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Assessing the impact of isolation and testing effect on the transmission dynamics of COVID-19.⋆,⋆⋆

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Abstract

The global effect of Covid19 and inadquacy of literature dealing with deterministic mathematical model on preventive measures on the transmisson dynamics of the disease is an exuding factor of endemicity in human population. Thus,this study focus on the formulaton of a new deterministic model incorperated with control measures for combating the transmission of the disease. It is shown that the model exhibit forward bifurcation,hence,the epidemiological requirement $R_o \prec 1$,is a neccessary and sufficient condition for the ellimination of the disease.The local and asymptotic stability of the endemic equilibrium point is investigated.Furthermore,it is shown that the disease free equilibrium is globaly asymptotically stable.Numerical simulation of the model suggest that high value of administered control measures without strict compliance ($\rho = 90\%$) to control measures is not a sufficent condition for the ellimination of COVID19.

Keywords: Forward Bifurcation, Isolaton Effect Effect , Global Asymptotc stabilitystrategies

1. Introduction

Deterministic mathematical models have been widely used to ascertain the spread and control of emerging and re-emerging human disease dating back to the of Bernoulli in 1760 and the likes of Ross, Kermacack and Mckendrick[21, 22]. The dynamics of these models is determined by the threshold quantity

⋆Sunday Akporugo@ Covid 19 Model.

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R_0 called the basic reproduction number. Which ascertain the number of new cases an index case can generate in a completely susceptible population[21].The phenomenon ,where the disease-free equilibrium loses its stability and a stable endemic equilibrium appears as Roincreases through one,is known as forward bi- furcation [23]. It is imperative to provide some background information on the burden of COVID-19. COVID-19 a viral infectious disease,declared by the WHO as a pandemic[1],is caused by a new type of coronavirus formely called 2019-nCOV by the WHO. It is the seventh member of the coronavirus family together with MERS-nCOV and SAR-nCOV,that can spread to human [2]. Despite concerted e ort by the government, WHO and international health organizations,COVID-19 still main- tains its exuding e ect to human population.An estimate of 634,835 infected in- dividuals with 29891 death cases was reported by the world health organization as of march 2020[3]. The symptoms of the infection include fever,cough,shortness of breath and diarrhea. In more severe cases,COVID-19 can cause pneumonia and even death[4]. There is no cure for COVID-19 for the moment but strict compliance to control measures can prevent its attenuating e ect on the human population. Several attempt has been made to study the transmission dynamics of COVID- 19. For example Moore et al used a deterministic mathematical model to present control strategies[5]. S. Zhang et al ,estimated the reproduction number of COVID-19 and the probable size on the diamond princess cruise ship[6]. The objective of this study is to design a new deterministic mathemati- cal model that assess the impact of preventive measures in the transmission dynamics of COVID-19.The resulting deterministic system of nonlinear di er- ential equations will be rigorously analysed to gain insight into the dynamical features.

2. MODEL FORMULATION

The total population of Nigeria at time t, denoted by $N(t)$ is divided into the mutually exclusive compartments of infectious individuals who are unware of their covit 19 status (I_u), infectious individuals who are aware of their COVIT 19 status(I_a), susceptible individuals (S), Suceptible individuals that observed isolation (S_i), infectious individuals that refuse to be quarantine (I_r), infectious individuals that comply to be quarantine (I_i), infectious individuals who recovers from COVIT 19 (R). The total population becomes:

$$N(t) = S + S_i + I_u + I_a + I_r + I_i + R.$$

The population of susceptible individuals is sourced by birth of children at rate Λ. Susceptible individuals acquires infection at a rate λ_t and adhere to quarantining at a rate σ_i. The population is further diminished by natural mortality at a rate μ. Thus , the differential compartment of the susceptible class will be

$$\frac{dS}{dt} = \Lambda - \mu S - \lambda_t S - \sigma_i S.$$

The population of isolated susceptible individuals got their from susceptible individuals who adhere to quarantine measures at a rate σ_i, despite lockdown, it was assumed that a fraction of the isolated susceptible individuals left their isolated zone (for greener pasture) and interacted with infected individuals who are unware of their COVIT 19 status at a rate σ_{mi}. The population suffer from natural death a rate μ.

$$\frac{dS_i}{dt} = \sigma_i S - \mu S_i - \sigma_{mi} S_i$$

The population of infectious individuals who are unware of their COVIT 19 status is generated following the infection acquired by susceptible individuals. The population is increase by isolated susceptible individuals who interacted with unware infectious COVIT 19 individuals. Individuals in the class comply to testing (to know their COVIT 19 status) at a rate α_t. I t was observed that individuals with strong immune system recovers from the disease at rate τ_u. The population is further decreased by natural death at rate μ. So that

$$\frac{dI_u}{dt} = \lambda_t S - \mu I_u + \sigma_{mi} S_i - \alpha_t I_u - \tau_u I_u.$$

