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SIMULATING MODELS FOR THE TRANSMISSION DYNAMICS OF A NOVEL CORONA VIRUS UNDER THE ADMINISTRATION OF AN IMPERFECT VACCINE IN NIGERIA

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Abstract: The spread of corona virus disease (COVID-19) to over 210 countries has resulted in a pandemic which has continued to generate severe public health concern and socio-economic burden worldwide. This study investigated the impact of some control strategies (face mask usage, social distancing and contact tracing) on the dynamics of Corona virus in the Nigerian population. A mathematical model was developed and analyzed to also examine the impact of an imperfect vaccine on the transmission dynamics of COVID-19 disease. The model was shown to be both locally and globally asymptotically stable. The model was extended to explore a relationship between vaccination rate and transmission dynamics of the disease. Numerical simulations suggest that an implementation of an effective face mask strategy as well as social distancing will greatly control community transmission. Also, widespread random testing could help in detecting, tracing and isolating symptomatic and asymptomatic cases, thereby reducing the transmission by contacts. More testing would imply an increase in the number of detected cases as well as prompt isolation of symptomatic and asymptomatic cases, thereby reducing community transmission. Furthermore, a simulation was done to measure the population impact level when an imperfect vaccine is administered. The simulation showed that corona virus burden in terms of the cumulative number of deaths, decreases with an increasing vaccine rate, and that, if the vaccine efficacy confers 70% protection

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and a large proportion of the susceptible class is vaccinated, then, it would have led to the elimination of the disease within a short period of time. However, if the vaccine efficacy level confers 10% to 40% protection against the disease, then it is not sufficient to curtail the disease in the near future.

Keywords: covid-19; vaccine; social distancing; face mask use; efficacy; testing.

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1. INTRODUCTION

Corona virus is a contagious virus that targets the human respiratory system. The disease is said to have emerged from Wuhan City, China, in late 2019, and first set of hospitalized patients were allegedly linked to a seafood market in Wuhan, Hubei province of China (Rothana and Byrareddy [1]). The spread of this disease to over 210 countries has resulted into a pandemic which has continued to generate severe public health concern and socio-economic burden worldwide. As at the 25th of January, 2022, the world has recorded about 352,796,704 total confirmed corona virus cases with 5,600,434 deaths globally, reported to World Health Organization. Also, a total of 9,620,105,525 doses of vaccines have been administered. (World Health Organization [2]).

Corona virus disease (COVID-19) is transmitted from human to human via direct contact with contaminated surfaces and through inhaling droplets from an infected person (Bai *et al* [3]). Presently, the control and mitigation efforts against the disease are focused on vaccination and the non-pharmaceutical interventions (NPIs) such as face mask use, social distancing, contact tracing, lockdown, quarantine of suspected cases and isolation of confirmed cases (Eikenberry *et al* [4], Ngonghala *et al* [5] and Iboi *et al* [6]).

Nigeria, the most populous country in Africa with a population of over 200 million people, has the potential of being one of the epicentres of COVID-19 in Africa. The first case of COVID-19 was reported on the 27th of February, 2020. As at March 30th, Nigeria has recorded about 131 cases with 121 cases on admission with 2 deaths (Nigeria Centre for Disease Control [7]. The growing number of corona virus cases necessitated the Federal government of Nigeria to implement a strict lockdown, first in three major states in the country (Lagos, Ogun and Abuja),

and later, the whole country, in order to minimize the rate of community transmission. Furthermore, due to the increase in the number of cases, the government extended the lockdown to include the rest of the country on the 27th of April, 2020. Later, the complete lockdown was then reduced to curfew from 8pm till 6am from 4th May to 17th May, 2020, with some states making adjustments to their own curfew time. The first phase of easing the lockdown ended on 1st June while the second phase ended on the 27th of July, 2020[8]. What was evident is that even after the lockdown, Nigeria is still recording new cases every day. Thus there is need to ascertain what measures the government can further put in place to ensure a drastic reduction in the disease burden rate. There is currently no perfect vaccine for COVID-19, although a number of organizations have started mass production of their novel vaccines (Knvul and Katie[9], Callaway[10] and Kirkpatrick[11]). Thus, there is need to investigate the impact of such an imperfect COVID-19 vaccine in Nigeria in the long run.

Various mathematical models have been formulated and used to study the transmission dynamics of corona virus disease. Chen *et al*[12] developed a mathematical model for simulating the phase-based transmissibility of a novel corona virus. Ferguson *et al*[13] also developed an agent based model to investigate the impact of NPIs on COVID-19 induced mortality, showing an alarming worst-case projection of number of cases for the US and Great Britain. Ngonghala *et al*[5] developed a comprehensive model for assessing the impact of the major NPIs (quarantine, isolation, social distancing, face mask usage in public, testing and contact tracing) on the control of COVID-19. Okuonghae and Omame[14] formulated a mathematical model for COVID-19 which examined the impact of various non- pharmaceutical control measures (NPIs) on the population dynamics of the novel Corona virus disease in Lagos, Nigeria.

This present study has investigated the impact of various control strategies (face mask usage, social distancing and contact tracing) on the dynamics of Corona virus in the Nigerian population. A mathematical model has also been developed and analyzed to examine the impact of an imperfect vaccine on the transmission dynamics of COVID-19 disease in Nigeria.

2. MODEL FORMULATION

The total population at time t denoted by $N(t)$ is divided into seven mutually exclusive sub-populations; the susceptible humans, $S(t)$, the exposed $E(t)$, the asymptomatic infectious $I_a(t)$, the symptomatic infectious $I_s(t)$, the self-isolated humans, $I_i(t)$, the detected infectious humans via testing and are isolated in the hospital for prompt treatment, $I_h(t)$and the recovered humans, $R(t)$. Thus, the total population is given by:

$$N(t) = \mathrm{S(t)} + \mathrm{E(t)} + I_a(t) + I_s(t) + I_i(t) + I_h(t) + R(t)(1) \quad (1)$$

Individuals acquire corona virus infection following effective contact with infected persons at a rate

$$\lambda = \frac{\beta(1-\varepsilon)(1-v)[I_s+\alpha I_a]}{N-(I_i+I_h)} \quad (2)$$

where β is the effective transmission rate, $0 \leq \varepsilon \leq 1$ represents the social distance compliance rate, $0 \leq v \leq 1$ measures the reduction rate in community contacts due to face mask use in the community. The parameter $0 \leq \alpha \leq 1$ accounts for rate of reduced infectiousness of humans in the asymptomatic class compared to humans in the symptomatic class.

The model for the transmission dynamics of corona virus disease in the population is given by the system of deterministic non-linear differential equations in (3). Table 1 describes the associated state variables and parameters, while Fig.1 gives the flow diagram of model (3).

$$\left.\begin{aligned}
\frac{dS}{dt} &= -\lambda \mathrm{S} \\
\frac{dE}{dt} &= \lambda \mathrm{S} - \theta \mathrm{E} \\
\frac{dI_s}{dt} &= \theta(1-\mathrm{k})\mathrm{E} - (\sigma_s + \sigma_h + r_1 + \delta_s)I_s \\
\frac{dI_a}{dt} &= \mathrm{k}\theta \mathrm{E} - r_2 I_a \\
\frac{dI_i}{dt} &= \sigma_i I_s - (r_3 + \delta_i)I_i \\
\frac{dI_h}{dt} &= \sigma_h I_s - (r_4 + \delta_h)I_h \\
\frac{dR}{dt} &= r_1 I_s + r_2 I_a + r_3 I_i + r_4 I_h
\end{aligned}\right\} \quad (3)$$

In model (3), susceptible individuals acquire COVID-19 following effective contact with individuals in the asymptomatic class (I_a) and symptomatic class (I_s) at λ rate. Newly infected individuals in the E class at the end of the incubation period, a proportion, $0 \leq k \leq 1$ of humans progress to the asymptomatic class at the rate $k\theta$, (where k is the proportion of humans who do not show clinical symptoms after the disease incubation period). The remaining proportion $1-k$ show clinical symptoms of corona virus at the end of the incubation period and progress to the symptomatic class at the rate $\theta(1-k)$.

Individuals in the symptomatic class become self-isolated (hospitalized) or recover at the rate $\sigma_s(\sigma_h)$ or r_1 respectively. The asymptomatic infectious humans become self-isolated (recovered) after detection at a rate $\sigma_s(r_2)$. Individuals in the self-isolated (hospitalized) class recover from the disease at the rate $r_3(r_4)$. The parameters δ_s, δ_i and δ_h accounts for the disease induced deaths in the symptomatic, self-isolation and hospitalized classes.

2.1 Basic Properties of Model (3)

In this section, we establish the dynamical properties of the corona virus model (3).

2.1.1 Positivity

For model (3) to be epidemiologically meaningful, it is pertinent to show that all the state variables are non-negative for all time. We claim the following:

Theorem 2.1

The system (3) preserves positivity of solutions. Thus the solution with positive initial conditions will remain positive for all time, $t > 0$.

Proof

$Let\ t_1 = Sup\{t > 0 : S > 0,\ E > 0, I_s > 0,\ I_a > 0,\ I_i > 0,\ I_h > 0,\ R > 0 \in [0, t]\}.$

Thus $t_1 > 0$.

From the first equation of model (3), we have

$$\int \frac{dS}{dt} = -\int \lambda \mathrm{S}$$

and

$$S(t_1) = S(0)\exp\left[-\int_0^{t_1}\lambda(u)du\right] > 0.$$

Similarly, it can be shown that $E > 0, I_s > 0,\ I_a > 0,\ I_i > 0,\ I_h > 0, and\ \ R > 0.$

Hence all solutions of model (3) remain positive for all non-negative initial conditions, as required.

