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RESEARCH ARTICLE

A Mathematical Model for the Control on the Transmission Dynamics of COVID-19 Pandemic Containing Asymptomatic and Symptomatic Classes

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ABSTRACT

In this research paper work, we developed a COVID-19 epidemic disease model fitted in Nigeria situation. In this model system, we divided Nigeria population into six subpopulations such as Susceptible population, Exposed population, Infected asymptomatic population, Infected symptomatic population, isolated symptomatic population, and the fully recovered population. Control measures parameter (hand sanitizers and nose masks) was incorporated into the model. We obtained the disease-free equilibrium and endemic equilibrium points. The basic reproduction number was obtained using the new generation matrix, the local and global stability was also obtained to be locally and globally asymptotically stable at $R_0<1$ for the DFE. We did numerical simulations using (Maple 17) software. The results showed the importance of the control measures and social distancing through graph.

Key words: Mathematical Model, Transmission Dynamics, Covid-19 Pandemic, asymptomatic, Symptomatic Classes

INTRODUCTION

Coronaviruses (CoV) are a large family of zoonotic viruses, that is, they are transmitted from animals to humans, and that cause symptoms ranging from the common cold to more serious illnesses such as Middle East respiratory syndrome (MERS) which is transmitted from dromedary to humans and severe acute respiratory syndrome (SARS) which is transmitted from civet to humans. Several known CoV that have not yet infected humans are circulating in some animals [1], [2].

The first case of the novel coronavirus, SARS coronavirus 2, was reported by Chinese health officials in Wuhan City in December 2019 [3]. CoV are a family of viruses that can cause illnesses, such as SARS and the MERS [4], [5]. The clinical spectrum of COVID-19 infection is broad, ranging from no symptoms to severe pneumonia. Approximately half of the COVID-19 patients (40–50%) in one study did not show any symptoms [6]. Other patients developed fever, body aches, nausea, or diarrhea (Center for Disease Control, 2020) typically 2–14 days after exposure to the virus. During the initial phase of COVID-19 in China (10–23 January 2020), only 14% of total infections were confirmed.

The remaining 86% were not identified or quarantined, contributing to a community spread in China. Later, on January 23, the Chinese government implemented a total lockdown of Wuhan City, which prevented further community spread [7], [8]. Due to this strict intervention, the number of new COVID-19 cases in China dropped to the single-digits in early March. Other countries, however, started to report an increasing number of confirmed cases. COVID-19 spread from Wuhan to the rest of China and neighboring Asian countries such as Thailand, Japan, Korea, Singapore, and Hong Kong. As of March 31, the number of confirmed cases worldwide had exceeded 820,000, and the number of deaths

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had reached more than 40,000 in more than 110 countries. The World Health Organization declared COVID-19 a pandemic on March 11, 2020 [9].

Nigeria, a country with approximately 200,000,000 populaces located in West Africa recorded its first case of COVID-19 in February 27, 2020, [2] and as at March 30, 2020 (22:00 WAT) 131 individuals have been infected with the virus. The total number of recoveries being 8 and deaths, 2. Lagos State (Nigeria) has a larger number of infected persons followed by the country's capital Abuja. At present, lock down have been declared in major cities of the country [10] and entry flights from countries with over 1000 cases have been banned (Stephanie, 2020) [11], [12].

In this current work, we developed a COVID-19 epidemic disease model fitted in Nigeria situation. In this model system, we divided Nigeria population into six subpopulations such as susceptible population, exposed population, infected asymptomatic population, infected symptomatic population, isolated symptomatic population, and the fully recovered population. Then using dynamical modeling analysis, our aim is to forecast the confirmed Nigeria COVID-19 cases in future specifically in different States in Nigeria. We also analyze the proposed disease model mathematically to understand transmission dynamics of the COVID-19 virus among humans.

MODEL FORMULATION

In developing the model, we assumed a homogenous mixing among the population. This implies that there are equal chances of transmitting the virus when there is an effective contact between the susceptible individual and the infected individual (both the Asymptomatic and Symptomatic individual). We represent the transmission of the disease using a set of Ordinary Differential Equation (ODE). The total population at time (t) denoted by $N(t)$ is divided into six mutually exclusive populations which are the susceptible (S), individuals who are exposed to COVID-19 (E), infected symptomatic individuals (I_S), infected asymptomatic individuals (I_A), isolated individuals (I), and fully recovered (R), such that $N(t)=S+E+I_A+I_S+R$

In formulating the model, we assumed that the total population at time t, is divided into susceptible (S), exposed (E), asymptomatic (I_A), symptomatic (I_S), isolated (I), and recovered (R).

The symptomatic and asymptomatic humans are equally infectious. Susceptible humans are recruited into (S) either by birth or immigration at rate Λ. A susceptible individual in S become exposed to Novel coronavirus and moved to E after getting into contact with an infectious human at a rate η, with

$$\eta = \beta \frac{\left(I_A + I_S\right)}{N} \tag{1}$$

where β is the effective contact rate. Control measure (Nose masks and Hand sanitizers) was used by the susceptible humans (S) population (N) at rate ($1–K\theta$) since it is not 100% effective. After the incubation period of the novel corona virus in the host, a proportion $\alpha \in [0,1]$ of the exposed human in (E) develops symptoms of COVID-19 and proceed to Symptomatic class I_S at a rate $\alpha\varepsilon$ while the remaining proportion ($1–\alpha$) does not develop symptoms of COVID-19 and becomes asymptomatic, thus moving to the class I_A at a rate $(1-\alpha)\varepsilon$; where ε is the disease (novel coronavirus) incubation rate in human. It is also assumed that, humans die from COVID-19 only when they have developed one or more symptoms of the virus. Therefore, individuals in I_A either developed symptoms naturally at a rate φ and moved to I_S or recover naturally due to their immunity at rate γ and move to R with permanent immunity. Individuals in I_S recovers due to treatment at home at rate τ_1 with permanent immunity into R or die due to the virus or complications at constant rate δ_1. Individuals in I_S who went to the hospital or got isolated moves to the isolation center I at a rate. Individuals at the isolation center I recovers due to treatment τ_2 with permanent immunity into R or die due to the virus/complications at the isolation center with constant rate δ_2. Table 1 present the notation and definition of variables and parameter used for the model.

MODEL DIAGRAM

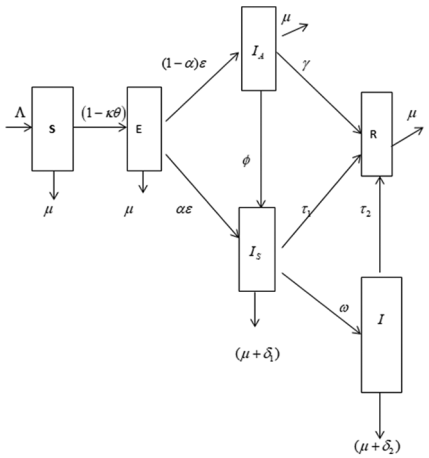

Figure 1: Schematic Diagram of the Model

THE MODEL EQUATION

Base on the assumption and interrelation between the variables and parameters in Figure 1, COVID-19 transmission dynamics can be described using ODE.

The SEI_AI_SIR Model with Vaccination

$$\begin{cases} \dfrac{dS}{dt} = \Lambda - (1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S - \mu S \\ \dfrac{dE}{dt} = (1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S - (\varepsilon+\mu)E \\ \dfrac{dI_A}{dt} = (1-\alpha)\varepsilon E - (\mu+\gamma+\phi)I_A \\ \dfrac{dI_S}{dt} = \alpha\varepsilon E + \phi I_A - (\delta_1+\mu+\tau_1+\omega)I_S \\ \dfrac{dI}{dt} = \omega I_S - (\delta_2+\mu+\tau_2)I \\ \dfrac{dR}{dt} = \gamma I_A + \tau_1 I_S + \tau_2 I - \mu R \end{cases} \tag{2}$$

with the initial conditions
$S(0)\geq 0, E(0)\geq 0, I_A(0)\geq 0, I_S(0)\geq 0, I(0)\geq 0, R(0)\geq 0$ (3)
and description of the state variables and the parameters used in the model are presented in table.

