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A Mathematical Model of COVID-19: Analysis and Identification of Parameters for Better Decision Making

Ouaténi Diallo[1], Yaya Kone[1], Chata Sanogo[1], Jérôme Pousin[2]

[1]Département de Mathématiques et Informatique, Faculté des Sciences et Techniques, Bamako, Mali
[2]Institut Camille Jordan, INSA, Lyon, France
Email: yayakone2000@yahoo.fr

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Abstract

Since the onset of the COVID-19 epidemic, the world has been impressed by two things: The number of people infected and the number of deaths. Here, we propose a mathematical model of the spread of this disease, analyze this model mathematically and determine one or more dominant factors in the propagation of the COVID-19 epidemic. We consider the *S-E-I-R* epidemic model in the form of ordinary differential equations, in a population structured in susceptibles *S*, exposed *E* as caregivers, travelers and assistants at public events, infected *I* and recovered *R* classes. Here we decompose the recovered class into two classes: The deaths class *D* and the class of those who are truly healed *H*. After the model construction, we have calculated the basic reproduction number $\mathbf{R}_0$, which is a function of certain number of parameters like the size of the exposed class *E*. In our paper, the mathematical analysis, which consists in searching the equilibrium points and studying their stability, is done. The work identifies some parameters on which one can act to control the spread of the disease. The numerical simulations are done and they illustrate our theoretical analysis.

Keywords

COVID-19, Mathematical Model, $\mathbf{R}_0$, Spread, Control Parameters, Malian Data

1. Introduction

All the presentations of evolution of the propagation of COVID-19 show an increasing proportion of the number of death. It seemed very important to manage the increase in the number of death because this one has a psychological impact

on the population. Otherwise, it is very important to find a strategy (mathematical, biological, clinical therapeutic, educational, behavioral changes, etc.) in order to avoid ulterior spread of this epidemic. In spite of their limit and insufficiency, mathematical models and computer simulations have become very useful in analysis of the spread and control of infectious diseases. They must together, build and test better elaborated theories to help complex biological systems to get quantitative conjectures and determine sensitivity parameters to control infectious diseases. Modeling is very crucial in epidemiology since in most cases we cannot perform biological experiments and do not have a pharmaceutical solution. Mathematical modeling must be used to develop and understand in a relevant way the epidemiological phenomenon, as well as to quantify the likely effects of different intervention strategies (see Li Li *et al.* [1]; M.E. Halloran *et al.* [2]; T. House *et al.* [3]).

An important aspect of the mathematical study in epidemiology is the formulation or design of the model. For the COVID-19, because of its complexity (type of contamination, duration of the disease before the death) the eradication of this epidemic remains a challenge for us. That is why, we propose here a new model which allows for complete mathematical analysis.

In the model, the class D that we consider as a class of removed is in fact the subpopulation of deceased whose real cause of death is another disease. The division of the class of removed into two classes is important; Transfers in class D are sensitive and even indicate the extent of the disease. That is why in the simulation, we are more interested in δ and μ.

The paper is organized as follows: After this introduction in section *1*, the model is presented in section *2*; In section *3*, we study the dynamic of the differential equations system which proceeds from the transfer diagram. We notice that, the basic reproduction number

$$\mathbf{R}_0 = \frac{\beta_{\max} E}{\delta + \gamma}$$

which depends on certain parameters or data, has a strong relationship between the basic reproduction rate $\mathbf{R}_0$ and the number of people exposed. The stability of the equilibrium points is studied. In section *4*, we propose some control strategies. Conclusions and discussions are given in section *5*.

2. The Model Construction

More complex epidemiological models, like most demographic models incorporating the entire population, susceptible as well as infected and recovered or without recovered, have been studied (see Anderson and May 1991 [4]; Roxana Lopez-Cruz [5]; Hethcote, H. W., van den Driessche, P. [6]; Liu, W. M., Levin, S. A., Iwasa, Y. [7]). We refer to these types of models to deepen the reflection about the models' construction and their analysis. The model which we consider here is based on the classical *S-E-I-R* model, where *S* denotes the susceptible class, *E* denotes the exposed class, *I* denotes the infected class and *R* is the recovered

class, but, we have separated this last class into two subgroups. D becomes the subpopulation of recovered who die from the disease in question and H denotes the subpopulation of recovered who are truly healed. The transfer between the mentioned classes and subgroups are schematically described by the following diagram noted (**Figure 1**):

