Original Research Article

Effective Management of COVID-19 in Nigeria: Investigating the Impact of Treatment and Prevention

ABSTRACT

In order to examine the controllability of Covid-19, a non-linear deterministic mathematical model that takes hospitalization, treatment, and prevention strategies into account is developed and examined. The model's solution has been tested for existence, uniqueness, and positivity; the findings demonstrate that the answer is both unique and exists. The effective reproduction number (ℓ) is a threshold parameter that we found to be significant. Covid-19 can be contained and eliminated from the population in a finite amount of time if Reff <1, which indicates the existence of a disease-free equilibrium that is locally and globally asymptotically stable. If Reff > 1, on the other hand, the illness infiltrates and becomes endemic in the population.

Key words: Stability, effective management, Reproduction Number, Model-fitting, Sensitivity analysis and Covid-19

1. INTRODUCTION

The infectious disease corona virus (COVID-19), which was first identified in Wuhan, the Chinese capital, in 2019, was the cause of the coronavirus pandemic of 2019–20. [6]. The World Health Organization received the first report on it on December 31, 2019 [15].

The most common symptoms of Covid-19 are fever, dry cough, and breathing difficulties; sore throat, muscle soreness, and sputum production are less common [16].Numerous research projects, including mathematical models to understand the virus's origin and spread, have been undertaken since its discovery. Nigeria is among the 210 nations impacted worldwide. On February 27, 2020, the first case was verified in Lagos State. The 44-year-old Italian citizen in this index case arrived back at a medical facility on February 26, 2020, having left Milan, Italy, on February 24 [16]. 2,558 cases had been reported nationwide as of May 3, 2020, spanning 35 states and the Federal Capital Territory (FCT). Of these, 1,767 (69%) are men; the most affected age group was 21 to 30 years old (23%); 210 (8%) had previously traveled abroad; 400 (15.6%) of the cases have been discharged; 87 deaths have been reported; the case fatality rate (CFR) of confirmed cases is now 3.4%, with regional variations ranging from 0 to 15.2%. Before the COVID-19 outbreak was reported in Africa, The WHO released guidance on epidemic preparedness after determining a clear connection between the continent and China. Nigeria is among the top thirteen nations deemed to be at high risk of importing COVID-19 due to a direct connection or a significant volume of travel to and from China. In order to prevent overcrowding in the healthcare system, the WHO also recommended that nations build their ability to quickly identify cases. At Level 3, the highest level of public health emergency in the nation, a multi-sectorial national emergency operation center led by the NCDC was triggered upon the discovery of the index case. The next step was the state-led contact deployment of Rapid Response Teams, tracking and additional reaction exercises. Additionally, the verified case was transported to a medical institution specifically meant to treat COVID-19 [16]. In March 2020, the rate of deaths per number of identified cases was 4.4%, ranging from 0.2% -15%, depending on age group and other health conditions. In China, reports of COVID-19 infections were 75,465 in February 2020 [6]. Different human coronaviruses are known to produce both common colds and more serious infections including Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS).The most recent revelation [15] is what causes Covid-19. Person-to-person transmission emerged as the main form of communication over time. While patients with symptomatic COVID-19 have traditionally been the main source of transmission, recent studies show that SARS-CoV-2 is also carried by asymptomatic patients and those who are in the incubation period. Symptoms may start to show up two days to two weeks after the virus is introduced [14]. The WHO has classified this virus as a pandemic because it has spread to many different countries [15]. COVID-19 swiftly expanded to several countries before the WHO classified it as a pandemic. The pandemic in China peaked in late January or early February 2020, according to estimates from a collaborative World Health Organization [15] fact-finding mission, and the number of new cases sharply decreased in early March. Several mathematical models have been used to understand the behavior of this virus.

The majority of people, particularly those at the local level, are unaware of how important it is to follow all control requirements. Some even think that COVID-19 is a tool the government uses to accomplish some vague goal. [16] claims daily new occurrences, implying that these safety measures are not followed. "There needs to be a very major adaptation" to the established measures we've been using to fight COVID-19, says [14], an epidemiologist and director of ICAP, a global health organization at Columbia University [11]. Low-income nations with failing healthcare systems struggle with large populations of impoverished people and cram megacities.

