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Modelling the Dynamics of COVID-19 Disease with Contact Tracing and Isolation in Ghana

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Abstract: We have formulated a mathematical model to investigate the transmission dynamics of the current novel COVID-19 disease outbreak in Ghana. The coronavirus originated from Wuhan,, China. Majority of people who contact the disease experience mild to moderate respiratory illness and recover. The elderly and people with underlying health issues experience severe complications. A plethora of measures have been taken by the government of Ghana to curtail the disease. The model considers, among other things, quarantining and testing of immigrants, contact tracing and isolation in the form of quarantining or hospitalization, as control measures in mitigating the spread of the pandemic. Our model considers the following classes: susceptible, exposed, infectious, quarantine, treatment and recovery class. The steady-state solution was calculated and the basic reproduction number for this model calculated and used as a threshold to determine the asymptotic behaviour of the model. Our analytical and numerical results show a close dependence of the basic reproductive number on epidemic parameters. The aim of this paper was to incorporate the various intervention strategies into the model and ascertain their impact on COVID-19. Some of the methods employed in the analysis include the Next Generation Matrix and the Jacobian Matrix. Our simulations results correlate well with data and indicate that early quarantine and a high quarantine rate are crucial to the control of COVID-19. Thus, current preventative measures, such as isolation, contact tracing and treatment are, indeed, critical components in the control of COVID-19 until appropriate cure or vaccine is found.

Keywords: COVID-19, Reproduction Number, Stability Analysis, Contract Tracing, Isolation

1. Introduction

COVID-19 is an infectious disease caused by a newly discovered coronavirus. This novel virus appears to have firstly reported in Wuhan, China late 2019. Ghana recorded its first case of coronavirus in March 2020 from an immigrant who visited the country. COVID-19 spreads from person-to-person and has grown to become a global pandemic. According to World Health Organization (WHO), most people infected with the COVID-19 virus experience mild to moderate respiratory illness and recover without requiring special treatment [1]. Adults and people with medical conditions, such as cardiovascular disease, diabetes, chronic respiratory disease, and cancer are more likely to develop serious complications after contracting the disease [1]. The array of symptoms of the novel coronavirus includes fever, muscle pain, cough, headaches, shortness of breath or difficulty in breathing and chills [2].

The rapid growth in the number of COVID-19 cases in China, Italy, Spain, USA, and Britain set up a strong alarm to the Ghana government and public health authorities. Following measures taken by other countries, the President of the Republic of Ghana initiated broadcasts and put in place drastic measures, such as closure of Ghana's borders and partial lockdown of Accra and Kumasi metropolitan areas in a bid to curtail the spread of the disease in March 2020 [3]. Newspapers, radio, and TV stations campaigned to educate the public on COVID-19 spread and prevention, although enforcing social distancing, especially in marketplaces remain a challenge.

With the advent of an epidemic, the first and foremost

question that arises in our mind is 'how do we, as a community, protect ourselves against the epidemic?' In fact, strict adherence to the infection control guidelines is essential to prevent the transmission of infection among the population in a community. Transmission of infection can be controlled by the identification and diagnosis of persons who may have encountered an infected person, called contact tracing and through the removal of infective individuals from the general population. Contact tracing and isolation strategies are critically important tools to control the outbreak of epidemics like Coronavirus [3].

The fundamental dilemma associated with the implementation of isolation and quarantine is how to predict the population level efficacy of individual quarantine: Which and how many individuals need to be quarantined to achieve effective control at the population level? [4]. Quarantine, defined loosely as the temporary removal (from their immediate abode or the general population) of people suspected of being exposed to a communicable disease, has historically been used as an effective basic public health control measure to prevent the spread of infectious diseases [5]. There are numerous issues pertaining to the logistic of the actual implementation of quarantine as a control strategy, such as who should be quarantined and for how long suspected people should be in quarantine (these have major socio-economic and public health implications) [6].

To gain insight into the mechanism of spread of COVID-19, numerous mathematical modelling techniques, typically of the form of deterministic systems of nonlinear differential equations, have been developed to study the transmission dynamics and control of COVID-19. Wu *et al.* [8], proposed a SEIR model to describe the transmission dynamics and fitted data from December 31, 2019 to January 28, 2020 in China. Pengpeng *et al.* [9], further established a new SEIR propagation dynamics model, which considered the weak transmission ability of the incubation period, the variation of the incubation period length, and the government intervention measures to track and isolate comprehensively. This model was further developed by Yang *et al.* [10] by including a new compartment for the concentration of the coronavirus in the environmental reservoir. Furthermore, Chang *et al.* [11], proposed an SIHRS model which incorporated awareness of media coverage, which plays an important role in preventing and controlling infectious diseases.

The spread of COVID-19 in Ghana, albeit on the low side, it is still significant compared to the etiology of the disease in other countries (see Figures 1 and 2).

To gain insight into the mechanism of spread of the disease, we have developed and analyzed a mathematical model. The model addresses the dynamics of coronavirus disease in a homogeneous population with immigration from outside into the susceptible Ghanaian population. The model addresses the impact of isolation, contact tracing and temporal immunity scenarios. We develop the full model system in Section 2 and analyse the model system in Section 3. In Section 4, we perform stability analysis and present a derivation of the basic reproductive number, a crucial parameter, which allows us to make more informed predictions about the severity of the disease. We present the numerical simulations based upon the Runge-Kutta method in Section 5, and we conclude by making some recommendations, based upon the model predictions in the Discussions and Conclusions in Section 6.