2.1.2 Boundedness

We now show that the region D is bounded with the following theorem

Theorem 2.2:

The region $D = \{(S,\ E, I_s,\ I_a,\ I_i,\ I_h,\ R)\epsilon R_+^7 : N(t) \leq S(0)\}$

is positively invariant for model (3) and attracts all positive solutions of the model.

Proof

We add all the equations of model (3), so that

$$\frac{dN}{dt} = \ -(\delta_s I_s\ + \delta_i I_i + \ \delta_h I_h);$$

which can be rewritten as

$$\frac{dN}{dt} \leq -\delta N\ ,\ \text{where } \delta = \min(\delta_s,\ \delta_i,\ \delta_h).$$

Thus by separation of variables, we have

$\int \frac{dN}{N} = -\int \delta\, dt$, which implies $N(t) \leq N(0)e^{-\delta t}$

Thus $N(t)$ approaches $N(0)\ as\ t \to \infty$. Hence the region D attracts all solutions in R_+^7 as required.

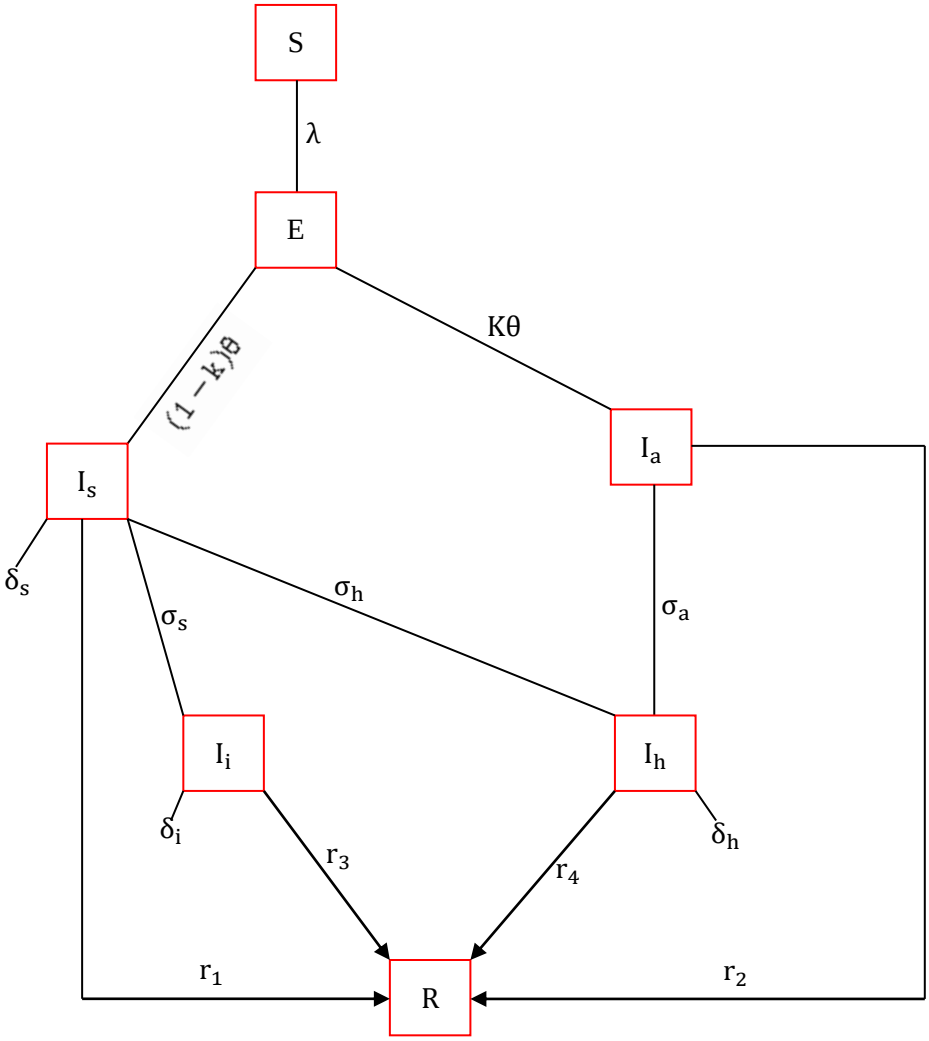


Figure 1: Flow Diagram of Model (3)

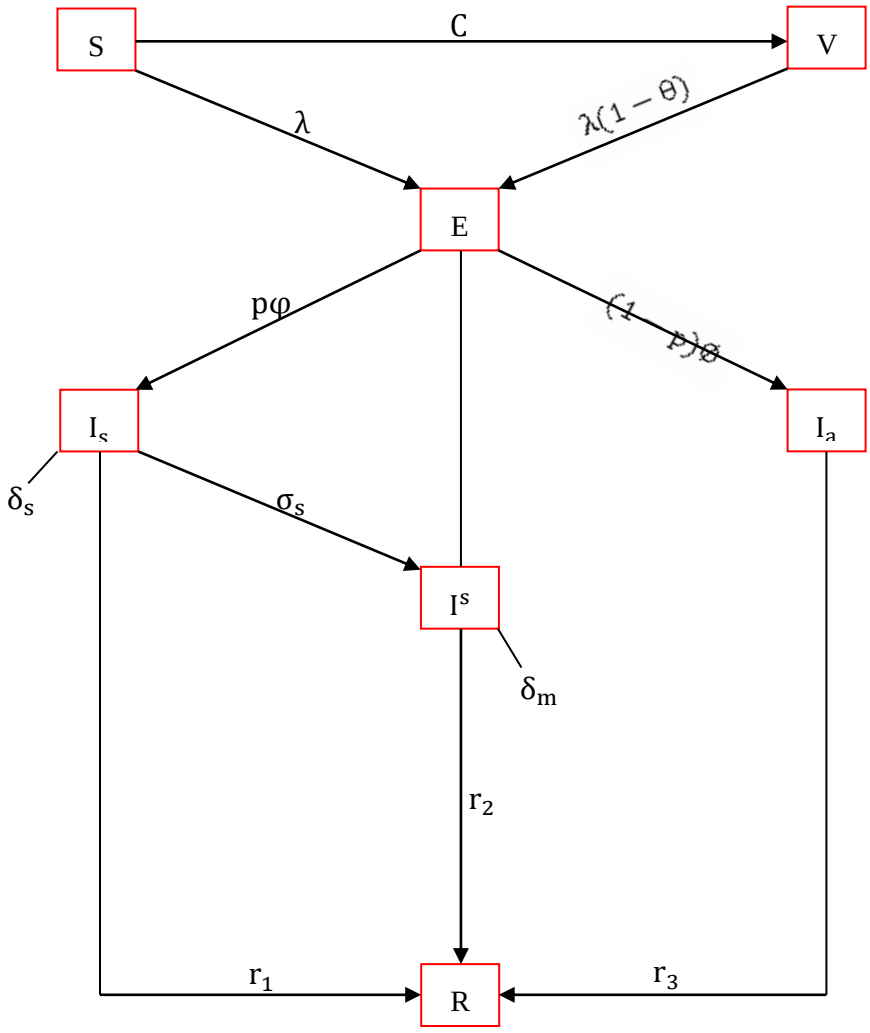


Figure 2: Flow Diagram of Model (14)

Table 1: Description of variables and parameters in model (3)

Variables	Interpretation
S	Susceptible humans
E	Exposed humans (newly infected humans with no sign of the disease)
I_s	Symptomatic infectious humans
I_a	Asymptomatic infectious humans
I_i	Individuals in self-isolation
I_h	Hospitalized individuals
R	Recovered individuals
B	Effective contact rate
ϵ	Social distance compliance rate
v	Rate of face mask use for reducing community contact
α	Modification parameter that accounts for reduction in infectiousness of humans in the I_a class compared to humans in the I_s class
σ_s, σ_h	Detection rate (via tracing and testing) for the I_s class
r_1, r_2, r_3, r_4	Recovery rates in the $I_s, I_a, I_i \; and \; I_h$ classes respectively
$\delta_s, \delta_i, \delta_h$	Disease induced death rates in the $I_s, I_i \; and \; I_h$ classes
θ	Efficacy of vaccine

Table 2: Baseline Values of Parameters used

Parameters	Values / Ranges	References
B	0.4355 [0.4,1.1]	Iboi *et al*[6]
θ	0.8 [0,1]	Iboi *et al*[6]
σ_s	0.025	Ferguson *et al*[13], Zhou *et al*[15]
σ_h	0.025	Ferguson *et al*[13], Zhou *et al*[15]
δ_s	0.015 [0.001,0.1]	Ferguson *et al*[13]
δ_h	0.015 [0.001,0.1]	Ferguson *et al*[13]
δ_i	0.015 [0.001,0.1]	Ferguson *et al*[13]
ε	0.1 [0,1]	Ngonghala *et al*[5]
α	0.5 [0,1]	Chen *et al*[12]
v	0.5 [0,1]	Estimated
r_1, r_2	0.013978 $[\frac{1}{30}, \frac{1}{3}]$	Tang *et al*[16]
r_3	0.07143 $[\frac{1}{30}, \frac{1}{3}]$	Tang *et al*[16]
r_4	0.0667 $[\frac{1}{30}, \frac{1}{3}]$	Chen *et al*[12], Cauchemez *et al*[17]
φ	0.1923 $[\frac{1}{14}, \frac{1}{3}]$	Iboi *et al*[6]
p	0.5 [0,1]	Chen *et al*[12]
δ_m	0.015 $[\frac{1}{10}, \frac{1}{30}]$	Ferguson *et al*[13]

2.2 Analysis of Model (3)

In this section, our major aim is to analyze model (3) so as to gain insights into the dynamics of model (3).

