.1098/rsif.2012.0921
- Roskilly, T., Mikalsen, R. (2015). Chapter Five: Closed-Loop Stability, Marine System Identification, Modeling and Control. Butterworth-Heinemann. <https://doi.org/10.1016/C2013-0-18786-7>.
- Shu T. L., Lin T. L., and Joseph M. R. (2020): A comparison to the 1918 influenza and how we can defeat it. doi:10.1136/postgradmedj-2020-139070
- Shujuan, M., Jiayue, Z., Minyan, Z., Qinging, Y., Wie G., Yixiang Z., Shi, Z., Maggie, H., Wang, Z. Y. (2020). Epidemiological parameters of coronavirus disease 2019: a pool analysis of publicly reported individual data of 1155 cases from seven countries. medRxiv. <https://doi.org/10.1101/2020.03.21.20040329>
- Sunday, N. A., Emmanuel, N., Louis, O., Michael U. (2023). Parameters Estimation of COVID-19 SEIR Model. *Asian Journal of Pure and Applied Mathematics*. Article no.AJPAM.1263
- Tyagi, S., Gupta, S., Abbas, S., Das K. P. and Riadh B. (2021). Analysis of infectious disease transmission and prediction through SEIQR epidemic model, *Nonauto. Dyn. Sys.*, no.1, 75–86.
- Tyagi, S., Martha, S. C., Abbas, S. and Debbouche, A. (2021). Mathematical modeling and analysis for controlling the spread of infectious diseases, *Chaos, Solitons and Fractals*, 144 Paper No.110707
- Wang, X., Pan, Y., Zhang, D., Daitao Z., Chen, L. J., Xinyu, L., Peng, Y., Quanyi, W., Raina, C. M. (2020). Basic epidemiological parameter values from data of real world in mega cities: the characteristics of Covid-19 in Beijing, China. *BMC Infec Dis* 20, 526. <https://doi.org/10.1186/s12879-020-05251-9>.
- Wu, J. T., Leung, K. and Leung, G. M. (2020). Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modeling study, *Lancet*, 395, pp.261–269
- Xu Z, Wu B, Topcu U. (2021). Control strategies for COVID-19 epidemic with vaccination, shield immunity and quarantine: A metric temporal logic approach. *PLoS ONE* 16(3): e0247660. <https://doi.org/10.1371/journal.pone.0247660>
- Yang, W., Zhang, D., Peng, L., Zhuge, C., Liu, L. (2020). "Rational evaluation of various epidemic models based on the COVID-19 data of China". arXiv:2003.05666v1 (<https://arxiv.org/abs/2003.05666v1>) [q-bio.PE (<https://arxiv.org/archive/q-bio>).