International Journal of Modern Computation, Information and Communication Technology 2021;4(1):18-24.
ISSN: 2581-5954
http://ijmcict.gjpublications.com

Research Article

Stability analysis of COVID-19 Model under certain constraints

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Abstract

In the present work, we present a mathematical model for the transmission dynamics of COVID-19 under certain constraints. The model formulated is designed into compartments which lead to a system of differential equations for the transmission dynamics of COVID-19 with control measures. The stabilities of the model are investigated at several instances. The results showed that the disease free equilibrium is locally asymptotically stable under assumed conditions on the parameters given in the model. It was then concluded from the results that putting on masks, proper and frequent sanitation and educational sensitization are effective methods of controlling COVID-19.

Keywords: COVID-19; Equilibrium; Control strategies; Stability.

Introduction

COVID-19 has been a persistent pandemic and continues to be a global world health issue. Despite the studies on this disease for over one year, it is estimated that approximately millions of people have died from COVID-19 and the dynamics of the disease indicate that it is intimately linked to serious inadequate access to clean water, of access to essential health services. Most cases of COVID-19 currently occur in developed countries. Currently, COVID-19 is severe in India and Bangladesh near the Bay of Bengal as well as in coastal regions of South America [1-7]. Cases in these regions tend to have seasonal circles, generally associated with fluctuations in water temperature, zooplankton levels and monsoon cycles [8].

These pandemics tend to coincide with dry weather and higher water temperatures while cases are reduced in winter. Preventative measures include vaccination, putting on masks, and washing hands well- all of which is assumed that people have easy access to these resources but since most existing models exclude the use of education based intervention in passing down the aforementioned strategies in fighting against the propagation of infectious diseases, this work is aimed to better understand the effects of this measure so as to gain useful guidelines to the effective prevention and intervention strategies against COVID-19.

Model formulation

In this study, we consider the SIRP epidemiological model for COVID-19 transmission by making reasonable improvement on the work of Fatima and Isthrinayagy [8] with the incorporation of human treatment, masking, sanitation and education based intervention which is assumed to be the control strategies. Consequently, we introduce another compartment into the model: the concentration of COVID-19 on body surface at time (t) denoted by $C_v(t)$. Let $S_H(t)$, $I_H(t)$, $R_H(t)$ and $P_H(t)$ represent the susceptible, the infected, recovered and the protected human populations respectively. The total human $N_H(t) = S_H + I_H + R_H + P_H$ is closed, which is a reasonable assumption for a relatively short period of time and for low mortality diseases like COVID-19. Various parameters and definitions are given in table 1.

The Susceptible population is generated either through birth or through immigration at rate Λ_H.They acquire infection and move to infected class at the rate:

Received: 30.04.2021; Received after Revision: 21.05.2021; Accepted: 23.05.2021
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$$\alpha = \frac{q_1 C_V}{C_V + K} + q_2 I_H \quad (1)$$

Where $q_1 and\ q_2$ = rates of attracting COVID-19 virus from the water droplets on body surfaces and through human to human interaction respectively.
C_v =Concentration of COVID-19 virus in body surface.
K = Concentration of COVID-19 in water droplets that yields 90% chance of getting it.
I_H = Total number of infected individuals.

Table 1. Parameters and definitions

Symbols	Definitions
Λ_H	Per capital birth rate of humans.
μ_H	Per capital natural death rate of humans.
d_H	COVID-19 induced death rate.
α_H	Rate of exposure to contaminated water.
ρ_H	Loss rate of immunity by recovered individuals.
β_H	Natural recovery rate.
ε	Rate of contribution of each infected person to the population of COVID-19 in the water droplets.
z_H	Recovery due to the use of treatment.
M	COVID-19 growth rate.
N	COVID-19 loss rate.
φ	Net death rate of COVID-19 ie m-n.
γ_H	Rate of exposure to education and its compliance.
η	Rate of death of COVID-19 as a result of water treatment.
K	Concentration of COVID-19 in water droplets that yield 90% chance of getting it.
$q_1$andq_2.	Rates of attracting COVID-19 from the body surface.

