Global Stability and Sensitivity Assessment of COVID-19 with Timely and Delayed Diagnosis in Ghana

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Global Stability and Sensitivity Assessment of COVID-19 with Timely and Delayed Diagnosis in Ghana

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Abstract. In this paper, we present the dynamical effects of timely and delayed diagnosis on the spread of COVID-19 in Ghana, using reported data from March 12 to June 19, 2020. The estimated basic reproduction number, $\mathcal{R}_0$, for the proposed model is 1.04. One of the main focus of this study is stability results and senesitivity assessment of the parameters. We show both theoretically and numerically that, the disease can be eliminated when the basic reproduction number is less or equal to a unity. Furthermore, we show that the disease persist whenever $\mathcal{R}_0 > 1$ or whenever there is a delay in the diagnoses of infected individuals in the community. To assess the most influential parameters in the basic reproduction number, we carried out global sensitivity analysis. The scatter plots and the partial rank correlation coefficient reveal that, the most positive sensitive parameter is the recruitment rate, followed by the relative transmissibility of exposed individuals; and that the most negative sensitive parameters are the proportion of the infectious with timely diagnosis, and the transition rate of self-quarantined individuals to the susceptible population. For public health benefit, our analysis suggests that, a reduction in the inflow of new individuals into the country or a reduction in the inter community inflow of individuals will reduce the basic reproduction number and thereby reduce the number of secondary infections (multiple peaks of the infection). COVID-19; Ghana; non-autonomous ODE; delayed diagnosis; basic reproduction number; Mathematical modeling

1 Introduction

COVID-19 was declared a pandemic in the first quarter of 2020 by the World Health Organization (WHO) see, e.g. [1]. The disease affects different people in different ways with most infected people developing mild to moderate illness. Most common symptoms are fever dry cough and tiredness whiles less common symptoms include aches and pains, sore throat, diarrhoea, conjunctivitis, headache, loss of taste or smell, a rash on skin or discolouration of fingers or toes [1,2]. It is well understood that the elderly with underlying medical problems are the most vulnerable people. COVID-19 is transmitted by means of contact (direct or indirect), droplet spray in short range transmission and aerosol in long-range transmission (airborne transmission) [15]. Globally, there were 100,285,517 confirmed cases with 2,149,461 confirmed death cases as on 26th January, 2021 [2].

In Africa, there were a total of 3,512,124 confirmed cases with 88,130 confirmed death cases where Ghana is among the top ten (10) most infected countries as on 26th January, 2021 [2]. As on 26th January, 2021, Ghana had 63,883 confirmed cases with 390 confirmed death cases and 59,553 recovered individuals. The first confirmed cases in Ghana were recorded on 12th of March, 2020 from two people who had returned from Norway and Turkey [6]. In Figure 1, we presented the logistic growth model for the cumulative cases of COVID-19 for Ghana on 25th January, 2021.

Several works have been studied concerning COVID-19 including a human-to-human model analysis, see, e.g. [4]. The transmission dynamics in Wuhan has also been studied and presented

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Fig. 1: Logistic model fit and cumulative trajectories for reported cases for Ghana.

in several articles with control measures and basic reproduction number well analyzed, see e.g. [19,7,16]. In an earlier article [14], we presented the control strategies to curb the virus using data from Wuhan. Measures to control the spread of COVID-19 are mostly avoiding human-to-human contacts, person protection and environmental disinfection. The diagnosis of COVID-19 is difficult and the incubation period of 2 – 14 days or 0 – 24 days is longer than most known coronaviruses or similar viruses which usually ranges between 1 to 10 days [13]. Due to the long incubation period, it results in a delay in diagnosis. This delay allows for human-to-human transmission as well as human-environment-human transmission.

In this article, we present the transmission dynamics of COVID-19 considering human-environment-human dynamics for Ghana. We have particularly considered Ghana from the anglophone west Africa to understand the effects of timely-delayed dynamics in this region of the sub-saharan continent. For mathematical feasibility, we will present the global stability analysis, the basic reproduction numbers, sensitivity assessment and numerical simulations of the proposed model.

The rest of the article is organized as follows; In Section 2, we present the model formulation and definition of parameters used. Section 3 concerns the existence and uniqueness as well as the positivity and boundedness of the solution. We present the analysis of disease-free equilibrium in Section 4 and the Endemic equilibrium in Section 5. The numerical results using data from Ghana

and corresponding parameters are presented in Section 6. Finally, the concluding remarks and recommendations are presented in Section 8.

2 Model formulation

Based on the model formulated in [19], we propose a modified version of the epidemiological compartment model that takes into account the recruitment of hosts and the natural death. Here, we note that the total human population size denoted as (N) is divided into susceptible (S) , self-quarantine susceptible (S_q) , exposed (E) , infectious with timely diagnosis (I_1) , infectious with delayed diagnosis (I_2) , hospitalized (H) and recovered (R) . The viral spread in the environment is denoted as (V) . Hence for the total human population at time t we have $N(t) = S(t) + S_q(t) + E(t) + I_1(t) + I_2(t) + H(t) + R(t)$. We also consider that all parameters are positive and it is only the I_1 , I_2 and H compartments which experiences disease induced death at a rate, d . The overall force of infection is given as $\lambda = \beta_e E + \beta_{i_1} I_1 + \beta_{i_2} I_2 + \beta_v V$ where the remainder of model parameters are presented in Table 1.

In Figure 2, we show the compartmental model describing the interaction between the human population and the pathogens in the environment.

Fig. 2: Diagram of COVID-19 Dynamics.

The description of the parameters used in the model for the COVID-19 transmission are given in Table 1. Following the compartmental transition diagram as shown in Figure 2, the eight state dynamical model describing the transmission dynamics of COVID-19 is given by

$$\begin{aligned}
 \frac{dS}{dt} &= \Lambda - \lambda S + q_1 S_q - (\mu + q)S, \\
 \frac{dS_q}{dt} &= qS - q_1 S_q - \mu S_q, \\
 \frac{dE}{dt} &= \lambda S - \omega E - \mu E, \\
 \frac{dI_1}{dt} &= \phi\omega E - \gamma_1 I_1 - \mu I_1 - dI_1, \\
 \frac{dI_2}{dt} &= (1 - \phi)\omega E - \gamma_2 I_2 - \mu I_2 - dI_2,
 \end{aligned} \tag{1}$$

Table 1: Description of parameters.