The population of infectious individual who are aware thier COVIT 19 status is sourced from unware COVIT 19 infectious individual who comply to testing. Individuals in this class were admitted to isolation centre at rate α_i. It was observed that some of this individuals recovers from the disease at a rate τ_a. Individuals suffers from natural death at rate μ. So that

$$\frac{dI_a}{dt} = \alpha_t I_u - \mu I_a - \alpha_i I_a - \tau_a I_a$$

The population of infectious individuals who refuse to be quarantine for COVIT 19, got its recruitment from isolated infectious individuals , where $0 < \rho < 1$,compliance rate of isolation from infectious COVIT19 individuals. The population suffers from natural death and recovers from the disease at a rate of μ and τ_r. So that

$$\frac{dI_r}{dt} = (1-\rho)\alpha_i I_a - \mu I_r - \tau_r I_r$$

The population of Isolated individauls is sourced from infectious COVIT 19 individuals who accepted isolation. The population suffers from natural death and recovers from the disease at μ and τ_i respectively. So that

$$\frac{dI_i}{dt} = \rho\alpha_i I_a - \mu I_i - \tau_i I_i$$

The population of infectious individuals who recovers from the disease is sourced from the respective recovery rate of each infectious class. The population suffer from natural mortality at a rate μ. So that

$$\frac{dR}{dt} = \tau_u I_u + \tau_a I_a + \tau_r I_r + \tau_i I_i - \mu R.$$

Table 1: Description of state variable

Variable	Interpretation
S	Susceptible individuals
S_i	Susceptible isolated individuals
I_u	Infectious individuals who are unaware of their COVIT 19 status
I_a	Infectious individuals who are aware of their COVIT 19 status
I_r	population of infectious individuals who refuse isolation
I_i	population of isolated infectious individuals
R	Population of infectious individual that recover from the COVIT 19

Table 2: Description of the variables and parameters of the model (1)

Parameter	Interpretation
Λ	Recruitment rate
μ	Natural mortality rate
σ_i	Rate of isolated susceptible individuals
σ_{mi}	Rate of interaction of isolated susceptible inviduals
α_t	Compliance to testing parameter
α_i	Compliance to isolation parameter
τ_u	Recovery rate on uninformed infectious individuals
τ_a	Recovery rate on informed infectious individuals
τ_i	Recovery rate on informed isolated infectious individuals
ρ	Compliance rate of informed infectious individauls
θ_i	Modification Parameter accounting for the reduction of COVIT 19 .
κ	Risk of infectioneous among uninformed infected individuals
η_a	Modification parameter of risk of infectioneous among informed infected individuals

Where

$$\lambda_t = \frac{\beta(1-\vartheta)\left[I_u + \eta_a I_a + \kappa I_r + \theta_i I_i\right]}{N}$$

Observing the definition and assumptions above ,the deterministic model of the transmission dynamics of COVIT 19 is represented by the non-linear differential equations.

$$\frac{dS}{dt} = \Lambda - \mu S - \lambda_t S - \sigma_i S.$$

$$\frac{dS_i}{dt} = \sigma_i S - \mu S_i - \sigma_{mi} S_i$$

$$\frac{dI_u}{dt} = \lambda_t S - \mu I_u + \sigma_{mi} S_i - \alpha_t I_u - \tau_u I_u. \tag{1}$$

$$\frac{dI_a}{dt} = \alpha_t I_u - \mu I_a - \alpha_i I_a - \tau_a I_a$$

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$$\frac{dI_r}{dt} = (1-\rho)\alpha_i I_a - \mu I_r - \tau_r I_r$$

$$\frac{dI_i}{dt} = \rho\alpha_i I_a - \mu I_i - \tau_i I_i$$

$$\frac{dR}{dt} = \tau_u I_u + \tau_a I_a + \tau_r I_r + \tau_i I_i - \mu R.$$

$$N(t) = S + S_i + I_u + I_a + I_r + I_i + R.$$

Where

$$\lambda_t = \frac{\beta(1-\vartheta)\left[I_u + \eta_a I_a + \kappa I_r + \theta_i I_i\right]}{N}$$

3. Basic properties

3.1. Boundedness of solution

The model (1) to be well posed it must satisfy the Lassalle's invariance principle which state that the solutions of the model (1) with positive initial data will remain positive for all $t \geq 0$. This is achieved below.

Lemma 1. *The region*

$$\Omega = \left\{(S, S_i, I_u, I_a, I_r, I_i, R)\epsilon\mathbb{R}_+^{\not\vdash}: \mathbb{N} \leq \frac{\not\geq}{\mu}\right\}$$

is positively invariant for the model (1).

Proof. Adding the equations in the model (1) gives

$$\frac{dN}{dt} = \Lambda - \mu N. \tag{2}$$

Hence , whenever $N > \frac{\Lambda}{\mu}$, then $\frac{dN}{dt} < 0$. Thus,It follows from the right hand side of the inequality (2.1) that $\frac{dN}{dt}$ is bounded by $\Lambda - \mu N$, a standard comparison theorem [1]can be used to show that

$$N(t) \leq N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1 - e^{-\mu t}).$$

If $N(0) \leq \frac{\Lambda}{\mu}$, then $N(t) \leq \frac{\Lambda}{\mu}$. Thus, Ω is a positively-invariant set under the flow described by model(1) so that no solution path leaves through any boundary of Ω . Hence it is suffiecient to consider the dynamics of the model in Ω. In this region the model can be considered as been epidemiologically and mathematically well-posed [2]. □

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3.2. Asymptptotic stability of Disease free Equilibrium (DFE)

