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Dynamic analysis of a mathematical model with health care capacity for COVID-19 pandemic

Süleyme Çakan

Üniversity, Department of Mathematics, Malatya, 44280, Turkey

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A B S T R A C T

The fact that no there exists yet an absolute treatment or vaccine for COVID-19, which was declared as a pandemic by the World Health Organization (WHO) in 2020, makes very important spread out over time of the epidemic in order to burden less on hospitals and prevent collapsing of the health care system. This case is a consequence of limited resources and is valid for all countries in the world facing this serious threat. Slowing the speed of spread will probably make that the outbreak last longer, but it will cause lower total death count. In this study, a new SEIR epidemic model formed by taking into account the impact of health care capacity has been examined and local and global stability of the model has been analyzed. In addition, the model has been also supported by some numerical simulations.

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1. Introduction

In today's world, many countries have faced with a global threat whose source is not precisely yet known: A novel coronavirus. The epidemic, which firstly started in the city of Wuhan, Hubei, China in early December of 2019, has rapidly spread to many countries in the world and has seriously shook up humanity. This new type outbreak has been named as the COVID-19 (coronavirus disease-2019) and determined as a pandemic by the WHO.

This pandemic has affect billions of people by forming very immense restrictions in their lives, movements, travels (in local, national and international) and social relationships. It has been taken unprecedented measures against to COVID-19, which is caused to many deaths, to intense stress and to changes in lifestyle and forms of work, by the local admininistrations and national governments of almost every countries. For instance, artial (local) or country-wide curfew, halting all means of unauthorised travel into and out of the cities or country, cancelling large events, extended schools closures, closing of workplaces and of major shopping centers, working remotely or, in particular, working alternately in formal organizations, obligation to use masks and gloves in crowded and common areas, disinfection of common active areas, restriction of number of people in public transport, isolation of suspected cases, information via public service announcement (public spot) etc. Also, social control measures have been extended up to houses by increased public awareness such as through good hygiene, social or physical distancing measures and not going out of the houses.

But, unfortunately, intense efforts of health authorities and governments in all of world countries has unable to prevent spreading of COVID-19. According to the reports of the WHO, since the outbreak of the pandemic, as of June 16, 2020, the total number of confirmed cases is 7890687 and the total number of deaths is 433404 in world-wide, [1]. As a result of increasing of infected cases day by day, density of hospitals (in particular, intensive care units) may increase quickly, and necessary and adequate care for patients may not be provided. Of course, the health systems belong to each countries has not to infinite sources. Therefore, exceeding to maximum level of this density in hospitals can lead to much more serious negative results. In the sense of this, to manage such a crisis situation, it is needed to various studies in different areas locally and globally. As a technique and a field, mathematical mod-
eling is one of these areas. The studies of mathematical modeling play a considerable role in analyzing the factors that may affect spreading of the disease. Here is, mathematical epidemiology exists for this purpose. Mathematical methods in epidemiology have a very momentous place in examining the behavioral dynamics of epidemic. Many mathematicians in worldwide interested in mathematical epidemiology are recently trying to contribute to the understanding of COVID-19. The references [2,3] and [4] are just a few of them.

This paper analyze the transmission dynamics of COVID-19 by composing a model considered of contribution (positive effect) rate to recovery of usage of health care capacity for COVID-19. The most important feature distinguishing this model from other models is that recovery rate and disease-induced death rate are variable during the outbreak. This variability arises from that these rates depend on the level of availability to opportunities provided by health care system to the infectious individuals. In this study, firstly the disease-free equilibria and endemic equilibria of the model are determined. Following, the value \( R_0 \) which is an extremely substantial threshold for the course of the disease in mathematical epidemic models is found. Then, according to the case of \( R_0 \), the local and global stabilities of these equilibria are analyzed by examined corresponding characteristic equation and by using LaSalle's Invariance Principle-Lyapunov's direct method, respectively.

\( R_0 \), called as the number of secondary infections or basic reproduction number, is the average number of new cases that a single case leads. So \( R_0 \) is a key value in the extinction or spreading of the disease in the population. The spreading of the disease in a population can be slowed by means that \( R_0 \) is reduced. If \( R_0 \) can be reduced then, even if same number of people will become infected, the outbreak will take longer. But, it should also not be ignored that the number of serious cases will spread out over time. Since no there exist any vaccine or specific drug for COVID-19 yet, spreading of the outbreak into time will provide a situation that will not strain the carrying capacity of hospitals and intensive care units.

Now let us examine the model in which we consider of treatment services provided by health institutions in coping with COVID-19.