Parameter	Description
Λ	Recruitment rate
q	Self-quarantined rate of the susceptible
q_1	Transition rate of self-quarantined individuals to the susceptible
β_e	Transmission rate from the exposed to the susceptible
β_{i_1}	Transmission rate from the infectious with timely diagnosis to the susceptible
β_{i_2}	Transmission rate from the infectious with delayed diagnosis to the susceptible
β_v	Transmission rate from the susceptible to the exposed (infected by virus)
$1/\omega$	Incubation period
ϕ	Proportion of the infectious with timely diagnosis
$1/\gamma_1$	Waiting time of the infectious for timely diagnosis
$1/\gamma_2$	Waiting time of the infectious for delayed diagnosis
μ	Natural human death rate
d	Disease-induced death rate
m	Recovery rate of the hospitalized
f_1	Virus released rate of the exposed
f_2	Virus released rate of the infectious with timely-diagnosis
f_3	Virus released rate of the infectious with delayed-diagnosis
d_v	Decay rate of virus in the environment

$$\begin{aligned}
\frac{dH}{dt} &= \gamma_1 I_1 + \gamma_2 I_2 - mH - \mu H - dH, \\
\frac{dR}{dt} &= mH - \mu R, \\
\frac{dV}{dt} &= f_1 E + f_2 I_1 + f_3 I_2 - d_v V.
\end{aligned}$$

3 Analysis of the model problem

The model (1) is described by a system of first order autonomous nonlinear differential equations. It can be rewritten in the matrix form as

$$X'(t) = F(X(t)), \quad (2)$$

where $X(t) := (S, S_q, E, I_1, I_2, H, R, V)^T$ and F is a smooth function defined from $\mathbb{R}^8$ by

$$F(X) := \begin{pmatrix} \Lambda - (\beta_e E + \beta_{i_1} I_1 + \beta_{i_2} I_2 + \beta_v V)S + q_1 S_q - (\mu + q)S \\ qS - q_1 S_q - \mu S_q \\ (\beta_e E + \beta_{i_1} I_1 + \beta_{i_2} I_2 + \beta_v V)S - \omega E - \mu E \\ \phi \omega E - \gamma_1 I_1 - \mu I_1 - dI_1 \\ (1 - \phi) \omega E - \gamma_2 I_2 - \mu I_2 - dI_2 \\ \gamma_1 I_1 + \gamma_2 I_2 - mH - \mu H - dH \\ mH - \mu R \\ f_1 E + f_2 I_1 + f_3 I_2 - d_v V \end{pmatrix},$$

where $X := (S, S_q, E, I_1, I_2, H, R, V) \in \mathbb{R}^8$. Since F is a smooth function, then F is locally lipschitz on $\mathbb{R}^8$. And we deduce the existence and uniqueness of the maximal solution to the Cauchy problem associated with the differential system (1) relating to the initial condition $(t_0, X_0) \in \mathbb{R} \times \mathbb{R}^8$.

Next, we consider the positivity of the solution. Here, we investigate the asymptotic behavior of orbits starting in the non-negative cone $\mathbb{R}_+^8$.

Theorem 1. *For any initial condition*

$(t_0 = 0, X_0 = (S(0), S_q(0), E(0), I_1(0), I_2(0), H(0), R(0), V(0)) \in \mathbb{R}_+^8)$, *the maximal solution* $([0, T[|X(t) = (S(t), S_q(t), E(t), I_1(t), I_2(t), H(t), R(t), V(t)))$ *of the Cauchy problem related with system (1) is non-negative.*

We define the set $\Delta := \{\tilde{t} \in [0, T[| X(t) > 0, \forall t \in]0, \tilde{t}[\}$. Since $(S, S_q, E, I_1, I_2, H, R, V)$ are continuous functions, then $\Delta \neq \emptyset$. Also, let $\tilde{T} := \sup \Delta$ and show that $\tilde{T} = T$. Assume $\tilde{T} < T$, then $S, S_q, E, I_1, I_2, H, R$ and V are simultaneously positive on $]0, \tilde{T}[$.

At least one of the following conditions is satisfied at time $\tilde{T}$: $S(\tilde{T}) = 0, S_q(\tilde{T}) = 0, E(\tilde{T}) = 0, I_1(\tilde{T}) = 0, I_2(\tilde{T}) = 0, H(\tilde{T}) = 0, R(\tilde{T}) = 0$ or $V(\tilde{T}) = 0$.

Assume $S(\tilde{T}) = 0$, then we deduce from the first equation of system (1)

$$\frac{d}{dt} \left(S e^{\int_0^t (\lambda(s) + \mu + q) ds} \right) = (\Lambda + q_1 S_q) e^{\int_0^t (\lambda(s) + \mu + q) ds}. \quad (3)$$

The integration of equation (3) from 0 to $\tilde{T}$ yields

$$S(\tilde{T}) = e^{-\int_0^{\tilde{T}} (\lambda(s) + \mu + q) ds} \left(S(0) + \int_0^{\tilde{T}} (\Lambda + q_1 S_q(t)) e^{\int_0^t (\lambda(s) + \mu + q) ds} dt \right) > 0.$$

Similarly, we can prove that $S(\tilde{T}) > 0, S_q(\tilde{T}) > 0, E(\tilde{T}) > 0, I_1(\tilde{T}) > 0, I_2(\tilde{T}) > 0, H(\tilde{T}) > 0, R(\tilde{T}) > 0$ and $V(\tilde{T}) > 0$. This is a contradiction to the previous claim that $S(\tilde{T}) = 0, S_q(\tilde{T}) = 0, E(\tilde{T}) = 0, I_1(\tilde{T}) = 0, I_2(\tilde{T}) = 0, H(\tilde{T}) = 0, R(\tilde{T}) = 0$ or $V(\tilde{T}) = 0$, if $\tilde{T} < T$. Then, $\tilde{T} = T$ and consequently the maximal solution $(S(t), S_q(t), E(t), I_1(t), I_2(t), H(t), R(t), V(t))$ of the Cauchy problem related with system (1) is positive. $\square$ Therefore, the variables of the system (1) are positive for all time $t > 0$. In other terms, solutions of the system (1) with nonnegative initial conditions will stay positive for all $t > 0$.

Next, we consider the invariant region of the model problem (1).