Positive Invariant Region

The entire population size N can be determined from equations 1.
The total population size is

$$N=S+E+I_A+I_S+I+R \tag{4}$$

Adding equation (1)

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI_A}{dt} + \frac{dI_S}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \tag{5}$$

$$\frac{dN}{dt} = \Lambda - \mu(\mathrm{S} + E + I_A + I_S + I + R) - (\delta_1 I_S + \delta_2 I) \tag{6}$$

In the absence of the disease (δ_1=δ_2=0) then (5) given
The positive invariant region can be obtained using the following theorem.

Theorem 1

The solutions of the system of equations (2) are feasible for t>0, if they enter the invariant region D is given as equation (7).

Proof

Let

$$D=(S,E,I_S,I_A,I,R)\in R^6 \tag{8}$$

Be any solution of the system of equations (2) with non-zero initial conditions.
Assuming there is no disease-induced deaths equation (8)

$$\frac{dN}{dt} \le \Lambda - \mu N \tag{9}$$

$$\frac{dN}{dt} + \mu N \le \Lambda \tag{10}$$

The integrating fact for equation (10) is multiplying both sides of equation (10) by give

$$\frac{dN}{dt} + \mu N e^{-\mu t} \le \Lambda e^{\mu t} \tag{11}$$

$$\frac{dN}{dt} \le \mu \tag{12}$$

Integrating both sides we have

$$N(t) \tag{13}$$

$$N(t) = \frac{\Lambda}{\mu} + c \tag{14}$$

Applying the initial condition t=0, $N(0)$=N_0

$$N_0 \le \frac{\Lambda}{\mu} + c \Rightarrow N_0 - \frac{\Lambda}{\mu} \le c \tag{15}$$

$$\rightarrow N \le \frac{\Lambda}{\mu} + \left(N_0 - \frac{\Lambda}{\mu} \right) e^{-\mu t} \tag{16}$$

Therefore, as t=∞ in (16) to humans N approaches $K = \frac{\Lambda}{\mu}$ (that is $N \rightarrow K = \frac{\Lambda}{\mu}$) the parameter $K = \frac{\Lambda}{\mu}$ is called the carrying capacity. Hence, all feasible solution set of the human of the model equation (2) enter the region.

$$D = \left\{ \begin{matrix} (S, E, I_S, I_A, I, R) \in R^6 : S > 0, E > 0, I_S > 0, I_A > 0, I > 0, \\ R > 0, N \le \frac{\Lambda}{\mu}) \end{matrix} \right\} \tag{17}$$

With is positively invariant (i.e., solution remain positive for all time t) and the model is epidemiologically meaningful and mathematically well pose.

Positive of Solutions

Since equation (2) represents the population in each compartment and all model parameters are all positive, then if lies in region *D* defined by

Theorem 2

Let the initial data for the model equation be given as this

$$S(0)\geq 0,\ E(0)\geq 0,\ I_S(0)\geq 0,\ I_A(0)\geq 0,\ I(0)\geq 0,\ R(0)\geq 0 \tag{18}$$

Then the solutions
($S(t)$, $E(t)$, $I_s(t)$, $I_A(t)$, $I(t)$, R) of the model equation with non-negative initial data with remain non-negative for at time $t>0$

Proof

For equation (2)

$$\frac{dS}{dt} = \Lambda - (1-\kappa\theta)\beta\frac{(I_A + I_S)}{N}S - \mu S \geq -\mu S \tag{19}$$

$$\Rightarrow \frac{dS}{dt} \geq -\mu S \tag{20}$$

By separating the variable and integrating equation we have;

$$\int \frac{ds}{s} \geq -\int \mu dt \tag{21}$$

We have,

$$\ln s \geq -u_t + c \tag{22}$$

Take the *e* of both sides

$$e^{lnS} \geq e^{-\mu t + c} \tag{23}$$

we have

$$S(t) \geq e^{-\mu t + c} \tag{24}$$

$$= S(t) \geq e^{-\mu t + c}.e^{c} \tag{25}$$

Let

$$e^{c} = A \tag{26}$$

$$S(t) \geq Ae^{-\mu t} \tag{27}$$

From equation let $t=0$ be initial population in the susceptible compartment $S(t)=S(0)=S_0$

$$S(0) \geq Ae^{-\mu(0)} \tag{28}$$

$$S(0) = A \tag{29}$$

$$S(t) \geq S(0)e^{-\mu t} \tag{30}$$

Similarly,

$$\begin{cases} E(t) \geq E(0)e^{-(\varepsilon+\mu)t} > 0 \\ I_A(\mathrm{t}) \geq I_A(0)e^{-(\mu+\gamma+\phi)t} > 0 \\ I_S(\mathrm{t}) \geq I_S(0)e^{-(\delta_1+\mu+\tau_1+\omega)t} > 0 \\ I(\mathrm{t}) \geq I(0)e^{-(\delta_2+\mu+\tau_2)t} > 0 \\ R(t) \geq R(0)e^{-\mu t} > 0 \end{cases} \tag{31}$$

Hence, from the above solutions, it is clear that the model solution is invariant and has positive results.

The Existence and Uniqueness of Solution

The validity and implementation of any mathematical model depend on whether the given system of equations has a solution, and if it has there is need to check if the solution is unique (Ayoade *et al.,* 2019).

Theorem 3.6.1

Let D denotes the region $\pi \in \Re^{+}$. Then the model system (3.2) to (3.7) has a unique solution if it is established that $\frac{\partial f_i}{\partial f_i}, \mathrm{i} = 1,2,3,4,5,6$ are continuous and bounded in D.

Proof

Let equations (2) be represented by $f_1, f_3, f_3, f_4, f_5, f_6$ and m_6 respectively
From equation (2), the following partial derivatives are obtain

$$\left.\begin{aligned} &\left|\frac{\partial f_1}{\partial S}\right| = \left|-((1-\kappa\theta)\eta+\mu)\right| < \infty, \left|\frac{\partial f_1}{\partial E}\right| = |0| < \infty, \\ &\left|\frac{\partial f_1}{\partial I_A}\right| = \left|-(1-\kappa\theta)\frac{\beta S}{N}\right| < \infty, \left|\frac{\partial f_1}{\partial I_S}\right| = \left|-(1-\kappa\theta)\frac{\beta S}{N}\right| < \infty, \\ &\left|\frac{\partial f_1}{\partial I}\right| = |0| < \infty, \left|\frac{\partial f_1}{\partial R}\right| = |0| < \infty \end{aligned}\right\} \tag{32}$$

The above partial derivatives exist, continuous and are bounded
From equation (3), we obtained the following partial derivatives

$$\left.\begin{aligned} &\left|\frac{\partial f_2}{\partial S}\right| = \left|(1-\kappa\theta)\eta\right| < \infty, \left|\frac{\partial f_2}{\partial E}\right| = \left|-(\mu+\varepsilon)\right| < \infty, \\ &\left|\frac{\partial f_2}{\partial I_A}\right| = \left|-(1-\kappa\theta)\frac{\beta S}{N}\right| < \infty, \left|\frac{\partial f_2}{\partial I_S}\right| = \left|-(1-\kappa\theta)\frac{\beta S}{N}\right| < \infty, \\ &\left|\frac{\partial f_2}{\partial I}\right| = |0| < \infty, \left|\frac{\partial f_2}{\partial R}\right| = |0| < \infty \end{aligned}\right\} \tag{33}$$

From equation (4), we obtained the following partial derivatives

$$\left.\begin{aligned} &\left|\frac{\partial f_3}{\partial S}\right| = |0| < \infty, \left|\frac{\partial f_3}{\partial E}\right| = \left|(1-\alpha)\varepsilon\right| < \infty, \\ &\left|\frac{\partial f_3}{\partial I_A}\right| = \left|-(\mu+\gamma+\phi)\right| < \infty, \left|\frac{\partial f_3}{\partial I_S}\right| = |0| < \infty, \\ &\left|\frac{\partial f_3}{\partial I}\right| = |0| < \infty, \left|\frac{\partial f_3}{\partial R}\right| = |0| < \infty \end{aligned}\right\} \tag{34}$$

The above partial derivatives exist, continuous and are bounded
From equation (5), we obtained the following partial derivatives

$$\left.\begin{aligned}
&\left|\frac{\partial f_4}{\partial S}\right| = |0| < \infty, \left|\frac{\partial f_4}{\partial E}\right| = |\alpha\varepsilon| < \infty \left|\frac{\partial f_4}{\partial I_A}\right| = |-\phi| < \infty, \\
&\left|\frac{\partial f_4}{\partial I_S}\right| = |-(\delta_1 + \mu + \tau_1 + \omega)| < \infty, \left|\frac{\partial f_4}{\partial I}\right| = |0| < \infty, \\
&\left|\frac{\partial f_4}{\partial R}\right| = |0| < \infty
\end{aligned}\right\} \tag{35}$$