1) Γ denotes the influx or recruitment in the susceptible subpopulation;

2) α denotes the rate of exposure of susceptible individuals to the disease;

3) $\beta(I,t)$ expresses the incidence function it may vary periodically with time. We take the usual case $\beta(I,t)=\beta(t)I$ (Glendinning, P., Perry L. P. [8]; Liu, W. M., Hethcote, H. W., Levin, S. A. [9]), where $\beta(t)$ (called the transmission rate) is either constant, or a periodic modulation about a constant value, here we take $\beta(t)=\beta_0\left(1+\beta_1\sin(\omega t)\right)$, β_0 is the probability of having contact with an infected individual and β_1 is the probability of being infected by this contact;

4) γ expresses the healing rate from the disease;

5) δ is supposed to be the death rates from the disease in the subpopulations of infected, and

6) μ is the death rate from another disease in reality;

7) η expresses the natural death rate.

The size of the population at time t is denoted by $N(t)$ and it is expressed as the following sum: $N(t)=S(t)+E(t)+I(t)+D(t)+H(t)$. These assumptions lead to the following structured *S*-*E*-*I*-[*D*/*H*] dynamic model.

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t}=\Gamma-\alpha S \\ \dfrac{\mathrm{d}E}{\mathrm{d}t}=\alpha S-\beta(I,t)E-\eta E \\ \dfrac{\mathrm{d}I}{\mathrm{d}t}=\beta(I,t)E-(\delta+\gamma)I \\ \dfrac{\mathrm{d}D}{\mathrm{d}t}=\delta I-\mu D \\ \dfrac{\mathrm{d}H}{\mathrm{d}t}=\gamma I-\eta H \end{cases} \tag{1}$$

3. The Model Dynamic

In the study of population dynamic, we use mathematical model in order to understand the interaction between the populations and calamities which threaten them of extinction. Among these calamities, one can identify predator-prey, ecological upheavals, epidemics, …, etc. In the case of epidemic, the mathematical models have developed indicators, such as the basic reproduction number or endemic threshold which enable us to know the strains of the phenomenon, the equilibrium points and their stability. We will calculate the basic reproduction number of (1), which will tell us the sensitive parameters of the spread of the disease and then we will analyze the stability of the equilibrium points.

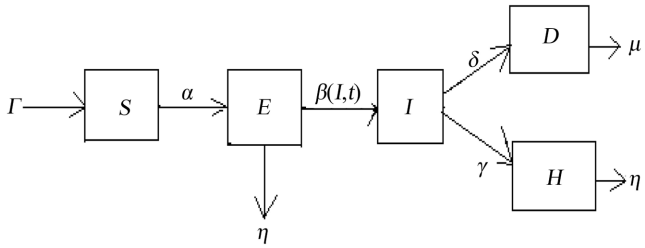

Figure 1. Transfer diagram between the classes.

3.1. The Basic Reproduction Number

We will use the technique due to Diekmann (1990) [10] and developed by Van den Driessche and Watmough (2002) [11] to calculate the basic reproduction number. So, we take $\beta(t)=\beta_{\max}=\max_{i\in[t_0,t]}\beta(i)$, a constant that expresses the transmission rate. The infective compartments being I, so that we start with the infective class, re-arranging the Equations in (1), which can be rewritten as follows:

$$\begin{cases} \dfrac{\mathrm{d}I}{\mathrm{d}t}=\beta_{\max}IE-(\delta-\gamma)I \\ \dfrac{\mathrm{d}S}{\mathrm{d}t}=\Gamma-\alpha S \\ \dfrac{\mathrm{d}E}{\mathrm{d}t}=\alpha S-\beta_{\max}IE-\eta E \\ \dfrac{\mathrm{d}D}{\mathrm{d}t}=\delta I-\mu D \\ \dfrac{\mathrm{d}G}{\mathrm{d}t}=\gamma I-\eta H \end{cases} \tag{2}$$

From (2) we obtain: $\mathcal{F}=\begin{pmatrix}\beta_{\max}IE\\0\\0\\0\\0\end{pmatrix}$ and $\mathcal{V}=\begin{pmatrix}(\delta+\gamma)I\\\alpha S-\Gamma\\\beta_{\max}IE-\alpha S+\eta E\\-\delta I+\mu D\\-\gamma I+\eta H\end{pmatrix}$

The derivatives of $\mathcal{F}$ and $\mathcal{V}$ are given by $F=(\beta_{\max}E)$, and $V=(\delta+\gamma)$ respectively.