Theorem 2. *The model problem (1) has solutions in the invariant region*

$$\Omega := \left\{ (S, S_q, E, I_1, I_2, H, R, V) \in \mathbb{R}_+^8, \quad N(t) \leq \frac{\Lambda}{\mu} \quad \text{and} \quad V(t) \leq (f_1 + f_2 + f_3) \frac{\Lambda}{\mu d_v} \right\}.$$

We first split model system (1) into two parts i.e. the human population $(S, S_q, E, I_1, I_2, H, R)$ and the viral spread in the environment V . Then, using model system (1), the dynamics of the total human population satisfy

$$\frac{dN}{dt} = \Lambda - \mu N - d(I_1 + I_2 + H) \leq \Lambda - \mu N. \quad (4)$$

Integrating the expression above, we deduce that

$$N(t) \leq \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu} \right) e^{-\mu t}, \quad \forall t \geq 0,$$

where $N(0)$ is the value of $N(t)$ at the beginning. We deduce that if $N(0) \leq \frac{\Lambda}{\mu}$, then $0 \leq N(t) \leq \frac{\Lambda}{\mu}$, $\forall t \geq 0$. Now using the fact that $I_1(t) \leq \Lambda/\mu, I_2(t) \leq \Lambda/\mu, E(t) \leq \Lambda/\mu$, the dynamics of the viral spread in the environment satisfy

$$\frac{dV}{dt} \leq (f_1 + f_2 + f_3) \frac{\Lambda}{\mu} - d_v V.$$

Integrating the expression above, we deduce that

$$V(t) \leq (f_1 + f_2 + f_3) \frac{\Lambda}{\mu d_v} + \left(V(0) - (f_1 + f_2 + f_3) \frac{\Lambda}{\mu d_v} \right) e^{-d_v t}, \quad \forall t \geq 0,$$

where $V(0)$ is the initial condition of $V(t)$. Thus, as $t \rightarrow +\infty$ we have

$$V(t) \leq (f_1 + f_2 + f_3) \frac{\Lambda}{\mu d_v}.$$

Thus the region Ω is positively invariant and attracting for the system (1). It is therefore sufficient to consider the dynamics of the flow generated by the system (1). Since each maximal solution of the Cauchy problem associated with (1) is positive and bounded, each solution of the model problem (1) is global. $\square$

4 Disease-free equilibrium and its stability

For the analysis of the spread of an infection, the disease-free equilibrium (DFE) exhibits a state in the population where the disease is not prevalent and thus it is very crucial. The disease-free equilibrium is deduced from the resolution of the system of equations in (1) by taking $E = 0$, $I_1 = 0$, $I_2 = 0$, $H = 0$ and $V = 0$. Thus, the disease-free equilibrium for model (1) satisfies the system following of equations:

$$\begin{cases} (\mu + q)S^0 - q_1 S_q^0 = \Lambda, \\ qS^0 - (\mu + q_1)S_q^0 = 0. \end{cases} \quad (5)$$

Solving the system of equations in 5 yields the disease-free equilibrium point:

$$Q^0 = (S^0, S_q^0, 0, 0, 0, 0, 0),$$

where $S^0 = \frac{\Lambda(\mu + q_1)}{(\mu + q)(\mu + q_1) - qq_1}$ and $S^0 + S_q^0 = \frac{\Lambda}{\mu}$ and $S_q^0 = \frac{\Lambda q}{(\mu + q)(\mu + q_1) - qq_1}$.

The linear stability of Q^0 depends on the basic reproductive number $\mathcal{R}_0$, which is defined as the average number of secondary cases caused by an infected individual during his/her infectivity period when he/she is introduced to a population of susceptible individuals without any intervention. We study the stability of the equilibrium through the next generation operator [9,23]. Recalling the notations in [23] for model (1), the matrices $\mathcal{F}$ of the new infection and $\mathcal{W}$ of the remaining transfer terms at the DFE for are given by

$$\mathcal{F} = \begin{bmatrix} (\beta_e E + \beta_{i_1} I_1 + \beta_{i_2} I_2 + \beta_v V) S \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{and} \quad \mathcal{W} = \begin{bmatrix} \omega E + \mu E \\ -\phi \omega E + \gamma_1 I_1 + \mu I_1 + d I_1 \\ -(1 - \phi) \omega E + \gamma_2 I_2 + \mu I_2 + d I_2 \\ -\gamma_1 I_1 - \gamma_2 I_2 + m H + \mu H + d H \\ -f_1 E - f_2 I_1 - f_3 I_2 + d_v V \end{bmatrix}.$$

The Jacobian matrices of $\mathcal{F}$ and $\mathcal{W}$ at Q^0 are respectively,

$$F = \begin{bmatrix} \beta_e S^0 & \beta_{i_1} S^0 & \beta_{i_2} S^0 & 0 & \beta_v S^0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad (6)$$

and

$$W = \begin{bmatrix} \mu + \omega & 0 & 0 & 0 & 0 \\ -\phi\omega & \mu + \gamma_1 + d & 0 & 0 & 0 \\ -(1-\phi)\omega & 0 & \mu + \gamma_2 + d & 0 & 0 \\ 0 & -\gamma_1 & -\gamma_2 & \mu + m + d & 0 \\ -f_1 & -f_2 & -f_3 & 0 & d_v \end{bmatrix} \quad (7)$$

Then, the basic reproduction number of model system (1) is

$$\mathcal{R}_0 = \rho(FW^{-1}) = \mathcal{R}_{0,e} + \mathcal{R}_{0,i_1} + \mathcal{R}_{0,i_2} + \mathcal{R}_{0,v}, \quad (8)$$

where $\mathcal{R}_{0,e} = \frac{\beta_e S^0}{\mu + \omega}$, $\mathcal{R}_{0,i_1} = \frac{\beta_{i_1} \phi \omega S^0}{(\mu + \omega)(\mu + \gamma_1 + d)}$, $\mathcal{R}_{0,i_2} = \frac{\beta_{i_2} (1 - \phi) \omega S^0}{(\mu + \omega)(\mu + \gamma_2 + d)}$, $\mathcal{R}_{0,v} = \frac{\beta_v f_3 (1 - \phi) \omega (\mu + \gamma_1 + d) S^0 + \beta_v (\mu + \gamma_2 + d) [f_1 (\mu + \gamma_1 + d) + f_2 \phi \omega] S^0}{d_v (\mu + \omega) (\mu + \gamma_1 + d) (\mu + \gamma_2 + d)}$ and $\rho(FW^{-1})$ is the spectral radius of FW^{-1} .