The number of infected individuals decreases through natural recovery from the disease at the rate of β_H and Z_H is the recovery due to the use of treatments. μ_H is natural death of an individual andd_H is the death rate induced by the disease. ρ_HIs the loss rate of immunity by the recovered individuals, ε is the rate of contribution of each infected person to the population of COVID-19 in the aquatic environment. ω is the net death rate of COVID-19 gotten by ω = m – n, where m is the COVID-19 growth rate and n is the COVID-19 loss rate.

Variables

S_H = Total number of susceptible individuals.
I_H = Total number of infected individuals.
R_H =Total number of recovered individuals.
P_H = The human population called the protected population.
N_H =Total population of humans.
C_V= Concentration of COVID-19 in body surface.

The compartmental diagram

The model assumptions are as follows:

a. Susceptible individuals acquire Cholera at a constant rate.
b. The death in the Infectious class is not only due to the infection but also natural.
c. Water treatment leads to the death of the COVID-19.
d. All parameters are considered non-negative.

Fig. 1 illustrates the compartmental flow diagram.

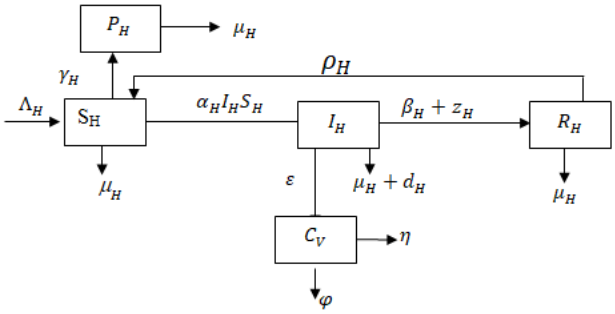

Fig. 1. Compartmental flow diagram

From the analysis and assumptions the following system is obtained:

$$\frac{dS_H}{dt} = \Lambda_H + \rho_H R_H - (\mu_H + \gamma_H) S_H - \frac{q_1 C_V}{C_V + K} S_H - q_2 I_H S_H \quad (2)$$

$$\frac{dI_H}{dt} = \frac{q_1 C_V}{C_V + K} S_H + q_2 I_H S_H - (\mu_H + d_H + \beta_H + z_H + \varepsilon) I_H \quad (3)$$

$$\frac{dR_H}{dt} = \beta_H R_H + z_H R_H - \mu_H R_H - \rho_H R_H \quad (4)$$

$$\frac{dP_H}{dt} = \gamma_H S_H - \mu_H P_H \quad (5)$$

$$\frac{dC_V}{dt} = \varepsilon I_H - (\varphi + \eta) C_V \quad (6)$$

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Invariant Region: All state variables remain non-negative all the time such that

$S_H(0) \geq 0, I_H(0) \geq 0, R_H(0) \geq 0, P_H(0) \geq 0, C_V \geq 0. \text{and} q_1 > q_2$ (7)

Existence of solution

The following theorem validates the existence of solution of the above models

Theorem 2.1. *Derrick and Groosman [10]*.Given IVP

$x' = f(t,x), \quad x(t_0) = x_0$ (8)

Let**D**denotes region

$|t - t_0| \leq a, \|x - x_0\| \leq b, x = (x_1, x_2, \dots, x_n)$

and suppose that $f(t,x)$ satisfies the Lipchitz condition

$\|f(t,x_1) - f(t,x_2)\| \leq k\|x_1 - x_2\|$ (9)

Whenever the pairs $(t,x_1)$and(t,x_2) belong to **D**, where$k$is a positive constant. Then, there is a constant $\delta > 0$ such that there exists a unique continuous vector solution $x(t)$ of the system in the interval$|t - t_0| \leq \delta$. The condition (9) is satisfied by the requirement that $\frac{\partial f_i}{\partial x_j}, i.j = 1,2, \dots, n$ be continuoous and bounded in D.