The inverse of V is given by $V^{-1}=\dfrac{1}{\delta+\gamma}$.

So, a calculation of FV^{-1} gives the well-known basic reproduction number: The number of secondary infections caused by an infective among a population of exposed in one infectious period. This one of the (1) models is:

$$\mathbf{R}_0=\frac{\beta_{\max}E}{\delta+\gamma}$$

3.2. Stability of the *DFE*

We consider the differential equations system (1), where $O\left(\frac{2}{3};0;0;0;0\right)$ is the

disease-free-equilibrium point. The Jacobian matrix at the disease-free-equilibrium is:

$$J=\begin{pmatrix} -\alpha & 0 & 0 & 0 & 0 \\ \alpha & -\eta & 0 & 0 & 0 \\ 0 & 0 & -(\delta+\gamma) & 0 & 0 \\ 0 & 0 & \delta & -\mu & 0 \\ 0 & 0 & \gamma & 0 & -\eta \end{pmatrix}$$

The eigenvalues equation is:

$$(-\eta-\lambda)(-\mu-\lambda)\begin{vmatrix} -\alpha-\lambda & 0 & 0 \\ \alpha & -\eta-\lambda & 0 \\ 0 & 0 & -(\delta+\gamma)-\lambda \end{vmatrix}=0$$

This is equivalent to:

$$(-\eta-\lambda)(-\mu-\lambda)(-(\delta+\gamma)-\lambda)(-\alpha-\lambda)(-\eta-\lambda)=0.$$

We obtain the eigenvalues which are: $\lambda_1=\lambda_4=-\eta$; $\lambda_2=-\mu$; $\lambda_3=-(\delta+\gamma)$; $\lambda_5=-\alpha$. So, at the disease-free-equilibrium, we have five negative eigenvalues.

In conclusion, the disease-free-equilibrium is stable.

3.3. Stability of the Endemic Equilibrium

A simple calculation gives us the endemic equilibrium point which is

$$P^*=\left(S^*;E^*;I^*;D^*;H^*\right)=\left(\frac{\Gamma}{\alpha};\frac{\delta+\gamma}{\beta};\frac{\Gamma}{\delta+\gamma};\frac{\delta\Gamma}{\mu(\delta+\gamma)};\frac{\gamma\Gamma}{\eta(\delta+\gamma)}\right)$$

The Jacobian matrix J at the endemic equilibrium point P^* is:

$$\begin{pmatrix} -\alpha & 0 & 0 & 0 & 0 \\ \alpha & \beta\left(\frac{\Gamma}{\delta+\gamma}\right)-\eta & \delta+\gamma & 0 & 0 \\ 0 & \beta\left(\frac{\Gamma}{\delta+\gamma}\right) & 0 & 0 & 0 \\ 0 & 0 & \delta & -\mu & 0 \\ 0 & 0 & \gamma & 0 & -\eta \end{pmatrix}$$

The eigenvalues equation is:

$$\begin{vmatrix} -\alpha-\lambda & 0 & 0 & 0 & 0 \\ \alpha & \beta\left(\frac{\Gamma}{\delta+\gamma}\right)-\eta-\lambda & \delta+\gamma & 0 & 0 \\ 0 & \beta\left(\frac{\Gamma}{\delta+\gamma}\right) & -\lambda & 0 & 0 \\ 0 & 0 & \delta & -\mu-\lambda & 0 \\ 0 & 0 & \gamma & 0 & -\eta-\lambda \end{vmatrix}=0$$

This is equivalent to:

$$(-\eta-\lambda)(-\mu-\lambda)\begin{vmatrix} -\alpha-\lambda & 0 & 0 \\ \alpha & \beta\left(\dfrac{\Gamma}{\delta+\gamma}\right)-\eta-\lambda & \delta+\gamma \\ 0 & \beta\left(\dfrac{\Gamma}{\delta+\gamma}\right) & -\lambda \end{vmatrix}=0$$

We find

$$(-\eta-\lambda)(-\mu-\lambda)\left[-\lambda^3+\lambda^2\left(\frac{\beta\Gamma}{\delta+\gamma}-\eta-\alpha\right)+\lambda\left(\beta\Gamma+\frac{\alpha\beta\Gamma}{\delta+\gamma}-\alpha\right)+\alpha\beta\Gamma\right]=0\text{; (3)}$$