Many mathematical models are being created to forecast future coronavirus disease 2019 (COVID-19) epidemics in the United States and globally. The predictability of these outbreaks greatly influences the speed and vigor of government response. While the relative effectiveness of different therapies in terms of infections is probably more dependable, estimates derived from models regarding COVID-19 might also add to ambiguity and concern. For example, it matters to know if Nigeria would experience tens of thousands or maybe hundreds of thousands of fatalities. Since the actions taken will, of course, determine the final numerical reality, the primary focus should be on the kinds of interventions that could help lower these numbers. Forecasting future health care demand requires model estimates, which include the number of beds that will be needed in intensive care units, the anticipated locations and times of ventilator shortages, and the number of healthcare professionals needed to respond appropriately. For planning purposes, short-term predictions might be quite important. However, concentrating on long-term "guesses" for these objectives is typically superfluous. Furthermore, national, state, and local policies are being made using predictions derived from computer models.

Significance of the study

Despite concerted efforts by government and non-governmental agencies to curb the spread of corona virus, the death rates have continued to be on the increase on a yearly basis. Many mathematical models have been formulated since the notice of this dead disease to study the transmission and control of the disease by incorporating, isolation and personal hygiene. Few of the models formulated have really looked at the impact of protection measures. In this work, we have formulated a mathematical model to study the control measures incorporating quarantine, protection and hospitalization.

The best result is achieved when these three control measures are combined and is applicable to our Nigeria environment.

2. PRELIMINARIES

We introduce a deterministic compartmental model that explains the dynamics of COVID-19 transmission when certain control measures are in place. The dynamics of the disease in Nigeria are captured by a system of nine (9) nonlinear ordinary differential equations that make up the model. The human population is split into nine (9) compartments in this model: Hospitalized (H), Quarantine class (Q), Dead (D), Recoveries (R), Exposed class (E), Symptomatically Infectious (Is), Susceptible (S), Protection class (A), Dead (D), and Asymptomatically Infectious (Ias).

MATERIAL AND METHODS

NONLINEAR SYSTEMS

Disease models in general are normally represented by systems of non-linear differential equations. An n^{th}-order system of continuous differential equations has the following form:

$$\left.\begin{aligned} \dot{x}_1(t) &= f_1\left(x_1(t), x_2(t), \ldots, x_n(t)\right), \\ \dot{x}_2(t) &= f_2\left(x_1(t), x_2(t), \ldots, x_n(t)\right), \\ \vdots \quad & \quad\ \vdots \qquad\quad \vdots \qquad\qquad \vdots \\ \dot{x}_n(t) &= f_n\left(x_1(t), x_2(t), \ldots, x_n(t)\right) \end{aligned}\right\}$$

which can be expressed in matrix form as;

$$\dot{\boldsymbol{x}}(t) = f\left(\boldsymbol{x}(t), t\right)$$

where $\boldsymbol{x} = (x_1, x_2, ..., x_n)^T$ and $f = (f_1, f_2, ..., f_n)^T$.

In general, one does not seek detailed solutions either in numerical or analytical form, but rather one seeks to characterize some aspects of system behaviour. For example one might ask whether there are equilibrium points and whether they are stable. In nonlinear systems, one might look, in addition to equilibrium points, for threshold effects. The approach therefore, includes characterizing in broad terms the critical aspects of the system behaviour.

The following is an existence theorem for solutions of the system (3.1).

1.1 Theorem

Let $\boldsymbol{x} = (x_1, x_2, ..., x_n)^T$ and $f\left(\boldsymbol{x}(t), t\right)$ denote the vector functions, $\left\{ f_1\left(x_1(t), x_2(t), \ldots, x_n(t)\right), \ldots, f_n\left(x_1(t), x_2(t), \ldots, x_n(t)\right)\right\}$. Suppose $f\left(\boldsymbol{x}(t), t\right)$ and $\partial f / \partial x_n, i = 1, 2, \ldots, n$, are continuous on the strip;

$$\Re = \left\{\left(X, t\right) \in \mathbb{R}^{n+1}; a \le t \le b, X \text{ arbitrary}\right\}$$

containing the point $\left(X_0, t_0\right)$. Assume further that there exists a positive constant *L* such that, for $i = 1, 2, \ldots, n$,

$$\left|\frac{\partial f}{\partial x_j}(\boldsymbol{x},t)\right| \le L, \text{ for all } (\boldsymbol{x},t) \in \Re$$

Then the initial value problem;

$$\dot{\boldsymbol{x}}(t) = f(\boldsymbol{x}(t),t), \quad \boldsymbol{x}(t_0) = x_0$$

has a unique solution on the entire interval $a \le t \le b$.