2.2.1 Disease-free equilibrium (DFE)

The corona virus model (3) has a DFE, obtained by setting the right hand sides of the equations in model (3) to zero, given by

$$\xi = (S^*, E^*, I_a^*, I_s^*, I_i^*, I_h^*, R^*) = (\mathrm{S}(0), 0, 0, 0, 0, 0, 0), \tag{4}$$

where $\mathrm{S}(0)$ is the initial total size of the population of susceptible individuals (so that $\mathrm{N}(0) = \mathrm{S}(0)$). The linear stability of the disease free equilibrium,ξ, can be established using the next generation operator method on model (3). Using the notations in Van den Driessche and Watmough[18], it follows that the associated non-negative matrix F (of new infections) and the matrix V (of transition terms) are respectively given by

$$F = \begin{bmatrix} 0 & \beta(1-\varepsilon)(1-V) & \beta\alpha(1-\varepsilon)(1-V) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \tag{5}$$

$$V = \begin{bmatrix} \theta & 0 & 0 \\ -\theta(1-k) & \sigma_s + \sigma_h + r_1 + \delta_s & 0 \\ -k\theta & 0 & r_2 \end{bmatrix} \tag{6}$$

Hence it follows that the control reproduction number of model (3), denoted by R_c is given by

$$R_c = \beta(1-\varepsilon)(1-V)\left[\frac{1-k}{\sigma_s+\sigma_h+r_1+\delta_s} + \frac{k\alpha}{r_2}\right] \tag{7}$$

The reproduction number R_c is the control reproduction number of model (3) which measures the average number of new corona virus cases generated by an infectious individual introduced into a population where some intervention strategies (social distancing, face mask usage and contact tracing) are implemented. We claim the following:

Theorem 2.3: the DFE, ξ of model (3) is locally asymptotically stable if $R_c < 1$ and unstable whenever $R_c > 1$.

The implication of theorem 2.3 is that the transmission of corona virus in the community can be effectively controlled in the community if the control strategies implemented can bring R_c

to a value less than unity. However it is pertinent to note that for epidemic models (with no birth or death demographic processes) such as model (3), having $R_c < 1$ is sufficient but not necessary for the elimination of the disease. This implies that even if $R_c > 1$, the disease will eventually die out. This is due to the fact that even if $R_c > 1$, some number of persons in the community can get infected when no control strategy is implemented. Some of these persons will recover from the infection, since recovery from the disease confers permanent natural immunity against future infection. This will lead to building community-wide natural herd immunity and the disease will eventually die out.

2.2.2 Interpretation of the Reproduction Number

As stated above, R_c is the control reproduction number of model (3) which is the sum of two reproduction numbers R_s and R_a. R_s is the product of the infection rate of susceptible individuals by symptomatic infectious individuals, the proportion of exposed individuals that survived the incubation period and moved to the symptomatic class (1-k) and the average duration in the symptomatic infectious class $\left(\frac{1}{\sigma_s+\sigma_h+r_1+\delta_s}\right)$. In the same vein, the reproduction number R_c is the product of the infectious rate of susceptible individuals, near the DFE, the proportion that survived the exposed class and moved to the asymptomatic infectious class (k) and the average duration in the asymptomatic class $\left(\frac{1}{r_2}\right)$.

We now seek to obtain the basic reproduction number of model (3) gotten by setting all public health intervention implemented in Nigeria to zero. Thus, the basic reproduction number is given by:

$$R_0 = R_c \setminus (\varepsilon = V = k = 0) = B\left[\frac{1-k}{\sigma_s+\sigma_h+r_1+\delta_s} + \frac{k}{r_2}\right] \quad (8)$$

R_0 represents the average number of secondary infections generated by a typical infected individual introduced into a completely susceptible sub-population during the period of the infectiousness of the individual.

2.2.3 Computation of the Final Size of the Pandemic

We now use the method of Kermack and Mckendrick[19] to determine the final size relation for the corona virus pandemic.

Let $x \in R_+^5$, $y \in R_+$ and $z \in R_+$ be the sets of infected, susceptible and recovered compartments of the model, respectively. It follows from model (3) that:

$x(t) = (E(t), I_a(t), I_s(t), I_i(t), I_h(t))^T$, $y(t) = S(t)$, and $z(t) = R(t)$ (9)

Using the notations in Arino, Brauer, Van Den Driessche, Watmough and Wu[20], model (3) reduces to:

$$\left.\begin{aligned} \frac{dx}{dt} &= \pi \mathrm{Dy}\beta(\mathrm{x},\mathrm{y},\mathrm{z})\mathrm{bx} - \mathrm{Vx} \\ \frac{dy}{dt} &= -\mathrm{Dy}\beta(\mathrm{x},\mathrm{y},\mathrm{z})\mathrm{bx} \\ \frac{dz}{dt} &= \mathrm{Wx} \end{aligned}\right\} \quad (10)$$

where β is the infection rate λ in model (3) (that is $\lambda = \beta(\mathrm{x},\mathrm{y},\mathrm{z})$), W is a k× n matrix with the property that (i,j)entry represents the rate at which individuals of the j^{th} infected compartment transits into the i^{th} compartment upon recovery, and the matrix V remains the transition terms.

Thus going by theorem 5.1 of Arino *et al*[20], the final epidemic size relation for model (3) is given by

$$Ln\left(\frac{S(0)}{S(\infty)}\right) \geq \frac{R_c}{S(0)}\big(S(0) - S(\infty)\big) + \frac{\beta(1-\varepsilon)(1-v)}{S(0)}\left[\frac{1}{\sigma_s+\sigma_h+r_1+\delta_s} I_s(0) + \frac{1}{r_2} I_a(0)\right] \quad (11)$$

Next we show the global asymptotic stability (GAS) of the disease-free equilibrium (DFE) of the model (3). We make the following proposal:

Theorem 2.4:

The DFE, ξ of model (3) is globally asymptotically stable whenever $\boldsymbol{R_c < 1}$.

Proof

Consider the Lyapunov function given by

$$L = \frac{\beta(1-\varepsilon)(1-v)(\sigma_s+\sigma_h+r_1+\delta_s)\alpha k+\beta(1-\varepsilon)(1-v)(1-k)r_2}{r_2(\sigma_s+\sigma_h+r_1+\delta_s)} E +$$

$$\frac{\alpha\beta(1-v)(1-\varepsilon)}{r_2} I_a + \frac{\beta(1-v)(1-\varepsilon)}{\sigma_s+\sigma_h+r_1+\delta_s)} I_s \quad (12)$$

Differentiating with respect to time, we have

$$\frac{dL}{dt} = \frac{\beta(1-\varepsilon)(1-v)(\sigma_s+\sigma_h+r_1+\delta_s)\alpha k+\beta(1-\varepsilon)(1-v)(1-k)r_2}{r_2(\sigma_s+\sigma_h+r_1+\delta_s)}\frac{dE}{dt} +$$

$$\frac{\alpha\beta(1-v)(1-\varepsilon)}{r_2}\frac{dI_a}{dt}+ \frac{\beta(1-v)(1-\varepsilon)}{\sigma_s+\sigma_h+r_1+\delta_s)}\frac{dI_s}{dt}$$

$$\frac{dL}{dt} = \beta(1-\varepsilon)(1-v)[\frac{1-k}{\sigma_s+\sigma_h+r_1+\delta_s} + \frac{k\alpha}{r_2}][\frac{\beta(1-\varepsilon)(1-k)(I_s+\alpha I_a)S}{N-(I_i+I_h)}] -$$

$$\alpha\beta(1-\varepsilon)(1-v)I_a - \beta(1-\varepsilon)(1-v)I_s$$

But for all time (t), we have that

$$S(t) \leq N-(I_i+I_h)\ and\ \beta(1-\varepsilon)(1-v)[\frac{1-k}{\sigma_s+\sigma_h+r_1+\delta_s} + \frac{k\alpha}{r_2}]$$

Thus,

$$\frac{dL}{dt} = \alpha\beta(1-v)I_a(R_c-1) + \beta(1-\varepsilon)(1-v)I_s([R_c-1)$$

$$\frac{dL}{dt} = [\beta(1-\varepsilon)(1-v)I_s + \alpha\beta(1-\varepsilon)(1-v)I_a](R_c-1)$$

Hence, $L < 1$ if and only if $R_c < 1$, and $L = 0$ if and only if $I_s = I_a = E = 0$.

Thus, L is a Lyapunov function for model (3).

Hence it follows by La Salle's principle that the DFE of model (3) is globally asymptotically stable whenever $R_c < 1$.

3. A VACCINATION MODEL FOR COVID-19

Currently, there are few approved vaccines for COVID-19. The development of new vaccines usually takes time, but a number of companies, government agencies and regulatory authorities have worked very hard to fast-track the mass availability of vaccines that provides some form of protection for COVID-19, and have been made available beginning from the end of year 2020 (Callaway, 2020[10] and Kirkpatrick, 2020)[11].