Let's make some assumptions:

1) $\Gamma=0$ corresponds mathematically to the influx equal to zero and practically to the closing of country borders; Equation (3) becomes

$$\lambda(-\eta-\lambda)(-\mu-\lambda)\left[-\lambda^2+\lambda(-\eta-\alpha)-\alpha\right]=0$$

We get one eigenvalue $\lambda_1=0$, two negative eigenvalues which are $\lambda_2=-\eta$ and $\lambda_3=-\mu$. As equation $\left[-\lambda^2+\lambda(-\eta-\alpha)-\alpha\right]=0$ has as discriminant $\Delta_1=(-\eta-\alpha)^2-4\alpha$, the eigenvalues λ_4 and λ_5 are: either negative reals, or conjugate complexes of negative real parts. Since the algebraic and geometric multiplicity of $\lambda_1=0$ coincide, we conclude that the endemic equilibrium is stable.

2) For $\Gamma\neq 0$, we return to the eigenvalues equation:

$$(-\eta-\lambda)(-\mu-\lambda)\left[-\lambda^3+\lambda^2\left(\frac{\beta\Gamma}{\delta+\gamma}-\eta-\alpha\right)+\lambda\left(\beta\Gamma+\frac{\alpha\beta\Gamma}{\delta+\gamma}\right)+\alpha\beta\Gamma\right]=0.$$

We have two negative eigenvalues which are: $\lambda_1=-\eta$ and $\lambda_2=-\mu$. The other three are possible solutions to the equation

$$\left[-\lambda^3+\lambda^2\left(\frac{\beta\Gamma}{\delta+\gamma}-\eta-\alpha\right)+\lambda\left(\beta\Gamma+\frac{\alpha\beta\Gamma}{\delta+\gamma}\right)+\alpha\beta\Gamma\right]=0.$$

The coefficient of $-\lambda^3$ being $-1<0$.

a) If $\Delta_2>0$, (here Δ_2 is the derivative of the discriminant of $f(\lambda)=\left[\lambda^2\left(\frac{\beta\Gamma}{\delta+\gamma}-\eta-\alpha\right)+\lambda\left(\beta\Gamma+\frac{\alpha\beta\Gamma}{\delta+\gamma}\right)+\alpha\beta\Gamma\right]=0$), six cases can arise, the existence of: a single positive root; a single negative root; a double negative root and a single positive root; three distinct positive roots; and a simple negative root and two positive roots. These roots are real and can be positive or negative according to the study of third degree polynomial functions. So, P^* can be stable, asymptotically stable or unstable for 1) according to the parameter values.

b) If $\Delta_2\leq 0$, four cases can arise: the existence of a single root greater than $\dfrac{\frac{\beta\Gamma}{\delta+\gamma}-\eta-\alpha}{3}$, a single root equal to $\dfrac{\frac{\beta\Gamma}{\delta+\gamma}-\eta-\alpha}{3}$, a triple root and a single

root less than $\frac{\frac{\beta\Gamma}{\delta+\gamma}-\eta-\alpha}{3}$. All these roots are reals greater than zero, then P^* is not stable.

3.4. Simulations

In our simulations, we used the Malian data as values of certain parameters. The standard situation in Mali is linked in **Figure 2(a)**. The figures: **Figure 2(b)**; **Figure 3(a)** and **Figure 3(b)**; **Figure 4(a)** and **Figure 4(b)** are obtained by varying the parameters β_0, δ and μ to see their impact on the spread of the disease. It appears from our observations that β_0 and β_1 are dominant parameters in the spread of the disease; δ and μ make it possible to control the number of deaths on two aspects: Finding a drug for the declared disease (this refers to medical research) and treating common diseases (so that μ is zero). **Figures 5(a)-(c)** indicates the evolution of the number of infected according to the values of β_0.