Theorem 2.2 (Uniqueness of solution) [9, 15, 16].

Let**D** denotes the region defined by $1 \leq \varepsilon \leq R$ such that$0 < R < \infty$,hold, then the solution of (2)-(6) is unique and bounded in the region**D**.

Proof

Let

$f_1 = \Lambda_H + \rho_H R_H - (\mu_H + \gamma_H)S_H - \frac{q_1 C_V}{C_V + K} S_H - q_2 I_H S_H.$ (10)

$f_2 = \frac{q_1 C_V}{C_V + K} S_H + q_2 I_H S_H - (\mu_H + d_H + \beta_H + Z_H + \varepsilon) I_H.$ (11)

$f_3 = \beta_H R_H + Z_H R_H - \mu_H R_H - \rho_H R_H.$ (12)

$f_4 = \gamma_H S_H - \mu_H P_H$ (13)

$f_5 = \varepsilon I_H - (\varphi + \eta) C_V$ (14)

It suffices to show that $\frac{\partial f_i}{\partial x_j}, i,j = 1,2, \dots .5$ are continuous.

Consider the partial derivatives:

For f_1;

$|\partial f_1/\partial S_H| = |-(\mu_H + \gamma_H)|.$

$|\partial f_1/\partial I_H| = 0 < \infty = |\partial f_1/\partial R_H| = |\partial f_1/\partial P_H| = |\partial f_1/\partial C_V|.$

Similarly;

$|\partial f_2/\partial I_H| = |-(\mu_H + d_H + \beta_H + Z_H + \varepsilon)|.$

$|\partial f_2/\partial S_H| = 0 < \infty = |\partial f_2/\partial R_H| = |\partial f_2/\partial P_H| = |\partial f_2/\partial C_V|.$

Similarly;

$|\partial f_3/\partial R_H| = |\beta_H + Z_H - \mu_H - \rho_H|.$

$|\partial f_3/\partial S_H| = 0 < \infty = |\partial f_3/\partial I_H| = |\partial f_3/\partial P_H| = |\partial f_3/\partial C_V|.$

Similarly;

$|\partial f_4/\partial P_H| = |-\mu_H|.$

$|\partial f_4/\partial S_H| = 0 < \infty = |\partial f_4/\partial I_H| = |\partial f_4/\partial R_H| = |\partial f_4/\partial C_V|.$

Finally;

$|\partial f_5/\partial C_V| = |-\varphi|.$

$|\partial f_5/\partial S_H| = 0 < \infty = |\partial f_5/\partial I_H| = |\partial f_5/\partial R_H| = |\partial f_5/\partial P_H|.$

It is clearly seen that the partial derivatives are continuous and bounded, implying that the solutions for (2)-(6) exists and are unique in the region D. Thus, the proof is complete.

Equilibrium state of the model

To show the disease-free equilibrium for the system (2)-(6), here, setting$\frac{N_H}{dt} = 0$, implying

$$\frac{dS_H}{dt} = \frac{dI_H}{dt} = \frac{dR_H}{dt} = \frac{dP_H}{dt} = \frac{dC_V}{dt} = 0$$

For disease-free state,

$$I_H = R_H = C_V = 0.$$

So that (2)-(6) has a disease free equilibrium state of the form:

$E_0 = (S_H, I_H, R_H, P_H, C_V) = \left(\frac{\Lambda_H}{\mu_H + \gamma_H}, 0, 0, \frac{\gamma_H \Lambda_H}{\mu_H(\mu_H + \gamma_H)}, 0\right)$ (15)

Estimation of the Basic Reproduction Number

The basic reproduction number denoted by R_0 is an important parameter used to study the behavior of model, this is defined as the expected number of secondary cases produced in a completely susceptible population, by a typical infective individual. This is a threshold that determines whether or not; an infection will spread through a given population.

$n = 1, m = 3$ so that $x = (I_H), Y = (S_H + R_H + P_H)$

where

$X = \{x_1, x_2, \dots, x_n\}$ represents n – infected host compartments.