The DFE of the model(1) is given by

$$\Pi_0 = (S^{**}, S_i^{**}, I_u^{**}, I_a^{**}, I_r^{**}, I_i^{**}, R^{**}) = ((S^{**}, S_i^{**}, 0, 0, 0, 0, 0)$$

where

$$S^{**} = \frac{\Lambda}{\mu + \sigma_i} \qquad S_i^{**} = \frac{\Lambda \sigma_i}{(\mu + \sigma_i)(\mu + \sigma_{mi})}.$$

The local stability of Π_0 can be established using the next generation operator method on (1)[3, 4] using the notation in [4],it follows that the matrices F and V,for the new infection terms and the remaining transfer terms are ,respectively ,given by

$$V = \begin{bmatrix} k_1 & 0 & 0 & 0 \\ -\alpha_t & k_2 & 0 & 0 \\ 0 & -(1-\rho)\,\alpha_i & k_3 & 0 \\ 0 & -\rho\alpha_i & 0 & k_4 \end{bmatrix} \quad and \quad F = \begin{bmatrix} \beta & \beta\eta_a & \beta\kappa & \beta\theta_i \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

where $k_1 = \mu + \alpha_t + \tau_u$ $k_2 = \mu + \alpha_i + \tau_a$ $k_3 = \mu + \tau_r$ $k_4 = \mu + \tau_i$. Hence , it follows from [4] that

$$R_c = \frac{\beta[k_3k_4(k_2 + \eta_a\alpha_t) + (\kappa(1-\rho)k_4 + \theta_i\rho k_3)\alpha_t\alpha_i}{k_1k_2k_3k_4}$$

Lemma 2. *The DFE of* (Π_0) *of the model* (1) *is locally asymptotically stable if* $R_c < 1$,*and unstable if* $R_c > 1$.

The threshold quantity R_c is the effective reproduction number of COVIT 19 [5, 2]. It represent the average number of secondary cases generated by a single infectious individual. The epidemiological implication of lemma2

is that when the threshold parameter is less than unity, a pertubation from the COVIT 19 infectious individual will not generated large outbreaks, and the disease goes into extinction.

3.3. Global asymptotic stability of DFE

Theorem 3. *The disease free equilibrium of the model is globally aymptotically stable in* Ω *whenever* $R_c \leq 1$.

Proof. Consider the Lyapunov function

$$L = \zeta_1 I_u + \zeta_1 I_a + \zeta_1 I_r + I_i.$$

where ζ_i is the coefficient of infectiousness.A thorough algebraic exercise gave the coefficient of infectiounes as follows

$$\zeta_1 = \frac{R_0 k_4}{\beta}$$

$$\zeta_1 = \frac{k_4}{\theta_i}[\frac{\eta_a}{k_2} + \frac{(1-\rho)\alpha_i\kappa}{k_2k_3} + \frac{\theta_i\rho\alpha_i}{k_2k_4}] \tag{3}$$

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$$\zeta_3 = \frac{\kappa k_4}{\theta_i k_3}$$

$$\dot{L}=\zeta_1 \dot{I}_u + \zeta_1 \dot{I}_a + \zeta_1 \dot{I}_r + \dot{I}_i. \tag{4}$$

A thorough algebraic simplification when the (2.2) is observed in (2.3) gives

$$\dot{L} \leq \frac{k_4}{\theta_i} (R_0 - 1) [I_u + \eta_a I_a + \kappa I_r + \theta_i I_i].$$

Hence,the derivative of the Lyapunov function is less than zero whenever the threshold parameter is less than equal one and all parameters and variables of the model are non-negative, iff all the infectious class in model (1) equal zero. It follows from Lasalle's invariance principle ,that every solution to the equations in model(1) with initial conditions in Ω converges to Π_0 as $t \to \infty$. The epidemiological implication is that if the quarantine and isolation measures are implemented such that its brings the threshold parameter below one then COVIT 19 will be elliminated in Nigeria. □

3.4. Existence and stability of endemic equilibrium point

In this secttion,the case of model(1) where at least one of the infected variables of the model (1) is non-zero shall be considered. This is attainable by solving model (1) at the endemic steady state. This is attainable as follows

$$S^{**} = \frac{\Lambda}{(\mu + \sigma_i + \lambda_t)}$$

$$S_i^{**} = \frac{\sigma_i \lambda_t}{(\mu + \sigma_{mi})(\mu + \sigma_i + \lambda_t)}$$

$$I_u^{**} = \frac{1}{k_1}[\frac{\sigma_{mi}\sigma_i \Lambda}{(\mu + \sigma_{mi})(\mu + \sigma_i + \lambda_t)} + \frac{\lambda_t \Lambda}{(\mu + \sigma_i + \lambda_t)}]$$

$$I_a^{**} = \frac{\alpha_t}{k_1 k_2}[\frac{\sigma_{mi}\sigma_i \Lambda}{(\mu + \sigma_{mi})(\mu + \sigma_i + \lambda_t)} + \frac{\lambda_t \Lambda}{(\mu + \sigma_i + \lambda_t)}]$$

$$I_r^{**} = \frac{(1-\rho)\alpha_i \alpha_t}{k_1 k_2 k_3}[\frac{\sigma_{mi}\sigma_i \Lambda}{(\mu + \sigma_{mi})(\mu + \sigma_i + \lambda_t)} + \frac{\lambda_t \Lambda}{(\mu + \sigma_i + \lambda_t)}]$$

$$I_r^{**} = \frac{\rho\alpha_i \alpha_t}{k_1 k_2 k_4}[\frac{\sigma_{mi}\sigma_i \Lambda}{(\mu + \sigma_{mi})(\mu + \sigma_i + \lambda_t)} + \frac{\lambda_t \Lambda}{(\mu + \sigma_i + \lambda_t)}]$$