4. Control of Epidemic

In general, the basic reproduction rate makes it possible to control an epidemic. The expression of our basic reproduction rate indicates that we can act on the following data: β_0, β_1, E and Γ, $(\delta+\gamma)$. The interpretation of these parameters to decrease $\mathbf{R}_0$, so controlling the disease is respectively to:

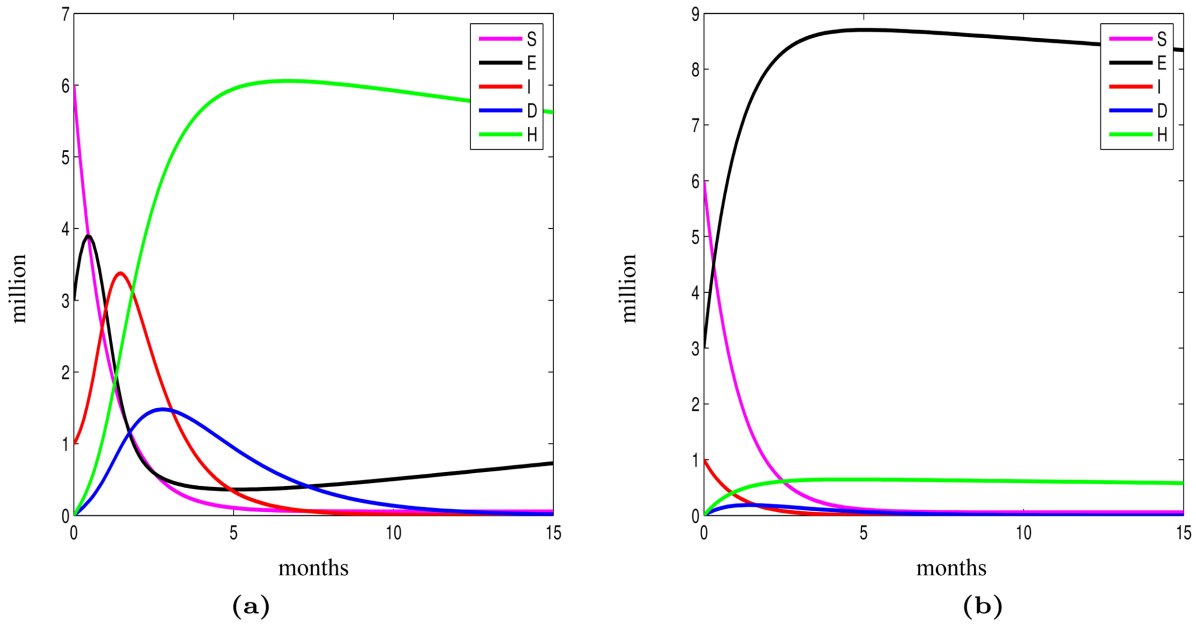

Figure 2. Simulation of system (1). (a) $\Gamma = 0.0533857$; $\alpha = 0.9557$; $\boxed{\beta_0 = 0.569625}$; $\beta_1 = 0.775$; $\omega = 0.125125$; $\eta = 0.01106$; $\delta = 0.369$; $\gamma = 0.70031$; $\mu = 0.45$; $t \in [0;15]$; $(S_0, E_0, I_0, D_0, H_0) = (06.00; 03.00; 01.00; 0.0; 0.0)$. (b) $\Gamma = 0.0533857$; $\alpha = 0.9557$; $\boxed{\beta_0 = 0.00569625}$; $\beta_1 = 0.775$; $\omega = 0.125125$; $\eta = 0.01106$; $\delta = 0.369$; $\gamma = 0.70031$; $\mu = 0.45$; $t \in [0;15]$; $(S_0, E_0, I_0, D_0, H_0) = (06.00; 03.00; 01.00; 0.0; 0.0)$.