2. The model and its qualitative and stability analysis

2.1. Model equations and nomenclature

We consider a time delayed SEIR epidemic model with compartments consisting of Susceptible (S) against to the disease COVID-19, Exposed (E) to the coronavirus, Infectious (I) and Recovered (R) individuals in total population (N).

All parameters used in the model are non-negative constants. Parameters \( b \) and \( d \) represent birth rate and natural death rate of all compartments, respectively. In the model, it is assumed that all newborns are included to the susceptible compartment. Also \( b \) is effective contact rate between susceptible and infectious individuals, \( \gamma \) is progression rate of exposed individuals into infectious population. Besides, \( \delta \) is transition rate of the exposed individuals who are not infectious to the class \( R \). The function \( c(t) \), which takes value in the interval of \([0, 1]\), represents the level of availability to opportunities provided by health care system to individuals who are become infectious at time \( t \). \( \alpha_1 \) is natural recovery rate of the infectious class, that is, this value is minimum recovery rate for the model. Also \( \alpha_2 c(t) \) is contribution rate to recovery of health care system. Thus clearly \( \alpha_1 + \alpha_2 \) is maximum recovery rate. Furthermore, \( \mu_1 \) is minimum disease-induced death rate and \( \mu_2 (1 - c(t)) \) is a factor increasing the disease-induced deaths due to can not benefit from health care system. So, it is clear that \( \mu_1 + \mu_2 \) is maximum death rate.

As it can be estimated, the case that \( c(t) \) tends to zero means that all hospital opportunities are almost consumed away, the case of \( c(t) = 1 \) says that all hospital opportunities can be used fully.

Additionally, the \( N(t), S(t), E(t), I(t), R(t) \) describe the numbers of individuals in the relevant compartments at time \( t \). These variables are clearly non-negative and \( N(t) = S(t) + E(t) + I(t) + R(t) \) for all \( t \geq 0 \).

In addition to, \( \tau \) is a time delay corresponding the latent period of the COVID-19. By the way, the term \( \tilde{E}(t, \tau) \) describes the number of exposed and still surviving individuals to coronavirus at the time \( t - \tau \). This term is mathematically explained with the expression \( \beta S(t - \tau)I(t - \tau)e^{-\delta \tau} \) and has been given in the following part with details.

With above descriptions and assumptions, the model, which is taken into account the effect of level of availability to opportunities provided by health care system to individuals, with a time delay representing a latent period is as follows:

\[
\frac{dS}{dt} = b - \beta S(t)I(t) - dS(t),
\]

\[
\frac{dE}{dt} = \beta S(t)I(t) - \gamma E(t, \tau) - dE(t) - dE(t, \tau),
\]

\[
\frac{dI}{dt} = \gamma E(t, \tau) - [\mu_1 + \mu_2 (1 - c(t))]I(t) - \alpha_1 I(t) - \alpha_2 c(t)I(t) - dI(t),
\]

\[
\frac{dR}{dt} = \alpha_1 I(t) + \alpha_2 c(t)I(t) + \delta E(t) - dR(t).
\]

(1)

where the evolution of the density in the exposed individuals is given by

\[
\left( \frac{\partial}{\partial t} + \frac{\partial}{\partial \tau} \right) \tilde{E}(t, \tau) = -d\tilde{E}(t, \tau).
\]

(2)

From the above descriptions, since \( \tilde{E}(t, 0) \) describes the number of exposed individuals to coronavirus at the time \( t \), we say that \( \tilde{E}(t, 0) \) corresponds to \( \beta S(t)I(t) \). Thus, considering the Eq. (2) with the boundary condition

\[
\tilde{E}(t, 0) = \beta S(t)I(t),
\]

from it's solution, we get

\[
\tilde{E}(t, \tau) = \beta S(t - \tau)I(t - \tau)e^{-\delta \tau}.
\]

Therefore the system (1) can be rearranged as follows:

\[
\frac{dS}{dt} = b - \beta S(t)I(t) - dS(t),
\]

\[
\frac{dE}{dt} = \beta S(t)I(t) - \gamma \beta S(t - \tau)I(t - \tau)e^{-\delta \tau} - (d + \delta)E(t),
\]

\[
\frac{dI}{dt} = \gamma \beta S(t - \tau)I(t - \tau)e^{-\delta \tau} - [\mu_1 + \mu_2 (1 - c(t))]I(t) - [\alpha_1 + \alpha_2 c(t)]I(t) - dI(t),
\]

\[
\frac{dR}{dt} = [\alpha_1 + \alpha_2 c(t)]I(t) + \delta E(t) - dR(t).
\]