The term $\mathcal{R}_{0,e}$ represents the average number of secondary cases caused by one exposed during its infectious period. Then the term $\mathcal{R}_{0,i_1}$ (respectively $\mathcal{R}_{0,i_2}$) represents the average number of secondary cases caused by one infectious timely diagnosis (respectively infectious with delayed diagnosis) during its infectious period. Similarly, the term $\mathcal{R}_{0,v}$ represents the average number of secondary cases caused by one virus in the environment during its infectious period.

The importance of the basic reproduction number is due to the result given in the next Lemma established from Theorem 2 in [23].

Lemma 1. *The DFE Q^0 of the system (1) is locally asymptotically stable whenever $\mathcal{R}_0 \leq 1$ and unstable whenever $\mathcal{R}_0 > 1$.*

The biological meaning of Lemma 1 is that a sufficiently small number of contaminated hosts will not induce an epidemic unless $\mathcal{R}_0 > 1$. Global asymptotic stability (GAS) of the DFE is required to better control the disease. In addition, the expansion of the basin of attraction of Q^0 is a more challenging task for the model under consideration, involving a fairly new result. For this purpose, we will use Theorems 2.1 and 2.2 of [21].

Theorem 1. *If $\mathcal{R}_0 \leq 1$, the DFE Q^0 of the system (1) is GAS in Ω . If $\mathcal{R}_0 > 1$, Q^0 is unstable, the system (1) is uniformly persistent and there exists at least one endemic equilibrium in the interior of Ω .*

The system (1) can be written as

$$\begin{aligned} \frac{dx}{dt} &= (F - W)x - f(x, y), \\ \frac{dy}{dt} &= g(x, y), \end{aligned} \quad (9)$$

where $x = (E, I_1, I_2, H, V)^T$ is the vector representing the infected classes, $y = (S, S_q, R)^T$ is the vector representing the uninfected classes, the matrices F and W are given as in (6) and (7) respectively, and

$$f(x, y) = \begin{bmatrix} \beta_e E(S^0 - S) + \beta_{i_1} I_1(S^0 - S) + \beta_{i_2} I_2(S^0 - S) + \beta_v V(S^0 - S) \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

and

$$g(x, y) = \begin{bmatrix} A - (\beta_e E + \beta_{i_1} I_1 + \beta_{i_2} I_2 + \beta_v V)S + q_1 S_q - (\mu + q)S \\ qS - q_1 S_q - \mu S_q \\ (\beta_e E + \beta_{i_1} I_1 + \beta_{i_2} I_2 + \beta_v V)S - \omega E - \mu E \end{bmatrix}.$$

Then,

$$W^{-1}F = \begin{bmatrix} A\beta_e S^0 & A\beta_{i_1} S^0 & A\beta_{i_2} S^0 & 0 & A\beta_v S^0 \\ B\beta_e S^0 & B\beta_{i_1} S^0 & B\beta_{i_2} S^0 & 0 & B\beta_v S^0 \\ C\beta_e S^0 & C\beta_{i_1} S^0 & C\beta_{i_2} S^0 & 0 & C\beta_v S^0 \\ D\beta_e S^0 & D\beta_{i_1} S^0 & D\beta_{i_2} S^0 & 0 & D\beta_v S^0 \\ E\beta_e S^0 & E\beta_{i_1} S^0 & E\beta_{i_2} S^0 & 0 & E\beta_v S^0 \end{bmatrix},$$

where

$$\begin{aligned} A &= \frac{1}{\mu + \omega}, \quad B = \frac{\phi\omega}{(\mu + \omega)(\mu + \gamma_1 + d)}, \quad C = \frac{(1 - \phi)\omega}{(\mu + \omega)(\mu + \gamma_2 + d)}, \\ D &= \frac{\omega[\gamma_1\phi(\mu + \gamma_2 + d) + \gamma_2(1 - \phi)(\mu + \gamma_1 + d)]}{(\mu + \omega)(\mu + \gamma_1 + d)(\mu + \gamma_2 + d)(\mu + m + d)}, \quad \text{and} \\ E &= \frac{f_3(1 - \phi)\omega(\mu + \gamma_1 + d) + (\mu + \gamma_2 + d)[f_1(\mu + \gamma_1 + d) + f_2\phi\omega]}{d_v(\mu + \omega)(\mu + \gamma_1 + d)(\mu + \gamma_2 + d)}. \end{aligned}$$

Let $(\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)$ be the left eigenvalue of $W^{-1}F$ and be given by

$$\omega_1 = \frac{\beta_e}{\beta_{i_1}}, \quad \omega_2 = 1, \quad \omega_3 = \frac{\beta_{i_1}}{\beta_v}, \quad \omega_4 = 0 \quad \text{and} \quad \omega_5 = 1, \quad (10)$$

since $(\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)W^{-1}F = \mathcal{R}_0(\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)$. We consider the following Lyapunov function

$$Q = (\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)W^{-1}(E, I_1, I_2, H, V)^T = \mathcal{A}E + \mathcal{B}I_1 + \mathcal{C}I_2 + \mathcal{D}V, \quad (11)$$

where $\mathcal{A} = \frac{\mathcal{R}_{0,e}}{\beta_{i_1}S^0} + \frac{\mathcal{R}_{0,i_1}}{\beta_{i_1}S^0} + \frac{\mathcal{R}_{0,i_2}}{\beta_vS^0} + \frac{\mathcal{R}_{0,v}}{\beta_vS^0}$, $\mathcal{B} = \frac{d_v + f_2}{d_v(\mu + \gamma_1 + d)}$, $\mathcal{C} = \frac{\beta_{i_2}d_v + f_3\beta_v}{\beta_vd_v(\mu + \gamma_2 + d)}$ and $\mathcal{D} = \frac{1}{d_v}$. Then the derivative of the Lyapunov function Q yields,

$$Q' = (\mathcal{R}_0 - 1)(\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)^T x - (\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)^T W^{-1}f(x, y).$$

Since $(\omega_1, \omega_2, \omega_3, \omega_4, \omega_5) \geq 0$, $W^{-1} \geq 0$ and $f(x, y) \geq 0$ in Ω , then $(\omega_1, \omega_2)^T W^{-1} f(x, y) \geq 0$. Therefore, $Q' \leq 0$ in Ω if $\mathcal{R}_0 \leq 1$ and Q is a Lyapunov function for the system (1). By La Salle's invariance principle [10,11], Q^0 is GAS in Ω .

