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Mathematical Analysis of Effect of Slow Progressor on Coronavirus Disease Dynamics Transmission

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A B S T R A C T

Coronavirus disease is a new respiratory virus that is not fully understood and information about both the pathogen and immunity in natural infection is lacking. This study aims to introduce a mathematical model construction regarding the transmission of coronavirus disease in human population by taking into consideration several epidemiology parameters that are closely identical with the real condition. The model was analyzed by identifying the endemicity parameters of coronavirus disease that is, the presence of disease-free equilibrium point and basic reproductive number. Furthermore, the sensitivity analysis was carry out to find out which parameter is the most dominant to affect the disease's endemicity. The results revealed that the contact rate β, and modification of undetected η_U in sequence showed the most dominant sensitivity index towards the basic reproductive number. Finally, results from simulation reveal that the slow progressor on susceptible individual should be totally reduced and increase on exposed individual for easily detection of infectious detected and infectious undetected.

Keywords:- COVID-19, Disease Free Equilibrium, Basic Reproduction Number, Global Stability Of Endemic And Sensitivity Analysis.

1. Introduction

The World Health Organization (WHO) stated that severe acute respiratory syndrome coronavirus -2 popularly known as COVID-19 was first reported in December 2019 in Wuhan City, China. Since the first diagnosed case in China, it has rapidly spread across the world through travellers returning from hotspots in Asia, Europe and the United States. COVID-19 pandemic was confirmed to have spread to Africa on 14 February 2020. Egypt Today reported that the first confirmed case was recorded in Egypt [2]. Around 1 AM on Friday 28 February 2020, Nigeria announced sub-Saharan Africa's first confirmed case [1]. This study mainly builds a dynamic statistical model based on time series analysis on the reported cases of COVID-19 transmission in Nigeria, and compares the prediction effects of these models. This will provide the general public, public health officials and any researcher with the exposure to the outbreak. Since the emergence of COVID-19 and its swift global spread, various pandemic simulation prediction models have sprung up. The Poisson regression model is a technique used to depict count data as a function of a set of predictor variables. In the last two decades it has been broadly used both in human and in veterinary epidemiology to examine the prevalence and mortality of chronic diseases.

Also, many governments worldwide are spending billions of the United States' dollars as well as soliciting aids from well-spirited individuals and organizations towards combating the COVID-19 pandemic. Furthermore, many countries have imposed compulsory self-quarantine and restricted movements of their citizenries (lockdown/sit at home), closure of businesses, and borders as preventive measures [1, 10, 4, 6, 8]. These interventions have succeeded greatly in curtailing the trans-border

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spread of the SARS-CoV-2 from country to country. Nevertheless, the emerging major problem in the spread of COVID-19 is human-to-human transmission in a heterogeneous community. Sadly, the implementation of these interventional policies of governments (e.g. total lockdown of movement, businesses, fear of quarantine/isolation), has thrown up another new challenge in the fight of the disease because of hunger and poverty especially in developing countries in sub-Saharan Africa where governments lack social securities. Therefore, there is the need to find cost-effective ways of halting the COVID-19 pandemic with minimal economic and social disruptions to avert impending catastrophic economic rupture.

[5] worked on impact of lockdown to control coronavirus disease transmission in Nigeria using mathematical modeling approach, the theoretical study of the model was provided and basic reproduction number which determines the extinction and the persistence of the infection and results show that in order to control transmission of corona virus disease total lockdown should imposed by federal governmental and individual compliance with COVID-19 guidelines are essential to control the infection.

Scholars are approaching this pursuit from two broad but complementary aspects of sciences; the Medical sciences and natural sciences. The medical scientists are busy trying to identify the source(s) of the disease, quicker ways of detecting the disease, treatment, and vaccine production [10, 3, 9]. The natural scientists are busy trying to proffer interventional measures through the development of mathematical models that will control the disease transmission especially now that there is no vaccine or known treatment.