(3)

2.2. Feasible positively invariant region

Now let us determine feasible region which is positively invariant will be enough to study mathematically and epidemiologically. Thus, all results about the model such as existence and uniqueness of equilibrium points, stability of system etc. can be only considered in this region.
The rate of change of the total population is seen by summing the all equations of system (3):
\[
\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt}
\]
\[
= b - dN - [\mu_1 + \mu_2 (1 - c(t))]I. \tag{4}
\]
Then we say
\[
N'(t) + dN \leq b.
\]
Taking into account the ordinary differential equation \(N'(t) + dN = b\) and solving with the classical way (using separation of variables), we obtain the solution \(N(t) = b/d + ce^{-dt}\). Obviously \(c = N(0) - b/d\) for the initial condition \(t = 0\), and hence time-varying population is in form
\[
N(t) = N(0)e^{-dt} + \frac{b}{d} \left(1 - e^{-dt}\right). \tag{5}
\]
Using Standard Comparison Theorem [5], the right side of the equality (5) is the maximal solution of Eq. (4). Thus for all \(t \geq 0\), we say
\[
N(t) \leq N(0)e^{-dt} + \frac{b}{d} \left(1 - e^{-dt}\right)
\]
Especially, when \(N(0) \leq b/d\), we can write \(N(t) \leq b/d\) for all \(t > 0\). Therefore for system (3) the region
\[
\Gamma = \left\{ (S(t), E(t), I(t), R(t)) \in \mathbb{R}^4 \mid N(t) \leq \frac{b}{d} \right\}
\]
is positively invariant. Consequently this region attracts all solutions of the system and this restricted region will be enough to consider of the dynamics of the model (3).

After of these specifications about the model, we will focus on qualitative and stability analysis of the model (3) in below subtitles. But first of all, let us immediately note that since the variables \(E(t)\) and \(R(t)\) do not appear in other remainder equations, we can only analyze the dynamics of the following binary system and that will be enough:
\[
\begin{align*}
\frac{dS}{dt} &= b - \beta S(t)I(t) - dS(t), \\
\frac{dI}{dt} &= \gamma \beta S(t) - \gamma I(t)(t - \tau)e^{-dt} - [\mu_1 + \mu_2 (1 - c(t))]I(t) + \alpha_1 + \alpha_2 c(t) + d[I(t)]
\end{align*}
\]
\[
\tag{6}
\]
Of course, \(\Gamma\) is a restricted and feasible region that sufficient to examining for model (6), too.

2.3. Equilibrium points and basic reproductive number

The system (6) always has a disease-free equilibrium point
\[
P_0 = (S_0, I_0) = \left(\frac{b}{d}, 0\right).
\]
Moreover, to obtain the endemic equilibria \(P_e = (S^*, I^*)\) of (6), \(S^*\) and \(I^*\) should satisfy the following algebraic equations:
\[
\begin{align*}
0 &= b - \beta S^* I^* - dS^*, \\
0 &= \gamma \beta S^* e^{-dt} - [\mu_1 + \mu_2 (1 - c(t))] + \alpha_1 + \alpha_2 c(t) + d[I^*].
\end{align*}
\]
Solving these equations, we get \(P_e = (S^*, I^*)\) such that
\[
S^* = \frac{\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d}{\gamma \beta e^{-dt}}
\]
\[
I^* = \frac{\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d}{\gamma \beta e^{-dt}} \times \left(b - \frac{\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d}{\gamma \beta e^{-dt}}\right).
\]
Utilizing from [6,7] and [8], by means of the next generation matrix method let us find the basic reproduction number \(R_0\) of the mentioned model.