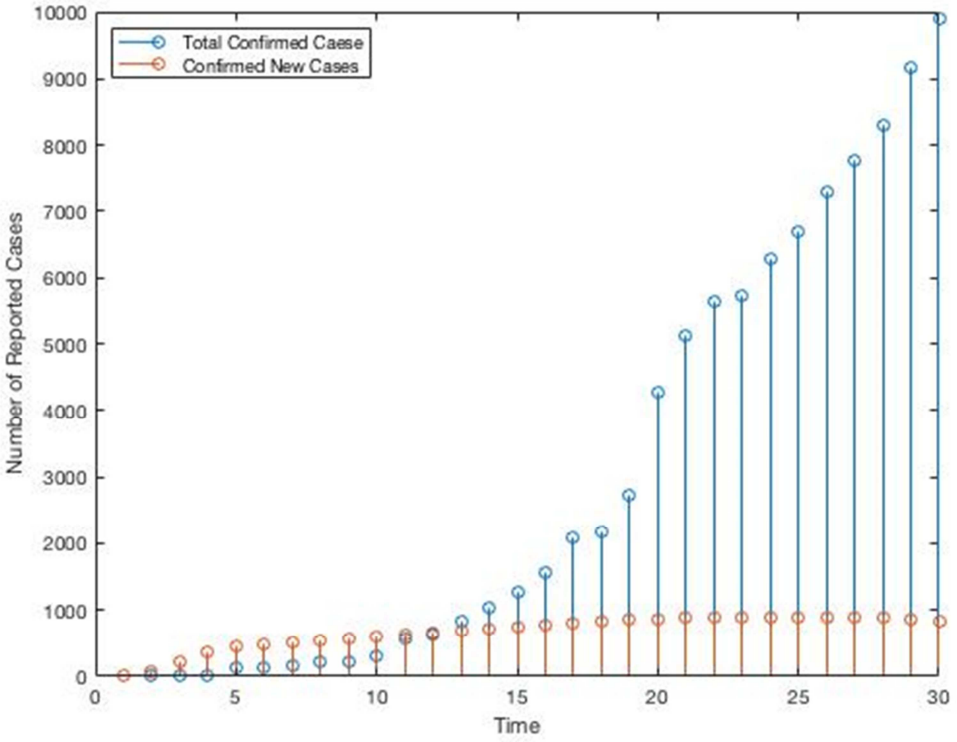

Figure 1. *Number of reported cases in Ghana, the orange stem denotes the new cases and the blue stem denotes the total cases.*

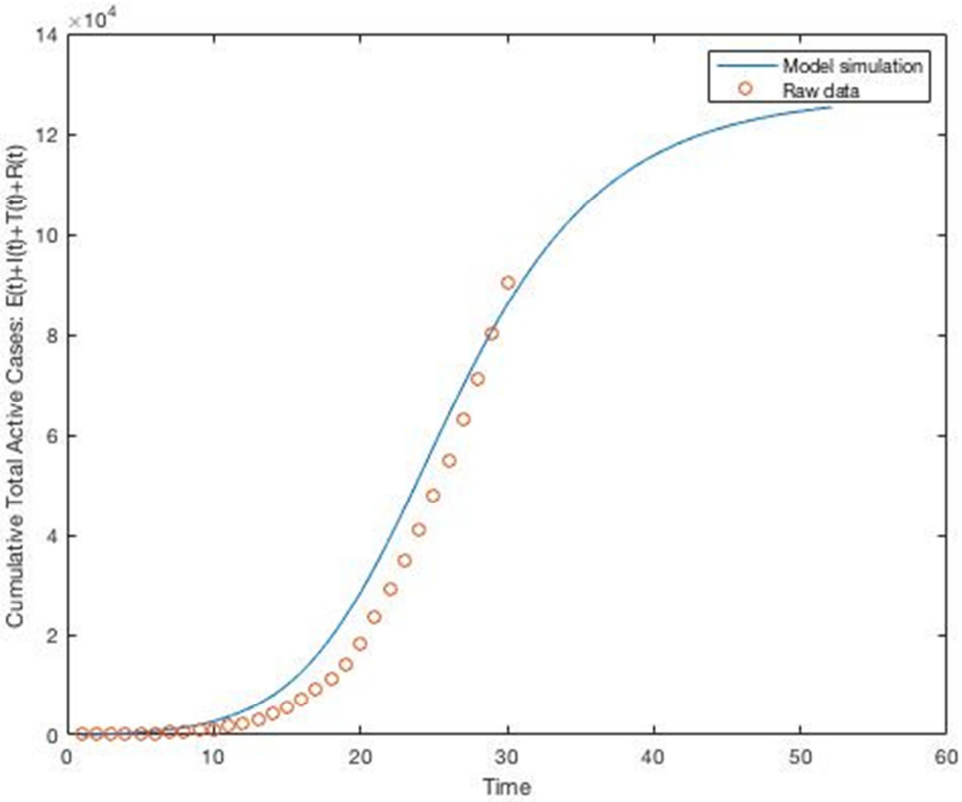

Figure 2. *Cumulative total active cases. Circles (in orange) denote the fitted data and solid line (in blue) denotes the simulation result.*

2. Model Design

Following the basic idea and structure of mathematical modeling in epidemiology [8, 12], our model describes the dynamics of six sub-populations (classes), namely susceptible, exposed, infective, quarantined, treated, and recovered individuals. We assume that only a fraction of the total newly infected contacts, are elucidated and that those individuals are isolated. The population is subdivided into the following six classes:

Susceptible S(t): members of the population who may become infected.

Exposed E(t): members of population infected by the coronavirus but are in the incubation period and are asymptomatic. The population exposed to COVID-19 is subtly infectious (either without infectivity or with very low infectivity).

Infectives *I*(t): members of the population who are infectious and symptomatic with strong infectivity but have not yet been quarantined.