$Y = \{y_1, y_2, \dots, y_n\}$ represent m – other host compartments.

$\frac{dx_i}{dt} = F_i(x,y) - V_i(x,y),$

$i = 1, \dots, n, \ \frac{dy_j}{dt} = G_j(x,y), \ j = 1, \dots, m$

F_i = rate at which new infected enter compartment i.

V_i= rate at which transfer of individuals out of and into ith compartments.

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$$\frac{dx}{dt} = F(x) - V(x)$$

$$F_i = \left(\frac{q_1 C_V}{C_V + K} + q_2 I_H\right) S_H; \quad V_i = (\mu_H + d_H + \beta_H + Z_H + \varepsilon) I_H$$

$$G_1 = \Lambda_H - \rho_H R_H - \left(\mu_H + \gamma_H + \frac{q_1 C_V}{C_V + K} + q_2 I_H\right) S_H$$

$$G_2 = (\beta_H + Z_H) R_H - (\mu_H + \rho_H) R_H$$

$$G_3 = \gamma_H S_H - \mu_H P_H$$

$$F = \begin{pmatrix} q_2 S_H & \frac{q_1 K S_H}{(C_V + K)^2} \\ 0 & 0 \end{pmatrix} \quad (16)$$

$$V = \begin{pmatrix} \mu_H + d_H + \beta_H + Z_H + \varepsilon & 0 \\ \varepsilon & (\varphi + \eta) \end{pmatrix} \quad (17)$$

$$R_0 = FV^{-1} = \begin{pmatrix} q_2 S_H & \frac{q_1 K S_H}{(C_V + K)^2} \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{\mu_H + d_H + \beta_H + Z_H + \varepsilon} & 0 \\ \frac{\varepsilon}{(\mu_H + d_H + \beta_H + Z_H + \varepsilon)} & \frac{1}{(\varphi - \eta)} \end{pmatrix}$$

The reproduction number with control measure is given *as*:

$$R_0 = \frac{q_1 k S_H}{(C_V + k)^2 (\varphi + \eta)} \quad (18)$$

if $R_0 < 1$ ⇒Asymptotically stable,$R_0 > 1$ ⇒ unstable.

Local Stability of the Disease-Free Equilibrium (DFE)

In what follows, the local stability of the DFE is established

Theorem 3.1[15-18]

The disease free-equilibrium of (2)-(6) is locally asymptotically stable if$R_0 < 1$and unstable otherwise.

Proof

The variational (Jacobian matrix) of the system formed by (2)-(6) at $E_0 = \left(\frac{\Lambda_H}{\mu_H + \gamma_H}, 0, 0, \frac{\gamma_H \Lambda_H}{\mu_H(\mu_H + \gamma_H)}, 0\right)$ is given by:

$$\frac{\partial f_1}{\partial S_H} = -(\mu_H + \gamma_H), \quad \frac{\partial f_1}{\partial I_H} = -q_2 S_H, \quad \frac{\partial f_1}{\partial R_H} = \rho_H, \frac{\partial f_1}{\partial C_V} = \frac{q_1 K S_H}{(C_V + K)^2}$$

$$\frac{\partial f_2}{\partial S_H} = \left(\frac{q_1 C_V}{C_V + K} + q_2 I_H\right), \quad \frac{\partial f_2}{\partial I_H} = q_2 S_H - (\mu_H + d_H + \beta_H + Z_H + \varepsilon),$$

$$\frac{\partial f_2}{\partial C_V} = \frac{q_1 K S_H}{(C_V + K)^2}, \quad \frac{\partial f_3}{\partial R_H} = \beta_H + Z_H - \mu_H - \rho_H$$

$$\frac{\partial f_4}{\partial S_H} = \gamma_H, \quad \frac{\partial f_4}{\partial P_H} = -\mu_H$$

$$\frac{\partial f_5}{\partial I_H} = \varepsilon, \quad \frac{\partial f_5}{\partial C_V} = -(\varphi + \eta)$$