Now, let us say \(X = (I, S)^T\). Then the model (6) can be expressed as
\[
\frac{dX}{dt} = F(X) - V(X), \tag{7}
\]
where
\[
F(X) = \begin{bmatrix}
\gamma \beta S(t) - (t - \tau)e^{-dt} \\
0
\end{bmatrix}
\]
and
\[
V(X) = \begin{bmatrix}
\mu_1 + \mu_2 (1 - c(t)))[I(t) + [\alpha_1 + \alpha_2 c(t)]I(t) + d[I(t)] \\
\beta S(t)I(t) + dS(t) - b,
\end{bmatrix}
\]
\[
X_0 = \left(\frac{b}{d}, 0\right)^T \] is the unique disease-free equilibrium point of the model (7).
The Jacobian matrices at the disease-free equilibrium point \(P_0 = (\frac{b}{d}, 0)\) of \(F(X)\) and \(V(X)\) by looked to the derivatives with respect to \(I\) and \(S\) are obtained as
\[
dF(P_0) = \begin{bmatrix}
\gamma \beta S_0 e^{-dt} & \gamma \beta I_0 e^{-dt} \\
0 & 0
\end{bmatrix}
\]
and
\[
dV(P_0) = \begin{bmatrix}
\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d & 0 \\
\beta S_0 & \beta I_0 + d,
\end{bmatrix}
\]
respectively. So \(F\) and \(V\) which are the new infection terms and the remaining transfer terms of the model, respectively; are determined as
\[
F = dF_{1 \times 1} = \left[\frac{b \beta y e^{-dt}}{d}\right]
\]
and
\[
V = dV_{1 \times 1} = \left[\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d\right].
\]
Also, characteristic polynomial of
\[
FV^{-1} = \begin{bmatrix}
\frac{b \beta y e^{-dt}}{d} \\
\frac{b \beta y e^{-dt}}{d(\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d)}
\end{bmatrix}
\]
is
\[
\det \left(\lambda I_1 - FV^{-1}\right) = \lambda - \frac{b \beta y e^{-dt}}{d(\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d)}.
\]
It follows from [6,7] and [8] that the basic reproduction number of the model (6) is the spectral radius (maximum eigenvalue) of the next generation matrix \(FV^{-1}\). In that case,
\[
R_0 = \left[\frac{b \beta y e^{-dt}}{d(\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d)}\right]. \tag{8}
\]
By the way, it is clearly seen that the endemic equilibrium point \(P_e\) can be rewritten as
\[
P_e = (S^*, I^*) = \left(\frac{b}{dR_0}, \frac{d}{b}\right) (R_0 - 1).
\]

2.4. Local asymptotic stability analysis of the equilibrium points

In this section, we show local stabilities of the disease-free and endemic equilibrium points by analyzing corresponding characteristic equation.

**Theorem 1.** If \(R_0 < 1\), then the disease-free equilibrium \(P_0\) is locally asymptotically stable in the positively invariant region \(\Gamma\).
**Proof.** The Jacobian matrix at the disease-free equilibrium point \( P_0 \) of the system (6) is
\[
J(P_0) = \begin{bmatrix}
-\beta_0 - d & -\beta S_0 \\
\gamma \beta_0 e^{-\alpha t} & \gamma \beta S_0 e^{-\alpha t} - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d]
\end{bmatrix}
\]
Putting \( S_0 = b/d \) and \( I_0 = 0, \) we write
\[
J(P_0) = \begin{bmatrix}
-d & -\beta S_0 \\
0 & \frac{b \beta_0 e^{-\alpha t}}{d} - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d]
\end{bmatrix}
\]
The characteristic equation which is correspond to this matrix is the following form:
\[
(-d - \lambda) \left( \frac{b \beta_0 e^{-\alpha t}}{d} - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d] - d - \lambda \right) = 0.
\]
This equation always has negative root \( \lambda_1 = -d. \) The other root of characteristic Eq. (9) is
\[
\lambda_2 = \frac{b \beta_0 e^{-\alpha t}}{d} - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d] - d = \frac{b \beta_0 e^{-\alpha t}}{d} \left( \frac{\beta_0}{\beta} (R_0 - 1) \right).
\]
\( \lambda_2 \) is negative for \( R_0 < 1, \) and thus the disease-free equilibrium point \( P_0 \) is locally asymptotically stable since two roots of Eq. (9) are negative. If \( R_0 = 1, \) then \( \lambda_2 = 0 \) and \( P_0 \) is stable. Also \( P_0 \) is unstable for \( R_0 > 1 \) since one of roots of Eq. (9) has positive real parts. □

**Theorem 2.** When \( R_0 > 1, \) the endemic equilibrium point \( P_\ast \) is locally asymptotically stable in the positively invariant region \( \Gamma. \)

**Proof.** The Jacobian matrix for system (6) at endemic equilibrium point \( P_\ast = (S_\ast, I_\ast) \) is
\[
J(P_\ast) = \begin{bmatrix}
-(\beta \gamma) - d \\
\gamma \beta S_\ast e^{-\alpha t} - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d]
\end{bmatrix}
\]
Using (8) and
\[
(S' , I') = \left( \frac{b}{d R_0} \frac{d}{\beta} (R_0 - 1) \right),
\]
we obtain the trace of \( J(P_\ast) \) as
\[
Tr(J(P_\ast)) = -d R_0 < 0.
\]
Also
\[
det(J(P_\ast)) = \frac{b \beta_0 e^{-\alpha t}}{d R_0} (R_0 - 1) > 0
\]
for \( R_0 > 1. \) This means that all eigenvalues of matrix \( J(P_\ast) \) have negative real parts and so the endemic equilibrium \( P_\ast \) is locally asymptotically stable in the set \( \Gamma \) for \( R_0 > 1. \) □

2.5. Global asymptotic stability analysis of the equilibrium points

To examine global properties of the equilibrium points belong to the model (6) we will use Lyapunov functional techniques and LaSalle’s Invariance Principle. It can be look to the references [9,10,11] for Lyapunov-LaSalle’s asymptotic stability theorem.