Quarantined Q(t): members of the population who have been infected, and have not been diagnosed, but have been quarantined. It includes individual from contact tracing.

Treatment T(t): members of the population who are infective, have been diagnosed and have been treated.

Recovered R(t): members of the population who have recovered from the disease with partial immunity against reinfection.

The schematic representation of the individual flow between the different classes is shown in Figure 3.

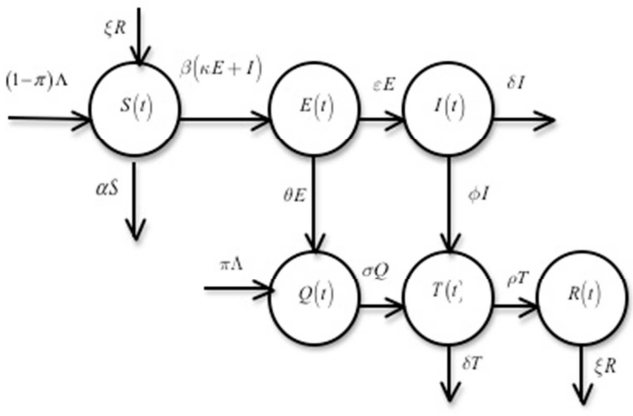

Figure 3. *Compartmental model of coronavirus disease with contact tracing and isolation.*

The variables S(t), E(t), I(t), Q(t), T(t), and R(t) are the numbers of the individuals in the six classes at time *t*, respectively. We assume that the epidemic process operates on a much faster time scale than natural deaths, and assume that the only deaths are due to disease. In Ghana, at present the number of exposed, infective, quarantined, diagnosed, and recovered classes appear to be small compared to the susceptible population. The susceptible group is increased through immigration rate of Λ, with a proportion π being the rate at which persons enter the quarantined group (Q) [17]. Susceptible group get infected through contact with infected persons with force of infection λ and through government intervention some are isolated at a rate of α. A person infected by coronavirus enters the exposed class and is in the incubation period. The incubation period lasts 2 to 14 days [13]. Some exposed individuals will enter the quarantined class at a rate of λ, because of contact tracing. The remaining exposed individuals will enter the infective class at a rate of ε. People in the quarantined and infective classes will enter the treatment class at a rate of σ and ϕ respectively, after obvious symptoms of COVID-19 appear and they are diagnosed eventually. Diagnosed group enters recovered class at a rate of ρ or die of the infection at a rate of δ. People with weakened immune systems might not develop full immunity after infection and be more likely to be reinfected with the same coronavirus. It is assumed that the recovered population again enters the susceptible population but with low risk of infection at the rate ξ.

From the model design and the schematic flow diagram (Figure 3) the model equations become:

$$\begin{cases} \dfrac{dS(t)}{dt} = (1-\pi)\Lambda + \xi R(t) - (\lambda(t)+\alpha)S(t) \\ \dfrac{dE(t)}{dt} = \lambda(t)S(t) - (\varepsilon+\theta)E(t) \\ \dfrac{dI(t)}{dt} = \varepsilon E(t) - (\phi+\delta)I(t) \\ \dfrac{dQ(t)}{dt} = \pi\Lambda + \theta E(t) - \sigma Q(t) \\ \dfrac{dT(t)}{dt} = \phi I(t) + \sigma Q(t) - (\rho+\delta)T(t) \\ \dfrac{dR(t)}{dt} = \rho T(t) - \xi R(t) \end{cases} \tag{1}$$

where $\lambda(t)$ is the infection rate is given by the following relationship:

$$\lambda(t) = \beta(\kappa E(t) + I(t)) \tag{2}$$

The model system (Equation 1) is able to encapsulate most of the salient features of the disease etiology in Ghana. Below, we provide analysis of the model and explore some ramifications.

3. Qualitative Analysis of Coronavirus Model

To find the positivity and boundedness of solutions throughout the work, we assume that the initial conditions of system (1) are non-negative:

$$\{S(0)\geq 0, E(0)\geq 0, I(0)\geq 0, Q(0)\geq 0, T(0)\geq 0, R(0)\geq 0 \text{ and } N(t) = S(t)+E(t)+I(t)+Q(t)+T(t)+R(t) \tag{3}$$

Our first lemma shows that the considered model (1) – (3) is biologically meaningful.

Lemma 1. The solutions $(S(t), E(t), I(t), Q(t), T(t), R(t))$ of system (1) are non-negative for all $t \geq 0$ with non-negative initial conditions (3) in R_6^+.

Proof. We have

$$\begin{cases} \left.\dfrac{dS(t)}{dt}\right|_{\psi(S)} = (1-\pi)\Lambda + \xi R(t) \geq 0, \\ \left.\dfrac{dE(t)}{dt}\right|_{\psi(E)} = \lambda(t)S(t) \geq 0, \\ \left.\dfrac{dI(t)}{dt}\right|_{\psi(I)} = \varepsilon E(t) \geq 0, \\ \left.\dfrac{dQ(t)}{dt}\right|_{\psi(Q)} = \pi\Lambda + \theta E(t) \geq 0, \\ \left.\dfrac{dT(t)}{dt}\right|_{\psi(T)} = \phi I(t) + \sigma Q(t) \geq 0, \\ \left.\dfrac{dR(t)}{dt}\right|_{\psi(R)} = \rho T(t) \geq 0. \end{cases}$$

where $\psi(v)=\{v(t)=0 \text{ and } S,E,I,Q,T,R\in C(\mathbb{R}_+^6)\}$ and $v\in\{S,E,I,Q,T,R\}$. Therefore, due to Lemma 2 in [14], any solution of system (1) is such that $(S(t),E(t),I(t),Q(t),T(t),R(t)\in\mathbb{R}_+^6)$ for $t\geq 0$.