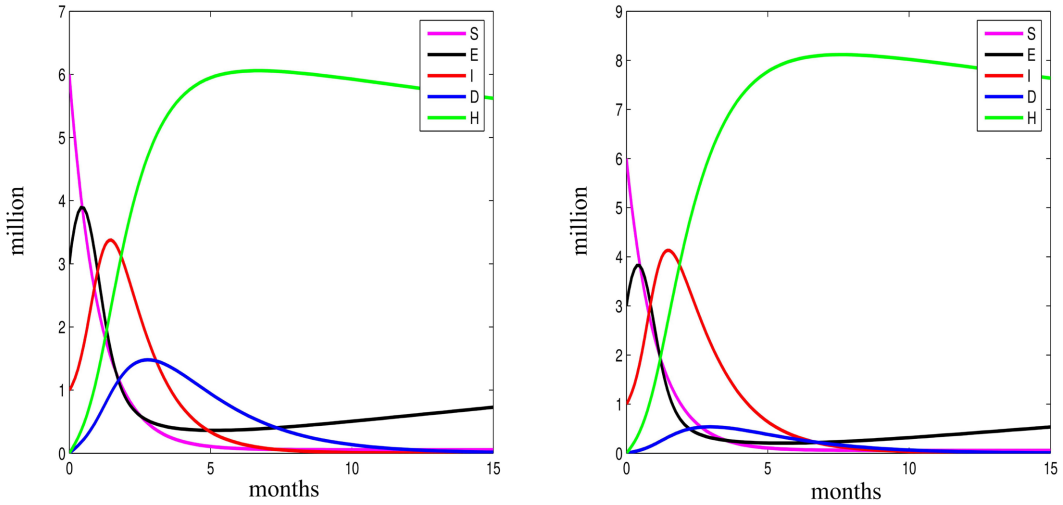

Figure 3. Simulation of system (1). (a) $\Gamma = 0.0533857$; $\alpha = 0.9557$; $\beta_0 = 0.569625$; $\beta_1 = 0.775$; $\omega = 0.125125$; $\eta = 0.01106$; $\boxed{\delta = 0.369}$; $\gamma = 0.70031$; $\mu = 0.45$; $t \in [0;15]$; $(S_0, E_0, I_0, D_0, H_0) = (06.00; 03.00; 01.00; 0.0; 0.0)$. (b) $\Gamma = 0.0533857$; $\alpha = 0.9557$; $\beta_0 = 0.569625$; $\beta_1 = 0.775$; $\omega = 0.125125$; $\eta = 0.01106$; $\boxed{\delta = 0.1069}$; $\gamma = 0.70031$; $\mu = 0.45$; $t \in [0;15]$; $(S_0, E_0, I_0, D_0, H_0) = (06.00; 03.00; 01.00; 0.0; 0.0)$.

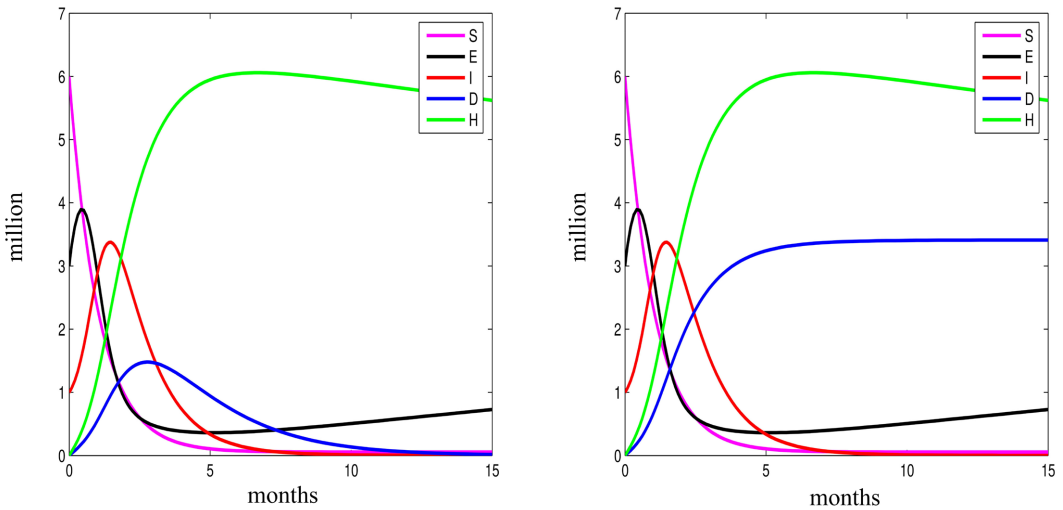

Figure 4. Simulation of system (1). (a) $\Gamma = 0.0533857$; $\alpha = 0.9557$; $\beta_0 = 0.569625$; $\beta_1 = 0.775$; $\omega = 0.125125$; $\eta = 0.01106$; $\delta = 0.369$; $\gamma = 0.70031$; $\boxed{\mu = 0.45}$; $t \in [0;15]$; $(S_0, E_0, I_0, D_0, H_0) = (06.00; 03.00; 01.00; 0.0; 0.0)$. (b) $\Gamma = 0.0533857$; $\alpha = 0.9557$; $\beta_0 = 0.569625$; $\beta_1 = 0.775$; $\omega = 0.125125$; $\eta = 0.01106$; $\delta = 0.369$; $\gamma = 0.70031$; $\boxed{\mu = 0}$; $t \in [0;15]$; $(S_0, E_0, I_0, D_0, H_0) = (06.00; 03.00; 01.00; 0.0; 0.0)$.