1.2 Definition (Equilibrium points)

A vector $\boldsymbol{X}$ is an equilibrium point for a dynamical system if once the state vector is equal to $\overline{\boldsymbol{x}}$ it remains equal to $\overline{\boldsymbol{x}}$ for all future time. Consider for example the system

$$\dot{\boldsymbol{x}}(t) = f(\boldsymbol{x}(t),t)$$

then an equilibrium point is a state $\overline{\boldsymbol{x}}$ satisfying

$f(\overline{x},t) = 0$ for all time *t*.

An analysis of a nonlinear dynamical system may devote considerable attention to the characterization of the equilibrium points. In the linear systems equilibrium points are basically solutions to linear equations. The nonlinear case is different in two essential respects:

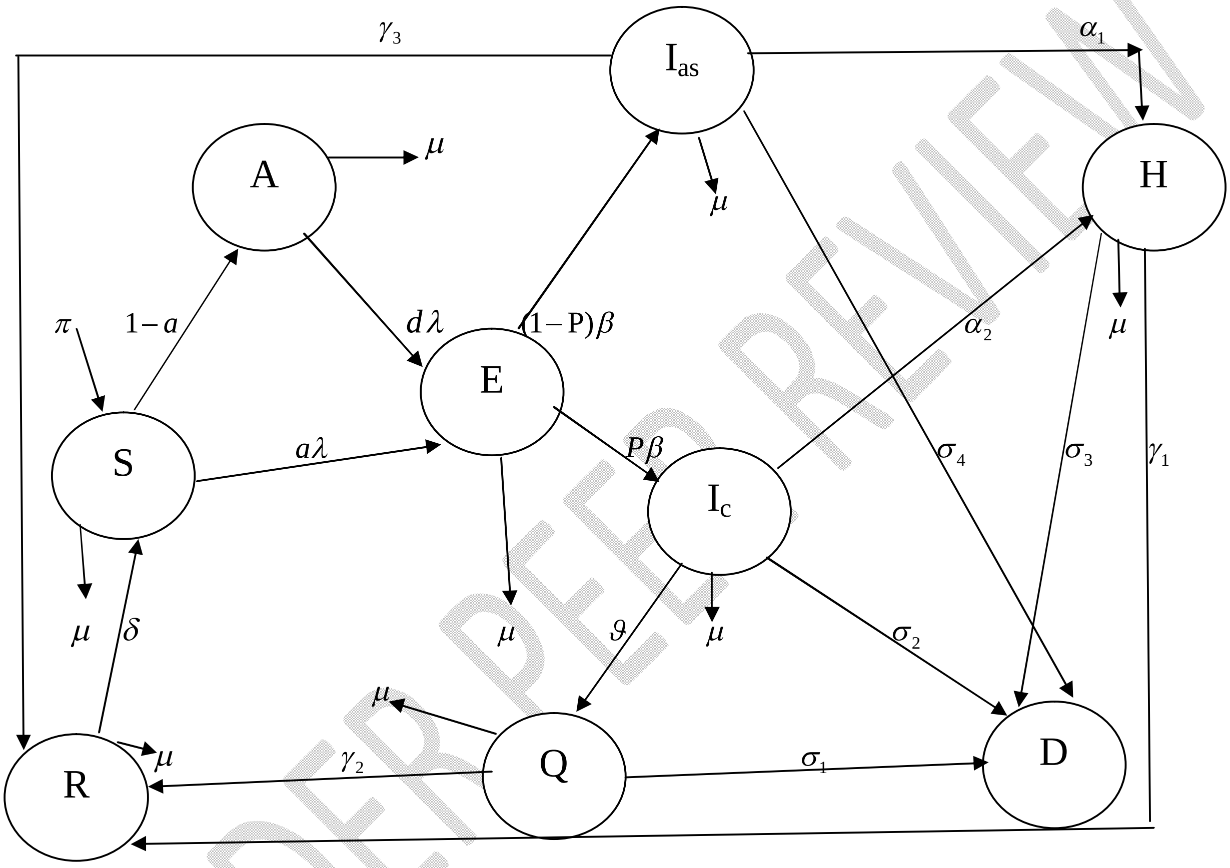
1. First, since the equilibrium points are solutions, in this case, to nonlinear equations, finding such solutions is somewhat more of an accomplishment than in the linear case.
2. The equilibrium point distribution is potentially more complex in the nonlinear case than in the linear

1.3 Remark: A system may have none, one or any number of equilibrium points in virtually a spatial pattern in state space.