Therefore, in this section, we develop a model for assessing the impact of COVID-19 vaccines on the Nigerian population. We assume that the COVID-19 vaccine are imperfect (that is, it would not offer 100% protection against corona virus infection in all humans in the

population). Hence, the basic COVID-19 model (3) is extended to include a population of vaccinated individuals, denoted by V(t), so that the total population is given by

$$N(t) = \mathrm{S(t)} + \mathrm{V(t)} + \mathrm{E(t)} + I_a(t) + I_s(t) + I_m(t) + R(t) \quad (13)$$

This subpopulation of vaccinated individuals is generated by the vaccination of susceptible individuals at the rate c. Since the vaccine is assumed to be imperfect, vaccinated individuals acquire infection at a rate $\lambda(1-\theta), where\ 0 \leq \theta \leq 1$is the vaccine efficacy. We merge the $I_i$and the I_h classes in the first model to obtain an isolated class denoted by I_m. This compartment includes those in self-isolation and those already hospitalized. From the foregoing, our new model is given by the following deterministic system of non-linear differential equations

$$\left.\begin{aligned}
\frac{dS}{dt} &= -\lambda \mathrm{S} - \mathrm{cS} \\
\frac{dV}{dt} &= \mathrm{cS} - (1-\theta)\mathrm{V} \\
\frac{dE}{dt} &= \lambda \mathrm{S} - \lambda(1-\theta)\mathrm{V} - \emptyset \mathrm{E} \\
\frac{dI_s}{dt} &= \mathrm{p}\emptyset \mathrm{E} - (\sigma_s + r_1 + \delta_s) I_s \\
\frac{dI_a}{dt} &= \emptyset(1-p)E - r_3 I_a \\
\frac{dI^s}{dt} &= \sigma_s I_s - (r_2 + \delta_m) I_m \\
\frac{dD}{dt} &= \delta_S I_s + \delta_h I_m \\
\frac{dR}{dt} &= r_1 \mathrm{I_s} + r_3 \mathrm{I_a} + r_2 I_m,
\end{aligned}\right\} \quad (14)$$

where

$$\lambda = \frac{\beta(1-\varepsilon)(1-k)[I_s + \alpha I_a]}{N - I^S} \quad (15)$$

The dynamics of the vaccination model (14) will be considered in the region

$$D_1 = \{ (S,\ V,\ E, I_s,\ I_a,\ I_m,\ R) \epsilon R_+^7 : N(t) \leq S(0) + V(0) \} \quad (16)$$

As done in section 2.1, the region D_1 can be shown to be positively-invariant and attracting all positive solutions.

3.1 Disease-free Equilibrium (DFE)

The DFE of the vaccination model (14) is given by

$$\xi_0 = (S^*,\ V^*,\ E^*,\ I_a^*,\ I_s^*,\ I_m^*,\ R^*) = (\mathrm{S}(0), V(0),\ 0,\ 0,\ 0,\ 0,\ 0) \quad (17)$$

where $S(0),\ and\ V(0)$, are the initial sizes of the population of susceptible and vaccinated individuals, respectively, so that

$$N(0) = S(0) + V(0) \tag{18}$$

Furthermore, the associated next generation matrices are given by

$$F = \begin{bmatrix} 0 & x & y \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \tag{19a}$$

$$where\ x = \beta(1-\varepsilon)(1-V)\frac{S^*}{N-I_m} + \beta(1-\varepsilon)(1-V)(1-\theta)\frac{V^*}{N-I_m}$$

$$\text{and } y = \beta\alpha(1-\varepsilon)(1-V)(1-\theta)\frac{S^*}{N-I_m} + \beta\alpha(1-\varepsilon)(1-V)(1-\theta)\frac{V^*}{N-I_m}$$

$$V = \begin{bmatrix} \emptyset & 0 & 0 \\ -p\emptyset & \sigma_s + r_1 + \delta_s & 0 \\ -\emptyset(1-p)\emptyset & 0 & r_3 \end{bmatrix} \tag{19b}$$

It follows that the control vaccination reproduction number for model (14) is given by

$$R_V = \frac{\beta(1-P)(1-\varepsilon)(1-v)}{(\sigma_s+r_1+\delta_s)}\left[\frac{S^*+(1-\theta)V^*}{N-I_m}\right] + \frac{\beta(P)(1-\varepsilon)(1-v)}{r_3}\alpha\left[\frac{S^*+(1-\theta)V^*}{N-I_m}\right] \tag{19c}$$

We propose the following from Theorem 2 of Van den Driessche and Watmough[18].

Theorem 3.1:

The disease-free equilibrium (DFE) of model (14) is locally asymptotically stable if $R_V < 1$ and unstable if $R_V > 1$.

The quantity R_V measures the average number of new corona virus cases generated by an infectious individual introduced into a population where a certain fraction is vaccinated (with an imperfect vaccine) against corona virus. The epidemiological implication of Theorem 3.1 is that a small influx of corona virus cases will not generate a COVID-19 outbreak if the control reproduction number R_V is less than unity.

We now turn to obtain the basic reproduction number obtained by setting all control parameters and state variables $(\varepsilon, c, v, \theta\ and\ V^*)$ to zero in (21). Thus, the basic reproduction number is given by

$$R_0^* = R_{\varepsilon=\theta=v=\theta=V^*=0} = \left[\frac{1-p}{\sigma_s+r_1+\delta_s} + \frac{p\alpha}{r_3}\right] \tag{20}$$

R_0^* represents the number of secondary infections generated by an infected individual introduced into a completely susceptible population during the individual duration of infectiousness.

3.2 Threshold Analysis and Vaccine Impact

It is pertinent to determine whether or not the widespread use of an imperfect vaccine in a community will always be beneficial or not. First, we consider the initial size of the population $S(0),\ and\ V(0)$. Let p_v denote the fraction of susceptible individuals and h_v be the fraction of vaccinated individuals at the disease-free steady state. Thus,

$$p_y = \frac{S(0)}{S(0)+V(0)} \tag{21}$$

$$h_y = \frac{V(0)}{S(0)+V(0)} \tag{22}$$

The parameters R_s given below denote the control reproduction number with the vaccinated subpopulation

$$R_s = \beta(1-\varepsilon)(1-v)[\frac{1-p}{\sigma_s+r_1+\delta_s} + \frac{p\alpha}{r_3}] \tag{23}$$

In the same vein, the reproduction number for a COVID-19 model with a wholly vaccinated population (model in which every member of the population is vaccinated) is given by

$$R_{0v} = \beta(1-\varepsilon)(1-v)(1-\theta)[\frac{1-p}{\sigma_s+r_1+\delta_s} + \frac{p\alpha}{r_3}] \tag{24}$$

It follows from (19), (21) and (22) that the control reproduction number R_v can be rewritten in terms of$p_y\ and\ h_y$ as

$$R_v = R_s p_y + (1-\vartheta)h_y R_s \tag{25}$$

$$R_v = R_s(p_y + h_y - \vartheta h_y) \tag{26}$$

$$R_v = R_s(1-\vartheta)h_y \tag{27}$$

Now we set $R_v = 1$ in (27) and solve for h_y to get

$$h_y = \frac{1}{\theta}\left[1 - \frac{1}{R_s}\right] = h_v^c \tag{28}$$

We thus propose the following:

Lemma 3.1:

The DFE of the vaccination model (14), $\xi_{o,}$ is locally asymptotically

stable if $h_y > h_v^c$, and unstable if $h_y < h_v^c$

Proof

It is obvious that $R_c < 1$ whenever $h_y > h_v^c$, so that the DFE $\xi_0$is locally asymptotically stable. In the same vein, $R_c > 1$ for $h_y < h_v^c$ and the DFE is unstable. This lemma implies that if the fraction of individuals vaccinated at steady-state exceeds the threshold level (h_v^c) then the DFE is locally asymptotically stable and consequently, the disease could be eliminated.

From the result obtained from (27) and (28) we have the following proposition:

Theorem 3.2:

The use of an imperfect vaccine for COVID-19 in a population will have the following

(i) Positive impact in the population if $h_y > h_v^c$ ($R_s < 1$)

(ii) Negative impact in the population if $h_y > h_v^c$ ($R_s > 1$)

(iii) No impact in the population if $h_y = h_v^c$ ($R_s = 1$)

Alternatively, we may assess the impact of an imperfect vaccine by using (23), (24) and (19). We first rewrite R_v as

$$R_v = R_s\ [1 - \frac{V}{N - I_m}\left[1 - \frac{R_{ov}}{R_s}\right]] \tag{29}$$

Using the notations by Elbasha and Gumel[21], a measure of the vaccine impact for the model (14) is defined in terms of the vaccine impact factor, denoted by

$$\Omega = \frac{V^*}{N - I_m}[1 - \frac{R_{0v}}{R_s}] \tag{30}$$

We claim the following result:

Theorem 3.3:

The use of an imperfect vaccine for corona virus in a population will have the following

i) Positive population impact level if $\Omega > 0$ ($R_v < R_s$)

ii) Negative population impact level if $\Omega < 0$ ($R_v > R_s$)

iii) No impact level if $\Omega = 0$ $(R_v = R_s)$

Proof

Using (30) in (29) gives $R_v = R_s[1 - \Omega]$ (31)

So that $1 - \Omega = \frac{R_v}{R_s}$ (32)

Thus, whenever $R_v < R_s$, then $1 - \Omega < 1$; so that $\Omega > 0$ (and the vaccine has a positive impact). Similarly, whenever $R_v >$ R_s, then $1 - \Omega > 1$; so that $\Omega < 0$ (and the vaccine would have a negative impact). Finally, if $R_v = R_s$, then $1 - \Omega = 1$; so that $\Omega = 0$ (and the vaccine has no impact.