The above partial derivatives exist, continuous and are bounded
From equation (6), we obtained the following partial derivatives

$$\left.\begin{aligned}
&\left|\frac{\partial f_5}{\partial S}\right| = |0| < \infty, \left|\frac{\partial f_5}{\partial E}\right| = |0| < \infty, \left|\frac{\partial f_5}{\partial I_A}\right| = |0| < \infty \\
&\left|\frac{\partial f_5}{\partial I_S}\right| = |\omega| < \infty, \left|\frac{\partial f_5}{\partial I}\right| = |-(\delta_2 + \mu + \tau_2)| < \infty, \\
&\left|\frac{\partial f_5}{\partial R}\right| = |0| < \infty
\end{aligned}\right\} \tag{36}$$

The above partial derivatives exist, continuous and are bounded
From equation (7), we obtained the following partial derivatives

$$\left.\begin{aligned}
&\left|\frac{\partial f_6}{\partial S}\right| = |0| < \infty, \left|\frac{\partial f_6}{\partial E}\right| = |0| < \infty, \left|\frac{\partial f_6}{\partial I_A}\right| = |\gamma| < \infty, \\
&\left|\frac{\partial f_6}{\partial I_S}\right| = |\tau_1| < \infty, \left|\frac{\partial f_6}{\partial I}\right| = |\tau_2| < \infty, \left|\frac{\partial f_6}{\partial R}\right| = |-\mu| < \infty
\end{aligned}\right\} \tag{37}$$

Since all the partial derivatives exist, bounded and defined, then system of equations (2)-(7) exists and has solution in $\Re^6$.

Basic Reproduction Number (R_0)

The basic reproduction number is an important threshold parameter that determines whether an infectious disease can invade the population.
To calculate (R_0), we use the next generation matrix approach (Diekmann *et al.,* 1990)

$$F_i = \begin{bmatrix} (1-\kappa\theta)\beta \dfrac{(I_A + I_S)}{N} S \\ 0 \\ 0 \\ 0 \end{bmatrix} \tag{38}$$

$$V_i = \begin{bmatrix} (\varepsilon+\mu)E \\ -(1-\alpha)\varepsilon E + (\mu+\gamma+\phi)I_A \\ -\alpha\varepsilon E - \phi I_A + (\delta_1+\mu+\tau_1+\omega)I_S \\ -\omega I_S + (\delta_2+\mu+\tau_2)I \end{bmatrix} \tag{39}$$

$$F = \begin{bmatrix} \frac{dF_1}{dE} & \frac{dF_1}{dI_A} & \frac{dF_1}{dI_S} & \frac{dF_1}{dI} \\ \frac{dF_2}{dE} & \frac{dF_2}{dI_A} & \frac{dF_2}{dI_S} & \frac{dF_2}{dI} \\ \frac{dF_3}{dE} & \frac{dF_3}{dI_A} & \frac{dF_3}{dI_S} & \frac{dF_3}{dI} \\ \frac{dF_4}{dE} & \frac{dF_4}{dI_A} & \frac{dF_4}{dI_S} & \frac{dF_4}{dI} \end{bmatrix} \tag{40}$$

$$V = \begin{bmatrix} \frac{dV_1}{dE} & \frac{dV_1}{dI_A} & \frac{dV_1}{dI_S} & \frac{dV_1}{dI} \\ \frac{dV_2}{dE} & \frac{dV_2}{dI_A} & \frac{dV_2}{dI_S} & \frac{dV_2}{dI} \\ \frac{dV_3}{dE} & \frac{dV_3}{dI_A} & \frac{dV_3}{dI_S} & \frac{dV_3}{dI} \\ \frac{dV_4}{dE} & \frac{dV_4}{dI_A} & \frac{dV_4}{dI_S} & \frac{dV_4}{dI} \end{bmatrix} \tag{41}$$

Therefore, the inverse

$$V^{-1} = \frac{adjo\,\text{int}}{\det er\,\min ant} \qquad F = \begin{bmatrix} 0 & \frac{(1-\kappa\theta)\beta}{(\frac{\Lambda}{\mu})}(\frac{\Lambda}{\mu}) & \frac{(1-\kappa\theta)\beta}{(\frac{\Lambda}{\mu})}(\frac{\Lambda}{\mu}) & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{42}$$

$$V = \begin{bmatrix} (\varepsilon+\mu) & 0 & 0 & 0 \\ -(1-\alpha)\varepsilon & (\mu+\gamma+\phi) & 0 & 0 \\ -\alpha\varepsilon & -\phi & (\delta_1+\mu+\tau_1+\omega) & 0 \\ 0 & 0 & -\omega & (\delta_2+\mu+\tau_2) \end{bmatrix} \tag{43}$$

Thus, the inverse of the matrix in (43) was obtained as;

$$V^{-1}=\begin{bmatrix} \frac{1}{(\varepsilon+\mu)} & 0 & 0 & 0 \\ \frac{(1-\alpha)\varepsilon}{(\varepsilon+\mu)(\mu+\gamma+\phi)} & \frac{1}{(\mu+\gamma+\phi)} & 0 & 0 \\ \frac{\varepsilon(\mu\alpha+\alpha\gamma+\phi)}{(\mu+\gamma+\phi)(\delta_1+\mu+\tau_1+\omega)(\varepsilon+\mu)} & \frac{\phi}{(\mu+\gamma+\phi)(\delta_1+\mu+\tau_1+\omega)} & \frac{1}{(\delta_1+\mu+\tau_1+\omega)} & 0 \\ \frac{\omega\varepsilon(\mu\alpha+\alpha\gamma+\phi)}{(\mu+\gamma+\phi)(\delta_1+\mu+\tau_1+\omega)(\varepsilon+\mu)(\delta_2+\mu+\tau_2)} & \frac{\omega\phi}{(\mu+\gamma+\phi)(\delta_1+\mu+\tau_1+\omega)(\delta_2+\mu+\tau_2)} & \frac{\omega}{(\delta_2+\mu+\tau_2)(\delta_1+\mu+\tau_1+\omega)} & \frac{1}{(\delta_2+\mu+\tau_2)} \end{bmatrix} \tag{44}$$

To compute the Eigen values

$$FV^{-1}=\begin{bmatrix} \frac{(1-\kappa\theta)\beta(1-\alpha)\varepsilon}{(\varepsilon+\mu)(\mu+\gamma+\phi)}+\frac{(1-\kappa\theta)\beta\varepsilon(\mu\alpha+\alpha\gamma+\phi)}{(\mu+\gamma+\phi)(\varepsilon+\mu)(\delta_1+\mu+\tau_1+\omega)} & \frac{(1-\kappa\theta)\beta}{(\mu+\gamma+\phi)}+ & & \\ 0 & 0 & & \\ 0 & 0 & & \\ 0 & 0 & & \end{bmatrix}$$

$$\begin{bmatrix} \frac{(1-\kappa\theta)\beta\phi}{(\mu+\gamma+\phi)(\delta_1+\mu+\tau_1+\omega)} & \frac{(1-\kappa\theta)\beta}{(\delta_1+\mu+\tau_1+\omega)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \tag{45}$$

Since it's an upper triangular matrix the determinant can be gotten by multiplying the leading diagonal.

$$-\Psi^3\left(\frac{(1-\kappa\theta)\beta(1-\alpha)\varepsilon}{(\varepsilon+\mu)(\mu+\gamma+\phi)}+\frac{(1-\kappa\theta)\beta\varepsilon(\mu\alpha+\alpha\gamma+\phi)}{(\mu+\gamma+\phi)(\varepsilon+\mu)(\delta_1+\mu+\tau_1+\omega)}-\Psi\right)=0 \tag{46}$$

Case 1:

$$-\Psi^3=0 \text{ And } \frac{(1-\kappa\theta)\beta(1-\alpha)\varepsilon}{(\varepsilon+\mu)(\mu+\gamma+\phi)}+\frac{(1-\kappa\theta)\beta\varepsilon(\mu\alpha+\alpha\gamma+\phi)}{(\mu+\gamma+\phi)(\varepsilon+\mu)(\delta_1+\mu+\tau_1+\omega)}-\Psi\neq 0 \tag{47}$$