Table 1: Description of the Parameter used in this model

parameter	***Description***
Π	rate of recruitment into the susceptible class
A	proportion of the susceptible class that are protected
C	rate of contact between infected class and those that are not protected
D	proportion of protected class that lose their protection
***c*0**	rate of contact between infected class and those that are protected
κ_1	probability that a contact with symptomatomatically infectious persons will result to infection
κ_2	probability that a contact with asymptomatomatically infectious persons will result to infection
α_1	the rate at which the asymptomatically infectious persons are hospitalized and treated
α_2	the rate at which the symptomatically infectious persons are hospitalized and treated
σ_1	death rate for self-isolated persons
σ_2	death rate for symptomatically infected persons
σ_3	death rate for hospitalized persons
σ_4	death rate for asymptomatically infected persons
P	proportion of exposed class that becomes symptomatically infectious
B	incubation rate of corona virus
γ_1	rate of recovery for hospitalized persons
γ_2	rate of recovery for self-isolated persons
γ_3	rate of recovery for asymptomatically infected persons
Q	the proportion of symptomatically infectious humans that self-isolate
Δ	proportion of recovered class that becomes susceptible
μ	human natural death rate

Diagram 1: A compartmentalized diagram showing the covid-19 model with control measures



Where $\lambda = c(k_1 I_s + k_2 I_{as})$

The model equations are;

$$\frac{dS(t)}{dt} - \pi + \delta R - ac(k_1 I_s + k_2 I_{as})S - (1-a)S - \mu S$$

$$\frac{dA(t)}{dt} = (1-a)S(t) - cd(k_1 I_s + k_2 I_{as})A - \mu A$$

$$\frac{dE(t)}{dt} = ac(k_1 I_s + k_2 I_{as})S + cd(k_1 I_s + k_2 I_{as})A - (\beta + \mu)E(t)$$

$$\frac{dI_{as}(t)}{dt} = (1-p)\beta E - (\alpha_1 + \sigma_4 + \gamma_3 + \mu)I_{as}(t)$$

$$\frac{dI_s(t)}{dt} = p\beta E - (\alpha_2 + \sigma_2 + q + \mu)I_s(t)(1) \qquad (1)$$

$$\frac{dH(t)}{dt} = \alpha_1 I_{as} + \alpha_2 I_s - (\sigma_3 + \gamma_1 + \mu)H(t)$$

$$\frac{dQ(t)}{dt} = qI_s - (\sigma_1 + \gamma_2 + \mu)Q(t)$$

$$\frac{dD(t)}{dt} = \sigma_1 Q + \sigma_2 I_s + \sigma_3 H + \sigma_4 I_{as}$$

$$\frac{dR_h(t)}{dt} = \gamma_1 H + \gamma_2 Q + \gamma I_{as} - (\delta + \mu)R_s(t)$$

Disease-free equilibrium

The equilibrium points of the model system are the steady state solutions obtained when the right hand of the system (1) is to zero. That is the solution to the equations

$$\pi + \delta R - ac(k_1 I_s + k_2 I_{as})S - (1-a)S - \mu S = 0,$$

$$(1-a)S(t) - cd(k_1 I_s + k_2 I_{as})A - \mu A = 0.$$

$$ac(k_1 I_s + k_2 I_{as})S + cd(k_1 I_s + k_2 I_{as})A - (\beta + \mu)E(t) = 0,$$

$$(1-p)\beta E - (\alpha_1 + \sigma_4 + \gamma_3 + \mu)I_{as}(t) = 0,$$

$$p\beta E - (\alpha_2 + \sigma_2 + q + \mu)I_s(t) = 0,$$

$$\alpha_1 I_{as} + \alpha_2 I_s - (\sigma_3 + \gamma_1 + \mu)H(t) = 0,$$

$$qI_s - (\sigma_1 + \gamma_2 + \mu)Q(t) = 0,$$

$$\sigma_1 Q + \sigma_2 I_s + \sigma_3 H + \sigma_4 I_{as} = 0,$$

$$\gamma_1 H + \gamma_2 Q + \gamma_3 I_{as} - (\delta + \mu)R_h(t) = 0,$$

Disease-free equilibrium points of the model are the solutions to (2) obtained when there is no disease in the population. That is the solution obtained when

$$A = E = I_{as} = I_s = H = Q = D = 0$$

$$E_0 = (S^*, \mathrm{A}^*, \mathrm{E}^*, \mathrm{I}^*{}_{\mathrm{as}}, \mathrm{I}^*{}_{\mathrm{s}}, H^*, \mathrm{Q}^*, \mathrm{D}^*, \mathrm{R}^*) = \left(\frac{\pi}{1-a+\mu}, \frac{(1-a)\pi}{\mu(1+\mu-a)}, 0, 0, 0, 0, 0, 0, 0\right)$$

The disease-free equilibrium is necessary in the determination of the basic reproduction number of the disease.