It is important and also easy to show that:

$$R_s - R_{0v} = \beta(1 - \varepsilon)(1 - v)\theta[\frac{1-p}{\sigma_s + r_1 + \delta_s} + \frac{p\alpha}{r_3}] > 0 \quad (33)$$

So that $R_0 > R_{0v}$. Thus, it follows from (30) that Ω is always positive. In other words, the vaccine will always have a positive impact in the population, leading to the following result:

Lemma 3.2:

The COVID-19 vaccine will always have a positive impact in the population.

4. NUMERICAL SIMULATIONS

The models (3) and (14) were numerically simulated, using the baseline parameters in table 2 to assess the impact of various intervention strategies evident in the model (social distancing, rate of face mask compliance and contact tracing) for the entire Nigerian population. For the purpose of our simulations we set our initial value for $S(0) = 200{,}000{,}000$. As at August 5th, 2020, the subpopulation of infected individuals $I_s(0) = 46{,}577$; hospitalized individuals, $I_h(0) = 12{,}446$; the total number of deaths $\mathrm{D}(0) = 945$ and the total number of recovered humans $\mathrm{R}(0) = 33{,}186$; while fixing all other state variables $\mathrm{E}(0) = I_a(0) = I_i(0) = 0$.

4.1 Effect of Social Distancing

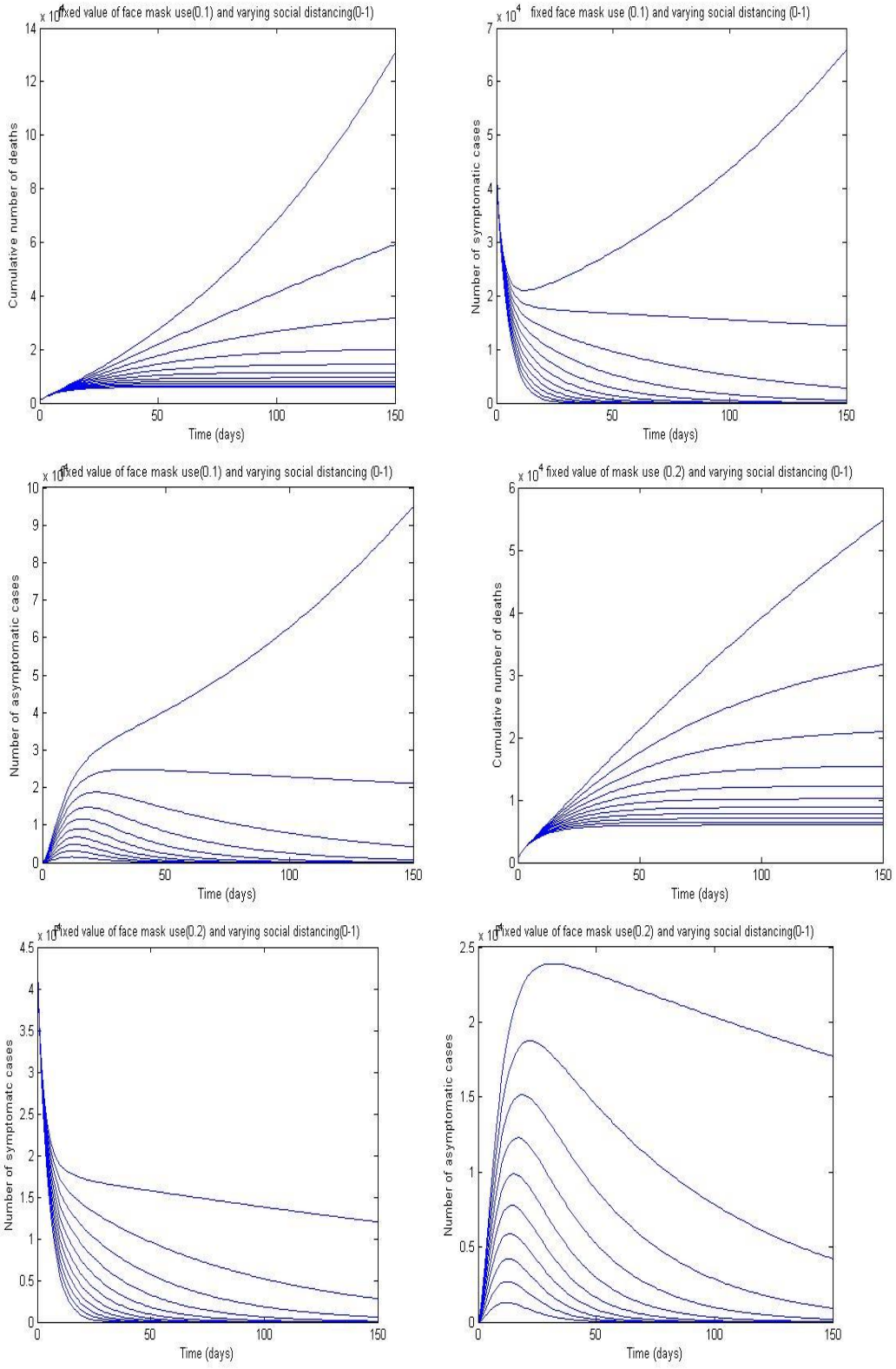
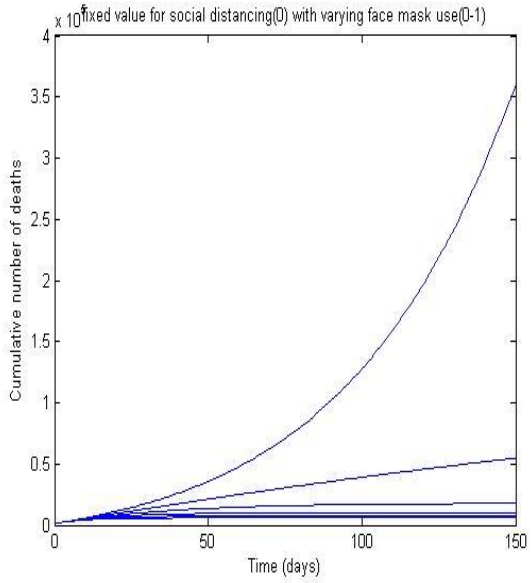
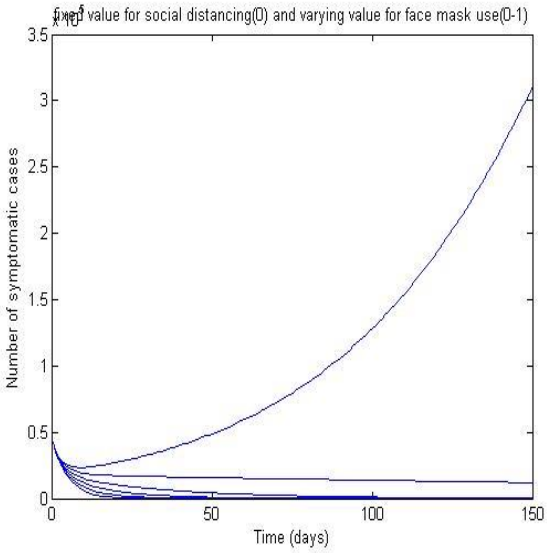


Figure 3: *simulation of model (3) by varying the value for social distancing (ε = 0-1) and the value of the rate of face mask compliance (v) is set at 0.1 and 0.2.*

From figure 3, we see that varying the rate of social distancing from 0 to 1 and setting the value of face mask compliance rate to 0.1 would mark a reduction in the cumulative number of deaths. This implies that even if a few percentage of humans comply to face mask use but all humans maintain social distancing it will result to a fewer number of deaths. This will also bring about a reduction in the number of new infections leading to a reduction in the disease burden. Increasing the percentage of the number of persons who comply with wearing face mask will further reduce the number of new cases as long as they maintain social distancing. If only 20% of the population comply to social distancing, the cumulative number of deaths will be a little below 60,000 by the end of January, 2020. Having about 80% of the population comply with social distancing will lead to a drastic reduction in the number of cumulative deaths caused by the disease. This simulation implies that as long as people comply to the use of face mask even if their compliance rate is moderate, as long as they maintain social distancing, the elimination of the disease from the population is feasible.