In this work, an epidemic model for COVID-19 with transmission routes from symptomatic infectious humans, asymptomatic infectious humans and hospitalized individuals is parameterized and analyzed based on the cumulative number of active cases reported in Nigeria. Moreover, optimal control theory is applied to the epidemiology of COVID-19 transmission in order to assess the optimal levels of time-dependent prevention and management measures that will significantly minimize the number of infectious humans in the population. The outbreak of COVID-19 in West Africa, especially in Nigeria happens to be the most severe in the history of epidemic recorded; hence, there is a need to explore the characteristics of this disease through mathematical modeling, in order to control further outbreak of the disease in Nigeria. Several researchers have developed some mathematical models to better improve our understanding of the dynamics and spread of corona virus disease in order to curb its prevalence and curtain the incessant outbreaks of the virus. This research was formulated and analyzed a mathematical model that studied the effect of each parameter and impart of detection rate on the dynamical spread of COVID-19 in the population as a whole.

2. Model Formulation and Analysis

In this study, a mathematical model of the spread and transmission of SARS-CoV-2 was formulated. The model subdivides the total population size at time t denoted as $N(t)$ into susceptible $S(t)$, exposed $E(t)$, infectious detected $I_D(t)$, infectious undetected $I_U(t)$, infectious isolated $I_S(t)$ and recovered class $R(t)$.

$$\lambda = \frac{\beta(\eta_D I_D + \eta_U I_U + \eta_S I_S)}{N}$$

From above expression it is assumed that the exposed and recovered individual respectively do not transmit the disease i.e. only infected detected, infected undetected and finally infected isolated are assumed capable of transmitting the COVID-19 to susceptible individual by putting all this assumptions together obtain the following model equations

$$\frac{dS}{dt} = \rho - \lambda S - \mu S + \phi R$$
$$\frac{dE}{dt} = \varepsilon\lambda S - (\kappa + \sigma_1 + \mu)E$$
$$\frac{dI_D}{dt} = (1-\varepsilon)\lambda S + \omega\kappa E - (\sigma_2 + \delta + \mu)I_D$$
$$\frac{dI_U}{dt} = (1-\omega)\kappa E - (\gamma_1 + \mu + \delta)I_U$$
$$\frac{dI_S}{dt} = \sigma_1 E + \sigma_2 I_D - (\gamma_2 + \delta + \mu)I_S$$
$$\frac{dR}{dt} = \gamma_1 I_U + \gamma_2 I_S - (\phi + \mu)R$$

Table 1.Description of variables

Variable	Description
S	Susceptible individual
E	Expose individual
I_D	Infectious detected individual
I_U	Infectious undetected individual
I_S	Infectious isolated individual
R	Recovered individual

Table 2. Description of Parameters

Parameter	Description
ρ	Recruitment rate
δ	Disease induced death rate
ω	Endogenous reactivation rate
κ	Progression rate from exposed to detected and undetected individual
ε	Slow progressor
$1-\varepsilon$	Fast progressor
γ_1	Recovery rate of infectious undetected individual
γ_2	Recovery rate of infectious isolated individual
μ	Natural death rate
σ_1	Isolation rate of exposed individual
σ_2	Isolation rate of infectious detected
$\eta_{D=}\eta_{U=}\eta_S$	Modification parameters
β	Contact rate
ϕ	Loss of immunity from recovered individual

3. Theoretical Analysis of the Model

It should be noted that the parameters of the formulated model (2.1) are non-negative since the model describes disease outbreak in human population. Therefore, it is suffices to state that solutions of the model (2.1) are non-negative too.

3.1 Disease free equilibrium (DFE)

In this section disease free equilibrium point is obtained at which the epidemic is eradicated from the population. Setting the right hand side of equation (2.1) to zero i.e. $I_D = I_U = I_S = 0$. It is given by $E_0 = \left(\frac{\rho}{\mu},0,0,0,0,0\right)$.

3.3 Basic reproduction number

The threshold parameter that governs the spread of a Covid-19 which is called the basic reproduction number is determined with the help of next generation matrix method so that it is the spectral radius of the next generation matrix FV^{-1}[11].