Much rigourous algebraic exercise gives

$$\lambda_t^{**} - (1 - R_0)A + \sigma_{mi}\sigma_i = 0 \tag{5}$$

where

$$A = \frac{1}{(k_3 k_4 (k_2 + \eta_a \alpha_t) + (\kappa(1-\rho)k_4 + \theta_i \rho k_3)\alpha_t \alpha_i)(k_3 k_4 k_2 + k_3 k_4 \alpha_t + k_4 \alpha_t \alpha_i + \rho k_4 \alpha_t \alpha_i)}$$

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It is obvious that the linear sytem (2.4) has a unique positive solution whenever $R_0 \geq 1$ and $A > \sigma_{mi}\sigma_i > 0$.

Theorem 4. *The endemic equilibrium of the model is locally asymptotically stable if* $|1 + R_0| > 1$.

Proof. Recall from (2.1) that

$$\frac{dN}{dt} = \Lambda - \mu N.$$

So that $N \to \frac{\Lambda}{\mu} = N^{**}$ as $t \to \infty$. Hence,using the substitution

$$S = N^{**} - (I_u, I_a, I_r, I_i)$$

where . The model(1), can be rewritten as □

$$\frac{dI_u}{dt} = {N^{**}}^{-1}[\beta(1-\vartheta)(I_u + \eta_a I_a + \kappa I_r + \theta_i I_i)][(N^{**} - (I_u, I_a, I_r, I_i)] - k_1 I_u. \tag{6}$$

$$\frac{dI_a}{dt} = \alpha_t I_u - k_2 I_a$$

$$\frac{dI_r}{dt} = (1-\rho)\alpha_i I_a - k_3 I_r$$

$$\frac{dI_i}{dt} = \rho\alpha_i I_a - k_4 I_i$$

Linearizing the model (2.2) around the endemic equilibrium point gives

$$\frac{dI_u}{dt} = [(x_2 - x_1) - k_1]I_u + (\eta_a x_2 - x_1)\, I_a + (\kappa x_2 - x_1)I_r + (\theta_i x_2 - x_1)$$

$$\frac{dI_a}{dt} = \alpha_t I_u - k_2 I_a$$

$$\frac{dI_r}{dt} = (1-\rho)\alpha_i I_a - k_3 I_r \tag{7}$$

$$\frac{dI_i}{dt} = \rho\alpha_i I_a - k_4 I_i$$

where

$$x_1 = \frac{\beta(1-\vartheta)\,[I_u + \eta_a I_a + \kappa I_r + \theta_i I_i]}{N}$$

$$x_2 = \frac{\beta S^{**}}{N}.$$

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The jacobian of the system evaluated at the EEP is given by

$$J = \begin{bmatrix} (x_2 - x_1) - k_1 & (\eta_a x_2 - x_1) & (\kappa x_2 - x_1) & (\theta_i x_2 - x_1) \\ \alpha_t & -k_2 & 0 & 0 \\ 0 & (1-\rho)\,\alpha_i & k_3 & 0 \\ 0 & \rho\alpha_i & 0 & k_4 \end{bmatrix}$$

It is imperative to show that system (2.3) has no solution of the form :

$$P(t) = P_0 e^{\omega t} \tag{8}$$

where $P_0 = (P_1, P_2, P_3, P_4)$ and $\omega, P_0 \epsilon \mathbb{C}$. Substitue the solution (2.4) into (2.3) gives

$$\omega P_1 = [(x_2 - x_1) - k_1]\, P_1 + (\eta_a x_2 - x_1)\, P_2 + (\kappa x_2 - x_1) P_3 + (\theta_i x_2 - x_1)\, P_4$$

$$\begin{aligned} \omega P_2 &= \alpha_t P_1 - k_2 P_2 \\ \omega P_3 &= \alpha_t P_2 - k_3 P_3 \\ \omega P_4 &= \alpha_t P_3 - k_4 P_4 \end{aligned} \tag{9}$$

Thorough algebraic simplification of system (2.5) gives the following system

$$\begin{aligned} [1 + F_1(\omega)]\, P_1 &= (HP)_1 \\ [1 + F_2(\omega)]\, P_2 &= (HP)_2 \\ [1 + F_3(\omega)]\, P_3 &= (HP)_3 \\ [1 + F_4(\omega)]\, P_4 &= (HP)_4 \end{aligned} \tag{10}$$

where

$$F_1(\omega) = \frac{\omega}{k_1} + \frac{x_1}{k_1}\left(1 + \frac{\alpha_t}{k_2 + \omega} + \frac{(1-\rho)\,\alpha_i \alpha_t}{(k_2 + \omega)(k_3 + \omega)} + \frac{\rho \alpha_i \alpha_t}{(k_4 + \omega)(k_2 + \omega)}\right)$$

$$F_2(\omega) = \frac{\omega}{k_2}$$

$$F_3(\omega) = \frac{\omega}{k_3}$$

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$$F_4(\omega) = \frac{\omega}{k_4}$$

$$H = \begin{bmatrix} \frac{x_2}{k_1} & \frac{\eta_a x_2}{k_1} & \frac{(1-\rho)\alpha_i \kappa x_2}{k_1} & \frac{x_2 \alpha_i \rho \theta_i}{k_1} \\ \frac{\alpha_t}{k_2} & 0 & 0 & 0 \\ 0 & \frac{(1-\rho)\alpha_i}{k_3} & 0 & 0 \\ 0 & \frac{\rho \alpha_i}{k_4} & 0 & 0 \end{bmatrix}$$