If $\mathcal{R}_0 > 1$, then $Q' = (\mathcal{R}_0 - 1)(\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)^T x > 0$ provided that $x > 0$ and $y = (S^0, S_q^0, 0)$. By continuity, $Q' > 0$ in the neighborhood of Q^0 . Solutions in positive cone sufficiently close to Q^0 move away from Q^0 , implying that Q^0 is unstable. Thus, the model system (1) is uniformly persistent [8,12]. Uniform persistence and the positively invariance of Ω imply the existence of an endemic equilibrium. $\square$ As a consequence of this result above,

we can confidently deduce that COVID-19 can be eradicated from the host community if the value of $\mathcal{R}_0$ can be reduced and retained less than the unity. Figure 3 shows the validation of the global stability analysis for the disease-free equilibrium point.

Fig. 3: 3a: Global stability when $\mathcal{R}_0 < 1$, 3b: Global stability when $\mathcal{R}_0 = 1$, in accordance with Theorem 1. Parameter values used are as given in Table 1, except $\gamma_2 = 1/10$, so that $\mathcal{R}_0 = 0.77 < 1$ and $\phi = 0.909$, so that $\mathcal{R}_0 = 0.95 \approx 1$.

5 Endemic equilibrium and its stability

Let $Q^* = (S^*, S_q^*, I_1^*, I_2^*, H^*, R^*, V^*)$ be the positive endemic equilibrium (EE) of model system (1). Then, the positive endemic equilibrium can be obtained by setting the right hand side of all equations in model system (1) to zero, giving:

$$\begin{cases} \Lambda - \lambda^* S^* + q_1 S_q^* - (\mu + q) S^* &= 0, \\ q S^* - q_1 S_q^* - \mu S_q^* &= 0, \\ \lambda^* S^* - \omega E^* - \mu E^* &= 0, \\ \phi \omega E^* - \gamma_1 I_1^* - \mu I_1^* - d I_1^* &= 0, \\ (1 - \phi) \omega E^* - \gamma_2 I_2^* - \mu I_2^* - d I_2^* &= 0, \\ \gamma_1 I_1^* + \gamma_2 I_2^* - m H^* - \mu H^* - d H^* &= 0, \\ m H^* - \mu R^* &= 0, \\ f_1 E^* + f_2 I_1^* + f_3 I_2^* - d_v V^* &= 0, \end{cases} \quad (12)$$

, where $\lambda^* = \beta_e E^* + \beta_{i_1} I_1^* + \beta_{i_2} I_2^* + \beta_v V^*$. Given the complexity of the system (12), we are going to try to determine an explicit formula for the endemic equilibrium point Q^* . To do this, we will

solve the system (12). After algebraic manipulations of this system, we obtain:

$$\begin{aligned} R^* &= \frac{m}{\mu} H^*, E^* = \frac{\mu + \gamma_1 + d}{\phi \omega} I_1^*, I_2^* = \frac{(1 - \phi)(\mu + \gamma_1 + d)}{\phi(\mu + \gamma_2 + d)} I_1^*, S_q^* = \frac{q_1 + \mu}{q} S^*, \\ H^* &= \frac{\gamma_1 \phi(\mu + \gamma_2 + d) + \gamma_2(1 - \phi)(\mu + \gamma_1 + d)}{\phi(\mu + \gamma_2 + d)(\mu + m + d)} I_1^*, \\ V^* &= \frac{f_1(\mu + \gamma_1 + d)(\mu + \gamma_2 + d) + f_2 \phi \omega(\mu + \gamma_2 + d) + f_3(1 - \phi) \omega(\mu + \gamma_1 + d)}{\phi \omega d_v(\mu + \gamma_2 + d)} I_1^*, \\ S^* &= \frac{d_v(\mu + \omega)(\mu + \gamma_1 + d)(\mu + \gamma_2 + d)}{\beta_e d_v(\mu + \gamma_1 + d)(\mu + \gamma_2 + d) + \beta_{i_1} \phi \omega d_v(\mu + \gamma_2 + d) + \beta_{i_2}(1 - \phi) \omega d_v(\mu + \gamma_1 + d)} \\ &\quad + \frac{d_v(\mu + \omega)(\mu + \gamma_1 + d)(\mu + \gamma_2 + d)}{\beta_v f_1(\mu + \gamma_1 + d)(\mu + \gamma_2 + d) + \beta_v f_2 \phi \omega(\mu + \gamma_2 + d) + \beta_v f_3(1 - \phi) \omega(\mu + \gamma_1 + d)}, \end{aligned}$$

and

$$I_1^* = \frac{\phi \omega [(q + \mu)(q_1 + \mu) - q q_1]}{(q_1 + \mu)(\mu + \omega)(\mu + \gamma_1 + d)} S^* (\mathcal{R}_0 - 1).$$

Lemma 1. *Model (1) has exactly one endemic equilibrium whenever $\mathcal{R}_0 > 1$.*

We establish the following result to analyze the stability of Q^* .

Theorem 1. *If $\mathcal{R}_0 > 1$, the endemic equilibrium Q^* is GAS in Ω .*

Consider the following Lyapunov function candidate:

$$\begin{aligned} L &= \left(S - S^* - S^* \ln \frac{S}{S^*} \right) + h_1 \left(S_q - S_q^* - S_q^* \ln \frac{S_q}{S_q^*} \right) + h_2 \left(E - E^* - E^* \ln \frac{E}{E^*} \right) \\ &\quad + h_3 \left(I_1 - I_1^* - I_1^* \ln \frac{I_1}{I_1^*} \right) + h_4 \left(I_2 - I_2^* - I_2^* \ln \frac{I_2}{I_2^*} \right) + h_5 \left(V - V^* - V^* \ln \frac{V}{V^*} \right), \end{aligned} \quad (13)$$

where h_1, h_2, h_3, h_4 and h_5 are positive constants to be determined later. Differentiating the function (13) with respect to time yields

$$\dot{L} = \left(1 - \frac{S^*}{S} \right) \dot{S} + h_1 \left(1 - \frac{S_q^*}{S_q} \right) \dot{S}_q + h_2 \left(1 - \frac{E^*}{E} \right) \dot{E} + h_3 \left(1 - \frac{I_1^*}{I_1} \right) \dot{I}_1 + h_4 \left(1 - \frac{I_2^*}{I_2} \right) \dot{I}_2 + h_5 \left(1 - \frac{V^*}{V} \right) \dot{V}. \quad (14)$$

