COVID-19 dynamics in Africa under the influence of asymptomatic cases and re-infection

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Abstract

Since December 2019 that coronavirus pandemic (COVID-19) has hit the world, with over 13 million cases recorded, only a little above 4.67 percent of the cases have been recorded in the continent of Africa. The percentage of cases in Africa rose significantly from 2 percent in the month of May 2020 to above 4.67 percent by the end of July 15, 2020. This rapid increase in the percentage indicates a need to study the transmission, control strategy, and the dynamics of COVID-19 in Africa continent. In this study, a nonlinear mathematical model to investigate the impact of asymptomatic cases on the transmission dynamics of COVID-19 in Africa is proposed. The model is analyzed, the reproduction number is obtained, the local, as well as the global, asymptotic stability of the equilibria were established. We investigate the existence of backward bifurcation and we present the numerical simulations to verify our theoretical results.

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1 Introduction

Coronavirus disease (COVID-19), initially referred to as 2019-nCoV or SARS-CoV-2, is a new strain of coronavirus that has caused fears in many countries of the world since its emergence in the city of Wuhan in December, 2019. The coronavirus is a family of viruses initially existing in animals but which was found to infect human with some respiratory infections. They were not expected to be deadly until the emergence of COVID-19, which has claimed over 500,000 human lives. Although the

the first case was recorded in Wuhan, China, it is not yet clear as to how the first human contracted the disease. However, some researchers opined that COVID-19 came from bats, wolf pulps or rats. The first human acquired the virus (from whichever source or means) and the transmission continues from human to human. COVID-19 spreads through infected droplets when humans sneeze, yawn or cough . The disease can also spread when human have contact with the surfaces contaminated with the virus and thereafter touches their nose, mouth, eyes or ears. The virus was declared a pandemic by the World Health Organization (WHO) on the 30th of January, 2020. As at 28th of June, 2020, over 10 million cases were recorded in over 200 countries and territories around the world. As at the time of this study, there are no specific treatments or vaccines for COVID-19, although different measures have been adopted to slow down the transmission of the disease and its mortality rate. The measures include; 1) advocacy on regularly washing of hands and covering of nose, 2) rapid tracing, finding and quarantining all confirmed cases to prevent further transmission, 4) physical distancing, 5) restrictions and temporary bans on non-essential travels and 6) proper clinical care for the patients. COVID-19 comes with a number of symptoms including high fever, cough, sneezing and running nose, fatigue, muscles and joint pains, shortness of breath, and sore throat. The period of incubation ranges from two to fourteen days and the average incubation is five to six days of infection. There have been few cases recorded of people who are infected but do not show any symptoms, this cases are referred to as asymptomatic cases. At the height of the disease, patient may develop a cardiovascular problems or neurologic complications, multi-organ failure and pneumonia, and finally, death. The more reliable diagnosing test that is been use is real-time reverse transcription polymerase chain reaction (rRT-PCR) while CT scans may also be helpful to diagnose COVID-19 [17, 18, 7, 8, 9, 10, 12, 20, 22, 23, 3].

Several mathematical models to study direct human-to-human and environmental transmission of COVD-19, to compare its spread with the spread of previous diseases, forecast local and international spread, etc. have been developed withing the short time. One common outcome of all these researches is that the disease would remain endemic for a long time; thus necessitating long-term disease prevention and intervention programs [1, 2, 6, 11, 14, 15, 16, 19, 21, 24, 27, 26, 28, 29, 30].

As the case is, it is not very clear whether a recovered individual can also be infected again. Some few cases have been recorded where they were initially considered recovered but later tested positive of COIVD-19 again. More so, several asymptotic cases of COVID-19 have been recorded but it is also not clear whether asymptomatic individual can transmit the disease to a susceptible individual. It becomes clear that even though there is no scientific justification as to whether an individual can be re-infected, it is only better to take into consideration the possibility of re-infection. As at May 25, 2020, Africa had only 114,223 confirmed cases of COVID-19 which had increased to 142,398 cases by May 30, 2020; a 24.7 percent increase in the number of confirmed cases. As at July 9, 2020, the number of recorded cases has risen to 523,782 which means about 359 percent increase in the number in confirmed cases. This is a rather rapid increase in the number of confirmed cases in Africa and at such increasing rate, there are worries that Africa may rise from the least-hit continent to become the worst-hit continent with the highest number of cases and the longest to recover from the pandemic.