Case 2:

$$-\Psi^3\neq 0 \text{ and } \frac{(1-\kappa\theta)\beta(1-\alpha)\varepsilon}{(\varepsilon+\mu)(\mu+\gamma+\phi)}+\frac{(1-\kappa\theta)\beta\varepsilon(\mu\alpha+\alpha\gamma+\phi)}{(\mu+\gamma+\phi)(\varepsilon+\mu)(\delta_1+\mu+\tau_1+\omega)}-\Psi=0 \tag{48}$$

We have;

$$\Psi_1=\Psi_2=\Psi_3=0 \text{ and } \Psi_4=\frac{(1-\kappa\theta)\beta(1-\alpha)\varepsilon}{(\varepsilon+\mu)(\mu+\gamma+\phi)}+\frac{(1-\kappa\theta)\beta(\mu\alpha+\alpha\gamma+\phi)\varepsilon}{(\mu+\gamma+\phi)(\varepsilon+\mu)(\delta_1+\mu+\tau_1+\omega)} \tag{49}$$

Since R_0 is the most positive value among the Eigen values we have;

$$R_0=\frac{(1-\kappa\theta)\beta(1-\alpha)\varepsilon}{(\varepsilon+\mu)(\mu+\gamma+\phi)}+\frac{(1-\kappa\theta)\beta(\mu\alpha+\alpha\gamma+\phi)\varepsilon}{(\mu+\gamma+\phi)(\varepsilon+\mu)(\delta_1+\mu+\tau_1+\omega)} \tag{50}$$

$$R_0=R_{0A}+R_{0S} \tag{51}$$

Where R_{0A} and R_{0S} are the basic reproduction number of the Asymptomatic and Symptomatic Humans, respectively.

Equilibrium Points of the Model At Equilibrium

$$\frac{dS}{dt}=\frac{dE}{dt}=\frac{dI_A}{dt}=\frac{dI_S}{dt}=\frac{dI}{dt}=\frac{dR}{dt}=0 \tag{52}$$

$$\begin{cases}\Lambda-(1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S-\mu S=0\\ (1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S-(\varepsilon+\mu)E=0\\ (1-\alpha)\varepsilon E-(\mu+\gamma+\phi)I_A=0\\ \alpha\varepsilon E+\phi I_A-(\delta_1+\mu+\tau_1+\omega)I_S=0\\ \omega I_S-(\delta_2+\mu+\tau_2)I=0\\ \gamma I_A+\tau_1 I_S+\tau_2 I-\mu R=0\end{cases} \tag{53}$$

is the steady state of (53) which can be obtained by solving (53)?
The diseased classes for human can be defined as E, I_S, I_A, I, R. In the absence of disease- or disease-free state, it implies that ($E=I_s=I_A=I=R=0$) and so (53) become $\Lambda=\mu S$ where $N=S+E+I_s+I_A+I+R$ but $I_s=I_A=0$ Therefore equation (53) reduced to

$$\Lambda=\mu S^*=0 \tag{54}$$

Which implies that

$$S^*=\frac{\Lambda}{\mu} \tag{55}$$

Then the disease-free equilibrium (DFE) ε_0
will be

$$A_0=(S^*,E^*,I_A{}^*,I_S{}^*,I^*,R^*)=(\frac{\Lambda}{\mu},0,0,0,0,0) \tag{56}$$

Stability Analysis of Disease-free Equilibrium

Given that $R_{00}=\dfrac{(1-\kappa\theta)\beta\alpha\varepsilon}{(\mu+\varepsilon)(\delta_1+\mu+\tau_1+\omega)}$, the Disease Free Equilibrium of the model is Locally Asymptomatically Stable if, R_{0s}, R_{0A}, $R_{00}<1$ and unstable if R_{0s}, R_{0A}, $R_{00}>1$

Proof: We can proof the theorem by constructing the Jacobian matrix for the model system evaluated at DFE and computing the Eigen values.
The Jacobian Matrix is given as;
Let,

$$\begin{vmatrix} -\mu-\Psi & 0 & -d\beta & -d\beta & 0 & 0 \\ 0 & -k_1-\Psi & d\beta & d\beta & 0 & 0 \\ 0 & 0 & \frac{-(-Ld\beta+k_1k_2)}{k_1}-\Psi & \frac{Ld\beta}{k_1} & 0 & 0 \\ 0 & 0 & 0 & -\frac{(Ld\beta\phi+Ld\beta k_3+d\beta\alpha\varepsilon-k_1k_2k_3)}{Ld\beta-k_1k_2}-\Psi & 0 & 0 \\ 0 & 0 & 0 & 0 & -k_4-\Psi & 0 \\ 0 & 0 & 0 & 0 & 0 & -\mu-\Psi \end{vmatrix} = 0 \quad (57)$$

From the leading diagonals we have

$$\left.\begin{aligned} \Psi_1 &= -\mu \\ \Psi_2 &= -(\varepsilon+\mu) \\ \Psi_3 &= -(\delta_2+\mu+\tau_2) \\ \Psi_4 &= -\mu \\ \Psi_5 &= -(\mu+\gamma+\phi)(1-R_{0A}) \\ \Psi_6 &= -\left(\frac{(\delta_1+\mu+\tau_1+\omega)(1-(\mathrm{R}_{0A}+R_{00}))-R_{0A}}{(1-R_{0A})}\right) \end{aligned}\right\} \quad (58)$$

The above Eigen values has a negative real part if and only if R_{0A}, R_{00}<1

Global Stability of Disease Free Equilibrium

Theorem 3
The disease free equilibrium of equations (53) is globally asymptotically stable provided R_0<1 and unstable if R_0>1
Proof: Referring to Castillo-Chaves *et al.* (2000), the system of equations (53) can be written as,

$$\begin{aligned} \frac{dx(t)}{dt} &= F(x,y), \\ \frac{dy(t)}{dt} &= G(x,y) \end{aligned} \quad (59)$$

Where $x=(S,E,I_S,I_A,I,R)\in\Re_+^6$ denote the different compartments of uninfected humans, $y=(E,I_S,I_A,I)\in\Re_+^4$ denote the different compartments of infected humans.

The disease free equilibrium (DFE)=(x_0,0), where

$$\mathrm{x}^* = \frac{\Lambda}{\mu} \quad (60)$$

We are required to proof that

$$\frac{dx(t)}{dt} = W(x,0),\ x^* \text{ is globally asymptotically stable, and}$$
$$G(x,y) = Uy - \hat{G}(x,y),\ \ \hat{G}(x,y)\geq 0 \text{ for } (x,y)\in\Omega$$

Case 1: Consider the uninfected subsystem,

$$\frac{dx}{dt} = W(\mathrm{x}, \mathrm{y}) = \begin{pmatrix} \Lambda - (1-\kappa\theta)\beta \dfrac{(I_A + I_S)}{N} S - \mu S \\ \gamma I_A + \tau_1 I_S + \tau_2 I - \mu R \end{pmatrix} \tag{61}$$

When y-0
it implies that $E=I_A=I_S=I=0$ we have

$$\frac{dx}{dt} = W(\mathrm{x}, 0) = \begin{pmatrix} \Lambda - \mu S \\ -\mu R \end{pmatrix} \tag{62}$$

From the equation above we have;

$$\frac{dS}{dt} = \Lambda - \mu S \tag{63}$$

And

$$\frac{dR}{dt} = -\mu R \tag{64}$$

Solving equation (62) first we have

$$\frac{dR}{dt} = -\mu R \tag{65}$$

Using separation method we have;

$$\frac{dR}{} = - \quad dt \tag{66}$$

Integrating both sides we have

$$\ln R = -\mu t + c \tag{67}$$

Taking the e of both sides we have;

$$e^{lnR} = e^{-\mu t + c} = \text{But } e^{ln} = 1$$

Then (67) is given as

$$R(t) = e^{-\mu t + c} \tag{68}$$

Also, by laws of indices we can write (68) as;

$$R(t) = e^{c}.e^{-\mu t} \text{ Let } A = e^{c}$$
$$R(t) = Ae^{-\mu} \tag{69}$$

At initial condition t=0 we have;

$$R(0) = A \tag{70}$$

Putting (68) into (69) we have;

$$R(t) = R(0)e^{-\mu t} \tag{71}$$

$$\lim_{t \to \infty} \mathrm{R(t)} = 0 \tag{72}$$

As $t \to \infty$, $R(t)$=0 Irrespective of the value of $R(0)$

Solving (62) next we have

$$\frac{dS}{dt} = \Lambda - \mu S \tag{73}$$

$$\frac{dS}{dt} + \mu S = \Lambda e^{\mu t} \tag{74}$$

Multiplying both sides by its integrating factor $e^{\int \mu dt}$ we have;