4.2 Effect of Face Mask Use in Public





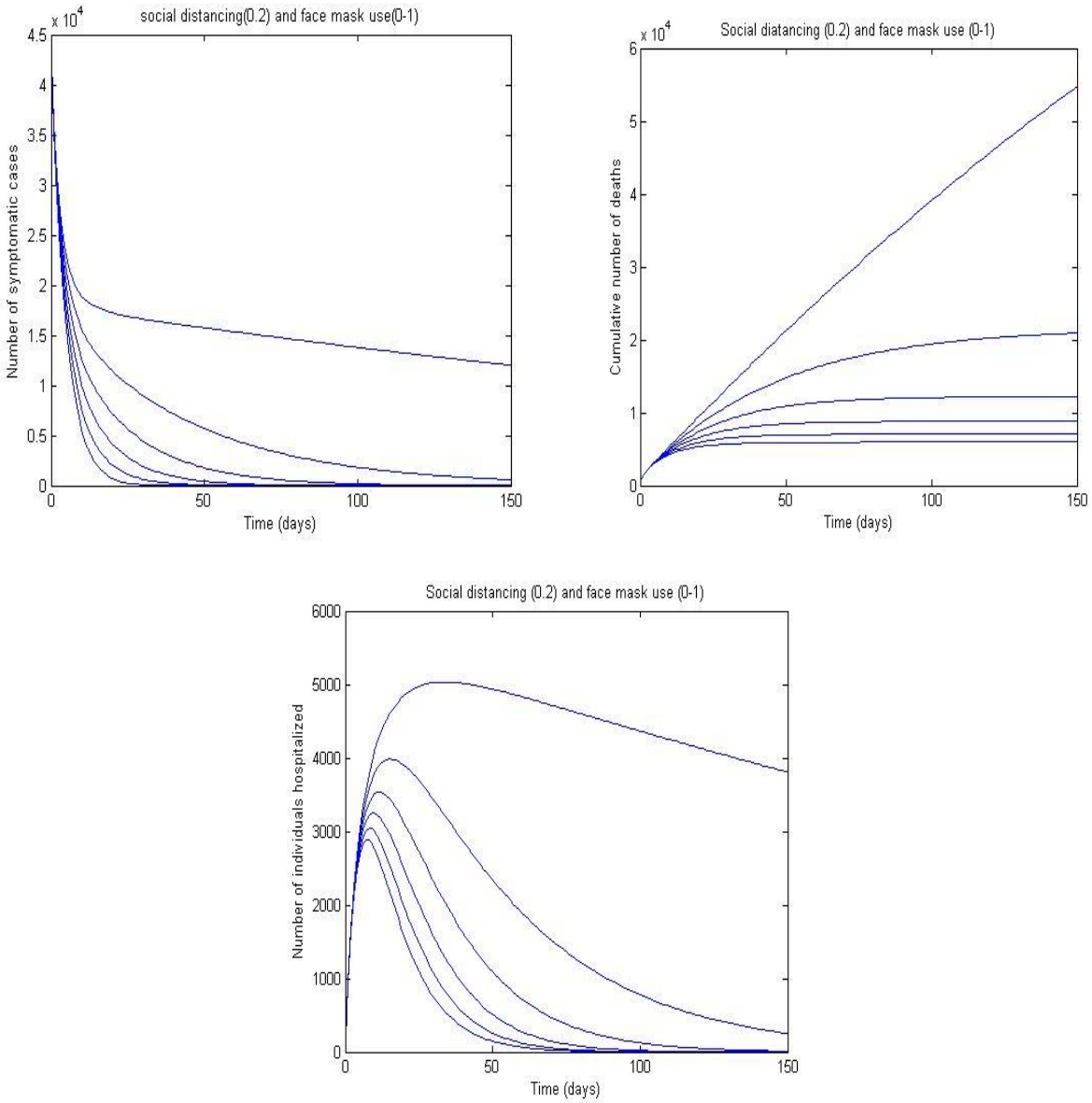
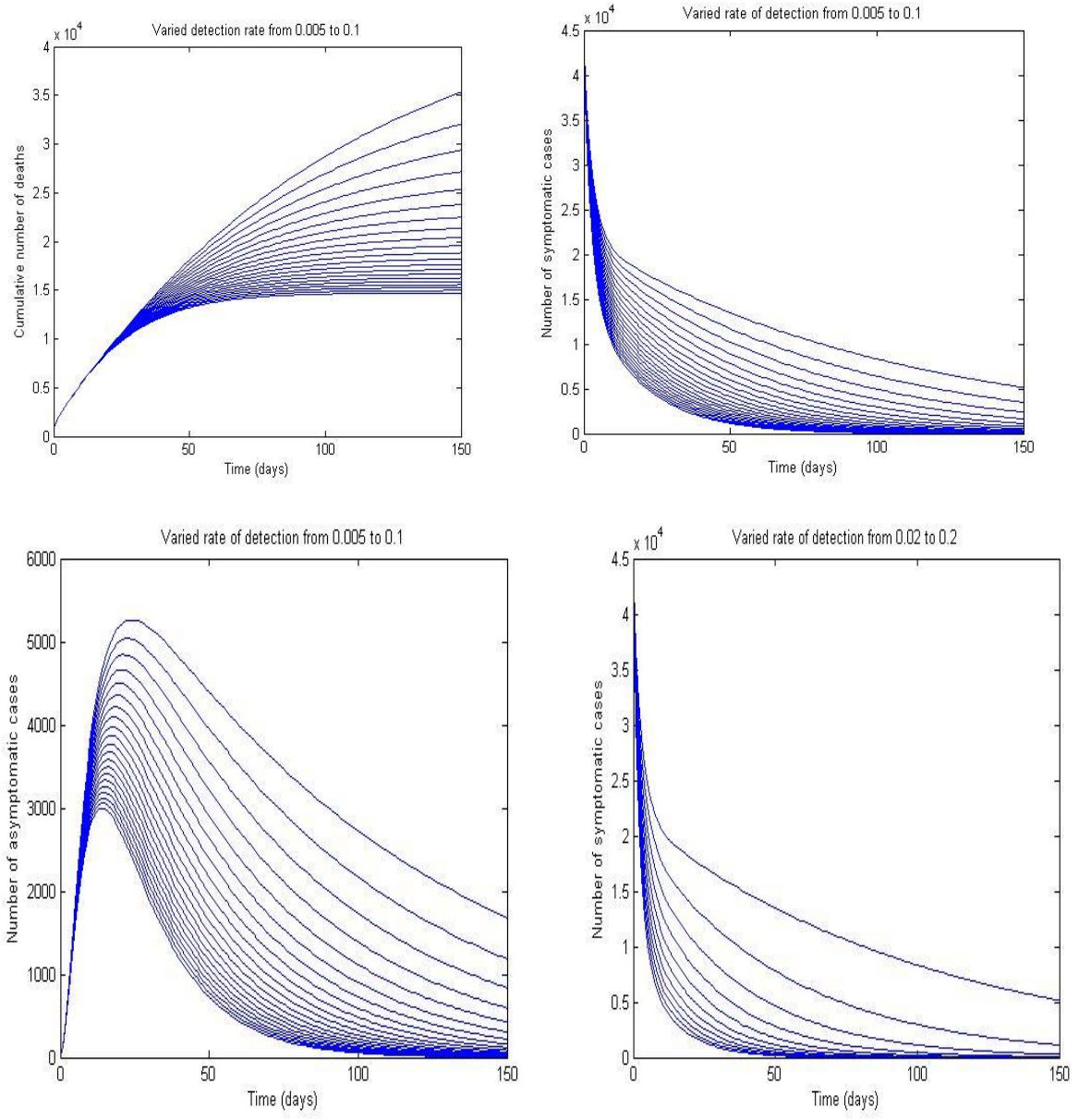


Figure 4: *Simulation of model (3) by varying the value for face mask public usage (v = 0-1) and the value of the rate of social distancing (ε) is set at 0.1 and 0.2.*

Figure 4 reveals that if people do not maintain social distancing and wear their mask in public, the cumulative number of deaths will be very high and we would have an increase in the number of infected persons which was actually the initial cause of the pandemic. If 20% of the population maintain social distance and 20% 0f the population also comply to face mask use in public, then the cumulative number of deaths caused by the disease will be reduced to a little

above 20,000 deaths by the end of January 2020. Our simulation show that even if people do not maintain social distancing as long as everyone comply to face mask use in the public, the disease can be eliminated by January, 2020. Thus, our simulation reveals that the use of face mask in the community can help curtail the widespread of the disease.

4.3 Effect of Contact Tracing



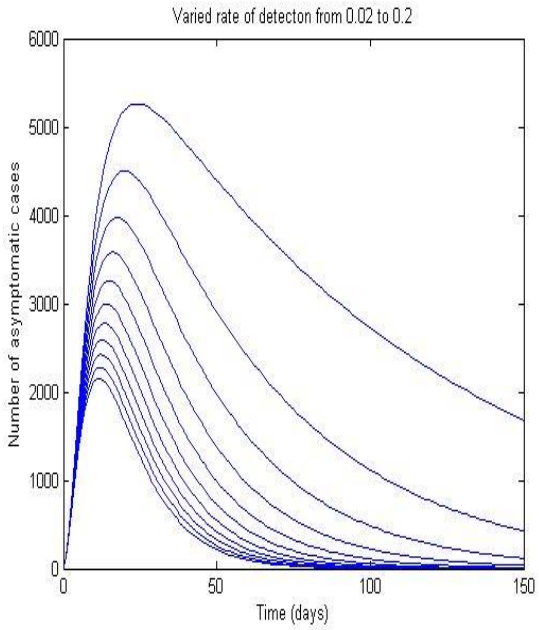
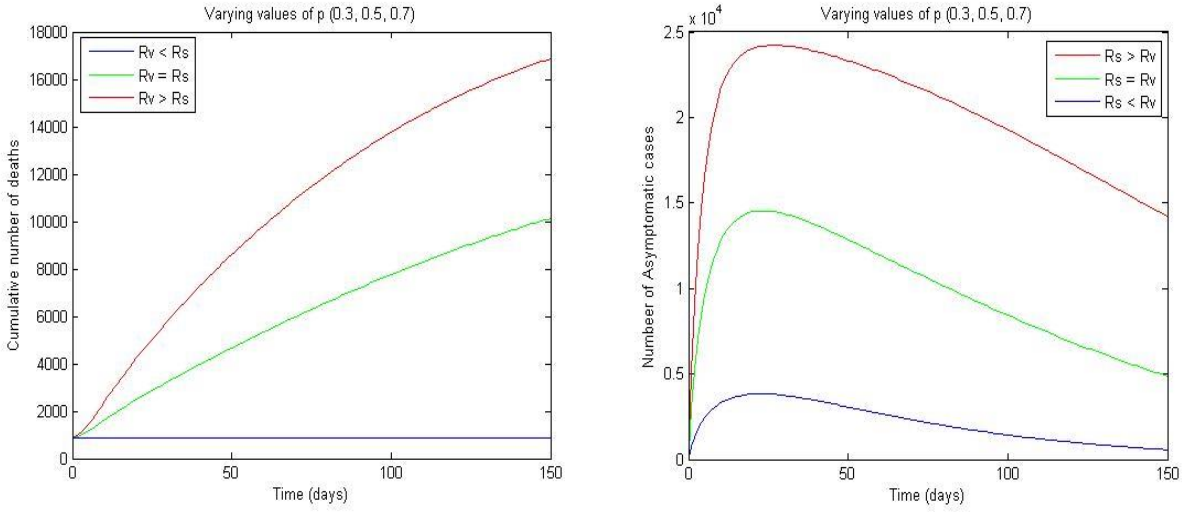