Motivated by the fact that no author has considered the impact of asymptomatic case with re-infection in the dynamics of COVID-19, this research is conducted to unravel the impact of asymptomatic cases on the dynamics of transmission of COVID-19, with possible cases of re-infection. This paper arranged as follows; the governing model is formulated in section 2, the stability analysis of the equilibria is carried out in section 3, and the numerical simulations and discussions are presented in section 4 before the conclusion in section 5.

2 The Model

In order to formulate the model, the following assumptions are made;

1. the population is divided into five different epidemiological compartments; susceptible human class (S), exposed human (E), symptomatic human class (I_s), asymptomatic human class (I_a) and the Recovered human class (R).
2. The influx rate into the population at any time is Λ.
3. the population is assumed to die naturally at a rate μ in each of the classes.
4. the disease is acquired when there is an interaction between a susceptible individual and an infected individual. Let the force of infection rate be

$$\lambda = \beta \left(\frac{I_s + I_a}{N} \right) \tag{2.1}$$

   where β is the transmission rate for both the symptomatic and asymptomatic population.
5. N is the total human population and is given by

$$N = S + E + I_s + I_a + R. \tag{2.2}$$

6. v is the progression rate from the exposed class to the infected classes.
7. a fraction p of infected human population is asymptomatic while the remaining fraction $(1 - p)$ is symptomatic.
8. the symptomatic (asymptomatic) population may die as result of the disease at a rate $\alpha_s(\alpha_a)$ and recover at the rate $r_s(r_a)$.
9. recovered individual may be re-infected as a result of continuous contact with the infected individuals.
10. the re-infection rate is given by ψ.

Combining the above assumptions, the model for the dynamics of COVID-19 with the asymptotic cases and possibility of re-infection is modeled by the following ordinary differential equations;

$$S' = \Lambda - \lambda S - \mu S \tag{2.3}$$
$$E' = \lambda S - (v + \mu)E + \psi \lambda R \tag{2.4}$$
$$I_s' = (1 - p)vE - (\alpha_s + r_s + \mu)I_s \tag{2.5}$$
$$I_a' = pvE - (\alpha_a + r_a + \mu)\, I_a \tag{2.6}$$
$$R' = r_a I_s + r_a I_a - \mu R - \psi \lambda R \tag{2.7}$$

where,

$$\lambda = \beta \left(\frac{I_s + I_a}{N} \right) \tag{2.8}$$

Let $S(t) + E(t) + I_s(t) + I_a(t) + R(t) = N(t)$. By adding equations (2.3 - 2.7), it becomes clear that

$$\frac{dN}{dt} = \Lambda - \mu N - \alpha_s I_s - \alpha_a I_a \leq \Lambda - \mu N \tag{2.9}$$

Then, it follows from (2.9) that

$$N(t) \leq \frac{\Lambda}{\mu} + e^{-\mu t} \left(N(0) - \frac{\Lambda}{\mu} \right) \tag{2.10}$$

and as $t \to \infty$, we have the feasible region of the system as

$$\mathcal{D} = \left\{ (S, E, I_s, I_a, R) \in \mathbb{R}_+^5 : \ N \leq \frac{\Lambda}{\mu} \right\},$$

it is positively invariant and sufficient to consider solutions in $\mathcal{D}$ for all $t \geq 0$. Therefore, the system (2.3 - 2.7) is mathematically and epidemiologically well-posed and it is sufficient to consider the dynamics of the flow generated by the system (2.3 - 2.7) in the domain $\mathcal{D}$. Since we are considering a disease transmission model of human population, we assume non-negativity of all the parameters and the states variables for the model.

3 Stability of Equilibria

In this section, the existence of the disease-free equilibrium (DFE) and the endemic equilibrium are established.

3.1 Local Asymptotic stability of the DFE and Reproduction Number

The disease-free equilibrium is

$$U^0 = \left(S^0, E^0, I_s^0, I_a^0, R^0\right) = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0\right). \tag{3.1}$$

The Reproduction number $\Re_0$ which ascertains the transmission ability of the disease [25] is obtained as

$$\Re_0 = \frac{\beta v \left((1-p)\left(\alpha_a + r_a + \mu\right) + p\left(\alpha_s + r_s + \mu\right)\right)}{\left(v + \mu\right)\left(\alpha_a + r_a + \mu\right)\left(\alpha_s + r_a + \mu\right)}. \tag{3.2}$$

The following lemma is well-known and also supports the results of this research.