Substituting equation (1) into equation (14) and using Equation (12) at the positive endemic equilibrium with further simplification yields

$$\begin{aligned} \dot{L} &= - (q_1 + \mu) \left(1 - \frac{1}{x_1} \right)^2 S + \beta_e S^* E^* \left(1 - \frac{1}{x_1} + x_3 - x_1 x_3 \right) + \beta_{i_1} S^* I_1^* \left(1 - \frac{1}{x_1} + x_4 - x_1 x_4 \right) \\ &\quad + \beta_{i_2} S^* I_2^* \left(1 - \frac{1}{x_1} + x_5 - x_1 x_5 \right) + \beta_v S^* V^* \left(1 - \frac{1}{x_1} + x_6 - x_1 x_6 \right) + q_1 S_q^* \left(x_2 + \frac{1}{x_1} - \frac{x_2}{x_1} - 1 \right) \\ &\quad + h_1 q S^* \left(x_1 - x_2 - \frac{x_1}{x_2} + 1 \right) + h_2 \beta_e S^* E^* \left(1 - x_1 - x_3 + x_1 x_3 \right) + h_2 \beta_{i_1} S^* I_1^* \left(1 - x_3 + x_1 x_4 - \frac{x_1 x_4}{x_3} \right) \\ &\quad + h_2 \beta_{i_2} S^* I_2^* \left(1 - x_3 + x_1 x_5 - \frac{x_1 x_5}{x_3} \right) + h_2 \beta_v S^* V^* \left(1 - x_3 + x_1 x_6 - \frac{x_1 x_6}{x_3} \right) \\ &\quad + h_3 \phi \omega E^* \left(1 + x_3 - x_4 - \frac{x_3}{x_4} \right) + h_4 (1 - \phi) \omega E^* \left(1 + x_3 - x_5 - \frac{x_3}{x_5} \right) + h_5 f_1 E^* \left(1 + x_3 - x_6 - \frac{x_3}{x_6} \right) \end{aligned}$$

$$+ h_5 f_2 I_1^* \left(1 + x_4 - x_6 - \frac{x_4}{x_6}\right) + h_5 f_3 I_2^* \left(1 + x_5 - x_6 - \frac{x_5}{x_6}\right), \quad (15)$$

where $x_1 = \frac{S}{S^*}$, $x_2 = \frac{S_q}{S_q^*}$, $x_3 = \frac{E}{E^*}$, $x_4 = \frac{I_1}{I_1^*}$, $x_5 = \frac{I_2}{I_2^*}$ and $x_6 = \frac{V}{V^*}$. Then equation (15) becomes

$$\begin{aligned} \dot{L} = & - (q_1 + \mu) \left(1 - \frac{1}{x_1}\right)^2 S + \beta_e S^* E^* + \beta_{i_1} S^* I_1^* + \beta_{i_2} S^* I_2^* + \beta_v S^* V^* - q_1 S_q^* + h_1 q S^* \\ & + h_2 \beta_e S^* E^* + h_2 \beta_{i_1} S^* I_1^* + h_2 \beta_{i_2} S^* I_2^* + h_2 \beta_v S^* V^* + h_3 \phi \omega E^* + h_4 (1 - \phi) \omega E^* + h_5 f_1 E^* \\ & + h_5 f_2 I_1^* + h_5 f_3 I_2^* + \left(-\beta_e S^* E^* - \beta_{i_1} S^* I_1^* - \beta_{i_2} S^* I_2^* - \beta_v S^* V^* + q_1 S_q^* \right) \frac{1}{x_1} \\ & + (h_1 q S^* - h_2 \beta_e S^* E^*) x_1 + (q_1 S_q^* - h_1 q S^*) x_2 + (\beta_e S^* E^* - h_2 \beta_e S^* E^* - h_2 \beta_{i_1} S^* I_1^* \\ & - h_2 \beta_{i_2} S^* I_2^* - h_2 \beta_v S^* V^* + h_3 \phi \omega E^* + h_4 (1 - \phi) \omega E^* + h_5 f_1 E^*) x_3 \\ & + (\beta_{i_1} S^* I_1^* - h_3 \phi \omega E^* + h_5 f_2 I_1^*) x_4 + (\beta_{i_2} S^* I_2^* + h_4 (1 - \phi) \omega E^* + h_5 f_3 I_2^*) x_5 \\ & + (\beta_v S^* V^* - h_5 f_1 E^* - h_5 f_2 I_1^* - h_5 f_3 I_2^*) x_6 + (-\beta_e S^* E^* + h_2 \beta_e S^* E^*) x_1 x_3 \\ & + (-\beta_{i_1} S^* I_1^* + h_2 \beta_{i_1} S^* I_1^*) x_1 x_4 + (-\beta_{i_2} S^* I_2^* + h_2 \beta_{i_2} S^* I_2^*) x_1 x_5 \\ & + (-\beta_v S^* V^* + h_2 \beta_v S^* V^*) x_1 x_6 - q_1 S_q^* \frac{x_2}{x_1} + h_1 q S^* \frac{x_1}{x_2} - h_3 \phi \omega E^* \frac{x_3}{x_4} - h_4 (1 - \phi) \omega E^* \frac{x_3}{x_5} \\ & - h_5 f_1 E^* \frac{x_3}{x_6} - h_5 f_2 I_1^* \frac{x_4}{x_6} - h_5 f_3 I_2^* \frac{x_5}{x_6} - h_2 \beta_{i_1} S^* I_1^* \frac{x_1 x_4}{x_3} - h_2 \beta_{i_2} S^* I_2^* \frac{x_1 x_5}{x_3} - h_2 \beta_v S^* V^* \frac{x_1 x_6}{x_3}. \end{aligned} \quad (16)$$