3.2 The Control Reproduction Number

$$\frac{dE(t)}{dt} = ac(k_1 I_s + k_2 I_{as})S + cd(k_1 I_s + k_2 I_{as})A - (\beta + \mu)E(t),$$

$$\frac{dI_{as}(t)}{dt} = (1 - p)\beta E - (\alpha_1 + \sigma_4 + \gamma_3 + \mu)I_{as}(t),$$

$$\frac{dI_s(t)}{dt} p\beta E - (\alpha_2 + \sigma_2 + q + \mu)I_s(t), (2)$$

$$\frac{dII(t)}{dt} = \alpha_1 I_{as} + \alpha_2 I_s - (\sigma_3 + \gamma_1 + \mu)H(t),$$

$$\frac{dQ(t)}{dt} = qI_s - (\sigma_1 + \gamma_2 + \mu)Q(t),$$

From the subsystem, we have

$$F = \begin{pmatrix} ac(k_1 I_s + k_2 I_{as})S + cd(k_1 I_s + k_2 I_{as})A \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, V = \begin{pmatrix} (\beta + \mu)E \\ (1 \quad p)\beta E \mid (\alpha_1 \mid \sigma_4 \mid \gamma_3 \mid \mu)I_{as} \\ -p\beta + (\alpha_2 + \sigma_2 + q + \mu)I_s \\ -\alpha_1 I_{as} - \alpha_2 I_s + (\sigma_3 + \gamma_1 + \mu)H \\ -qI_s + (\sigma_1 \end{pmatrix} \quad (3)$$

Then, F is the Jacobian matrix of F evaluated at the disease-free equilibrium and V is the Jacobian matrix of V evaluated at the disease-free equilibrium. Hence, we have

$$F = \begin{pmatrix} 0 & \frac{ac\kappa_2\pi}{(1-a+\mu)} + \frac{dc\kappa_2\pi(1-a)}{\mu(1+\mu-a)} & \frac{ac\kappa_1\pi}{(1-a+\mu)} + \frac{dc\kappa_1\pi(1-a)}{\mu(1+\mu-a)} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \quad (4)$$

and

$$V=\begin{pmatrix} \beta+\mu & 0 & 0 & 0 & 0 \\ -(1-p)\beta & \alpha_1+\sigma_4+\gamma_3+\mu & 0 & 0 & 0 \\ -p\beta & 0 & \alpha_2+\sigma_2+q+\mu & 0 & 0 \\ 0 & -\alpha_1 & -\alpha_2 & \sigma_3+\gamma_1+\mu & 0 \\ 0 & 0 & -q & 0 & \sigma_1+\gamma_2+\mu \end{pmatrix} \tag{5}$$

The inverse of V is non-negative, and is given by

$$V^{-1}=\begin{pmatrix} \frac{1}{\beta+\mu} & 0 & 0 & 0 & 0 \\ \frac{(1-p)\beta}{(\beta+\mu)(\alpha_1+\sigma_4+\gamma_3+\mu)} & \frac{1}{(\alpha_1+\sigma_4+\gamma_3+\mu)} & 0 & 0 & 0 \\ \frac{(\alpha_1(1-p)\beta(\alpha_2+\sigma_2+q+\mu)+p\beta\alpha_2(\alpha_1+\sigma_4+\gamma_3+\mu)}{(\beta+\mu)(\alpha_1+\sigma_4+\gamma_3+\mu)(\alpha_2+\sigma_2+q+\mu)(\sigma_3+\gamma_1+\mu)} & \frac{\alpha_1}{(\alpha_1+\sigma_4+\gamma_3+\mu)(\sigma_3+\gamma_1+\mu)} & \frac{\alpha_2}{(\alpha_2+\sigma_2+q+\mu)(\sigma_3+\gamma_1+\mu)} & \frac{1}{(\sigma_3+\gamma_1+\mu)} & 0 \\ \frac{pq\beta}{(\beta+\mu)(\alpha_2+\sigma_2+q+\mu)(\sigma_1+\gamma_2+\mu)} & 0 & \frac{q}{(\alpha_2+\sigma_2+q+\mu)(\sigma_1+\gamma_2+\mu)} & 0 & \frac{1}{\sigma_1+\gamma_2+\mu} \end{pmatrix} \tag{6}$$