Lemma 1. *The disease-free equilibrium U^0 of system (2.3 - 2.7) always exists and U^0 is locally asymptotically stable whenever $\Re_0 < 1$ and unstable if $\Re_0 > 1$.*

Next is to examine the reproduction number $\Re_0$ by evaluating the impact of the progression rate v and asymptomatic case detection rate p. Now, the rate of change of $\Re_0$ with respect to v is;

$$\frac{\partial \Re_0}{\partial v} = \frac{\beta\mu\left((1-p)(\alpha_a + r_a + \mu) - p(\alpha_s + r_s + \mu)\right)}{\left(v + \mu\right)^2\left(\alpha_a + r_a + \mu\right)\left(\alpha_s + r_s + \mu\right)}, \tag{3.3}$$

from which it can easily be inferred that the progression rate v will have a positive impact in controlling the spread of COVID-19 if $(0.5 < p \leq 1)$, otherwise the progression rate v will have a negative impact on the spread of COVID-19. Also, consider the rate of change of $\Re_0$ with respect to p,

$$\frac{\partial \Re_0}{\partial p} = -\frac{v\beta\left((\alpha_a + r_a + \mu) + (\alpha_s + r_s + \mu)\right)}{\left(v + \mu\right)\left(\alpha_a + r_a + \mu\right)\left(\alpha_s + r_s + \mu\right)}, \tag{3.4}$$

from which it is clear that

$$\frac{\partial \Re_0^2}{\partial p} < 0,$$

implying that increase in testing strategy to detect asymptomatic cases of COVID-19 will have a positive impact on the reduction of COVID-19 burden in a population.

Theorem 2. *The system (2.5) has a unique endemic equilibrium if* $\Re_0 > 1$.

Proof. The endemic equilibrium point (EEP) corresponding to the system (2.3 - 2.7) expressed in terms of the equilibrium value of the force of infection λ^* is given as

$$U^* = (S^*, E^*, I_s^*, I_a^*, R^*)\,. \tag{3.5}$$

where

$$S^* = \frac{\Lambda}{(\lambda^* + \mu)},\ E^* = \frac{\lambda^* S^* + \psi\lambda^* R^*}{(v+\mu)},\ I_s^* = \frac{(1-p)vE^*}{(\alpha_s + r_s + \mu)},\ I_a^* = \frac{pvE^*}{(\alpha_a + r_a + \mu)}, \tag{3.6}$$

$$R^* = \frac{\left(r_s\left(\alpha_a + r_a + \mu\right)(1-p) + r_a\left(\alpha_s + r_a + \mu\right)\right)v\Lambda\lambda^*}{(\lambda^* + \mu)\left(\left(\alpha_a + r_a + \mu\right)(\psi\lambda^* + \mu) - \left(r_s\left(\alpha_a + r_a + \mu\right)(1-p) + r_a\left(\alpha_s + r_a + \mu\right)\right)v\psi\lambda^*\right)} \tag{3.7}$$

and the EEP force of infection is

$$\lambda^* = \beta\left(\frac{I_s^* + I_a^*}{N^*}\right) \tag{3.8}$$

substituting (3.6) and (3.7) into the equation (3.8), we have

$$C_1^0\lambda^{*2} + C_2^0\lambda^* + C_3^0 = 0 \tag{3.9}$$

where

$$\begin{aligned} C_1^0 =& \frac{\Lambda}{(v+\mu)}\psi\left(pv\left(\alpha_s + r_s + \mu\right)(1 - r_a) + (1-p)\left(\alpha_a + r_a + \mu\right)(1 - r_s)\,v\right. \\ &\left. +2\left(\alpha_s + r_s + \mu\right)\left(\alpha_a + r_a + \mu\right)\right) \end{aligned} \tag{3.10}$$

$$\begin{aligned} C_2^0 =& v\Lambda\left(r_s\left(\alpha_a + r_a + \mu\right)(1-p) + r_a\left(\alpha_s + r_s + \mu\right)p\right)\left(1 - \frac{\mu\psi}{(v+\mu)}\right) \\ &+ \frac{\mu v\Lambda}{(v+\mu)}\left(\left(1-p\right)\left(\alpha_a + r_a + \mu\right) + p\left(\alpha_s + r_s + \mu\right)\right)(1 - \beta\psi) \\ &+ \frac{\mu\Lambda}{(v+\mu)}\left(\frac{2\left(1-p\right)v}{(\alpha_s + r_s + \mu)} + \psi\left(\alpha_s + r_s + \mu\right)\left(\alpha_a + r_a + \mu\right)\right) \end{aligned} \tag{3.11}$$

$$C_3^0 = \mu\Lambda\left(\alpha_s + r_s + \mu\right)\left(\alpha_a + r_a + \mu\right)\left(\frac{\mu}{(v+\mu)} - \Re_0\right) \tag{3.12}$$