If P is a solution of (2.6) *then*it is possible to find a minimal positive real number (ϕ),such that $\|P\| \leq \phi \Psi_E$.It is important to state that H becomes stable if $Re(\omega) < 0$. Assume by contradiction that $Re(\omega) \geq 0$. There are two cases to consider .

Case 1

For the case $\omega = 0$,equation (2.6) becomes a homogeneous linear system in the variables of P. The determinant of the system is given by

$$\Delta_c =$$

It follows that system (2.6)has a unique solution given by $P = 0$ and this solution correspond to the DFE ,since the determinant of the system (2.6) is negative whenever R_c >1, and trivial whenever $R_c = 1$.

Case 2

Consider the case $Re(\omega) > 0$ (by assumption), then $|1 + P_i(\omega)| > 1$. Let $P(\omega) = mini\,|1 + P_i|$,then $P(\omega) > 1$ and $\frac{\phi}{P(\omega)} < \phi$. Since ϕ is a minimal positive real number such that $\|P\| \leq \phi \Psi_E$, then

$$\|P\| > \frac{\phi \Psi_E}{P(\omega)} < \phi \tag{11}$$

On the reverse , by taking the norm of both sides of the second equation (2.4), we have

$$P(\omega)\|P_2\| \leq |1 + P_2(\omega)|\,\|P_2\|$$

$$= \|(HP)_2\| \leq H\|P_2\| \leq \phi H (\Psi_E)_2$$

$$= (\Psi_E)_2 - \phi I_a^{**} \tag{12}$$

It implies that (2.8) contradicts (2.7). Hence $Re(\omega) < 0$. Thus,all eigenvalues of the characteristics equation associated with the linearized system will have a negative real part, so that the unique endemic equilibrium, Ψ_E is locally asymptotically stable . The epidemiological implication of the theorem (1) is that COVIT 19 will persist in the population if $R_c > 1$.

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3.5. Global stability of endemic equilibrium point.

Consider the force of infection in its explosive state

$$\lambda_t = \frac{\beta(1-\vartheta)\left[I_u + \eta_a I_a + \kappa I_r + \theta_i I_i\right]}{N}$$

were all mofication parameter equal one i.e $\eta_a = \theta_i = \kappa = 1$. The epidemiological implication is that infectious individuals with low response to isolation and quarantine measures do not modify their behaviour for the spread of the disease.

Lemma 5. *The region* $\Omega = \{(S, S_i, I_u, I_a, I_r, I_i, R)\epsilon S(t) \leq S^{**}\}$ *is positively invariant and attracting for model (1).*

Proof. Omitted □

Theorem 6. *Consider the model (1). The associated unique endemic equiiibrium of the model is GAS in* Ω^{**}/Ω *if the threshold parameter is observed for all modification parameters equal one and* $S < S^{**}$.

Proof. Consider the following non-linear Lyapunov function (Goh-Volterra type):

$$F = S - S^{**} - S^{**} In\left(\frac{S}{S^{**}}\right) + S_i - S_i^{**} - S_i^{**} In\left(\frac{S_i}{S_i^{**}}\right) + I_u - I_u^{**} - I_u^{**} In\left(\frac{I_u}{I_u^{**}}\right) +$$

$$\left(\frac{\beta S}{k_2} + \frac{\beta S(1-\rho)\alpha_i}{k_2 k_3} + \frac{\beta S \rho \alpha_i}{k_2 k_4}\right)\left(I_a - I_a^{**} - I_a^{**} In\left(\frac{I_a}{I_a^{**}}\right)\right) + \frac{\beta S}{k_3}\left(I_r - I_r^{**} - I_r^{**} In\left(\frac{I_r}{I_r^{**}}\right)\right) \tag{13}$$

$$\frac{\beta S}{k_4}\left(I_i - I_i^{**} - I_i^{**} In\left(\frac{I_i}{I_i^{**}}\right)\right).$$

With Lyapunov derivatives ,

$$\dot{F} = \dot{S} - \frac{S^{**}}{S}\dot{S} + \dot{S}_i - \frac{S_i^{**}}{S_i}\dot{S}_i + \dot{I}_u - \frac{I_u^{**}}{I_u}\dot{I}_u + \left(\frac{\beta S}{k_2} + \frac{\beta S(1-\rho)\alpha_i}{k_2 k_3} + \frac{\beta S \rho \alpha_i}{k_2 k_4}\right)\left(\dot{I}_a - \frac{I_a^{**}}{I_a}\dot{I}_a\right)$$

$$\frac{\beta S}{k_3}\left(\dot{I}_r - \frac{I_r^{**}}{I_r}\dot{I}_r\right) + \frac{\beta \dot{S}}{k_4}\left(I_i - \frac{I_i^{**}}{I_i}\dot{I}_i\right). \tag{14}$$