The next generation matrix is therefore given by

$$K=FV^{-1}=\begin{pmatrix} \frac{\alpha k_2\pi(1-p)\beta}{(1-\alpha+\mu)(\beta+\mu)(\alpha_1+\sigma_4+\gamma_3+\mu)}+\frac{\alpha k_1\pi p\beta}{(1-\alpha+\mu)(\beta+\mu)(\alpha_2+\sigma_2+q+\mu)} & \frac{\alpha\pi}{(1-\alpha+\mu)(\alpha_1+\sigma_4+\gamma_3+\mu)} & \frac{\alpha\pi}{(1-\alpha+\mu)(\alpha_2+\sigma_2+q+\mu)} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

(7)

The eigenvalues of K are 0,0,0,0 and

$\frac{(1-p)\beta\alpha c K_2\pi}{(1-\alpha+\mu)(\beta+\mu)(\alpha_1+\sigma_4+\gamma_3+\mu)}+\frac{p\beta\alpha c K_1\pi}{(1-\alpha+\mu)(\beta+\mu)(\alpha_2+\sigma_2+q+\mu)}$. Therefore, the basic reproduction number of the disease is

$R_0 = \frac{(1-p)\beta acK_2\pi}{(1-a+\mu)(\beta+d)(\alpha_1+\sigma_4+\gamma_3+\mu)} + \frac{p\beta acK_1\pi}{(1-a+\mu)(\beta+\mu)(\alpha_2+\sigma_2+q+\mu)}$. The basic reproduction number can be written in the form

$$R_0 = R_{0a} + R_{0s}$$

Where $R_{0a} := \frac{(1-p)\beta acK_2\pi}{(1-a+\mu)(\beta+\mu)(\alpha_1+\sigma_4+\gamma_3+\mu)}$ is the average number of people that would be asymptomatically infected by a single infectious individual, where $R_{0s} := \frac{p\beta acK_1\pi}{(1-a+\mu)(\beta+\mu)(\alpha_2+\sigma_2+q+\mu)}$ is the average number of people that would be

asymptomatically infected by single infectious individual.

3.3 STABILITY OF DISEASE-FREE EQUILIBRIUM

The stability or otherwise of the disease-free equilibrium point, E_0 is determined by the sign of the real part of all the eigenvalues of the Jacobian matrix of $f(X)$ evaluated at E_0. Let $J(E_0)$ be the Jacobian matrix of $f\left(X(t)\right)$ evaluated at E_0. If all the eigenvalues of $J(E_0)$ have negative real parts, then E_0 is unstable. Therefore, we need to show that all the eigenvalues of $J(E_0)$ have negative real part. First, we write $f(X(t))$ in the form

$$f(X(t)) = \begin{pmatrix} f_1 \\ f_2 \\ f_3 \\ f_4 \\ f_5 \\ f_6 \\ f_7 \\ f_8 \\ f_9 \end{pmatrix} = \begin{pmatrix} \pi + \delta R - ac(k_1 I_s + k_2 I_{as})S - (1-a)S - \mu S \\ (1-a)S - cd(k_1 I_s + k_2 I_{as})A - \mu A \\ ac(k_1 I_s + k_2 I_{as})S + cd(k_1 I_s + k_2 I_{as})A - (\beta + \mu)E \\ (1-p)\beta E - (\alpha_1 + \sigma_4 + \gamma_3 + \mu)I_{as} \\ P\beta - (\alpha_2 + \sigma_2 + q + \mu)I_s \\ \alpha_1 I_{as} + \alpha_2 I_s - (\sigma_3 + \gamma_1 + \mu)H \\ qI_s - (\sigma_1 + \gamma_2 + \mu)Q \\ \sigma_1 Q + \sigma_2 I_s + \sigma_3 H + \sigma_4 I_{as} \\ \gamma_1 H + \gamma_2 Q + \gamma_3 I_{as} - (\delta + \mu)R \end{pmatrix} \qquad (8)$$

The Jacobian matrix of $f(X)$ valuated at the disease-free equilibrium point E_0 is

$$J(E_o) = \begin{pmatrix} (-d+1-a) & 0 & 0 & -ack_2 S^* & -ack_1 S^* & 0 & 0 & 0 & \delta \\ 1-a & -d & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\beta+d) & ack_2 S^* & ack_1 S^* & 0 & 0 & 0 & 0 \\ 0 & 0 & (1-p)\beta & -G_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & p\beta & 0 & -G_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \alpha_1 & \alpha_2 & -G_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & q & 0 & -G_4 & 0 & 0 \\ 0 & 0 & 0 & \sigma_4 & \sigma_2 & \sigma_3 & \sigma_1 & 0 & 0 \\ 0 & 0 & 0 & \gamma_3 & 0 & \gamma_1 & \gamma_2 & 0 & -(\delta+\mu) \end{pmatrix} \quad (9)$$