□

Solving the polynomial (3.9) gives the components of the EEP. Observe that the coefficients C_1^0 and C_2^0 are positive and $\Re_0 > 1$ implies that $C_3^0 < 1$.

3.2 Backward Bifurcation Analysis

Set the variables such that

$$S = x_1, E = x_2, I_s = x_3, I_a = x_4, R = x_5$$

and re-write the equation (2.5) as

$$\frac{dX}{dt} = G = (g_1, g_2, g_3, g_4, g_5)$$

such that

$$x_1'(t) = g_1 = \Lambda - \lambda_x x_1 - \mu x_1 \tag{3.13}$$
$$x_2'(t) = g_2 = \lambda_x x_1 - (v+\mu)\, x_2 + \psi \lambda_x x_5 \tag{3.14}$$
$$x_3'(t) = g_3 = (1-p) v x_2 - (\alpha_s + r_s + \mu)\, x_3 \tag{3.15}$$
$$x_4'(t) = g_4 = pv x_2 - (\alpha_a + r_a + \mu)\, x_4 \tag{3.16}$$
$$x_5'(t) = g_5 = r_s x_3 + r_a x_4 - \mu x_5 - \psi \lambda_x x_5 \tag{3.17}$$

where,

$$\lambda_x = \beta \left(\frac{x_3 + x_4}{x_1 + x_2 + x_3 + x_4 + x_5} \right) \tag{3.18}$$

Let $\beta = \beta^0$ be the bifurcation parameter for the system (3.13 - 3.17), then when $\Re_0 = 1$,

$$\beta^0 = \frac{(v+\mu)(\alpha_s + r_s + \mu)(\alpha_a + r_a + \mu)}{v\left((1-p)(\alpha_a + r_a + \mu) + p(\alpha_s + r_s + \mu)\right)}. \tag{3.19}$$

The Jacobian matrix associated to the model (3.13 - 3.17) is

$$J(U_0)\,|_{\beta=\beta^0} = \begin{pmatrix} -\mu & 0 & -\beta & -\beta & 0 \\ 0 & -(v+\mu) & \beta & \beta & 0 \\ 0 & (1-p)v & -(\alpha_s + r_s + \mu) & 0 & 0 \\ 0 & pv & 0 & -(\alpha_a + r_a + \mu) & 0 \\ 0 & 0 & r_s & r_a & -\mu \end{pmatrix} \tag{3.20}$$

We investigate the possibility of backward bifurcation at $\Re_0 = 1$ using the Centre Manifold theorem [4, 25], and show that the Jacobian $\left(J_{\beta^0}\right)$ at $\beta = \beta^0$ of the system (3.13 - 3.17) possesses right eigenvectors given as $u = [u_1, u_2, u_3, u_4, u_5]^T$ by multiplying the Jacobian matrix (3.20) with u. We further express each of the vectors in terms u_2 as

$$u_1 = -\frac{u_2}{\mu(v+\mu)} \Re_0 \tag{3.21}$$
$$u_3 = \frac{(1-p)v}{(\alpha_s + r_s + \mu)} u_2 \tag{3.22}$$
$$u_4 = \frac{pv}{(\alpha_a + r_a + \mu)} u_2 \tag{3.23}$$
$$u_5 = \frac{v}{\mu} \left(\frac{r_s(1-p)}{(\alpha_s + r_s + \mu)} + \frac{r_a p}{(\alpha_a + r_a + \mu)} \right) u_2 \tag{3.24}$$

Similarly, we show that the Jacobian $\left(J_{\beta^0}\right)$ at $\beta = \beta^0$ of the system (3.13 - 3.17) possesses left eigenvectors given as $w = [w_1, w_2, w_3, w_4, w_5]$ by multiplying the Jacobian matrix (3.20) with w, we further express each of the vectors in terms w_2 as

$$w_1 = 0,\ w_3 = \frac{\beta}{(\alpha_s + r_s + \mu)} w_2,\ w_4 = \frac{\beta}{(\alpha_a + r_a + \mu_a)} w_2,\ w_5 = 0. \tag{3.25}$$