Considering the expressions

$$h_2 \beta_e S^* E^* = \beta_e S^* E^*, \quad h_2 \beta_{i_1} S^* I_1^* = \beta_{i_1} S^* I_1^*, \quad h_2 \beta_{i_2} S^* I_2^* = \beta_{i_2} S^* I_2^*, \quad \text{and} \quad h_2 \beta_v S^* V^* = \beta_v S^* V^*,$$

we have $h_2 = 1$, thus the coefficients of $x_1 x_3$, $x_1 x_4$, $x_1 x_5$ and $x_1 x_6$ are all 0. By setting the coefficients of x_2 , x_3 , x_4 , x_5 , and x_6 to 0 and solving for h_1 , h_3 , h_4 and h_5 yields

$$\begin{aligned} h_1 &= \frac{q_1 S_q^*}{q S^*}, \quad h_3 = \frac{\beta_{i_1} S^* I_1^* (f_1 E^* + f_2 I_1^* + f_3 I_2^*) + \beta_v f_2 S^* V^* I_1^*}{\phi \omega E^* (f_1 E^* + f_2 I_1^* + f_3 I_2^*)}, \\ h_4 &= \frac{\beta_{i_2} S^* I_2^* (f_1 E^* + f_2 I_1^* + f_3 I_2^*) + \beta_v f_3 S^* V^* I_1^*}{(1 - \phi) \omega E^* (f_1 E^* + f_2 I_1^* + f_3 I_2^*)} \quad \text{and} \quad h_5 = \frac{\beta_v S^* V^*}{f_1 E^* + f_2 I_1^* + f_3 I_2^*}. \end{aligned}$$

Therefore, $\dot{L}$ can be rewritten as

$$\begin{aligned} \dot{L} = & - (q_1 + \mu) \left(1 - \frac{1}{x_1}\right)^2 S - \beta_e S^* E^* \left(x_1 + \frac{1}{x_1} - 2\right) \\ & - \beta_{i_1} S^* I_1^* \left(x_3 - x_4 + \frac{1}{x_1} + \frac{x_1 x_4}{x_3} - 2\right) - \beta_{i_2} S^* I_2^* \left(x_3 - x_5 + \frac{1}{x_1} + \frac{x_1 x_5}{x_3} - 2\right) \\ & - \beta_v S^* V^* \left(x_3 - x_6 + \frac{1}{x_1} + \frac{x_1 x_6}{x_3} - 2\right) - q_1 S_q^* \left(\frac{x_1}{x_2} + \frac{x_2}{x_1} - x_1 - \frac{1}{x_1}\right) \\ & - h_3 \phi \omega E^* \left(x_4 - x_3 - 1 + \frac{x_3}{x_4}\right) - h_4 (1 - \phi) \omega E^* \left(x_5 - x_3 - 1 + \frac{x_3}{x_5}\right) \\ & - h_5 f_1 E^* \left(x_6 - x_3 - 1 + \frac{x_3}{x_6}\right) - h_5 f_2 I_1^* \left(x_6 - x_4 - 1 + \frac{x_4}{x_6}\right) - h_5 f_3 I_2^* \left(x_6 - x_5 - 1 + \frac{x_5}{x_6}\right). \end{aligned}$$

Thus, using the arithmetic-geometric means inequality, we can see that $\dot{L}$ is less or equal to zero with equality only if $x_1 = 1$, $x_2 = 1$, $x_3 = 1$, $x_4 = 1$, $x_5 = 1$ and $x_6 = 1$. By LaSalle's invariance principle the largest invariant set in Ω , contained in

$$\{(S, S_q, E, I_1, I_2, H, R, V) \in \Omega \mid \dot{L} = 0\}$$

is reduced to the endemic equilibrium Q^* . Then, we conclude that the endemic equilibrium is globally asymptotically stable in Ω [5,22]. $\square$

Figure 4 shows the validation of the global stability analysis for the endemic equilibrium point.

Fig. 4: Global stability when $\mathcal{R}_0 > 1$, in accordance with Theorem 1. Parameter values used are as given in Table 1, except $\phi = 0.8$, so that $\mathcal{R}_0 = 2.06 > 1$.

6 Numerical Results

In this section, we present numerical simulations of the proposed model (1) using parameter estimates from COVID-19 data for Ghana [24]. In Figure 5, we present the fitted model, the cumulative cases and residual plot for Ghana using 100 data points. The initial conditions are taken on the date of the first confirmed cases i.e. 12th March, 2020. The incubation periods of COVID-19 is known to be 2–14 days. On 12th March, 2020, the first two COVID-19 cases was reported in Ghana, hence, we took the initial hospitalized to be two i.e. $H(0) = 2$, the total population of Ghana was 30,417,856. It is assumed that, there were no recoveries, but equal number of exposed, timely, and delayed people as the first two detected cases during the initial stages. Therefore, the initial values for Ghana are given by $S(0) = 30,417,848$ and $S_q(0) = 0$, $E(0) = 2$, $I_1(0) = 2$, $I_2(0) = 2$, $H(0) = 2$, $R(0) = 0$, $V(0) = 0$. From the data fitting, as shown in Figure 5 and Table 2, the computed reproduction number, $\mathcal{R}_0$, for the 100 data points is given as $\mathcal{R}_c = 1.0410$. In what follows, we show the global sensitivity analysis and other numerical outputs of the model using the obtained parameters in Table 1.

7 Global sensitivity analysis

In this section we obtained the graphical representation for the 18 parameters in basic reproduction number, $\mathcal{R}_0$, using scatter plots and Latent Hypercube Sampling (LHS). Scatter plots are used to obtain the correlations of the various parameters in the basic reproduction number, $\mathcal{R}_0$. It also gives undeniable visual connection of the various parameters in $\mathcal{R}_0$. It can vary from -1 (perfect negative

Fig. 5: Model fit for Ghana during the time window 12 March, 2020 to 19 June, 2020 .