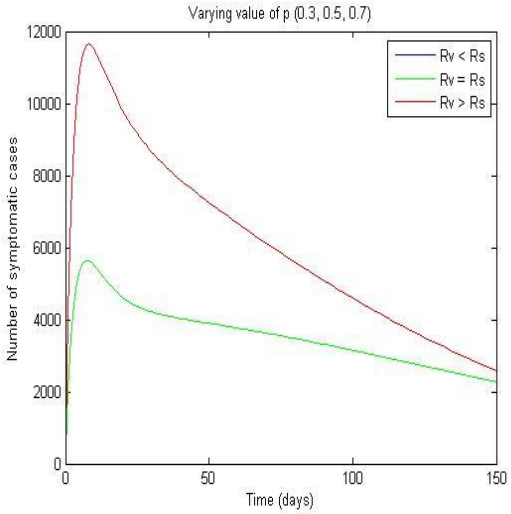
Figure 5: *simulation of model (3) by varying the value for detection rate (via contact tracing from 0.005-0.1 and 0.02 to 0.2).*

Figure 5 reveals that the detection and isolation of individuals infected with corona virus will aid in reducing the cumulative number of deaths as contact with infectious humans will become limited. This will in turn decrease the number of new cases.

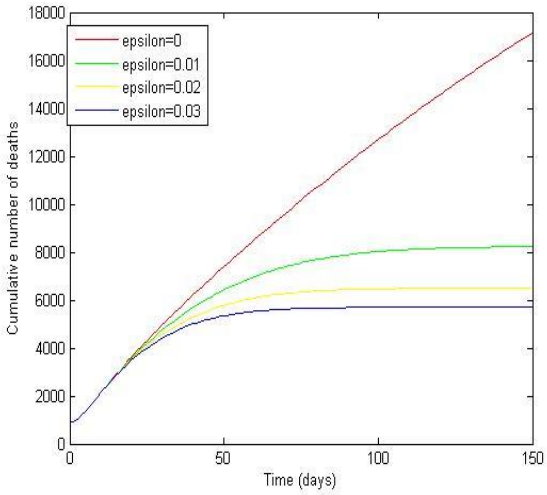
4.3 Effect of Vaccination on the Population

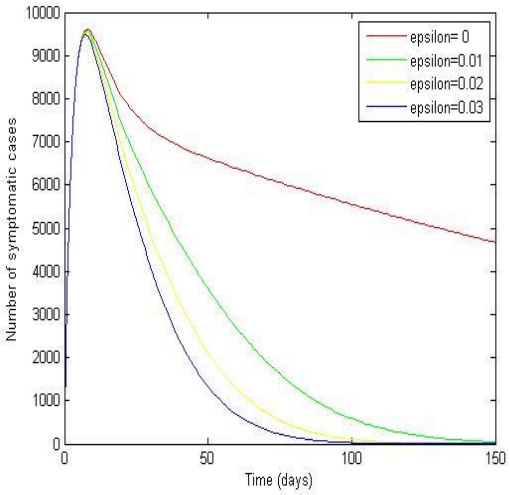
a)

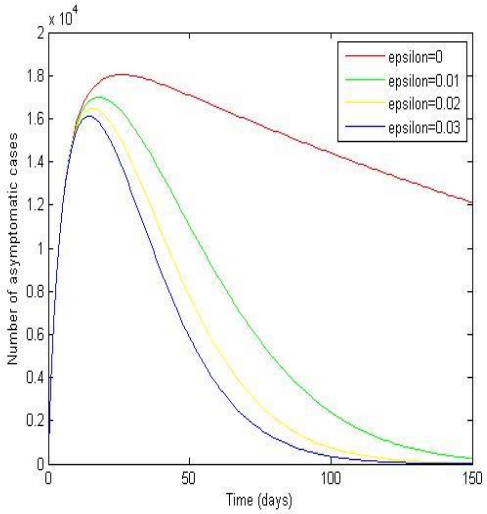


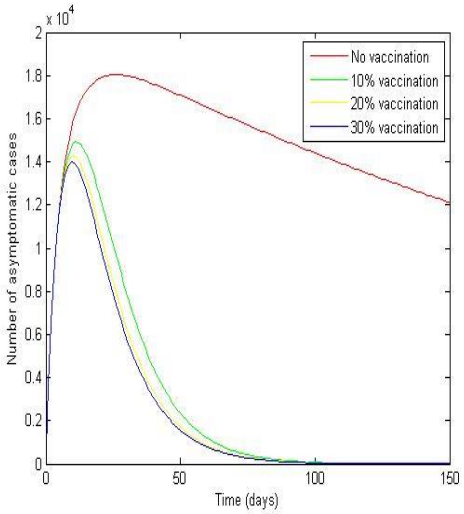

Varying value of p (0.3, 0.5, 0.7)
Rv < Rs
Rv = Rs
Rv > Rs
Number of symptomatic cases
Time (days)

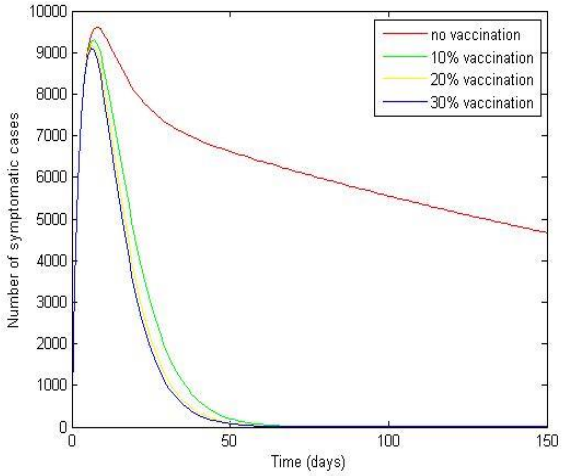
b)

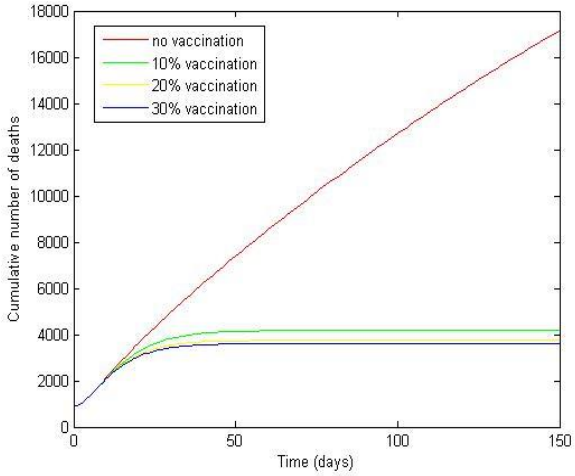

epsilon=0
epsilon=0.01
epsilon=0.02
epsilon=0.03
Cumulative number of deaths
Time (days)

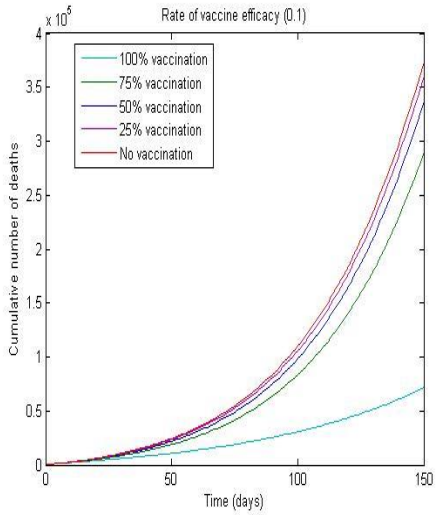

epsilon= 0
epsilon=0.01
epsilon=0.02
epsilon=0.03
Number of symptomatic cases
Time (days)

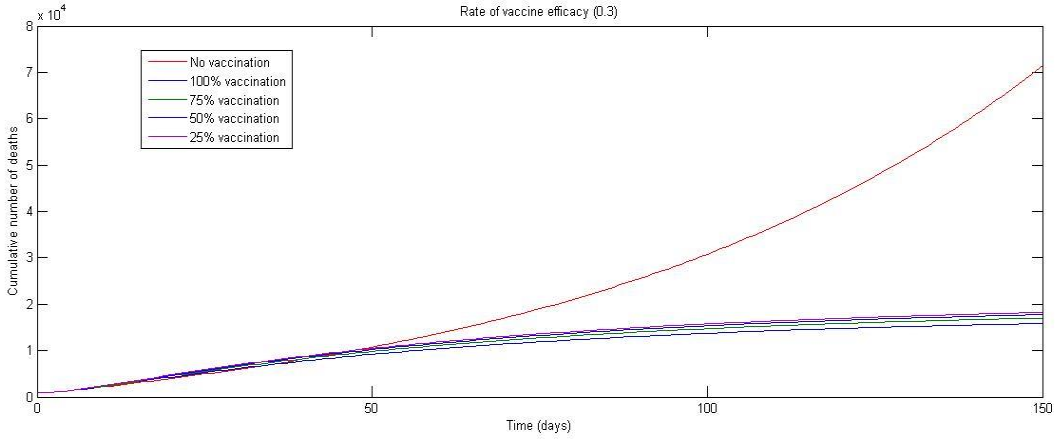

x 10^4
epsilon=0
epsilon=0.01
epsilon=0.02
epsilon=0.03
Number of asymptomatic cases
Time (days)


x 10^4
No vaccination
10% vaccination
20% vaccination
30% vaccination
Number of asymptomatic cases
Time (days)


no vaccination
10% vaccination
20% vaccination
30% vaccination
Number of symptomatic cases
Time (days)


no vaccination
10% vaccination
20% vaccination
30% vaccination
Cumulative number of deaths
Time (days)