Following the work of [5] for computation of a and b, the corresponding non-zero partial derivatives are

$$a = \sum_{k,i,j=1}^{n} w_k u_i u_j \frac{\partial^2 g_k}{\partial x_i \partial x_j}(0,0),\ b = \sum_{k,i=1}^{n} w_k u_i \frac{\partial^2 g_k}{\partial x_i \partial \beta}(0,0),$$

and thus

$$a = \left(-(K_1 + K_2 + K_3 + K_4) + \psi K_4\right) w_2 u_2^2, \text{ and } b = \left(\frac{(1-p)v}{(\alpha_s + r_s + \mu)} + \frac{pv}{(\alpha_a + r_a + \mu)} \right) w_2 u_2 > 0$$

where

$$K_1 = \frac{2\beta\mu v}{\Lambda}\left(\frac{(1-p)}{(\alpha_s + r_s + \mu)} + \frac{p}{(\alpha_a + r_a + \mu)}\right)$$
$$K_2 = \frac{4\beta\mu(1-p)v^2}{\Lambda(\alpha_s + r_s + \mu)}\left(\frac{(1-p)}{(\alpha_s + r_s + \mu)} + \frac{p}{(\alpha_a + r_a + \mu)}\right)$$
$$K_3 = \frac{4\beta\mu p^2 v^2}{\Lambda(\alpha_a + r_a + \mu)}$$
$$K_4 = \frac{2\beta v^2}{\Lambda}\left(\frac{(1-p)}{(\alpha_s + r_s + \mu)} + \frac{p}{(\alpha_a + r_a + \mu)}\right)\left(\frac{r_s(1-p)}{(\alpha_s + r_s + \mu} + \frac{r_a p}{\alpha_a + r_a + \mu}\right)$$

and $a > 0$ if and only if

$$\psi > 1 + \frac{K_1 + K_2 + K_3}{K_4}$$

but $a < 0$ if and only if

$$\psi < 1 + \frac{K_1 + K_2 + K_3}{K_4}$$

Hence we establish these results with the following theorem:

Theorem 3. *For $\Re_0 = 1$, where w_1, w_2, w_3, w_4, w_5 and u_1, u_2, u_3, u_4, u_5 are defined as equations (3.25) and (3.21 - 3.24), then*

1. *the system (3.15) undergoes a backward bifurcation if $a > 0$*
2. *the system (3.15) undergoes a transcritical bifurcation if $a < 0$.*
3. *the endemic equilibrium U^* is locally asymptotically stable for $\Re_0 > 1$ and $a < 0$.*

3.3 Global Asymptotic Stability (GAS) of the Disease-free Equilibrium (DFE)

The Global asymptotic stability of the DFE is shown by considering the system (2.3 - 2.7) without re-infection (i.e $\psi = 0$), then we observe the last equation is independent of the first four equations; therefore, we reduce the system of equations to

$$S' = \Lambda - \lambda S - \mu S, \tag{3.26}$$
$$E' = \lambda S - (v + \mu)E, \tag{3.27}$$
$$I_s' = (1-p)vE - (\alpha_s + r_s + \mu)I_s, \tag{3.28}$$
$$I_a' = pvE - (\alpha_a + r_a + \mu)\, I_a, \tag{3.29}$$

where

$$\lambda = \frac{\beta\,(I_s + I_a)}{N} \tag{3.30}$$

Theorem 4. *The disease-free equilibrium of the system (3.26 - 3.29), without re-infection is globally asymptotically stable in $\mathcal{D}$ whenever $\Re_0 \leq 1$.*