Where $G_1 = \alpha_1 + \sigma_4 + \gamma_3 + \mu, G_2 = \alpha_2 + \sigma_2 + q + \mu, \sigma_3 + \gamma_1 + \mu, G_4 = \sigma_1 + \gamma_2 + \mu$. The eigenvalues of $J(E_0)$ are $0, -\mu, -(\mu + 1 - a), -(\delta + \mu)$ and the eigenvalues of the sub-matrix

$$J_s(E_0) = \begin{pmatrix} -(\beta+d) & ack_2 S^* & ack_1 S^* & 0 & 0 \\ (1-p)\beta & -(\alpha_1+\sigma_4+\gamma_3+\mu) & 0 & 0 & 0 \\ p\beta & 0 & -(\alpha_2+\sigma_2+q+\mu) & 0 & 0 \\ 0 & \alpha_1 & \alpha_2 & -(\sigma_3+\gamma_1+\mu) & 0 \\ 0 & 0 & q & 0 & -(\sigma_1+\gamma_2+\mu) \end{pmatrix} \quad (10)$$

3.5 Sensitivity Analysis of the Basic Reproduction Number

Table 2: Sensitivity Indices number of the disease

PARAMETER	***SENSITIVITY INDEX***
C	+0.9992
C0	+0.0007646
***K*₂**	+0.2082
***K*₁**	+0.0002669
Π	+1
B	+0.0272
D	+0.00076469
A	+1.014
***A*₁**	-0.1237
***A*₂**	-0.2224
***Σ*₂**	-0.07113
***Σ*₄**	-0.0552
Q	-0.4719
P	-0.447
***Γ*₃**	-0.4719

We can now discuss the result of the sensitivity analysis as performed above. The parameters $a, c, \kappa_1, \kappa_2, \pi, \beta, d$ with positive sensitivity indices represent the parameters whose values must be reduced in order to control the spread of Covid-19. On the other hand, the parameters $\alpha_1, \alpha_2, \sigma_2, \sigma_4, q, p, \gamma_3$ with negative sensitivity indices are the parameters whose values must be increased if the spread of covid-19 is to be halted. From table 1 above, we see that the parameter with the highest positive sensitivity index is a, the proportion of susceptible that are not protecting themselves from covid-19 infection. The value, +1.014 , of the sensitivity index of a shows that personal protection and other forms of protection including vaccination, play important role in the control of spread of the disease. Reducing the value of a entails reducing the number of people that expose themselves to covid-19 infection. This reduces the basic reproduction.

4. NUMERICAL SIMULATION OF THE RESULTS

We present the numerical results of the above experiment as follows:

Numerical Result for the Optimal Control Problem and Discussion

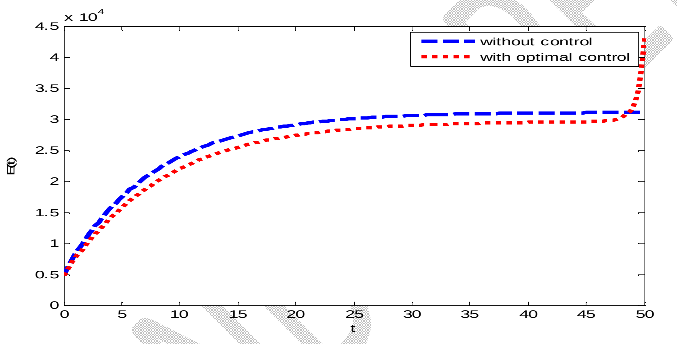


Figure 1: Graph of Exposed Humans

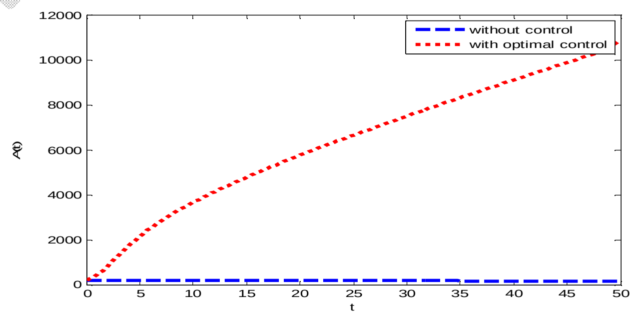
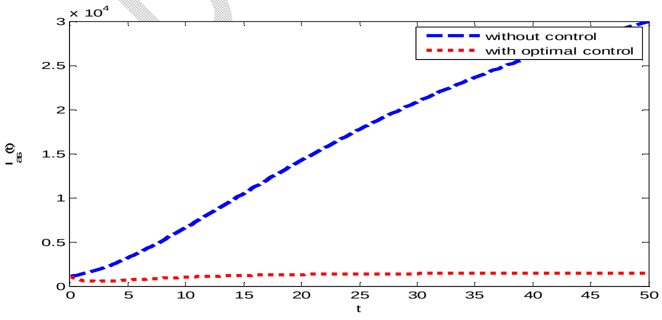