The infection components in this model are E, I_D, I_U, I_S. The new infection matrix F and the transition matrix V are given by

$$F=\begin{pmatrix}0 & \varepsilon\beta\eta_D & \varepsilon\beta\eta_U & \varepsilon\beta\eta_S\\ 0 & (1-\varepsilon)\beta\eta_D & (1-\varepsilon)\beta\eta_U & (1-\varepsilon)\beta\eta_S\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\end{pmatrix}, V=\begin{pmatrix}a_1 & 0 & 0 & 0\\ -\omega\kappa & a_2 & 0 & 0\\ -(1-\omega)\kappa & 0 & a_3 & 0\\ -\sigma_1 & -\sigma_2 & 0 & a_4\end{pmatrix}$$

Thus

$$R_0=\frac{\beta\begin{pmatrix}\omega\varepsilon\kappa a_2a_4\eta_U+\omega\varepsilon\kappa a_3a_4\eta_D+\omega\varepsilon\kappa a_3\eta_s\sigma_2+\varepsilon\kappa a_2a_4\eta_U-\varepsilon a_1a_3a_4\eta_D-\varepsilon a_1a_3\eta_S\sigma_2\\ +\varepsilon a_2a_3\eta_s\sigma_1+a_1a_3a_4\eta_D+a_1a_3\eta_S\sigma_2\end{pmatrix}}{a_1a_2a_3a_4}$$

3.4 Global stability of the endemic equilibrium point

Theorem 3.5 the endemic equilibrium E^* of the model (2.1) is globally asymptotically stable If $R_0>1$,

Proof: To prove the global asymptotic stability of the endemic equilibrium, use method of lyapunov functions.

Define by:

$$V(S,E,I_D,I_U,I_S,R)=\left(S-S^*\ln\frac{S}{S^*}\right)+\left(E-E^*\ln\frac{E}{E^*}\right)+\left(I_D-I_D^*\ln\frac{I_D}{I_D^*}\right)+\left(I_U-I_U^*\ln\frac{I_U}{I_U^*}\right)$$

$$+\left(I_S-I_S^*\ln\frac{I_S}{I_S^*}\right)+\left(R-R^*\ln\frac{R}{R^*}\right).$$

Find the derivative of V

$$\frac{dV}{dt}=\left(1-\frac{S^*}{S}\right)\frac{dS}{dt}+\left(1-\frac{E^*}{E}\right)\frac{dE}{dt}+\left(1-\frac{I_D^*}{I_D}\right)\frac{dI_D}{dt}+\left(1-\frac{I_U^*}{I_U}\right)\frac{dI_U}{dt}+\left(1-\frac{I_S^*}{I_S}\right)\frac{dI_S}{dt}+\left(1-\frac{R^*}{R}\right)\frac{dR}{dt}$$

Substituting the value of $\frac{dS}{dt}, \frac{dE}{dt}, \frac{dI_D}{dt}, \frac{dI_U}{dt}, \frac{dI_S}{dt}, \frac{dR}{dt}$ from (2.1)

$$\frac{dV}{dt}=\left(1-\frac{S^*}{S}\right)(\rho-\lambda S-\mu S+\phi R)+\left(1-\frac{E^*}{E}\right)(\varepsilon\lambda S-(\kappa+\sigma_1+\mu)E)+\left(1-\frac{I_D^*}{I_D}\right)((1-\varepsilon)\lambda S+\omega\kappa E-(\sigma_2+\delta+\mu)I_D)$$

$$+\left(1-\frac{I_U^*}{I_U}\right)((1-\omega)\kappa E-(\gamma_1+\mu+\delta)I_U)+\left(1-\frac{I_S^*}{I_S}\right)(\sigma_1E+\sigma_2I_D-(\gamma_2+\delta+\mu)I_S)+\left(1-\frac{R^*}{R}\right)(\gamma_1I_U+\gamma_2I_S-(\phi+\mu)R) \quad (2.2)$$

Endemic point of system (2.1) give

$$\rho=\lambda S^*+\mu S^*-\phi R^*$$

$$\kappa+\sigma_1+\mu=\frac{\varepsilon\lambda S^*}{E^*}$$

$$\sigma_2+\delta+\mu=\frac{(1-\varepsilon)\lambda S^*+\omega\kappa E^*}{I_D{}^*}$$

$$\gamma_1+\mu+\delta=\frac{(1-\omega)\kappa E^*}{I_U{}^*} \quad (2.3)$$

$$\gamma_2+\delta+\mu=\frac{\sigma_1E^*+\sigma_2I_D{}^*}{I_S{}^*}$$

$$\phi+\mu=\frac{\gamma_1I_U{}^*+\gamma_2I_S{}^*}{R^*}$$

Substituting (2.3) into (2.2)