At disease free state E_0:

$$\begin{pmatrix} -(\mu_H + \gamma_H) & \frac{-q_2 \Lambda_H}{\mu_H + \gamma_H} & \rho_H & 0 & 0 \\ 0 & \frac{q_2 \Lambda_H}{\mu_H + \gamma_H} - (\mu_H + d_H + \beta_H + z_H + \varepsilon) & 0 & 0 & 0 \\ 0 & 0 & \beta_H + z_H - \mu_H - \rho_H & 0 & 0 \\ \mu_H & 0 & 0 & -\mu_H & 0 \\ 0 & \varepsilon & 0 & 0 & -(\varphi + \eta) \end{pmatrix}$$

The characteristic equation using $|A - 1\lambda|$, we obtain

$$-(\mu_H + \gamma_H + \lambda) \begin{vmatrix} \frac{q_2 \Lambda_H}{\mu_H + \gamma_H} - (\mu_H + d_H + \beta_H + z_H + \varepsilon + \lambda) & 0 & 0 & 0 \\ 0 & \beta_H + z_H - \mu_H - \rho_H - \lambda & 0 & 0 \\ 0 & 0 & -(\mu_H + \lambda) & 0 \\ \varepsilon & 0 & 0 & -(\varphi + \eta + \lambda) \end{vmatrix} = 0$$

From which the following eigenvalues are obtained

$$\lambda_1 = -(\mu_H + \gamma_H), \lambda_2 = -\mu_H, \lambda_3 = (\varphi + \eta), \lambda_4 = \beta_H + Z_H - \mu_H - \rho_H$$

So that

$$\left(\frac{q_2 \Lambda_H}{\mu_H + \gamma_H} - (\mu_H + d_H + \beta_H + Z_H + \varepsilon)\right) < 0 \quad (19)$$

So that

Dividing both side of (19) by $(\mu_H + d_H + \beta_H + Z_H + \varepsilon)$we obtain

$$\frac{q_2 \Lambda_H}{(\mu_H + \gamma_H)(\mu_H + d_H + \beta_H + Z_H + \varepsilon)} < 1 \quad (20)$$

Biologically, by **Theorem 3.1**, COVID-19 can be removed from the community (when$R_0 < 1$) if the initial mass of the population of the model are in the basin of attraction of E_0. To ensure that elimination of COVID-19 is independent of the initial sizes of the populations. It is necessary to show that the disease-free equilibrium is globally asymptotically stable.

Conditions for Global Stability of the disease free-equilibrium

In this section, conditions that if met, guarantee the global asymptotic stability of the disease free state are listed. Set the model equation in the form:

$$\frac{dx}{dt} = F(X, Z) \quad (21)$$

$$\frac{dz}{dt} = G(X, Z), \quad G(X, 0) = 0.$$

Where $X \in R^m$ denotes the number of uninfected individuals and $Z \in R^n$denotes the number of /infected individuals including the latent, infectious etc.$U_0 = (x^*, 0)$ denotes the disease free equilibrium of this system.

The conditions (H1) and (H2) below must be met to guarantee local asymptotic stability.

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(H1) $\frac{dx}{dt} = F(X,0)$, x^* is globally asymptotically stable.

(H2) $G(X,Z) = AZ - \hat{G}(X,Z), \quad \hat{G}(X,Z) \geq 0$ for $(X,Z) \epsilon \Omega$.

Where $A = \frac{\partial G}{\partial Z}(X^*,0)$ is an M-matrix (the off diagonal elements of $A$are nonnegative) and Ω is the region where the model makes biological sense.

Then the disease free-disease equilibrium $x_0 = (X^*,0)$ is globally asymptotically stable provided that $R_0 < 1$.