Table 2: Model parameters for the COVID-19 in Ghana

Parameter	Value	Source
Λ	1319.294	[18]
q	0.0333	Fitted
q_1	1.6945×10^{-5}	Estimated
β_e	6.0380×10^{-8}	Fitted
β_{i_1}	3.8196×10^{-8}	Fitted
β_{i_2}	1.4286×10^{-5}	Fitted
β_v	4.00199×10^{-8}	[4]
ω	1/5.2	[20]
ϕ	0.9000	Fitted
γ_1	0.5000	Fitted
γ_2	0.0714	Fitted
μ	4.2578×10^{-5}	[20]
d	0.006139	Estimated
m	0.9815	Fitted
f_1	0.0178	Fitted
f_2	0.3115	Fitted
f_3	4.6131×10^{-5}	Fitted
d_v	0.3117	[17]

correlation) through 0 (no correlation) to +1 (perfect positive correlation). LHS is known to be a Monte Carlo sampling method. It divides the various parameters into equal even intervals and indiscriminately draws one sample from each equal interval once. LHS is usually carried out with partial rank correlation coefficient (PRCC) to estimate the nonlinearity between the parameters, and also the unmodulated, relationship between model parameters [3,25]. Using the LHS with 2500 samples from a uniform distribution, the parameters in the basic reproduction number $\mathcal{R}_0$, were employed to obtain the global sensitivity of the various parameters in $\mathcal{R}_0$. Figures 6a to 6c depict the scatter relation of the various parameters in the basic reproduction number. particularly, Figure 6a shows the relation of $\Lambda, q_1, \mu, q, \omega$, and d_v to the logarithmic relation of $\mathcal{R}_0$. We realise that each sample point in Λ and μ has a 100% clear direction with the basic reproduction number. Figures 6b and 6c give an undetermined relation of the other parameters to $\mathcal{R}_0$. Using the PRCC plot in Figure 6d, we noticed that the parameters contributing to the growth of the basic reproduction number are

$\Lambda, \beta_e, q_1, d, f_2, \beta_{i_2}, f_1, \gamma_2, f_3$, and β_{i_1} (ordered in order of magnitude). While, $\phi, q, \omega, \gamma_1, \mu, d_v, d$ and m , contribute to the decline of the basic reproduction number, $\mathcal{R}_0$ (ordered in order of magnitude). Among the positive parameters, Λ and β_e are the most dominant parameters, hence it suggests that a reduction in the number of new inflow Λ , and the interaction of exposed individuals β_e , in the population will reduce the rate of the virus spread in the local community or the basic reproduction number faster then the other parameters. Among the negative parameters, ϕ, q, ω and γ_1 are the most dominant parameters, hence, it suggest that, an increase in these parameters will reduce the rate of the virus spread in the local community or the basic reproduction number faster then the other parameters, μ, d_v, d and m . Therefore, in Figures 7 and 8 we show the graphical trajectories of the parameters on the infected classes.

Fig. 6: Global sensitivity analysis plot for COVID-19 model with timely-delayed diagnosis

In Figures 7a-7d, we show the impact of the rate of recruitment Λ , and the rate of relative transmissibility of exposed individuals β_e , on the model. We noticed in Figure 7a that an increase in Λ , will have a direct increase in the number of new infections whiles Figure 7b shows that, a decline in Λ , will help eradicate the disease in Ghana. In Figures 7c and 7d, we notice that an

Fig. 7: Sensitivity analysis plot for COVID-19 model with timely-delayed diagnosis, using Λ , and β_e .

increase in the relative transmissibility of exposed individuals will have an exponential growth in the number of secondary infections. Hence, we suggest that all persons should keep to the regular washing of hands with soap and alcohol based sanitizer whenever they use public facilities, since this will help reduce the spread of the virus by exposed individuals. In Figures 8a and Figure 8b, we showed the dynamical effects of varying the proportion of the infectious with timely diagnosis and self-quarantined rate of the susceptible individuals. Figure 8a indicates that, an increase in the proportion of the infectious with timely diagnosis reduces the basic reproduction number and that a 100% detection of infected individuals on time will have the basic reproduction reducing to 0.025, resulting in a complete eradication of the disease within 100 days. In Figure 8b we noticed that the willingness of individuals to practice self-quarantine has a major role in reducing the disease spread in Ghana. In Figure 8c we show the dynamical effect of incubation period of the disease on the number of timely-delayed diagnosis individuals. We noticed that an increase in the number of incubation period reduce the number of timely-delayed diagnosis individuals. Figure 8d shows the dynamical effects of delayed diagnosis on the number of exposed individuals. The Figure 8d shows

that, a reduction in time delayed reduces the number of exposed individuals, hence, we suggest that the government should increase their efforts in diagnoses so to reduce the number of infected individuals in each community.

Fig. 8: Sensitivity analysis plot for COVID-19 model with timely-delayed diagnosis, using ϕ, q, ω and γ_2 .

8 Conclusion

In this article, we presented a COVID-19 model that considers self-quarantined individuals, delay in diagnosis and environmental transmission and analysed the transmission dynamics of the pandemic in Ghana. The global stability analysis of the proposed model was shown to be globally asymptotically stable when $R_0 \leq 1$ and when $R_0 > 1$. The numerical simulations of the model suggest that, the recruitment rate positively increase the number of new infections, likewise the rate of transmissibility of exposed individuals. Figure 7c and 7d shows that, an increase in the relative transmissibility of exposed individuals will have an exponential growth in the number of secondary

infections. Hence, we suggest that all persons should keep to the regular washing of hands with soap and alcohol based sensitizer whenever they use public facilities, since this will help reduce the spread of the virus by expose individuals. We also noticed from Figure 8d that, timely diagnosis can reduce the number of exposed individuals in Ghana, hence, we suggest that the government should increase their efforts in diagnoses so to reduce the number of infected individuals in each community.

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Figures

Figure 1

Logistic model t and cumulative trajectories for reported cases for Ghana.

Figure 2

Diagram of COVID-19 Dynamics.

Figure 3

3a: Global stability when $R_0 < 1$, 3b: Global stability when $R_0 = 1$, in accordance with Theorem 1. Parameter values used are as given in Table 1, except $\beta_2 = 10$, so that $R_0 = 0.77 < 1$ and $\beta_2 = 0.909$, so that $R_0 = 0.95 < 1$.

Figure 4

Global stability when $R_0 > 1$, in accordance with Theorem 1. Parameter values used are as given in Table 1, except $\beta = 0.8$, so that $R_0 = 2.06 > 1$.

(a) Model fit

(b) Residual plot.

Figure 5

Model fit for Ghana during the time window 12 March, 2020 to 19 June, 2020 .

Figure 6

Global sensitivity analysis plot for COVID-19 model with timely-delayed diagnosis

(a)

(b)

(c)

(d)

Figure 7

Sensitivity analysis plot for COVID-19 model with timely-delayed diagnosis, using A ; and e .

Figure 8

sensitivity analysis plot for COVID-19 model with timely-delayed diagnosis, using ϕ ; q ; ω and γ_2 .