Proof. Consider the Lyapunov function associated with system (3.26 - 3.29)

$$L_1 = A_1 E + A_2 I_s + A_3 I_a, \tag{3.31}$$

where

$$A_1 = v\left((1-p)\left(\alpha_a + r_a + \mu\right) + p\left(\alpha_s + r_s + \mu\right)\right), \tag{3.32}$$

$$A_2 = \left(v + \mu\right)\left(\alpha_a + r_a + \mu\right), \tag{3.33}$$

$$A_3 = \left(v + \mu\right)\left(\alpha_s + r_s + \mu\right). \tag{3.34}$$

The time derivative of the Lyapunov function of the system (3.28) at DFE is

$$L_1' = A_1 E' + A_2 I_s' + A_3 I_a'. \tag{3.35}$$

Substituting equation (3.26 - 3.29) and (3.33), we obtain

$$L_1' = \left(v + \mu\right)\left(\alpha_a + r_a + \mu\right)\left(\alpha_s + r_s + \mu\right)\left(I_s + I_a\right)\left[\beta\frac{S}{N}\left(\frac{v\left((1-p)\left(\alpha_a + r_a + \mu\right) + p\left(\alpha_s + r_s + \mu\right)\right)}{\left(v + \mu\right)\left(\alpha_a + r_a + \mu\right)\left(\alpha_s + r_a + \mu\right)}\right) - 1\right]$$

and since $S \leq N$ in the domain $\mathcal{D}$ that forms the invariant set, then

$$L_1' \leq \left(v + \mu\right)\left(\alpha_a + r_a + \mu\right)\left(\alpha_s + r_s + \mu\right)\left(I_s + I_a\right)\left(\Re_0 - 1\right). \tag{3.36}$$

Clearly, $L_1' \leq 0$, if $\Re_0 \leq 1$. It follows that L_1 is a Lyapunov function in the domain $\mathcal{D}$. Hence, according to Lasalle's Invariance Principle [13] we have that

$$\left(E(t), I_s(t), I_a(t)\right) \to (0, 0, 0) \qquad \text{as } t \to \infty, \tag{3.37}$$

and as a result, every trajectory produced by the system (3.26 - 3.29) tends to the disease-free equilibrium point U^0 with $\psi = 0$ and for $\Re_0 \leq 1$. It is inferred from the analysis above that, if the assumption excludes re-infection (i.e $\psi = 0$) then we can conclude that the system (3.26 - 3.29) is globally asymptotically stable whenever $\Re_0 \leq 1$ at the DFE. This implies that eradication of COVID-19 from a population of no re-infection is obtainable whenever $\Re_0 \leq 1$,therefore , the $\Re_0 \leq 1$ is required and sufficient to effectively control COVID-19 in any population. □

3.4 Global Asymptotic Stability (GAS) of Endemic Equilibrium point (EEP)

Theorem 5. *For the system (3.26 - 3.29), if $\Re_0 > 1$ then the unique endemic equilibrium state $U^* = (S^*, E^*, I_s^*, I_a^*)$ is globally asymptotically stable in the domain $\mathcal{D}$.*

Proof. Consider the system (3.26 - 3.29) together with the force of infection and the reproduction number $\Re_0$. Hence whenever $\Re_0 > 1$, the unique EEP (U^*) exist. We represent the Lyapunov function L_2 for the EEP as

$$L_2 = \left(S - S^* - S^* \ln\frac{S}{S^*}\right) + \left(E - E^* - E^* \ln\frac{E}{E^*}\right) + R_1\left(I_s - I_s^* - I_s^* \ln\frac{I_s}{I_s^*}\right) + R_2\left(I_a - I_a^* - I_a^* \ln\frac{I_a}{I_a^*}\right) \tag{3.38}$$

where,

$$R_1 = \frac{\tilde{\beta}}{\left(\alpha_s + r_s + \mu\right)} S^* \; R_2 = \frac{\tilde{\beta}}{\left(\alpha_a + r_a + \mu\right)} S^* \tag{3.39}$$

and equation (3.30) is taken as

$$\tilde{\lambda} = \tilde{\beta}(I_s + I_a). \tag{3.40}$$

Putting (3.26-3.29) and , (3.39) into the time derivative of L_2, we have,

$$L_2' = \tilde{\beta} S^* I_s^* \left(3 - \frac{S^*}{S} - \frac{E}{E^*}\frac{I_s^*}{I_s} - \frac{S}{S^*}\frac{E^*}{E}\frac{I_s}{I_s^*}\right) + \tilde{\beta} S^* I_a^* \left(3 - \frac{S^*}{S} - \frac{E}{E^*}\frac{I_a^*}{I_a} - \frac{S}{S^*}\frac{E^*}{E}\frac{I_a}{I_a^*}\right) + \mu S^* \left(2 - \frac{S}{S^*} - \frac{S^*}{S}\right).$$