Let

$$X = (S_H, R_H, P_H), \; Z = (I_H, C_V)^T$$

$$F(X,0) = \begin{pmatrix} \Lambda_H - (\mu_H + \gamma_H)S_H \\ R_H(\beta_H + Z_H) - R_H(\mu_H + \rho_H) \\ \gamma_H S_H - \mu_H P_H \end{pmatrix}$$

Checking out for linearity of $F(X,0)$, we obtain:

$$S_H(t) = e^{-\int_0^t (\mu_H+\gamma_H)dt}\left(S_H(0) + \int_0^s \Lambda_H e^{\int_0^t (\mu_H+\gamma_H)dt} ds\right), R_H = R_H(0) e^{\int_0^t ((\beta_H+Z_H)-(\mu_H+\rho_H))dt}$$

$$P_H(t) = e^{\int_0^t \mu_H dt}\left(P_H(0) + \int_0^s \gamma_H S_H e^{\int_0^t \mu_H dt} ds\right).$$

Next we show that condition (H2) is less than or equal to zero as follows:

$$G(X,Z) = \begin{pmatrix} \frac{q_1 C_V}{C_V + K} S_H + q_2 I_H S_H - (\mu_H + d_H + \beta_H + z_H + \varepsilon) I_H \\ \varepsilon I_H - (\varphi + \eta) C_V \end{pmatrix}$$

$$AZ = \begin{pmatrix} q_2 S_H - (\mu_H + d_H + \beta_H + z_H + \varepsilon) & \frac{q_1 K S_H}{(C_V + K)^2} \\ \varepsilon & -(\varphi + \eta) \end{pmatrix} \begin{pmatrix} I_H \\ C_V \end{pmatrix}$$

$$\hat{G} = \begin{pmatrix} \frac{K}{(C_V + K)^2} \\ 0 \end{pmatrix}$$

Here, $K > 0$. Clearly, $\frac{K}{(C_V+K)^2} > 0$, so that $\hat{G} \geq 0$, thus satisfying H2. It is also clear that x^* is a g.a.s equilibrium if $\frac{dx}{dt} = F(x,0)$. Hence, by the above theorem U_0 is g.a.s.

Results and Discussion

Numerical results of this model are in a graph form. Using parameter values stated in table 2, Mathematica software was used to run the test. Figure 2 shows that proper enlightenment on masking, sanitation and social distancing on the population prone with COVID-19 will reduce the spread of the infection thereby bringing the population to a healthy state.

We noticed from the graph that when the population is exposed and well educated on the do's and don'ts, the recovery rate of the infected humans grows exponentially leading to a drastic reduction on the number of people infected with the disease and on the concentration of the virus.

Table 2. Parameters, description and value

Para-meter	Description	Value	Refe-rence
Λ_H	Per capital birth rate of humans.	0.590 (day^{-1})	10
μ_H	Per capital natural death rate of humans	0.761 (day^{-1})	11
d_H	Cholera induced death rate	0.499 (day^{-1})	10
α_H	Rate of exposure to body surface water droplets	0.680	13
ρ_H	Immunity waning rate	0.524 (day^{-1})	8
z_H	Rate of recovery of individuals due to treatment	0.998 (day^{-1})	9
β_H	Natural recovery rate	0.010 (day^{-1})	6
H	Death rate of COVID-19 due to reinfection.	0.472	11
E	Rate of contribution of each infected person	0.258	11
Φ	Net death rate of COVID-19	0.163	9
γ_H	Rate of exposure to education and its compliance	0.854	Estim ated
q_1 and q_2	Rates of attracting of COVID-19	0.017 (day^{-1})	14
H	Death of COVID-19 due to non-masking	0.950	Esti-mated
d_H	Disease induced death rate.	0.348 (day^{-1})	14
$S_H(0)$	Susceptible individuals in the population	19999000	Esti-mated
$I_H(0)$	Infected individuals in the population	109980	Esti-mated
N_H	Total human population	189098098100	Esti-mated
C_V	Concentration of COVID-19 in water droplets	0.992	11
K	Half saturation of COVID-19 in water droplets	100	9