1) Decrease travel or cancellation to reduce the probability of having contact with an infected person (which corresponds to the confinement measure);

2) Protect yourself to avoid that in case of contact with an infected person, there is no contamination (which corresponds to the wearing of gloves, masks and regular washing or disinfection of hands);

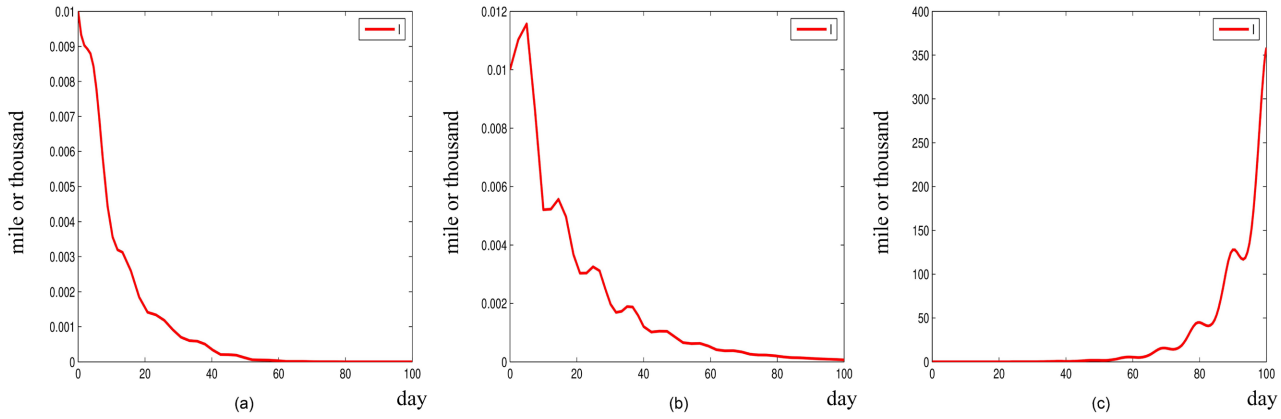

Figure 5. Infected curve. (a) $\Gamma = 0.1$; $\alpha = 0.2$; $\boxed{\beta_0 = 0.3}$; $\beta_1 = 0.3$; $\omega = 0.6$; $\eta = 0.01$; $E = 0.9$; $\delta = 0.3$; $\gamma = 0.1$; $\mu = 0.01$; $t \in [0;100]$; $I_0 = 01.00$. (b) $\Gamma = 0.1$; $\alpha = 0.2$; $\boxed{\beta_0 = 0.35}$; $\beta_1 = 0.3$; $\omega = 0.6$; $\eta = 0.01$; $E = 0.9$; $\delta = 0.3$; $\gamma = 0.1$; $\mu = 0.01$; $t \in [0;100]$; $I_0 = 01.00$. (c) $\Gamma = 0.1$; $\alpha = 0.2$; $\boxed{\beta_0 = 0.5}$; $\beta_1 = 0.3$; $\omega = 0.6$; $\eta = 0.01$; $E = 0.9$; $\delta = 0.3$; $\gamma = 0.1$; $\mu = 0.01$; $t \in [0;100]$; $I_0 = 01.00$.

3) Reduce the size of the class E, which amounts to reducing the number of people exposed to the disease (this corresponds to the screening and isolation of people tested positive);

4) Close the country borders; we saw in 3.3 that when $\Gamma = 0$ (which corresponds to the closing of country borders), that the endemic equilibrium is stable;

5) Increase the recovered rate (death + healed); this means reducing the treatment time and increasing the cure rate. This decreases the size of the I class and therefore reduces the risk of the epidemic spreading;

6) Treat common illnesses.

5. Conclusion and Discussion

Managing an epidemic has never been easy, especially when it is not known. But, for their control, many epidemics have common measures such as yourself protection measures. In the case of COVID-19, controlling the size of the class E of the exposed individual seems important for us. This is the screening piste. The other pistes are no less important, but screening seems more effective and even has a favorable link with other control measures to reduce the spread of the epidemic. We plan to work on the impact of treatment time on the spread of the disease in our next paper.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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