Rate of vaccine efficacy (0.1)
x 10^5
100% vaccination
75% vaccination
50% vaccination
25% vaccination
No vaccination
Cumulative number of deaths
Time (days)


Rate of vaccine efficacy (0.3)
x 10^4
No vaccination
100% vaccination
75% vaccination
50% vaccination
25% vaccination
Cumulative number of deaths
Time (days)

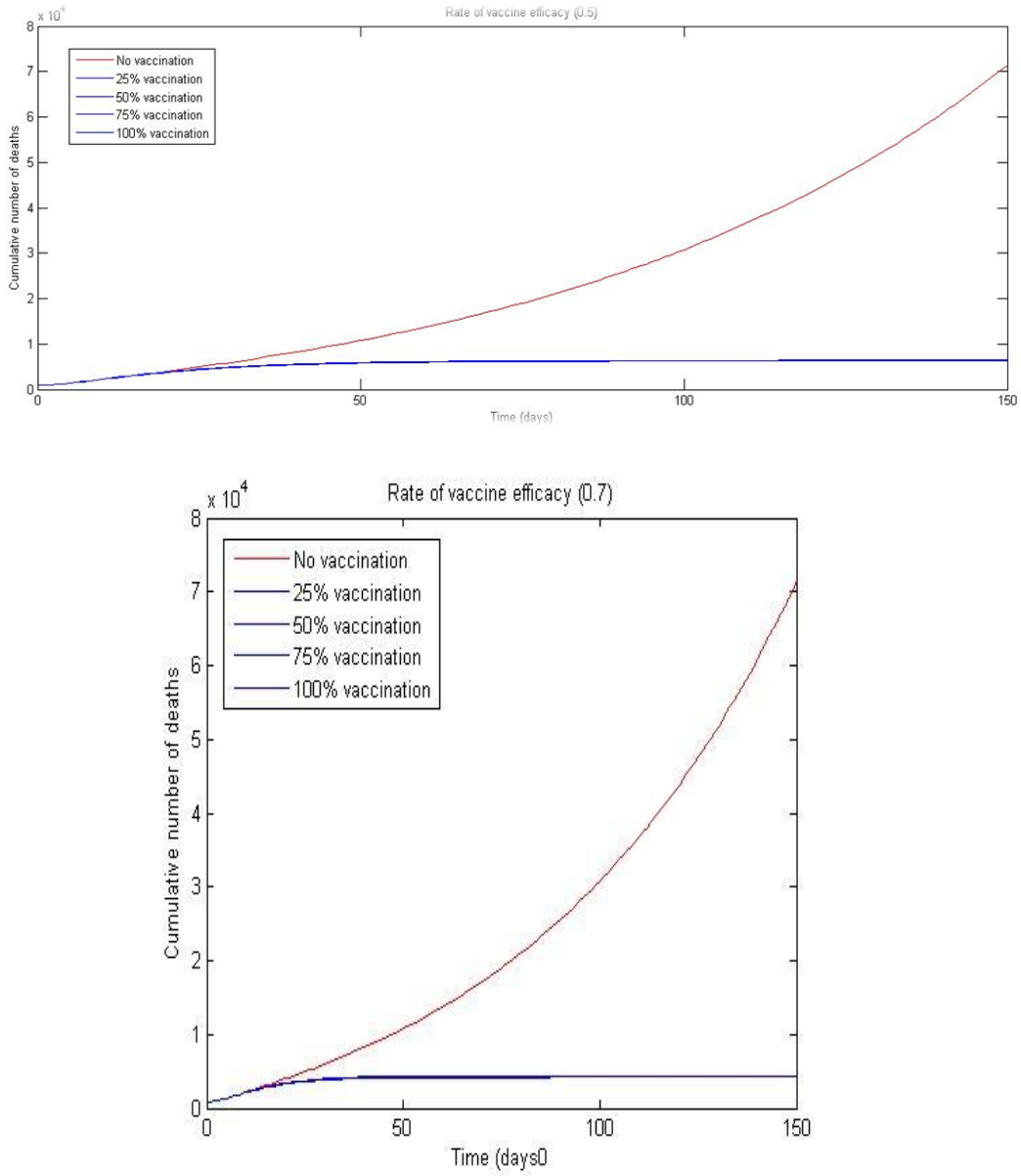


Figure 6: *simulation of model (3) by varying the value for the rate of vaccination (10% to 30% rate of vaccination) as well as varying the rate of vaccine efficacy from 0.1 to 0.7.*

The result of theorem 3.2 was numerically simulated in figure 6a, showing an increase in the cumulative COVID-19 induced mortality when $R_v < R_s$ (a negative impact in the population) and a decrease when $R_v > R_s$ (a positive impact in the population). Figure 6a also reveals that by the end of January 2021, the number of asymptomatic (symptomatic) cases will be a little below 15,000 (4,000) whenever $R_v > R_s$which implies a negative impact. The number of cumulative death will be reduced drastically if $R_v < R_s$which will imply a positive impact in the population.

Figure 6b reveals that for the worst case scenario without vaccination with c = 0, Nigeria would record a high number of daily deaths (above 16,000) at the end of January, 2021. With a vaccination rate of 0.01 to 0.03 would lead to a drastic reduction in the number of daily deaths at the end of January, 2021. Achieving 10% vaccination of the population would record a little above 4,000 daily deaths while 30% vaccination of the population would record a drastic reduction in the number of daily deaths by the end of January, 2020. In the same vein, achieving 30% vaccination of the population, would record a drastic reduction in the number of infected individuals. Our simulations also reveals that a vaccine efficacy rate of 0.1 will only reduce the daily number of deaths to 75,000 if a 100% vaccination of susceptible individuals is achieved. If the rate of vaccine efficacy confers 20% protection against the disease, then the daily number of deaths will be reduced to 15,000 if 100% vaccine coverage is achieved. The simulations also show that if the vaccine efficacy confers 50% protection against corona virus, then the daily deaths will be drastically reduced.

4.4 Discussion of Result

A novel corona virus emerged from Wuhan, Hubei Province in China in December, 2019. The virus has generated serious pandemic due to its spread to over 210 countries of the world with over 350 million confirmed cases and 5 million deaths globally as at the 25th of January, 2022. Also, over 9 billion doses of vaccines with controversial efficacy have been administered. We developed and analyzed the transmission dynamics of the novel corona virus with several control strategies (social distancing, face mask use in public as well as contact tracing). The model was extended to include a vaccinated subpopulation so as to assess the potential impact of an imperfect vaccine against COVID-19 disease in Nigeria. We assumed that the vaccine is not guaranteed to provide 100% protection against the disease.

The developed models were rigorously analyzed to gain insight into the transmission dynamics of the disease. The DFE of model (3) without a vaccinated subpopulation was found to be both locally and globally asymptotically stable when the control reproduction number is less than unity. The implication of this is that the transmission of corona virus in the community can be effectively controlled in the community if the control strategies implemented can bring the

threshold (R_c)to a value less than unity. Similarly, the DFE of the vaccination model (14) is also locally asymptotically stable when the threshold is less than unity. Vaccination against corona virus may lead to the effective control of the disease if the vaccine efficacy and nationwide coverage of the vaccine are high enough. In particular, if the vaccine efficacy and nationwide coverage of the vaccine is able to bring the control reproduction number to a value less than unity.

Our numerical simulation reveals that as long as people comply with the use of face mask reasonably and maintain social distancing, the elimination of the disease from the population is feasible. Similarly, our simulations also show that even if people do not maintain social distancing as long as everyone comply to face mask use in the public, the disease can be eliminated within a reasonable time frame. Thus an implementation of an effective face mask strategy as well as social distancing will greatly reduce community transmission. Also, widespread random testing can contribute in detecting, tracing and isolating symptomatic and asymptomatic cases their by reducing the transmission by contacts that would be spreading the disease in the population. More tests would imply an increase in the number of detected cases as well as rapid isolation of symptomatic and asymptomatic cases, thus, reducing community transmission.

Furthermore, our simulation was done to measure the population impact at which an imperfect vaccine is administered. The result revealed that the corona virus burden in terms of the cumulative number of deaths decreases with an increasing vaccine rate. Our simulation showed that if the vaccine efficacy confers 70% protection and a large proportion of the susceptible class are vaccinated, then, it will lead to the elimination of the disease by 2021. If the vaccine efficacy level confers 10% to 40% protection against the disease, then it is not sufficient to curtail the disease.

In summary, this study has explained the prospects of controlling corona virus disease in Nigeria. It shows that combining various intervention strategies such as face mask use in public, social distancing, contact tracing (detection of corona virus cases) as well as the administration of an imperfect vaccine will help in controlling or eliminating the disease in the population.

Attaining a very high vaccine coverage (80% and above) with an imperfect vaccine that confers at least 70% protection against the disease will lead to the elimination of the disease.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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