Lemma 2 shows that it is enough to consider the dynamics of the flow generated by (1) – (3) in a certain region Ω.

Lemma 2. *Let*

$$\Omega=\left\{(S,E,I,Q,T,R)\in\Re_+^6 \middle| 0\leq S(t)+E(t)+I(t)+Q(t)+T(t)+R(t)\leq\Lambda\right\} \tag{4}$$

then the region Ω *is positively invariant for model (1) with non-negative initial conditions (3) in* $\mathbb{R}_+^6$.

Proof. Adding the six equations of system (1) gives

$$N'(t)=S'(t)+E'(t)+I'(t)+Q'(t)+T'(t)+R'(t)=\Lambda-\sigma S(t)-\delta(I(t)+T(t))\leq\Lambda$$

For this reason, equation (3) defines the biologically feasible region for the population. From (1) and (3), we know that $N(t)$ is bounded for all $t\geq 0$. Therefore, every solution of system (1) with initial conditions in Ω remains in Ω for all $t\geq 0$. This is shown to be positively invariant and globally attracting in $\mathbb{R}_+^6$ with respect to system equation (1).

4. Equilibrium Points and Basic Reproduction Number

The disease – free equilibrium (DFE) of system equation (1) is given by

$$E^0=(S^0,E^0,I^0,Q^0,T^0,R^0)=\left(\frac{\Lambda(\rho\pi+a_2-\pi a_2)}{\alpha a_2},0,0,\frac{\pi\Lambda}{\sigma},\frac{\pi\Lambda}{a_2},\frac{\rho\pi\Lambda}{a_2\xi}\right) \tag{5}$$

Next, we compute the basic reproduction number *R*0.

Proposition 1: (Basic reproduction number of system of Equations (1)). *The basic reproduction number of model* (1) *is given by*

$$R_0=\frac{\beta\Lambda(\rho\pi+a_2-\pi a_2)(\kappa a_1+\varepsilon)}{a_2a_1a_0\alpha} \tag{6}$$

where

$$a_0=\varepsilon+\theta,\quad a_1=\phi+\delta,\quad a_2=\rho+\delta$$

Proof. Let consider +that $\mathcal{F}_i(t)$ is the rate of appearance of new infections in the compartment associated with index *i*, $\mathcal{V}_i(t)$ is the rate of transfer of infections into the compartment associated with index *i*.

From system Equations (1), we write down the equations with infection, $E(t)$, $I(t)$ and $T(t)$. This leads to the system

$$\begin{cases}\dfrac{dE(t)}{dt}=\lambda(t)S(t)-(\varepsilon+\theta)E(t)\\ \dfrac{dI(t)}{dt}=\varepsilon E(t)-(\phi+\delta)I(t)\\ \dfrac{dT(t)}{dt}=\phi I(t)+\sigma Q(t)-(\rho+\delta)T(t)\end{cases} \tag{7}$$

In this way, the matrices $\mathcal{F}_i(t)$, and $\mathcal{V}_i(t)$, associated with model (7), are given by

$$\mathcal{F}_i(t)=\begin{bmatrix}\beta S(t)(\kappa E(t)+I(t))\\ 0\\ 0\end{bmatrix} \text{ and } \mathcal{V}_i(t)=\begin{bmatrix}a_0E(t)\\ a_1I(t)-\varepsilon E(t)\\ a_2T(t)-\phi I(t)-\sigma Q(t)\end{bmatrix}$$

Partial differentiation of $\mathcal{F}_i(t)$, and $\mathcal{V}_i(t)$, with respect to $E(t)$, $I(t)$ and $T(t)$ gives:

$$F(t)=\begin{bmatrix}\beta\kappa S(t) & \beta S(t) & 0\\ 0 & 0 & 0\\ 0 & 0 & 0\end{bmatrix} \text{ and } \mathrm{V}(t)=\begin{bmatrix}a_0 & 0 & 0\\ -\varepsilon & a_1 & 0\\ 0 & -\phi & a_2\end{bmatrix}$$

In the disease-free equilibrium E^0 defined by (4), we obtain the matrices F_0 and V_0 given by

$$F_0 = \begin{bmatrix} -\frac{\beta\kappa\Lambda\left(\pi a_2 - \pi\rho - a_2\right)}{\alpha a_2} & -\frac{\beta\Lambda\left(\pi a_2 - \pi\rho - a_2\right)}{\alpha a_2} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{ and } V_0 = \begin{bmatrix} a_0 & 0 & 0 \\ -\varepsilon & a_1 & 0 \\ 0 & -\phi & a_2 \end{bmatrix}$$

The inverse of V_0 is calculated as

$$V_0^{-1} = \begin{bmatrix} \frac{1}{a_0} & 0 & 0 \\ \frac{\varepsilon}{a_0 a_1} & \frac{1}{a_1} & 0 \\ \frac{\varepsilon\phi}{a_0 a_1 a_2} & \frac{\phi}{a_1 a_2} & \frac{1}{a_2} \end{bmatrix}$$

then

$$F_0 V_0^{-} = \begin{bmatrix} -\frac{\beta\kappa\Lambda\left(\pi a_2 - \pi\rho - a_2\right)}{\alpha a_2 a_0} & -\frac{\beta\Lambda\left(\pi a_2 - \pi\rho - a_2\right)\varepsilon}{\alpha a_2 a_1 a_0} & -\frac{\beta\Lambda\left(\pi a_2 - \pi\rho - a_2\right)}{\alpha a_2 a_1} & 0 \\ 0 & & 0 & 0 \\ 0 & & 0 & 0 \end{bmatrix}$$

The basic reproduction number of model (1) which is the spectral radius of $F_0 V_0^{-}$ is given by

$$R_0 = \frac{\beta\Lambda\left(\rho\pi + a_2 - \pi a_2\right)\left(\kappa a_1 + \varepsilon\right)}{a_2 a_1 a_0 \alpha}$$

Now we prove the existence of an endemic equilibrium when R_0 given by (6) is greater than one.