$$e^{\mu t}\left(\frac{dS}{dt} + \mu S\right) = \Lambda e^{\mu t} \tag{75}$$

By virtue of product rule in reverse we have;

$$\frac{d}{dt}(Se^{\mu t}) = \Lambda e^{\mu t} \tag{76}$$

Multiplying both sides by *dt* and integrating both sides we have;

$$S(\mathrm{t})e^{\mu t} = \frac{\Lambda}{\mu}e^{\mu t} + c \tag{77}$$

Dividing both sides by $e^{\mu t}$ we have;

$$S(\mathrm{t}) = \frac{\Lambda}{\mu} + ce^{-\mu t} \tag{78}$$

At initial condition t=0 we have;

$$S(0) - \frac{\Lambda}{\mu} = c \tag{79}$$

Inputting (76) into (75) we have;

$$S(\mathrm{t}) = \frac{\Lambda}{\mu} + \left(S(0) - \frac{\Lambda}{\mu}\right)e^{-\mu t} \tag{80}$$

$$\lim_{t\to\infty} S(\mathrm{t}) = \frac{\Lambda}{\propto} \tag{81}$$

It implies that as $t\to\infty$, $S \to \frac{\Lambda}{\propto}$ regardless of the value of $S(0)$.

Therefore,

$x^* = \left(\frac{\Lambda}{\propto}, 0\right)$ is globally Asymptomatically stable

Condition 2: Consider an infected subsystem

$$\frac{dy}{dt} = G(\mathrm{x},\mathrm{y}) = \begin{pmatrix} (1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S-(\varepsilon+\mu)E \\ (1-\alpha)\varepsilon E-(\mu+\gamma+\phi)I_A \\ \alpha\varepsilon E+\phi I_A-(\delta_1+\mu+\tau_1+d)I_S \\ \omega I_S-(\delta_2+\mu+\tau_2)I \end{pmatrix} \tag{82}$$

From the condition 2 above given that

$$G(x,y) = Uy - \hat{G}(x,y)$$

It follows that $U = \left(\dfrac{dG}{dy}\right)_{A_0}$ recall from above at DFE

$$S \approx N \to \frac{\Lambda}{\propto}$$

$$U = \begin{pmatrix} -(\varepsilon+\mu) & (1-\kappa\theta)\beta & (1-\kappa\theta)\beta & 0 \\ (1-\alpha)\varepsilon & -(\mu+\gamma+\phi) & 0 & 0 \\ \alpha\varepsilon & \phi & -(\delta_1+\mu+\tau_1+d) & 0 \\ 0 & 0 & \omega & -(\delta_2+\mu+\tau_2) \end{pmatrix} \tag{83}$$

$y = \begin{pmatrix} E \\ I_A \\ I_S \\ I \end{pmatrix}$ Then we have;

$$Uy = \begin{pmatrix} (1-\kappa\theta)\beta(I_A+I_S)-(\varepsilon+\mu)E \\ (1-\alpha)\varepsilon E-(\mu+\gamma+\phi)I_A \\ \alpha\varepsilon E+\phi I_A-(\delta_1+\mu+\tau_1+d)I_S \\ \omega I_S-(\delta_2+\mu+\tau_2)I \end{pmatrix} \tag{84}$$

From the condition, we have;

$$\hat{G}(\mathrm{x},\mathrm{y}) = Uy - G(\mathrm{x},\mathrm{y}) = \begin{pmatrix} (1-\kappa\theta)\beta(I_A+I_S)-(\varepsilon+\mu)E \\ (1-\alpha)\varepsilon E-(\mu+\gamma+\phi)I_A \\ \alpha\varepsilon E+\phi I_A-(\delta_1+\mu+\tau_1+d)I_S \\ \omega I_S-(\delta_2+\mu+\tau_2)I \end{pmatrix} - \begin{pmatrix} (1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S-(\varepsilon+\mu)E \\ (1-\alpha)\varepsilon E-(\mu+\gamma+\phi)I_A \\ \alpha\varepsilon E+\phi I_A-(\delta_1+\mu+\tau_1+d)I_S \\ \omega I_S-(\delta_2+\mu+\tau_2)I \end{pmatrix} \tag{85}$$

$$\hat{G}(\mathrm{x},\mathrm{y}) = \begin{pmatrix} (1-\kappa\theta)\beta(I_A+I_S)\left(1-\dfrac{S}{N}\right) \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{86}$$

Since $S \le N, 1-\left(\dfrac{S}{N}\right) \ge 0$ implies $\hat{G}(\mathrm{x},\mathrm{y}) \ge 0$ .Hence the two conditions C1 and C2 of Lemma 1 are satisfied.

This shows that the system is globally asymptotically stable for the DFE

ENDEMIC EQUILIBRIUM POINTS OF THE MODEL

The equilibrium state in the presence of infection is known as the Endemic equilibrium.

Let $B_0 = (S^{**}, E^{**}, I_A^{**}, I_S^{**}, I^{**}, R^{**})$ be the Endemic equilibrium points.

To solve for the Endemic equilibrium points $I_A = I_S \neq 0$

$$\begin{pmatrix} S^{**} \\ E^{**} \\ I_A^{**} \\ I_S^{**} \\ I^{**} \\ R^{**} \end{pmatrix} = \begin{pmatrix} \frac{\Lambda}{K} \\ \frac{\Lambda\eta}{KL} \\ \frac{\Lambda Q\varepsilon\eta}{LKM} \\ \frac{\Lambda\eta\varepsilon(M\alpha - Q\phi)}{MLKN} \\ \frac{\Lambda\omega\eta(M\alpha + Q\phi)}{NMLKP} \\ \frac{\Lambda(\mathrm{M}\alpha\varepsilon(\mathrm{P}\tau_1 + \omega\tau_2) + Q\varepsilon(\gamma\,\mathrm{PN} + \mathrm{P}\phi\tau_1 + \omega\phi\tau_2))}{PNMLK\mu} \end{pmatrix} \tag{87}$$

Where, $K = (\eta + \mu),\ L = (\mu + \varepsilon),\ M = (\mu + \gamma + \phi),$
$N = (\delta_1 + \mu + \tau_1 + \omega),\ P = (\delta_2 + \mu + \tau_2)$

ANALYTICAL SOLUTION OF EQUATION (4.4.1) USING HOMOTOPY PERTURBATION METHOD

The system of equation

$$\begin{cases} \frac{dS}{dt} + (1-\kappa\theta)\beta\frac{(I_A + I_S)}{N}S + \mu S - \Lambda = 0 \\ \frac{dE}{dt} - (1-\kappa\theta)\beta\frac{(I_A + I_S)}{N}S + (\varepsilon + \mu)E = 0 \\ \frac{dI_A}{dt} - (1-\alpha)\varepsilon E + (\mu + \gamma + \phi)I_A = 0 \\ \frac{dI_S}{dt} - \alpha\varepsilon E - \phi I_A + (\delta_1 + \mu + \tau_1 + d)I_S = 0 \\ \frac{dI}{dt} = \omega I_S - (\delta_2 + \mu + \tau_2)I = 0 \\ \frac{dR}{dt} - \gamma I_A - \tau_1 I_S - \tau_2 I + \mu R = 0 \end{cases} \tag{88}$$

With the initial conditions given as;
$S(0)=S_0$, $E(0)=E_0$, $I_A(0)=I_{A0}$, $I_S(0)=I_{S0}$, $I(0)=I_0$, $R(0)=R_0$ Defining the solution

$$\left.\begin{aligned} S &= u_0 + pu_1 + p^2u_2 + \ldots \\ E &= v_0 + pv_1 + p^2v_2 + \ldots \\ I_A &= w_0 + pw_1 + p^2w_2 + \ldots \\ I_S &= x_0 + px_1 + p^2x_2 + \ldots \\ I &= y_0 + py_1 + p^2y_2 + \ldots \\ R &= z_0 + pz_1 + p^2z_2 + \ldots \end{aligned}\right\} \tag{89}$$