Figure 2: Graph of the protected class



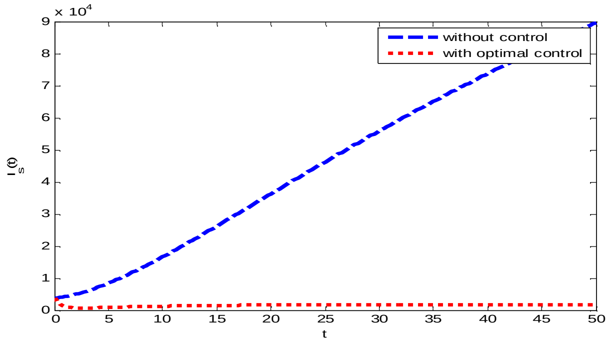


Figure 3: Graph of Asymptomatically infectious Humans

Figure 4: Graph of Symptomatically infectious Human

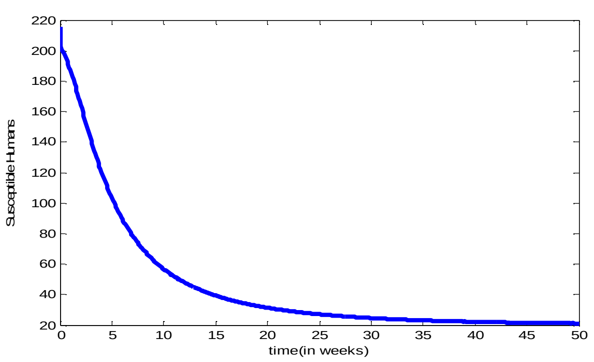


Figure 5 : Graph of Susceptible humans

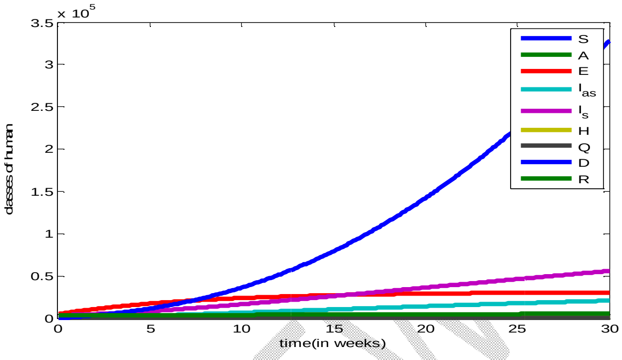


Figure 6: Graph for all the classes of Humans

Figure 1. Shows the relationship between the exposed human against time for the cases where the hospitalized human and the protected populations are varied.

Figure 2. Shows a case if optimal control is applied then the disease will reduce drastically in the class **Figure 3** shows the relationship between the asymptomatically infected human population against time for the cases where the treatment rates and the protection varied, which shows a decline in the number of asymptomatically infected human.

Figure 4. Since treatment is now administered to the sick the level of infected people reduces causing a slight increase in the number susceptible and those who are recovering.

Figure 5. The graph shows that when people are admitted and treated there's a great increase in the number of susceptible because asymptomatic and symptomatic infectious individuals has been reduced, and this increases the rate of recovery.

Figure 6. The diagram showing the effect of the susceptible population on the reproduction numbers, with the blue curve indicating the susceptible on the effective reproduction number with optimal control measures.

CONCLUSION

It can be concluded that as long as there are no interventions to control the spread of the disease, the disease will not be wiped out from the population. It was also observed that that the best combination is protection, hospitalized and quarantine. We further noted that there is a direct correlation between asymptomatically class and the reproduction numbers, that is, as the rate of secondary infective increase also the rate of symptomatic increases. We encourage a health policy that will cover the best combination of protection, hospitalized and quarantine even on time.

We finally observed that when treatment, quarantine and hospitalized policy is strictly adhered to, the disease will be completely wiped out of the population and thus reducing the rate of infection which increases the recovery rate in all classes

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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Details of the AI usage are given below:

1.

2.

3.

(Option 1)

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