Proposition 2: (Endemic equilibrium). *If the basic reproduction number* (6) *is such that* $R_0 > 1$*, then the model* (1) *has an endemic equilibrium given by*

$$E^1 = \left(S^*, E^*, I^*, Q^*, T^*, R^*\right) \tag{8}$$

where

$$\begin{cases} S^* = \frac{a_0 a_1 \Lambda\left(\rho\pi + a_2 - \pi a_2\right)}{\tilde{D}} \\ E^* = \frac{a_1 \lambda\Lambda\left(\rho\pi + a_2 - \pi a_2\right)}{\tilde{D}} \\ I^* = \frac{\varepsilon\lambda\Lambda\left(\rho\pi + a_2 - \pi a_2\right)}{\tilde{D}} \\ Q^* = \frac{\Lambda\left(a_1 a_2\left(\phi\lambda - \phi\lambda\pi - a_0\lambda\pi + a_0\alpha\pi\right) - \pi\rho\phi\lambda\varepsilon\right)}{\sigma\tilde{D}} \\ T^* = \frac{\Lambda\left(a_1\left(\phi\lambda - \phi\lambda\pi - a_0\lambda\pi + a_0\alpha\pi\right) + \varepsilon\phi\lambda\left(1-\pi\right)\right)}{\tilde{D}} \\ R^* = \frac{\rho}{\xi}T^* \end{cases}$$

and $\tilde{D} = a_2 a_1 a_0 \alpha - a_2 a_1 a_0 \lambda - \rho\phi\varepsilon\lambda - \rho\phi\lambda a_1$

Proof. To obtain the Endemic Equilibrium $E^1 = \left(S^*, E^*, I^*, Q^*, T^*, R^*\right)$, we let $\lambda^* = \beta\left(\tau E^* + I^*\right)$. It follows, by solving the equations in (1) at steady-state that

$$\begin{cases} S^* = \frac{a_0 a_1 \Lambda\left(\rho\pi + a_2 - \pi a_2\right)}{a_2 a_1 a_0 \alpha - a_2 a_1 a_0 \lambda - \rho\phi\varepsilon\lambda - \rho\phi\lambda a_1} \\ E^* = \frac{a_1 \lambda\Lambda\left(\rho\pi + a_2 - \pi a_2\right)}{a_2 a_1 a_0 \alpha - a_2 a_1 a_0 \lambda - \rho\phi\varepsilon\lambda - \rho\phi\lambda a_1} \\ I^* = \frac{\varepsilon\lambda\Lambda\left(\rho\pi + a_2 - \pi a_2\right)}{a_2 a_1 a_0 \alpha - a_2 a_1 a_0 \lambda - \rho\phi\varepsilon\lambda - \rho\phi\lambda a_1} \\ Q^* = \frac{\Lambda\left(a_1 a_2\left(\phi\lambda - \phi\lambda\pi - a_0\lambda\pi + a_0\alpha\pi\right) - \pi\rho\phi\lambda\varepsilon\right)}{\sigma\left(a_2 a_1 a_0 \alpha - a_2 a_1 a_0 \lambda - \rho\phi\varepsilon\lambda - \rho\phi\lambda a_1\right)} \\ T^* = \frac{\Lambda\left(a_1\left(\phi\lambda - \phi\lambda\pi - a_0\lambda\pi + a_0\alpha\pi\right) + \varepsilon\phi\lambda\left(1-\pi\right)\right)}{a_2 a_1 a_0 \alpha - a_2 a_1 a_0 \lambda - \rho\phi\varepsilon\lambda - \rho\phi\lambda a_1} \\ R^* = \frac{\rho}{\xi}T^* \end{cases} \tag{9}$$

Substituting E^* and I^* in (9) into $\lambda^* = \beta\left(\kappa E^* + I^*\right)$ gives the following quadratic equation (in terms of λ^*):

$$\Psi_0\left(\lambda^*\right)^2 + \Psi_1\lambda^* = 0 \tag{10}$$

with

$$\Psi_0 = -\left(a_2 a_1 a_0 + \rho\phi\varepsilon + \rho\phi a_1\right) \text{and } \Psi_1 = 1 - R_0$$

By solving for λ^* in (10) and substituting the positive values of λ^* into the expressions in (9) the endemic equilibria of the model (1) can then be obtained. It should be noted that $\Psi_0 > 0$ and $\Psi_1 < 0$ whenever $R_0 > 1$. Hence, the following result is established.