We construct an homotopy:

$$\begin{cases} (1-\mathrm{p})\dfrac{dS}{dt} + p\left(\dfrac{dS}{dt} + (1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S + \mu S - \Lambda\right) = 0 \\ (1-\mathrm{p})\dfrac{dE}{dt} + p\left(\dfrac{dE}{dt} - (1-\kappa\theta)\beta\dfrac{(I_A+I_S)}{N}S + (\varepsilon+\mu)E\right) = 0 \\ (1-\mathrm{p})\dfrac{dI_A}{dt} + p\left(\dfrac{dI_A}{dt} - (1-\alpha)\varepsilon E + (\mu+\gamma+\phi)I_A\right) = 0 \\ (1-\mathrm{p})\dfrac{dI_S}{dt} + p\left(\dfrac{dI_S}{dt} - \alpha\varepsilon E - \phi I_A + (\delta_1+\mu+\tau_1+d)I_S\right) = 0 \\ (1-\mathrm{p})\dfrac{dI}{dt} + p\left(\dfrac{dI}{dt} - \omega I_S + (\delta_2+\mu+\tau_2)I\right) = 0 \\ (1-\mathrm{p})\dfrac{dR}{dt} + p\left(\dfrac{dR}{dt} - \gamma I_A - \tau_1 I_S - \tau_2 I + \mu R\right) = 0 \end{cases}$$

If $p\rightarrow 1$, we recall the solution of the series
Substituting equation (4) into equation (3), we will have;

$$\begin{cases} (1-\mathrm{p})(u'_0 + pu'_1 + p^2u'_2 + \ldots) + \mathrm{p}\left(\begin{array}{l}(u'_0 + pu'_1 + p^2u'_2 + \ldots) + (1-\kappa\theta)\beta((w_0 + pw_1 + p^2w_2 + \ldots + x_0 + \\ px_1 + p^2x_2 + \ldots)(u_0 + pu_1 + p^2u_2 + \ldots) + \mu(u_0 + pu_1 + p^2u_2 + \ldots) - \Lambda\end{array}\right) = 0 \\ (1-\mathrm{p})(\mathrm{v}'_0 + pv'_1 + p^2\,\mathrm{v}'_2 + \ldots) + \mathrm{p}\left(\begin{array}{l}(\mathrm{v}'_0 + pv'_1 + p^2\,\mathrm{v}'_2 + \ldots) - (1-\kappa\theta)\beta((w_0 + pw_1 + p^2w_2 + \ldots + x_0 + px_1 + \\ p^2x_2 + \ldots)(u_0 + pu_1 + p^2u_2 + \ldots)) + (\varepsilon+\mu)(\mathrm{v}_0 + pv_1 + p^2v_2 + \ldots)\end{array}\right) = 0 \\ (1-\mathrm{p})(\mathrm{w}'_0 + pw'_1 + p^2\,\mathrm{w}'_2 + \ldots) + \mathrm{p}\left(\begin{array}{l}(\mathrm{w}'_0 + pw'_1 + p^2\,\mathrm{w}'_2 + \ldots) - (1-\alpha)\varepsilon(v_0 + pv_1 + p^2v_2 + \ldots) \\ +(\mu+\gamma+\phi)(w_0 + pw_1 + p^2w_2 + \ldots)\end{array}\right) = 0 \\ (1-\mathrm{p})(\mathrm{x}'_0 + px'_1 + p^2\,\mathrm{x}'_2 + \ldots) + \mathrm{p}\left(\begin{array}{l}(\mathrm{x}'_0 + px'_1 + p^2\,\mathrm{x}'_2 + \ldots) - \alpha\varepsilon(v_0 + pv_1 + p^2v_2 + \ldots) - \phi(w_0 + pw_1 \\ +p^2w_2 + \ldots) + (\delta_1+\mu+\tau_1+d)(x_0 + px_1 + p^2x_2 + \ldots)\end{array}\right) = 0 \\ (1-\mathrm{p})(\mathrm{y}'_0 + py'_1 + p^2\,\mathrm{y}'_2 + \ldots) + \mathrm{p}\left(\begin{array}{l}(\mathrm{y}'_0 + py'_1 + p^2\,\mathrm{y}'_2 + \ldots) - \omega(\mathrm{x}_0 + px_1 + p^2x_2 + \ldots) \\ +(\delta_2+\mu+\tau_2)(y_0 + py_1 + p^2y_2 + \ldots)\end{array}\right) = 0 \\ (1-\mathrm{p})(\mathrm{z}'_0 + pz'_1 + p^2\,\mathrm{z}'_2 + \ldots) + \mathrm{p}\left(\begin{array}{l}(\mathrm{z}'_0 + pz'_1 + p^2\,\mathrm{z}'_2 + \ldots) - \gamma(w_0 + pw_1 + p^2w_2 + \ldots) - \tau_1(\mathrm{x}_0 + px_1 \\ +p^2x_2 + \ldots) - \tau_2(y_0 + py_1 + p^2y_2 + \ldots) + \mu(z_0 + pz_1 + p^2z_2 + \ldots)\end{array}\right) = 0 \end{cases}$$

We now compare the identical powers of p as follow:

$$
\begin{cases}
S(\mathrm{t}) = \mathrm{S}_0 + \begin{pmatrix} \Lambda - (1-\kappa\theta)\beta \\ (I_{A0} + I_{S0})S_0 - \mu S_0 \end{pmatrix} t + \\
\begin{pmatrix} -(1-\kappa\theta)\beta \begin{pmatrix} (\Lambda - (1-\kappa\theta)\beta(I_{A0} + I_{S0})S_0 - \mu S_0)I_{A0} + ((1-\alpha)\varepsilon E_0 - (\mu+\gamma+\phi)I_{A0})S_0 \\ +(\Lambda - (1-\kappa\theta)\beta(I_{A0} + I_{S0})I_{S0} + (\alpha\varepsilon E_0 + \phi I_{A0} - (\delta_1 + \mu + \tau_1 + d)I_{S0})S_0 \end{pmatrix} \\ +\mu(\Lambda - (1-\kappa\theta)\beta(I_{A0} + I_{S0})S_0 - \mu S_0) \end{pmatrix} \frac{t^2}{2} \\
E(t) = E_0 + \begin{pmatrix} (1-\kappa\theta)\beta(I_{A0} + \\ I_{S0})S_0 - (\varepsilon+\mu)E_0 \end{pmatrix} t + \\
\begin{pmatrix} (1-\kappa\theta)\beta \begin{pmatrix} (\Lambda - (1-\kappa\theta)\beta(I_{A0} + I_{S0})S_0 - \mu S_0)I_{A0} + ((1-\alpha)\varepsilon E_0 - (\mu+\gamma+\phi)I_{A0})S_0 \\ +(\Lambda - (1-\kappa\theta)\beta(I_{A0} + I_{S0})I_{S0} + (\alpha\varepsilon E_0 + \phi I_{A0} - (\delta_1 + \mu + \tau_1 + d)I_{S0})S_0 \end{pmatrix} \\ +(\varepsilon+\mu)((1-\kappa\theta)\beta(I_{A0} + I_{S0})S_0 - (\varepsilon+\mu)E_0) \end{pmatrix} \frac{t^2}{2} \\
I_A(\mathrm{t}) = I_{A0} + \begin{pmatrix} (1-\alpha)\varepsilon E_0 \\ -(\mu+\gamma+\phi)I_{A0} \end{pmatrix} t + \begin{pmatrix} (1-\alpha)\varepsilon((1-\kappa\theta)\beta(I_{A0} + I_{S0})S_0 - (\varepsilon+\mu)E_0 \\ -(\mu+\gamma+\phi)((1-\alpha)\varepsilon E_0 - (\mu+\gamma+\phi)I_{A0}) \end{pmatrix} \frac{t^2}{2} \\
I_S(\mathrm{t}) = I_{S0} + \begin{pmatrix} \alpha\varepsilon E_0 + \phi I_{A0} \\ -(\delta_1 + \mu + \tau_1 + d)I_{S0} \end{pmatrix} t + \begin{pmatrix} \alpha\varepsilon((1-\kappa\theta)\beta(I_{A0} + I_{S0})S_0 - (\varepsilon+\mu)E_0) \\ +\phi((1-\alpha)\varepsilon E_0 - (\mu+\gamma+\phi)I_{A0}) \\ -(\delta_1 + \mu + \tau_1 + d) \\ (\alpha\varepsilon E_0 + \phi I_{A0} - (\delta_1 + \mu + \tau_1 + d)I_{S0}) \end{pmatrix} \frac{t^2}{2} \\
I(\mathrm{t}) = I_0 + \left(\omega I_{S0} - (\delta_2 + \mu + \tau_2)I_0\right) t + \begin{pmatrix} \omega(\alpha\varepsilon E_0 + \phi I_{A0} - (\delta_1 + \mu + \tau_1 + d)I_{S0}) \\ -(\delta_2 + \mu + \tau_2)(\omega I_{S0} - (\delta_2 + \mu + \tau_2)I_0) \end{pmatrix} \frac{t^2}{2} \\
R(\mathrm{t}) = R_0 + \left(\gamma I_{A0} + \tau_1 I_{S0} + \tau_2 I_0 - \mu R_0\right) t + \begin{pmatrix} \gamma((1-\alpha)\varepsilon E_0 - (\mu+\gamma+\phi)I_{A0}) \\ +\tau_1(\alpha\varepsilon E_0 + \phi I_{A0} - (\delta_1 + \mu + \tau_1 + d)I_{S0}) \\ +\tau_2(\omega I_{S0} - (\delta_2 + \mu + \tau_2)I_0) \\ -\mu(\gamma I_{A0} + \tau_1 I_{S0} + \tau_2 I_0 - \mu R_0) \end{pmatrix} \frac{t^2}{2}
\end{cases}
$$