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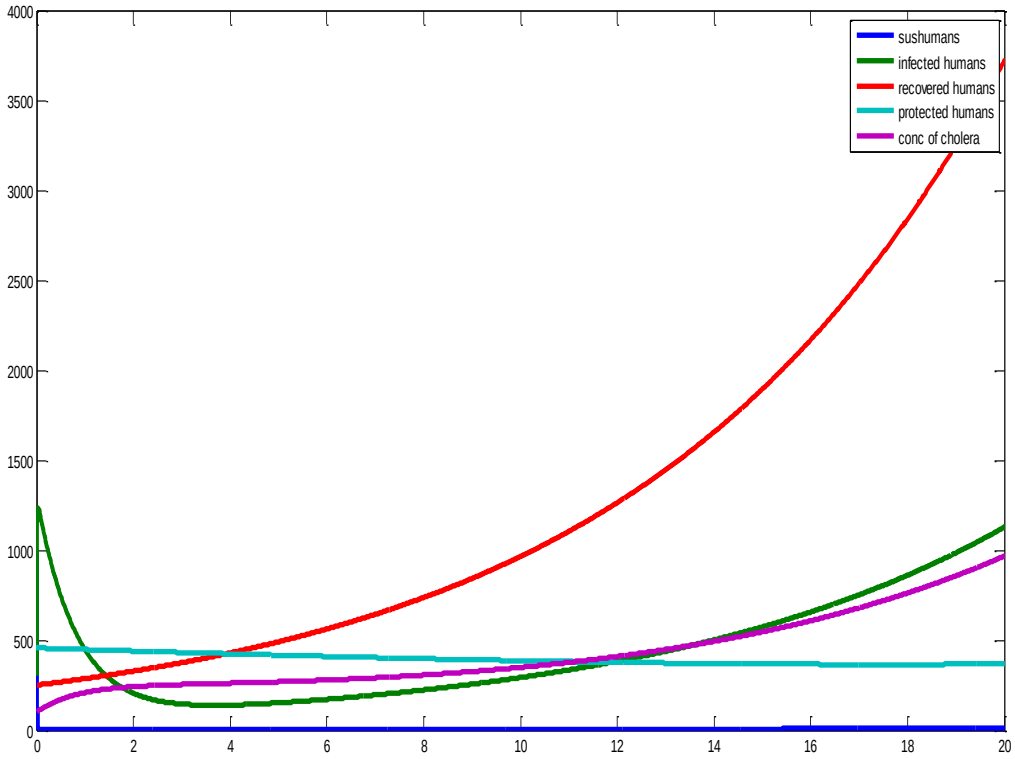

Fig. 2. The graph of education based intervention on a population prone to COVID-19 at time t

With this, the protected humans who are knowledgeable are not dragged into the struggle of living right since the understand it's effect. Consistency on this practice eventually leads to gradual dying out of the disease, bringing the population to a healthy state.

Conclusions

In this research work, we modeled education base intervention as an added control measure alongside with water treatment and environmental sanitation in the dynamics of COVID-19 in humans, there exists a disease free-equilibrium state.

$$E_0 = (S_H, I_H, R_H, P_H, C_V) = \left(\frac{\wedge_H}{\mu_H+\gamma_H}, 0, 0, \frac{\gamma_H \wedge_H}{\mu_H(\mu_H+\gamma_H)}, 0\right)$$

From the findings, the equilibrium point is stable when $R_0 < 1$, and unstable when $R_0 > 1$. Showing that the control recommended will help to eradicate the emergence of new infectious disease. This research work extends results from existing models by bringing in the education based intervention measure. We proved the existence of the model and it having a unique solution. Using the next generation matrix method, we determined the basic reproduction number R_0. We showed that the disease free equilibrium is locally asymptotically stable when $R_0 < 1$ causing the disease to disappear. Numerically we proved that educating the people should not be a program that should be done skeletally but with intense responsibility so as to achieve effectiveness in curbing COVID-19 from any population under the invasion. Lastly, social distancing should be considered seriously in the next research as a major contributor to spread of the disease.

Conflicts of interest

Authors declare no conflict of interest.

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