Existence and Stability of Equilibrium Solutions

Theorem 1: (Stability of the DFE (5)). *The disease-free equilibrium* E^0 *of model* (1) *is locally asymptotic stable, if* $R_0 < 1$*;*

Proof. We study the stability of the disease-free equilibrium by using the linearization method presented in [15]. The Jacobian matrix of the system (1) in a point (S, E, I, Q, T, R) is given by:

$$J = \begin{bmatrix} -\beta(\kappa E + I) - \alpha & -\beta S\kappa & -\beta S & 0 & 0 & \xi \\ \beta(\kappa E + I) & \beta S - a_1 & \beta S & 0 & 0 & 0 \\ 0 & \varepsilon & -a_1 & 0 & 0 & 0 \\ 0 & \theta & 0 & -\sigma & 0 & 0 \\ 0 & 0 & \phi & \sigma & -a_2 & 0 \\ 0 & 0 & 0 & 0 & \rho & -\xi \end{bmatrix} \tag{11}$$

At the disease-free equilibrium $E^0 = \left(\frac{\Lambda(\rho\pi + a_2 - \pi a_2)}{\alpha a_2}, 0, 0, \frac{\pi\Lambda}{\sigma}, \frac{\pi\Lambda}{a_2}, \frac{\rho\pi\Lambda}{a_2\xi}\right)$, the jacobian matrix will give as

$$J_{E^0} = \begin{bmatrix} -\alpha & \frac{\beta\kappa\Lambda(a_2\pi - \rho\pi - a_2)}{a_2\alpha} & \frac{\beta\Lambda(a_2\pi - \rho\pi - a_2)}{a_2\alpha} & 0 & 0 & \xi \\ 0 & \frac{\beta\kappa\Lambda(a_2\pi - \rho\pi - a_2)}{a_2\alpha} - a_1 & \frac{\beta\kappa\Lambda(\rho\pi + a_2 - a_2\pi)}{a_2\alpha} & 0 & 0 & 0 \\ 0 & \varepsilon & -a_1 & 0 & 0 & 0 \\ 0 & \theta & 0 & -\sigma & 0 & 0 \\ 0 & 0 & \phi & \sigma & -a_2 & 0 \\ 0 & 0 & 0 & 0 & \rho & -\xi \end{bmatrix} \tag{12}$$

Therefore, the eigenvalues are $-\alpha, -\xi, -\sigma, -a_2$, $-K\left(B + \sqrt{C}\right)$ and $-K\left(B - \sqrt{C}\right)$, where

$K = \frac{1}{2a_2\alpha}$, $B = \Lambda\beta\kappa(a_2\pi - \pi\rho - a_2) + a_2\alpha(a_0 + a_1)$,

$$\begin{aligned} C = {} & \Lambda^2\beta^2\kappa^2\left(a_2^2\pi^2 + a_2^2 + 2a_2\rho\pi + \rho^2\pi^2 - 2\rho\pi^2 a_2 - 2a_2^2\pi\right) \\ & + \Lambda\beta\kappa\alpha\left[2a_2^2(\pi - 1)(a_0 - a_1) + 2a_2\rho\pi(a_1 - a_0)\right] \\ & + 4\Lambda\beta\alpha\varepsilon\left(a_2\rho\pi + a_2^2 - a_2^2\pi\right) + a_2^2\alpha^2\left(a_1^2 + a_0^2 + 2a_0a_1\right) \end{aligned}$$

The first five eigenvalues are all negative, but we do not know whether $-K\left(B - \sqrt{C}\right)$ is negative. Imposing negativity condition leads to $B > \sqrt{C}$.

This implies,

$$B^2 - C > 0 \tag{13}$$

Simplifying equation (13) further leads to

$$4\beta\Lambda a_2\alpha(\kappa a_1 + \varepsilon)(\pi a_2 - \rho\pi - a_2) + 4a_2^2 a_1 a_0\alpha^2 > 0$$

Dividing through by the positive expression $4a_2^2 a_1 a_0\alpha^2$ yields

$$\frac{4\beta\Lambda a_2\alpha(\kappa a_1 + \varepsilon)(\pi a_2 - \rho\pi - a_2)}{4a_2^2 a_1 a_0\alpha^2} + 1 > 0$$

Multiplying through by -1 and simplifying gives

$$\frac{\beta\Lambda(\kappa a_1 + \varepsilon)(\rho\pi + a_2 - \pi a_2)}{a_2 a_1 a_0\alpha} - 1 < 0$$

Hence the disease-free equilibrium is asymptotically stable provided $R_0 < 1$.

5. Numerical Simulations

In this section, we carry out some numerical simulations for

the dynamics of the current COVID-19 outbreak disease model in Ghana. Although the disease is not yet well understood, much data has been collected during the COVID-19 epidemic. Based on the cumulative number of confirmed cases in Ghana from March 23, 2020 to April 24, 2020 [3] in shown graphically in Figures 1 and 2.

To illustrate the feasibility of the obtained results in our model system (Equation 1), we choose the following initial population classes, (t=0), $\left(S(t),E(t),I(t),Q(t),T(t),R(t)\right)$ respectively as ($2.45\text{x}10^{05}$, 100, 2, 0, 0, 0). The parameter values used for the model simulations are shown in Table 1. Based upon the parameter choices, the basic reproduction number becomes $R_0 = 0.5116 < 1$. By Theorem 1 the disease-free equilibrium is asymptotically stable, and the disease dies out (Figures 4-5, see also Figures 1-2).