Table 1: Notation and definition of variables and parameter

Variable	Definition
S (t)	The population of susceptible human at a given time (*t*)
E (t)	The population of exposed human at a given time (*t*)
IA (t)	The population of infectious asymptomatic human at a given time (*t*)
IS (t)	The population of infectious asymptomatic human at a given time (*t*)
I (t)	The population of isolated asymptomatic human at a given time (*t*)
R (t)	The population of recovered human at a given time (*t*)
Parameter	**Definition**
Λ	Recruitment rate of individuals into the population (Birth and immigration)
β	Effective contact rate between susceptible human and infectious human population
κ	Compliance level to usage of hand sensitizer
θ	Compliance level to usage of nose mask
ε	Disease incubation rate in humans (susceptible or exposed)
α	Proposed of exposed human
γ	Natural recovery rate of the asymptomatic infected *i*
τ_1	Compliance rate of infectious humans to drug
μ	Natural death rate of humans
φ	Rate at which asymptomatic human develops the symptoms
δ_1	COVID-19 induced death rate to infectious human population at home
τ_2	Compliance rate of infectious human to drugs and care at the infectious center
δ_2	COVID-19 induced death rate to infectious human isolation center
ω	The rate at which individual visit the isolation center

NUMERICAL SIMULATION AND RESULTS

In this chapter, the model will be analyzed using the parameter values as well as estimated initial values of the susceptible, exposed, infected, recovered, and vaccinated individuals. The results obtained will be discussed.
MATLAB was used to get the numerical solution of the model using ode 45.
Table 2 parameter and estimated values for initial conditions for the SEI_SI_AIR models.

Table 2: Variables and model parameters values

Parameter and variable	Value	Source
$S(t)$	211,660,928	Worldometer (2021)
$E(t)$	196,763,667	NCDC 29 2021
$I_A(t)$	14,549,903	Estimated
$I_S(t)$	104855	Estimated
$I(t)$	69904	Estimated
$R(t)$	165047	NCDC 3, 2021
Λ	0.02537	Assumed
β	0.0805	Ahmed *et al*. (2021)
ε	0.004	Assumed
α	0.3	Assumed
γ	0.05	Assumed
τ_1	0.0016728	Ahmed *et al*. (2021)
M	0.0106	Ahmed *et al*. (2021)
φ	0.01	Assumed
δ_1	0.0016728	Ahmed *et al*. (2021)
τ_2	0.00200000	Assumed
δ_2	0.0015	Assumed
ω	0.1	Assumed

NCDC (2021)

DISCUSSION OF RESULTS

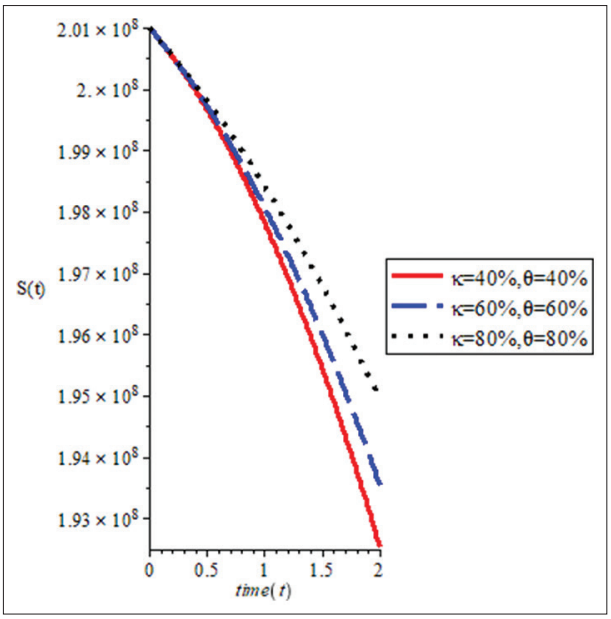

Figure 2: Is the graph of susceptible individuals against time varying the percentage of compliance level of both Hand sanitizer and Nose mask. It is observed that the population susceptible individual increases as the rate of the compliance rate of Hand sanitizer and Nose mask increases.

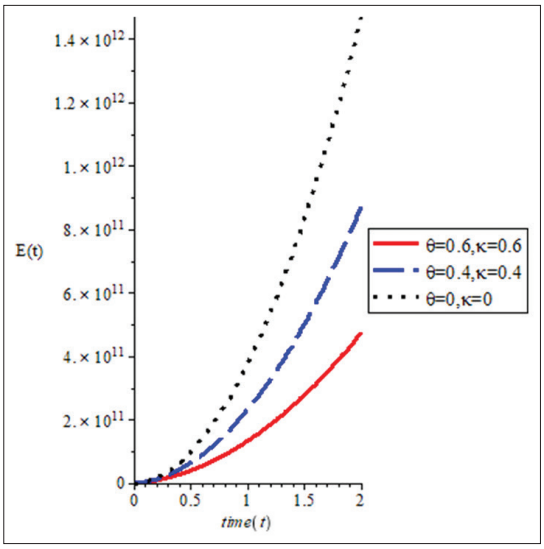

Figure 3: Is the graph of exposed individuals against time for different compliance level. It is observed that the population of exposed individuals increases as the compliance rate to Hand sanitizer and nose mask decreases.

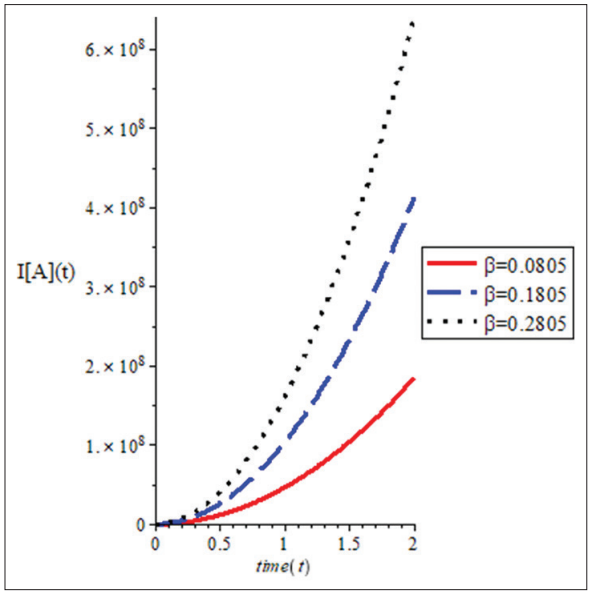

Figure 4: Is the graph of Infected Asymptomatic Individuals against time at different contact rate. It is observed that the population of the asymptomatic individuals increases as the contact rates increases.

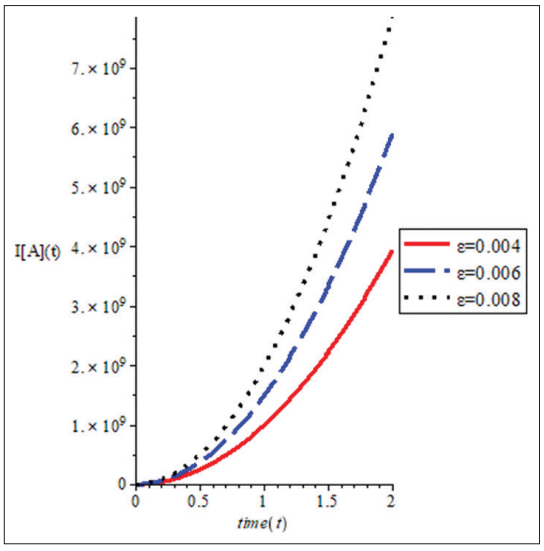

Figure 5: Is the graph of infected asymptomatic Individuals against time at different COVID-19 incubation rate. It is observed that the population of the asymptomatic individuals increases as the COVID-19 incubation period increases.