$$\frac{dV}{dt}=\left(1-\frac{S^*}{S}\right)(\lambda S^*+\mu S^*-\phi R^*-\lambda S-\mu S+\phi R)+\left(1-\frac{E^*}{E}\right)(\varepsilon\lambda S-\frac{\varepsilon\lambda S^*}{E^*}E)+\left(1-\frac{I_D^*}{I_D}\right)((1-\varepsilon)\lambda S+\omega\kappa E-$$
$$\{\frac{(1-\varepsilon)\lambda S^*+\omega\kappa E^*}{I_D{}^*}\}I_D)+\left(1-\frac{I_U^*}{I_U}\right)((1-\omega)\kappa E-\frac{(1-\omega)\kappa E^*}{I_U{}^*}I_U)+\left(1-\frac{I_S^*}{I_S}\right)(\sigma_1 E+\sigma_2 I_D-\{\frac{\sigma_1 E^*+\sigma_2 I_D{}^*}{I_S{}^*}\}I_S)+$$
$$\left(1-\frac{R^*}{R}\right)(\gamma_1 I_U+\gamma_2 I_S-\{\frac{\gamma_1 I_U{}^*+\gamma_2 I_S{}^*}{R^*}\}R)$$

Where $S=S^*, E=E^*, I_D=I_D^*, I_U=I_U^*, I_S=I_S^*, R=R^*$ obtain $\frac{dV}{dt}=0$. Hence by LaSalle's invariance principle every solution of system (2.1) with initial condition in $\Pi=\{(S,E,I_D,I_U,I_S,R)\in R_+^6\}$ it follows that E^* is globally asymptotically stable.

4. Sensitivity of the Model to Parameters

It is important to determine how sensitive the COVID-19 model (2.1) is to changes in each of its parameters in order to suggest intervention strategies that will help in bringing down the infection trajectory. In other words, carrying out sensitivity analysis will help in providing insights into what should be done to prevent the outbreak of the novel coronavirus [5]. The normalized forward sensitivity index of the reproduction number with respect to its parameters was computed which defined as:

$$X_P^{R_0}=\frac{\partial R_0}{\partial P}\times\frac{P}{R_0}$$

Sensitivity values for each parameter involved in R_0 is calculated and result were presented in the table below.

Table 3. Sensitivity indices with the parameters

Parameter	Sensitivity value
β	1.000
η_U	0.5731
ρ	0.2963
δ	-0.2397
ω	0.2963
κ	0.1465
ε	0.0009
γ_1	-0.0008
γ_2	-0.0008
μ	-0.0008
σ_1	-0.0008
σ_2	-0.3942
ϕ	0.000
η_D	0.2405
η_S	0.1862

The most sensitive parameter is contact rate (β), follow by modification of undetected (η_U) and so on. All of these parameters play a significant role in the dynamical spread or in controlling of the Corona virus disease in the community.

5. Numerical Simulation Results

Numerical simulation of the model (2.1) employing the parameter values given in table 4 with their initial conditions are evaluated using the Runge kutta method embedded in mathematical software (Maple18). $S(0)=2069617$, $E(0)=304064$, $I_D(0)=44942$,

$I_U(0) = 14323$ $I_S(0) = 35902$ and $R(0) = 44942$ with following parameters:

Table 4. Parameters Values

Parameter	Value
ρ	271.23/days
δ	0.7/days
ω	0.09/days
κ	0.1429/days
ε	0.7/days
γ_1	0.05
γ_2	0.1
μ	0.000031
σ_1	0.07143
σ_2	0.04762
$\eta_D = \eta_U = \eta_S$	0.10
β	0.2
ϕ	0.0051