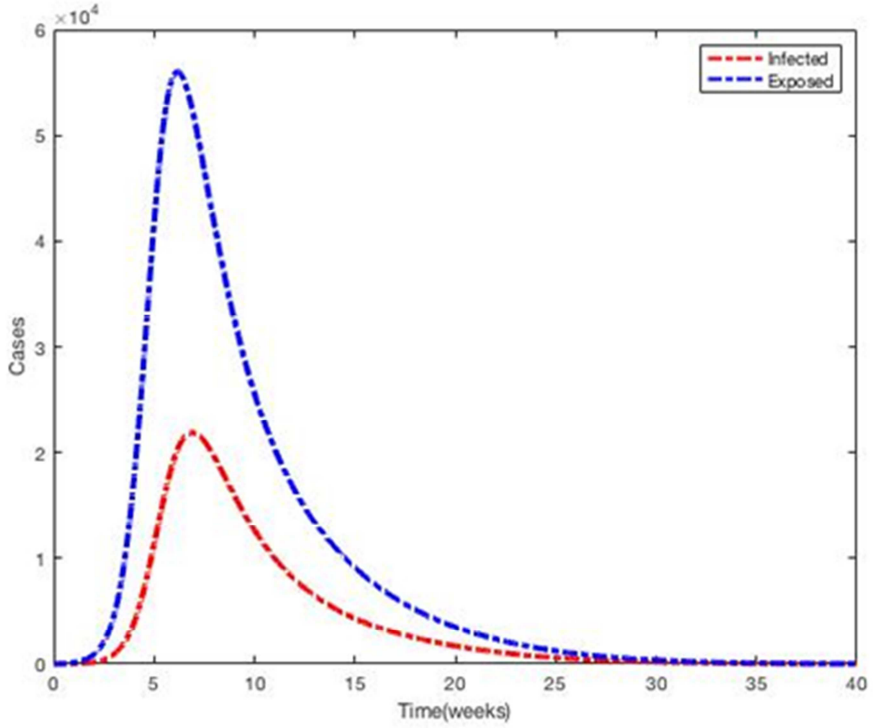

Figure 4. *Simulation result for the outbreak in Ghana using the constant transmission rates given in the Table 1.*

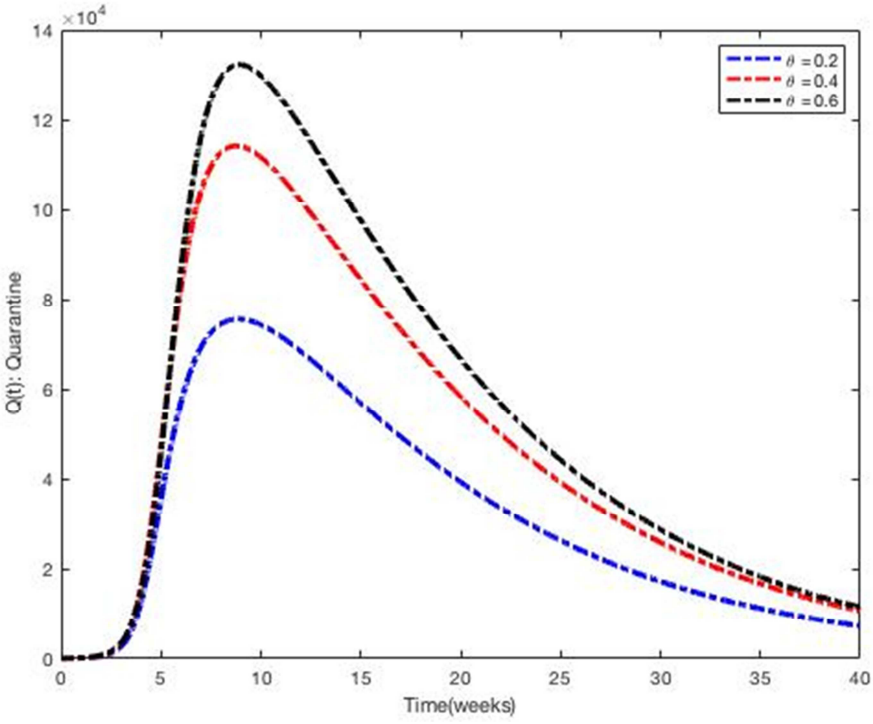

Figure 5. *The influence of contact tracing for quarantine.*

Table 1. *Description and baseline values of model parameters.*

Par.	Description	Baseline Values	Reference
Λ	Immigrant migration rate	100/day	Assumed
π	Fraction of recruited immigrant	0.6/day	Assumed
α	Isolation rate due to government intervention	0.2/day	Assumed
β	Transmission coefficient	$6.64\text{x}10^{-03}$/day	Estimated
κ	Relative infectiousness of Individuals with a Latent Infection	0.328/day	Assumed
ε	Progression rate from exposed to infectious class	0.003/day	Assumed
θ	Contact tracing rate for exposed individuals	0.2 – 1.0 per day	Varied
σ	Progression of infected persons in the quarantine class to treatment class	0.05 – 0.1 per day	Varied
ϕ	Rate of hospitalization of infectives	1/10 per day	Assumed
ρ	Recovery rate	0.095/day	Estimated
δ	Per Capita Covid-19 induced death rate	0.03/day	[13]
ξ	Per capita loss of immunity	0.0002	Assumed

6. Discussion

In this paper, we have presented a mathematical model to look into the current COVID-19 epidemic in Ghana. We developed a new SEIQTR model well suited for the characteristics of COVID-19 in Ghana. In the absence of vaccination, our model employs social distancing, quarantining of immigrants, contact tracing and hospitalization as measures for controlling the disease. In particular we included in the Quarantine class immigrants and suspected cases from contact tracing. Those who tested positive progressed into the treatment class or were hospitalized.

The basic reproduction number, which describes the number of secondary infections produced by an infective, was calculated. Thus, if $R_0 < 1$, Covid-19 dies out. This is highly desirable since Covid-19 is causing havoc in Ghana. On the other hand, $R_0 > 1$ is indicative of an epidemic. Steady-state analysis was carried out on the model. The disease-free equilibrium is locally asymptotically stable provided $R_0 < 1$ and the endemic equilibrium exist, if $R_0 > 1$.

To mitigate the COVID-19 disease spread in Ghana, after carefully choosing parameters and the initial values, we carried out model simulations to illustrate COVID-19 disease transmission dynamics. Our simulation results correlate well with the raw data shown in Figure 2. The modelling, analysis and simulations in this paper form a simple, mathematical approach to the study of COVID-19 disease transmission in Ghana.