At steady state of model , it can be shown that □

$$\Lambda = \mu S^{**} - \lambda_t S^{**} - \sigma_i S^{**}.$$

$$K_1 I_u^{**} = \lambda_t S^{**} + \sigma_{mi} S_i^{**}$$

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$$K_2 I_a^{**} = \alpha_t I_u^{**} \tag{15}$$

$$K_3 I_r^{**} = (1-\rho)\alpha_i I_a^{**}$$

$$K_4 I_i^{**} = \rho\alpha_i I_a^{**}.$$

Next, observe the derivatives of the infectious class in (1) and the steady state in (2.14) into (2.12),gives

$$\dot{F} = \mu S^{**}(2 - \frac{S^{**}}{S} - \frac{S}{S^{**}}) + \mu S_i^{**}(2 - \frac{S_i^{**}}{S_i} - \frac{S_i}{S_i^{**}}) + \sigma_i S^{**}(2 - \frac{S^{**}}{S} - \frac{S_i^{**}}{S_i}\frac{S}{S^{**}})$$

$$BS^{**}I_a^{**}(2 - \frac{S^{**}}{S} - \frac{I_a^{**}}{I_a}\frac{I_u}{I_u^{**}})$$

$$BS^{**}I_r^{**}(3 - \frac{S^{**}}{S} - \frac{I_a^{**}}{I_a}\frac{I_u}{I_u^{**}} - \frac{I_r^{**}}{I_r}\frac{I_a}{I_u^{**}}) + BS^{**}I_i^{**}(4 - \frac{S^{**}}{S} - \frac{I_a^{**}}{I_a}\frac{I_u}{I_u^{**}} - \frac{I_i^{**}}{I_i}\frac{I_a}{I_a^{**}} - \frac{I_u^{**}}{I_u}\frac{I_i}{I_i^{**}})$$

Since the arithmetic mean exceeds the geometric mean , the following inequalities hold:

$$2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \leq 0 \qquad 2 - \frac{S_i^{**}}{S_i} - \frac{S_i}{S_i^{**}} \leq 0,$$

$$2 - \frac{S^{**}}{S} - \frac{I_a^{**}}{I_a}\frac{I_u}{I_u^{**}} \leq 0,$$

$$3 - \frac{S^{**}}{S} - \frac{S_i^{**}}{S_i}\frac{S}{S^{**}} \leq 0, \qquad 3 - \frac{S^{**}}{S} - \frac{I_a^{**}}{I_a}\frac{I_u}{I_u^{**}} - \frac{I_r^{**}}{I_r}\frac{I_a}{I_u^{**}} \leq 0,$$

$$4 - \frac{S^{**}}{S} - \frac{I_a^{**}}{I_a}\frac{I_u}{I_u^{**}} - \frac{I_i^{**}}{I_i}\frac{I_a}{I_a^{**}} - \frac{I_u^{**}}{I_u}\frac{I_i}{I_i^{**}} \leq 0.$$

Thus $\dot{F} \leq 0$ for $R_{c/mofidicationparameters=1} > 1$. Hence , F is a Lyapunov function. It follows by lasalles invariance principle that every solution to the equation of the model (1) approaches the associated unique endemic equilibrium of the model as $t \to \infty$for $R_c > 1$.

Isolotation and testing effect with 80% compliance rate

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Table 3: Values of Parameters used for simulation

Parameter	Nominal value	Reference
β	0.45	Estimimated
μ	0.001	Estimimated
σ_i	0.05	Estimimated
σ_{mi}	0.03	Estimimated
α_t	0.06	Estimimated
α_i	0.6	Estimimated
τ_u	0.014	Estimimated
τ_a	0.013	Estimimated
τ_i	0.016	Estimimated
ρ	(0,1]	Estimimated
θ_i	0.014	Estimimated
κ	0.7	Estimimated
η_a	0.01	Estimimated

Table 4: Threshold Values in the absence of control measures

Case of reproduction number	Reproduction number	% of transmission
With control parameters	0.5802	1.000
Without control parameter	1.1353	1.959
Total	1.7155	2.959

Consider the case of model(1) without control measures. Table 3, gives the outcome of the reproduction number when the contact rate is fixed at f 0.5. It is established that the epidemiological requirement of the threshold parameter is not satisfied for the ellimination of Covid19. Thus, the need of control measures is imperative for combating the disease.Next,observed the reproduction number with control parameters.

Table 5: Isolotation and testing effect on transmission of COVID 19

α_i	α_t	R_c
0.45	0.5	1.16275
0.65	0.8	1.22718
0.811	0.9	1.284

When $\beta = 0.45$, $\rho = 0.5(50\%)$, its infer from table 4,high values of isolation and testing parameter will not attenuate the infection number at the observed compliance rate.The contour plot below display the dynamics of the infection at high values of administered control parameter.

3.5 Global stability of endemic equilibrium point. 14

Contour plot of reproducton number wth low compliance rate.