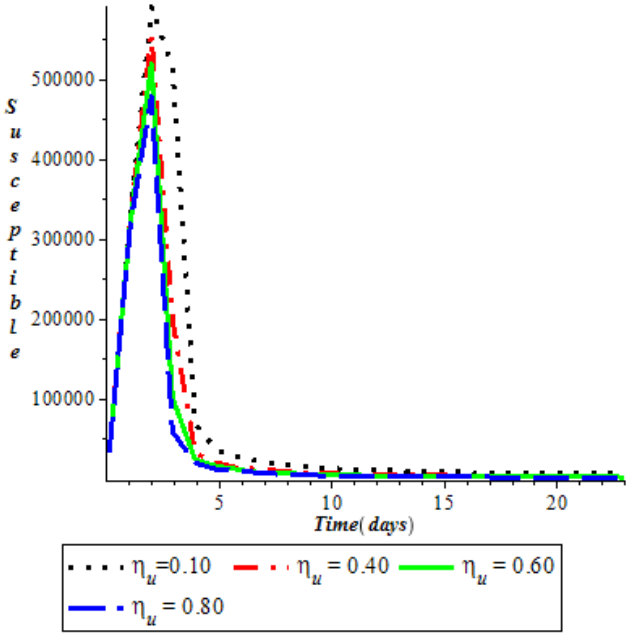

Fig. 1 Effect of modification parameters of infectious undetected on susceptible class