It is often very difficult to validate epidemiological simulation models due to the lack of reliable field data. However, Ministry of Health Ghana (MOH) has constantly reported the COVID-19 cases in Ghana since the first case was confirmed in Ghana. The COVID-19 epidemic data was obtained from MOH's website [3]. Figure 2 shows the number of people infected with COVID-19 virus in Ghana verses the cumulative total active cases. The trend of the raw data is succinctly expressed by the essential features of our COVID-19 model proposed in this paper. Thus, our model, with an ample degree of confidence, can be used to study the dynamics of the disease in Ghana.

In Figure 1, the number of confirmed new cases of COVID-19 in Ghana appears to grow and cumulative number continue to increase (Figure 2), albeit slowly. This must be a welcoming news for Ghana, but we cannot be over-optimistic. Although social intervention strategies are working, traders in the marketplaces still pose a problem. For better results, social distancing and the use of nose mask must be made compulsory. Contact tracing should be enhanced and all immigrants quarantined and tested. Figure 4 show that the number of exposed individual and infectives will continue to increase and attain a peak and then gradually become endemic. Figure 5 shows the simulated results in different contact tracing ratios. We can see that the spread of novel COVID-19 can be effective controlled when quarantine rate larger than 0.2. When $\sigma = 0.2$, the number of quarantine population reach the peak value 70,000 at week 8 and is smaller than other situations.

7. Conclusion

Our model is simple, yet it encapsulates the salient features of COVID-19 transmission dynamics, see for example, [16], where another simple model was used to describe tuberculosis disease dynamics. We included in the model the control measures adopted by the president of Ghana to fight this pandemic. This paper does not consider cases of COVID-19 infection to healthcare and frontline workers who contracted the disease in their line of duty. These healthcare workers have close contact with infected persons and form a high-risk group. How to include COVID-19 transmission in health care workers in our model is an important question and it would be important to learn what new phenomena might appear if these factors were considered.

Given the current trend of the disease progression and the stark prediction by WHO, the disease will continue to persist and become endemic. The results of our study indicate that Ghana must be prepared to fight the infectious disease much longer. The most important thing that can aid our effort at combating COVID-19 is testing. Ghana must be able to test a higher proportion of the population. Given the deficit in our budget, help will be needed from individuals, companies, and donor countries. In addition, attempt should be made at finding a vaccine or a cure. The latter will play a pivotal role in eliminating the disease.

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References

[1] J. Bryner, 1st known case of coronavirus traced back to November in China, https://www.livescience.com/first-case-coronavirus-found.html, Accessed April 18, 2020.

[2] Centers for Disease Control and Prevention, Symptoms of Coronavirus. https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html. Accessed April 18, 2020.

[3] Ministry of Health, Ghana, COVID-19 Ghana's outbreak response management update. https://ghanahealthservice.org/covid19/#.

[4] G. Chowell, P. W. Fenimore, M. A. Castillo-Garsow, C. Castillo-Chavez, SARS out-breaks in Ontario, Hong Kong and Singapore: the role of diagnosis and isolation as a control mechanism. *J Theor Biol*. 2003; 224: 1-8.

[5] J. M. Drazen, R. Kanapathipillai, E. W. Campion, E. J. Rubin, S. M. Hammer and S. Morrissey, Ebola and quarantine. *New England Journal of Medicine*, 371, (2014), 2029-2030.

[6] M. A. Safi and A. B. Gumel, Mathematical analysis of a disease transmission model with quarantine, isolation and an imperfect vaccine, *Computers and Mathematics with Applications*, 61 (2011) 3044–3070.

[7] N. T. J. Bailey, The Mathematical Theory of Infectious Diseases, Second Edition, Hafner, New York, (1975).

[8] J. T. Wu, K. Leung, and G. M. Leung, Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study, *Lancet*, 395 (2020), 689–697.

[9] S. Pengpeng, C. Shengli and F. Peihua, SEIR Transmission dynamics model of 2019 nCoV coronavirus with considering the weak infectious ability and changes in latency duration. medRxiv preprint doi: https://doi.org/10.1101/2020.02.16.20023655.

[10] C. Yang and J. Wang, A mathematical model for the novel coronavirus epidemic in Wuhan, China. *Mathematical Biosciences and Engineering* Volume 17, Issue 3, 2708–2724.

[11] X. Chang, M. Liu, Z. Jin and J. Wang, Studying on the impact of media coverage on the spread of COVID-19 in Hubei Province, China. *Mathematical Biosciences and Engineering* Volume 17, (2020) Issue 4, 3147–3159.

[12] V. Capasso, Mathematical structures of epidemic systems, In Lecture Notes in Biomathematics, Volume 97, (1993), Springer-Verlag, Berlin.

[13] C. Huang, Y. Wang, X. Li, L. Ren, J. Zhao and Y. Hu, "Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China." *The Lancet* 395 (10223): (2020) 497-506. https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30183-5/fulltext.

[14] X. Yang, L. Chen and J. Chen, Permanence and positive periodic solution for the single-species nonautonomous delay diffusive models, *Comput. Math. Appl.*, 32, (1996) 109–116.

[15] P. van den Driessche and J. Watmough, Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission, *Math. Biosc.*, 180, (2002), 29–48.

[16] D. E. Bentil and J. D. Murray, *Modelling Bovine Tuberculosis Infection in Badgers*. Journal of Animal Ecology, 62, (1993), 239–250.

[17] E. N. Wiah, O. D. Makinde and I. A. Adetunde, Optimal Control of Hepatitis B Virus Disease in a Population with Infected Immigrants, *Eng. Math. Let*, (2015): 8 ISSN: 2049-9337.