Since arithmetic mean is greater than or equal to geometric mean, we conclude that the following inequalities hold

$$\tilde{\beta}S^*I_s^*\left(3-\frac{S^*}{S}-\frac{E}{E^*}\frac{I_s^*}{I_s}-\frac{S}{S^*}\frac{E^*}{E}\frac{I_s}{I_s^*}\right)\leq 0,$$
$$\tilde{\beta}S^*I_a^*\left(3-\frac{S^*}{S}-\frac{E}{E^*}\frac{I_a^*}{I_a}-\frac{S}{S^*}\frac{E^*}{E}\frac{I_a}{I_a^*}\right)\leq 0,$$
$$\mu S^*\left(2-\frac{S}{S^*}-\frac{S^*}{S}\right)\leq 0$$

it then means that

$$L_2'\leq 0$$

if $\Re_0 > 1$ and the re-infection is negligible, then by Lassalle's invariance principle, U^* is globally asymptotically stable. □

4 Numerical Simulation

In this section, a numerical simulation of the COVID-19 cases in Africa is investigated. Data used are obtained from https://www.worldometers.info/coronavirus/ which publishes daily updates on the cases of COVID-19 containing the number of new cases, number of disease-induced death and the number of recovered individuals. Over 1.3 billion people are living in Africa with increasing birth rate. Thus we assume the influx rate Λ to be based on the number of births per day. Following the data, as at May 25, the following parameter values are obtained; $\Lambda = 19823210$, $\beta = 0.000085044$, $\mu = 0.0039$, $v = 0.167$, $w = 0.000000056$, $p = 0,\ 0.3,\ 0.9$, $\alpha_s = 0.0000017595$, $\alpha_a = 0.00000075407$, $r_s = 0.00032395$,$r_a = 0.000010337$ respectively.

Figure (4.1) shows the dynamics of the Exposed class, Symptomatic human class and asymptomatic human class as the rate of re-infection increases. Considering that re-infection is possible, then as the rate of re-infection increases, then both the symptomatic and asymptomatic human classes continue to increase. More so, the exposed class initial continues to increase but later starts to flatten out. The impact of asymptomatic population on the spread of COIVD-19 is illustrated in figure (4.2). It can be seen that as the p increases, the asymptomatic human class increases whereas the symptomatic cases decrease.

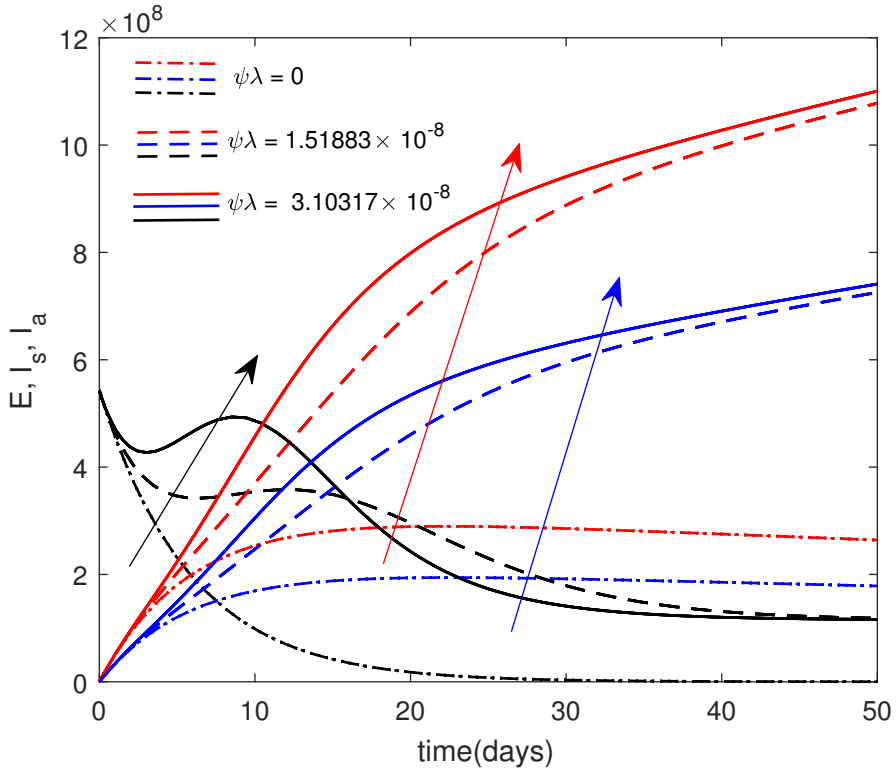

Figure 4.1: Graph of numerical solutions showing exposed population (black = E, blue= I_a, red=I_s)