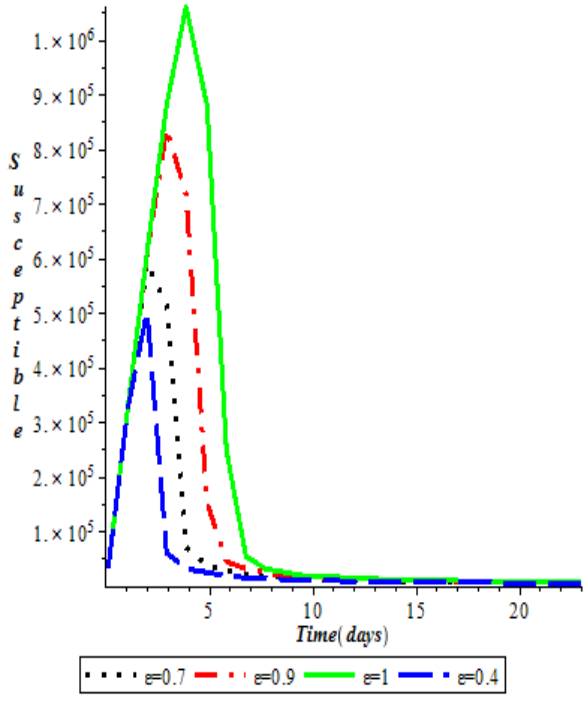

Fig. 2(a) Effect of slow progressor on susceptible class

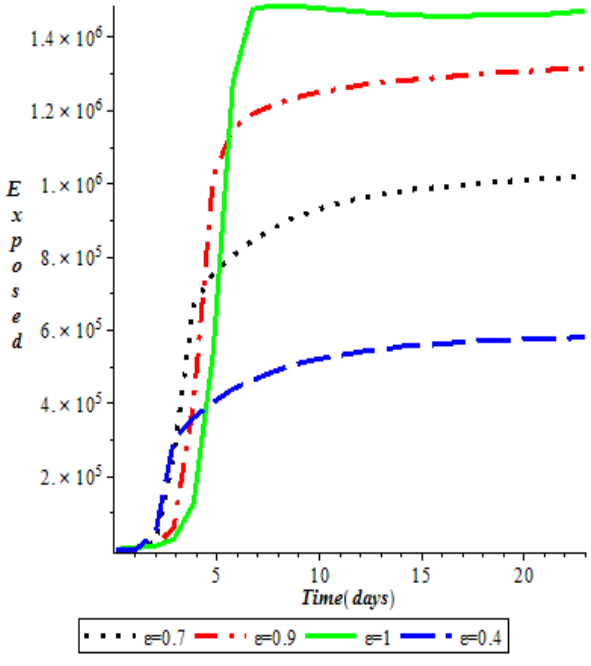

Fig. 2(b) Effect of slow progressor on exposed class

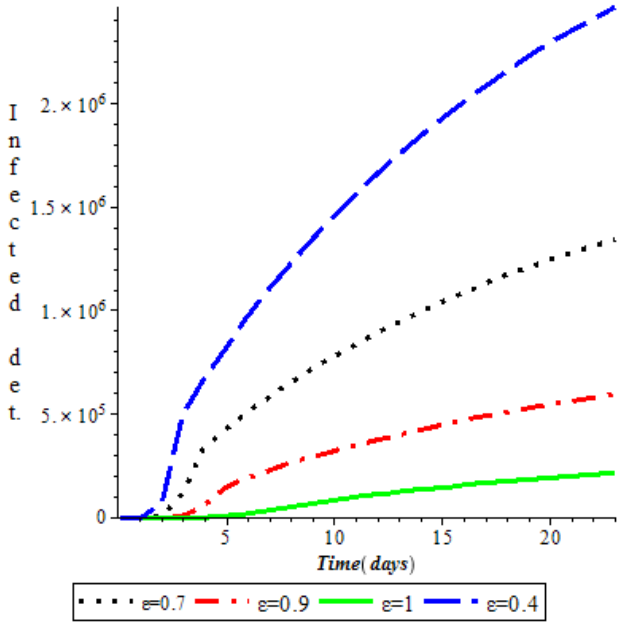

Fig. 2(c) Effect of slow progressor on infected detected class

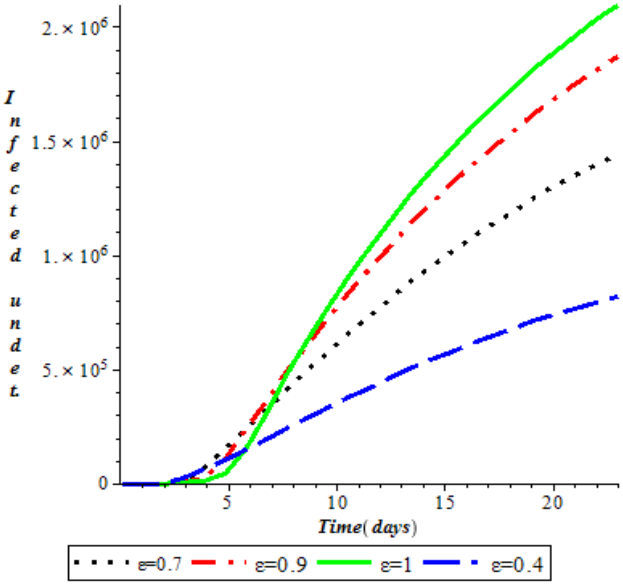

Fig. 2(d) Effect of slow progressor on infected undetected class

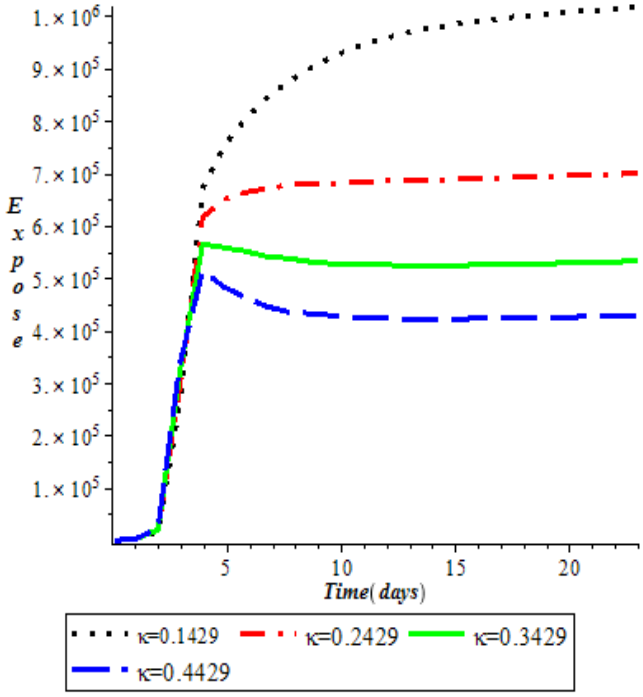

Fig. 3(a) Effect of progression rate on exposed class

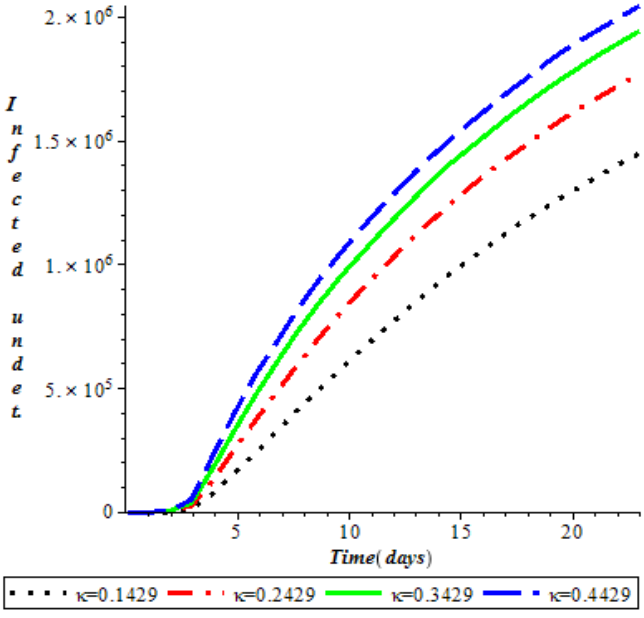

Fig. 3(b) Effect of progression rate infected undetected class

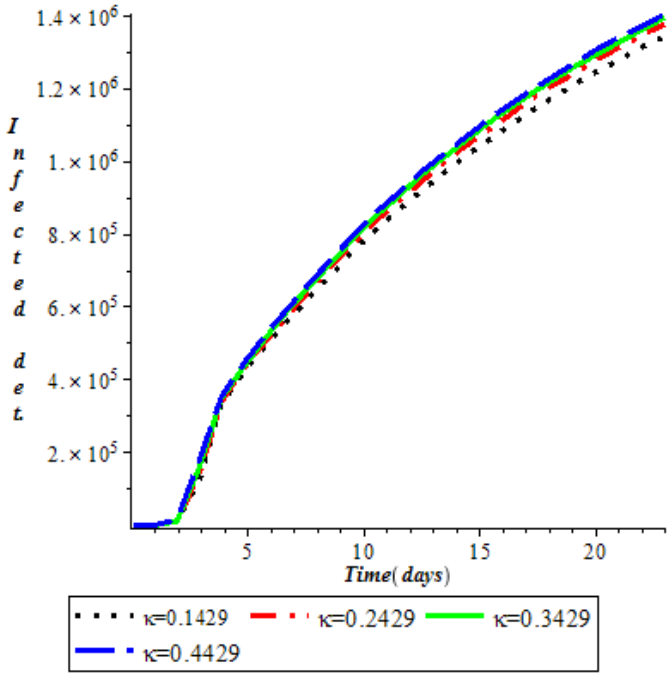

Fig. 3(c) Effect of progression rate on infected detected class

6. Discussion of Result

Figure 1, illustrate the effect of modification parameter of undetected on susceptible population as parameter (η_U) increases the population reduces.

In figure 2(a) susceptible population increases initially due to recruitment rate of individual into the system but later decreases and remain steady as a result of increasing in slow progressor(ε)

In the same way in figure 2(b) when slow progressor (ε) was increased on exposed population, the symptoms of exposed individual was increased as a result of that infected individual was able to detect and move to isolation class.

Also in figure 2(c) infectious detected individual is reducing due to increase in slow progressor due to that infectious is reducing in population.

In figure 2(d) infectious undetected population increases because those infectious already who are unable to detect are now detect due to increasing in slow progressor (ε).

In figure 3(a) the population of expose individual is reducing because of increasing in progression (κ) rate of exposed to infectious detected, as a result of that the disease is reducing within the community.

In figure 3(b) because of increasing in progression (κ) rate of exposed individual, the infectious undetected class increases as a result of detecting infectious undetected.

Finally, in figure 3(c) there is no significant difference on infectious detected individual as a result of increasing in progression rate (κ).

7. Conclusion

A mathematical model based on S, E, I_D, I_U, I_S, R was formulated and analyze to study the spread of COVID-19 evolution. The basic reproduction number was computed using the next generation matrix, stability analysis was performed and the results reveal that the disease free equilibrium is locally and globally stable. The results of sensitivity analysis revealed that the contact rate β, and modification of undetected η_U in sequence showed the most dominant sensitivity index towards the basic reproductive number in that case the contact rate between the susceptible and infectious individual should be minimized. Finally, results from simulation reveal that the slow progressor on susceptible individual should be totally reduced and increase on exposed individual for easily detection of infectious detected and infectious undetected.

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