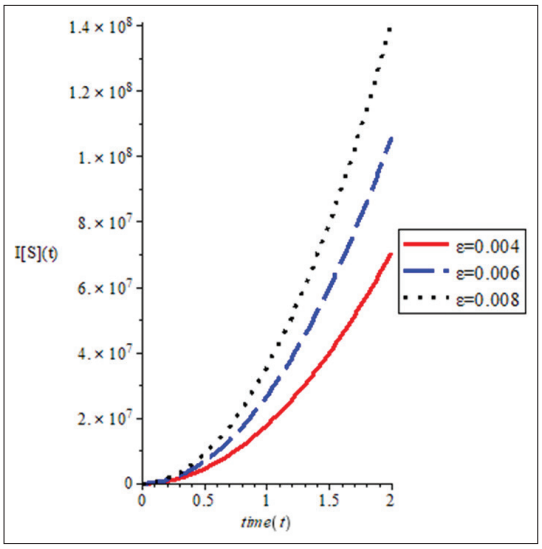

Figure 6: Is the graph of infected symptomatic individuals against time for different COVID-19 incubation rate. It is observed that the population of the symptomatic individuals increases as the COVID-19 incubation rates increases.

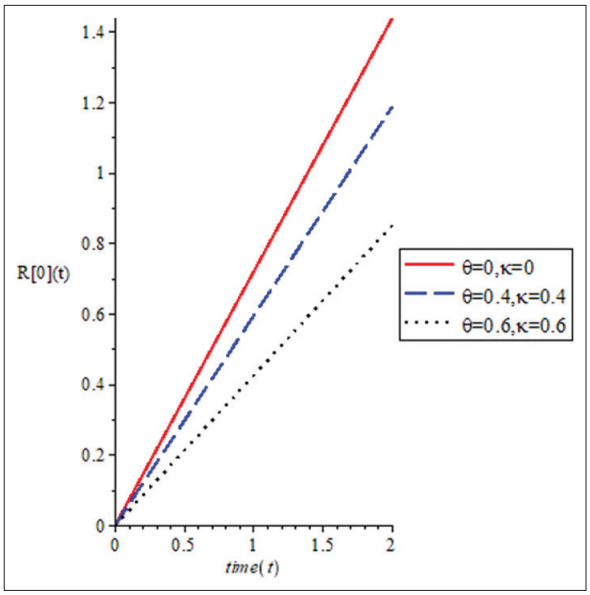

Figure 7: Is the graph of infected asymptomatic individuals against time at different contact rate. It is observed that the population of the asymptomatic individuals increases as the contact rates increases.

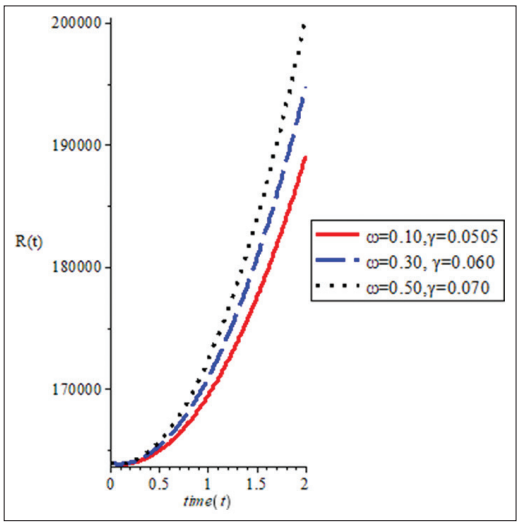

Figure 8: Is the graph of recovery individuals against time varying both the rate at which Individual moves to the isolation center and natural recovery rate of the asymptomatic individuals. It is observed that the population of recovery individuals increases as their compliance rate to go to the isolation center and natural recovery rate increases.

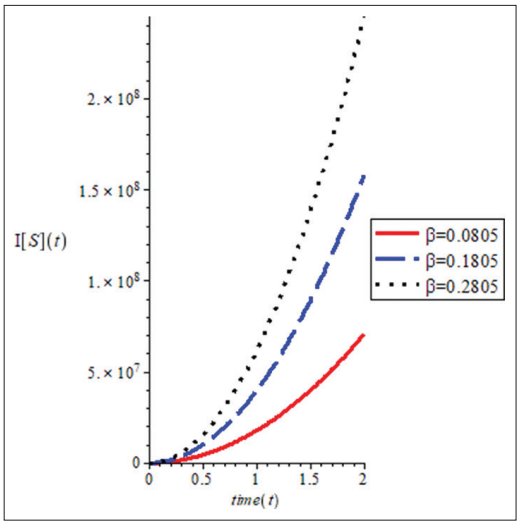

Figure 9: Is the graph of recovery individuals against time varying both the treatment rate at the isolation center and treatment using self-medication. It is observed that the population of recovery individuals increases as the treatment rate at the isolation center and treatment using self-medication increases.

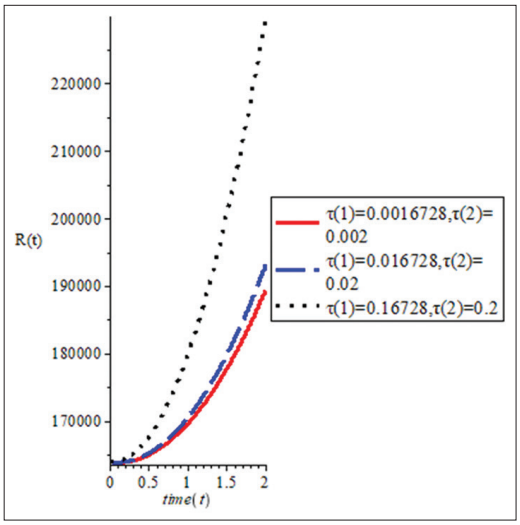

Figure 10: Graph of the basic reproduction number against time varying at different compliance level to hand sanitizers and nose masks. It is observed that the decrease in the compliance level to safety measures leads to an increase in the Basic Reproduction Number. At (0–40) % compliance rate to safety measures the Basic Reproduction number spiked above one. This implies that there would be an outbreak of the disease if there are no compliance to safety measures.

SUMMARY

COVID-19 virus is the most dreadful diseases that could be transmitted from human. To curb its spread a mathematical model was proposed in this work so as to understand the transmission dynamics of the disease and to proffer solution by introducing treatment to facilitate the prevention of the spread of the virus.
The population under consideration was a non-constant population. The EI_SI_AI models were considered and the disease free points were obtained. Their basic reproduction number were obtained using the next generation matrix approach. The stability of the disease free points were analyzed. With estimated values for parameters and initial numbers of the population classes,
MATLAB was used to get the numerical solution of the model using ode45.

CONCLUSION

In this study, the mathematical model for the control of the transmission dynamics and simulation of coronavirus (COVID-19) was developed using a system of first order differential equations. The model

has two equilibrium states; Disease-Free Equilibrium (DFE) and Endemic Equilibrium (EE). The basic reproduction number R_0 of the model was obtained. The Disease-Free Equilibrium (DFE) was analyzed on both the local and global stability. The result from the analysis of the DFE showed that, the DFE is locally asymptotically stable and the DFE is globally asymptotically stable if $R_0<1$. The model equations were solved analytically using Homotopy Perturbation Method (HPM). The solutions from the Homotopy Perturbation Method (HPM) were used for the graphical simulation.

Variables and parameters were estimated from the analytical solution. The analytical solutions of the model were presented graphically to have a better understanding of the model. Figures 1-10 are the different graph of the solution using the populations of human against time with different parameters of the model. Maple software was used to carry out the graphical solutions.

In Figure 1, it is observed that the susceptible individuals increases as the compliance level of Hand sanitizer and Nose mask increases per day which makes the population less exposed to the Novel coronavirus (4.9), Figure 9 also shows that as the treatment rate for Isolated symptomatic individuals increases the recovery population increase, thereby its observed that the disease will be eradicated completely from the population with time.

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