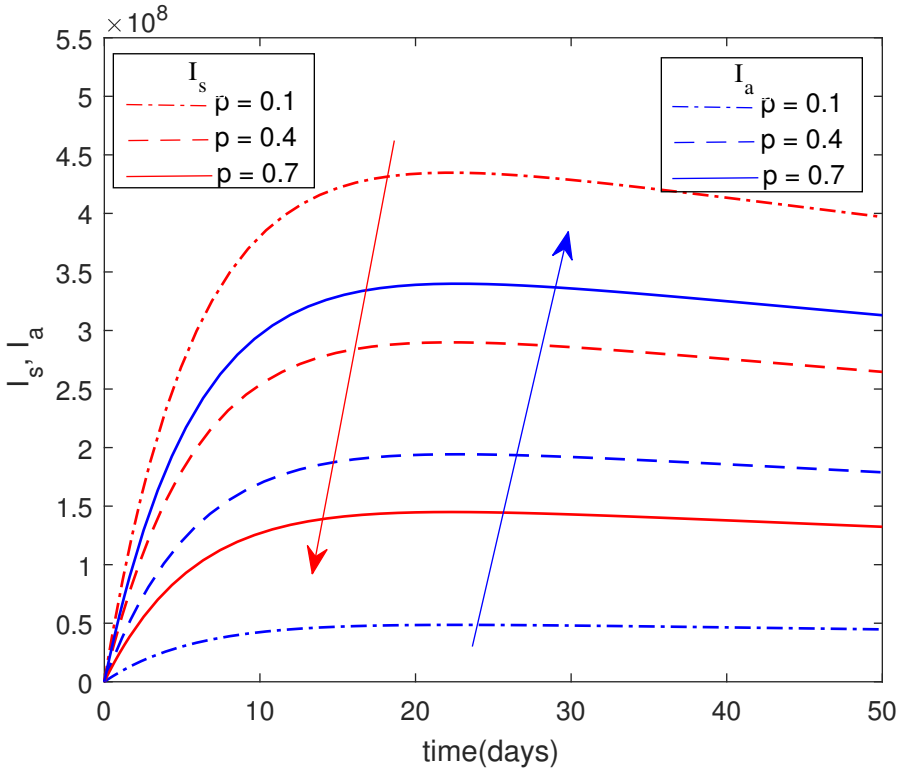

Figure 4.2: Graph of numerical solutions showing asymptomatic infected population

5 Discussion and Conclusion

We have presented a mathematical model to investigate the COVID-19 transmission dynamics in Africa. The impact of asymptomatic case detection (p) and possible re-infection rate on the dynamics of COVID-19 is incorporated into our model to form a system of five (5) non-linear ordinary differential equations. The analysis of this model is conducted by obtaining the reproduction number $\Re_0$. Existence of backward bifurcation is tested and the local asymptotic stability of the disease free equilibrium and the endemic equilibrium whenever the reproduction number $\Re_0 < 1$ and $\Re_0 > 1$ respectively are established. The global asymptotic stability of the disease free equilibrium and the endemic equilibrium for the model, without the re-infection, is also established. The reproduction number is examined in respect to some parameters.

The results here indicate that as the asymptomatic case detection $p \to 1$, the progression of COVID-19 is impacted positively. The impact of the asymptomatic case detection rate (p) is also examined on the reproduction number, and it is observed that $\Re_0$ is a decreasing function of p, which eventually have a positive impact on the control of the disease. More so, as the rate of re-infection increases, both the asymptomatic and symptomatic cases rise significantly.

Our numerical simulations results show that repeated and increase testing to detect people living with the disease will be very effective in containing and reducing the burden of COVID-19 in Africa. In addition, since it has not been confirmed whether a recovered individual can be re-infected, then enforcing a living condition where recovered individuals are not allowed to mix with the susceptible or exposed individuals will help in containing the spread of COVID-19. However, from the figures (4.1) and (4.2), it is clear that the disease may remain in Africa for a long time. This supports what was

speculated about this disease and we need to prepare for a longer period to fight COVID-19 as we wait for new vaccines which is the most feasible intervention to reduce and possibly eradicating the disease.

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