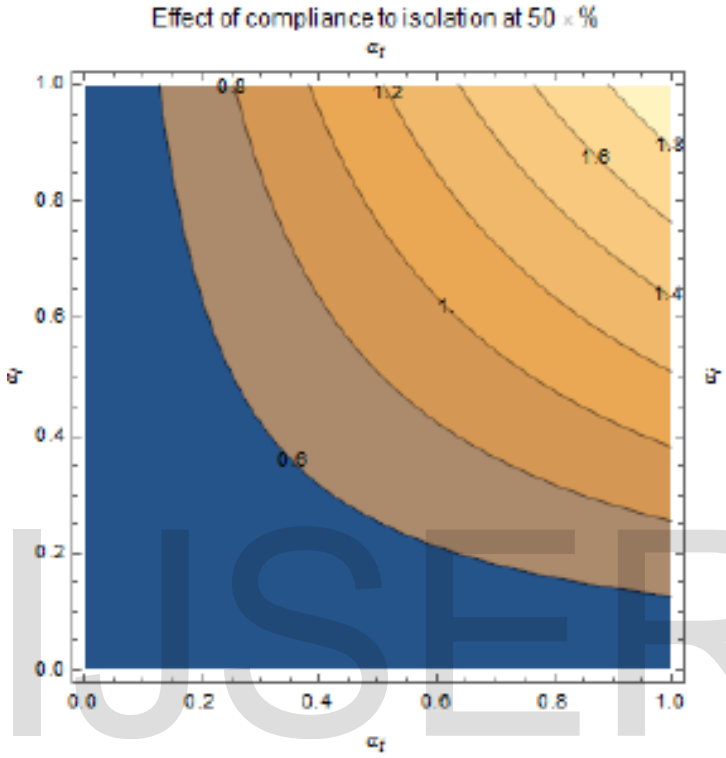

Figure 1:

Table 6: Isolotation and testing effect with 80% compliance rate

α_i	α_t	R_c
0.45	0.5	0.812293
0.65	0.8	1.22718
0.811	0.9	1.284

When $\beta = 0.45$, $\rho = 0.8(80\%)$.Same values of control parameters as define in Fig(3.1),attenuate the infection number at the observed compliance rate.The contour plotbelow display the dynamics of the infection at high values of administered control parameter.It is therefore imperative to state that high values of administered control parameters (isolation and testing) is only a neccessary but never a sufficient condition for the ellimination of COVID-19. The epidemiological implication is that strict monitoring to the alderance of control measures must be employed for effective combat of COVID-19. As display in the contour plot(Figure 3.2),the threshold parameter for the transmission of the disease is less than one.

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Contour plot of reproducton number wth high compliance rate.

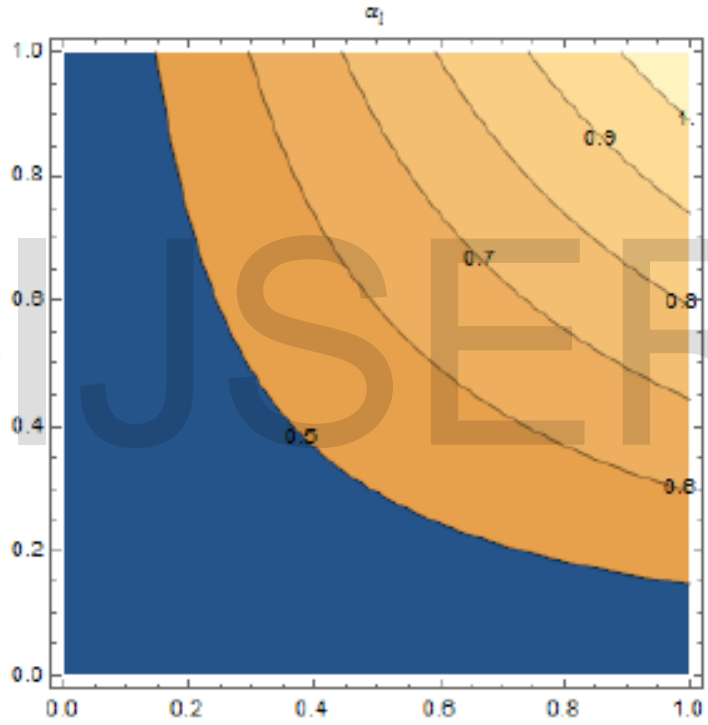

Figure 2:

Dynamics Of Infected Population With Low Compliance Rate.

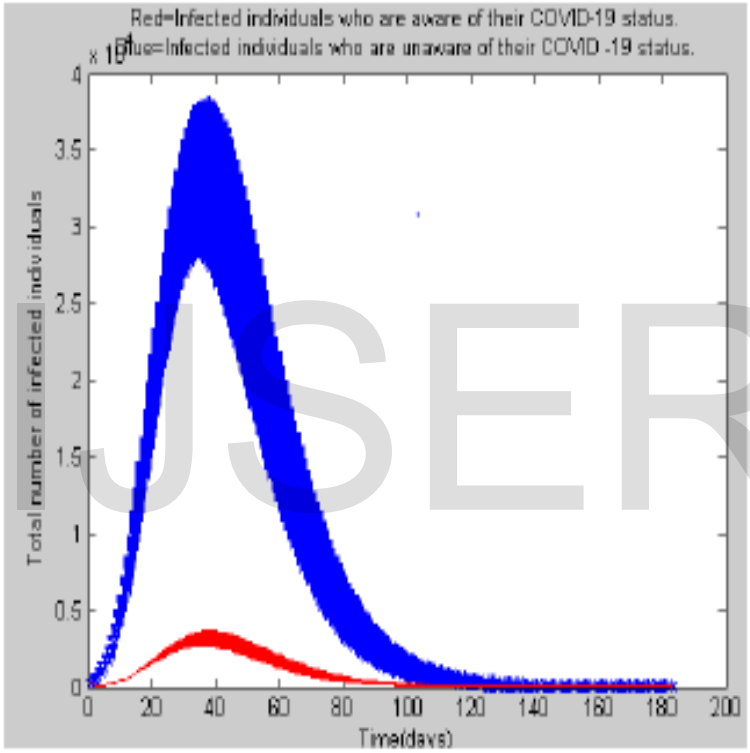

Figure 3:

From the plot dynamics above(Fig.3.7),the disease burden associated with infectious individuals who are aware their COVID-19 status have a low response for the transmission of the disease than its counter part. Thus, testing as a control measure is indespensable in curtailing COVID-19.$\beta = 0.45$,$\alpha_t = 0.02(98.0\%)$.

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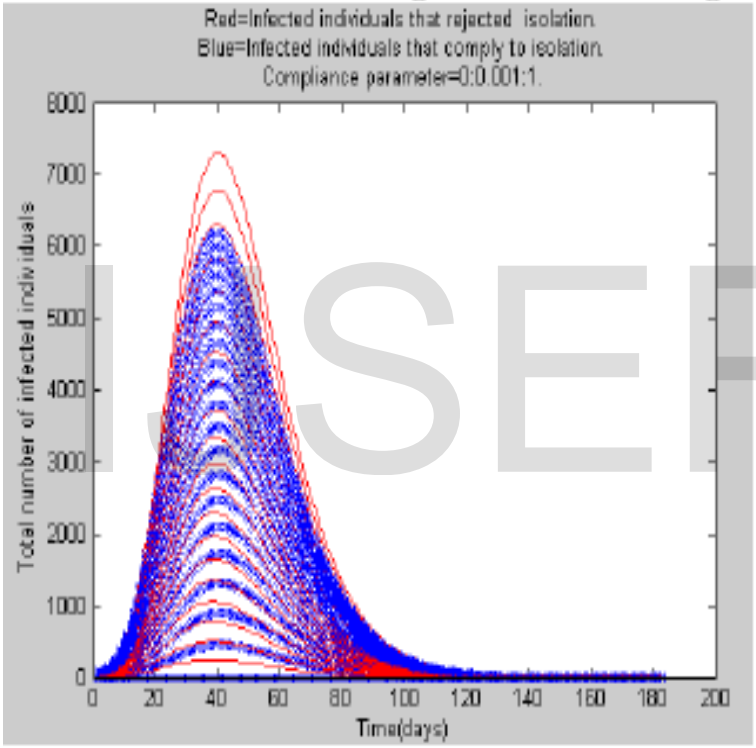
Dynamics Of Infected Population With High Compliance Rate.
Fig3.4.$\beta = 0.45, \alpha_t = 0.04, \alpha_i = 0.01, \rho =$ 0.001.

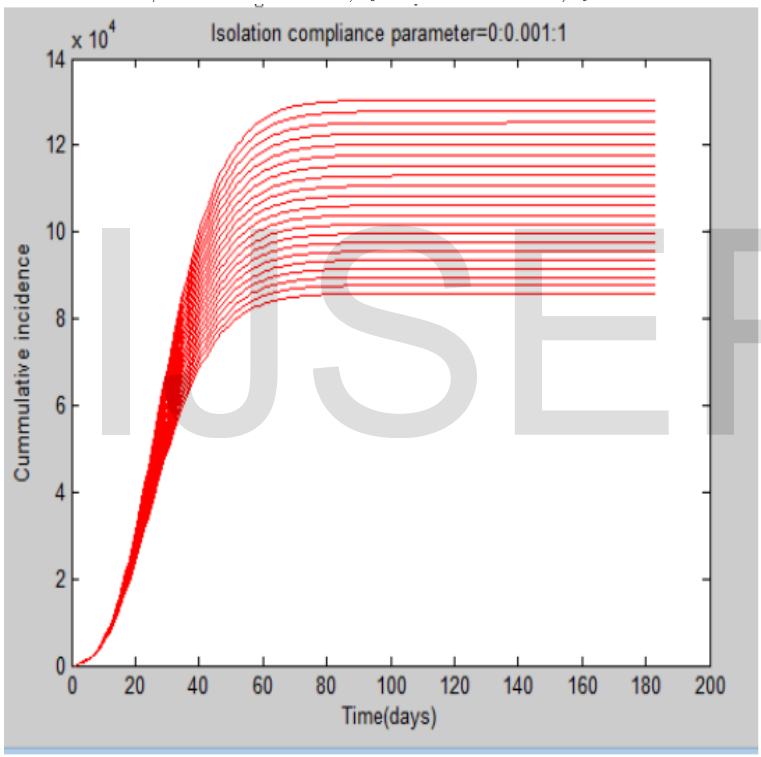


High level of administered control strategies with strict compliance to isolation,reduces the endemic equilibrium point as defined in fig3.4.

3.5 Global stability of endemic equilibrium point. 18

Cummulative Incidence Plot

Figure 4: $\beta = 0.45, \alpha_t = 0.04, \alpha_i = 0.01, \rho =$ 0.001



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