**Theorem 3.** For \( R_0 < 1, \) the disease-free equilibrium point \( P_0 \) of system (6) is globally asymptotically stable in \( \Gamma. \)

**Proof.** Let us define a positive function \( L \) as
\[
L(t) = I(t) + \gamma \beta e^{-\alpha t} \int_{t-\tau}^{t} S(t) I(t) dt.
\]
Computing the time derivative of \( L, \) we obtain
\[
\frac{dL}{dt} = \frac{dI}{dt} + \gamma \beta e^{-\alpha t} S(t) I(t) - \gamma \beta e^{-\alpha t} S(t - \tau) I(t - \tau) dt
\]
\[
= \gamma \beta S(t - \tau) I(t - \tau) e^{-\alpha t} - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d] I(t)
\]
\[
+ \gamma \beta S(t) I(t) e^{-\alpha t} - \gamma \beta S(t - \tau) I(t - \tau) e^{-\alpha t}
\]
\[
= I(t) (\gamma \beta e^{-\alpha t} S(t) - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d])
\]
\[
\leq I(t) \left( \frac{b \beta_0 e^{-\alpha t}}{d} - [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d] \right)
\]
\[
= I(t) [\mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d] (R_0 - 1).
\]
When \( R_0 < 1, \) \( dL/dt \leq 0 \) and then we say that \( L \) is a Lyapunov function for system (6). By LaSalle’s Invariance Principle, solutions of (6) has limit in the largest invariant subset of
\[
\{ (S(t), I(t)) : (S(t), I(t)) \text{ is a solution of } \frac{dL}{dt} = 0 \}.
\]
Also it can be easily seen that this subset consists only the disease-free equilibrium point \( P_0. \) So \( P_0 \) is globally asymptotically stable in \( \Gamma. \) □

**Theorem 4.** If \( R_0 > 1, \) the unique endemic equilibrium point \( P_\ast \) of system (6) is globally asymptotically stable in the positively invariant region \( \Gamma. \)

**Proof.** To analyse the global stability of the endemic equilibrium point \( P_\ast = (S_\ast, I_\ast) \), we construct the function defined by
\[
L(t) = L_1(t) + L_2(t) + L_3(t)
\]
such that
\[
L_1(t) = S_\ast \phi \left( \frac{S(t - \tau)}{S_\ast} \right).
\]
\[
L_2(t) = e^{\alpha t} \frac{I(t)}{I_\ast}.
\]
\[
L_3(t) = \beta S_\ast I_\ast \int_{t-\tau}^{t} \phi \left( \frac{I(t)}{I_\ast} \right) dt.
\]
Where \( \phi \) is defined as \( \phi(z) = z - 1 - \ln z \) for \( z > 0 \) and clearly \( \phi(z) \geq 0. \) Also especially \( \phi(0, \infty)) \rightarrow [0, \infty) \) has global minimum \( \phi(1) = 0. \) Therefore it is clear that \( L(t) \geq 0. \)

Let us survey to the sign of the derivative of the function \( L, \) which we define with three components: \( L_1, L_2 \) and \( L_3 \) sake for the clarity in the operations. Calculating the derivatives of \( L_1, L_2 \) and \( L_3 \) with respect to time by used the related equalities in (6), we obtain followings, respectively.
\[
\frac{dL_1}{dt} = S_\ast \left( \frac{S'(t - \tau)}{S_\ast} - \frac{S(t - \tau)}{S(t - \tau)} \right)
\]
\[
= S'(t - \tau) \left( 1 - \frac{S_\ast}{S(t - \tau)} \right)
\]
\[
= b - \beta S(t - \tau) I(t - \tau)
\]
\[
-dS(t - \tau) - \frac{b S_\ast}{S(t - \tau)} + \beta I(t - \tau) S_\ast + d S_\ast.
\]
\[
\frac{dL_2}{dt} = \frac{e^{\alpha t}}{\gamma} \left( \frac{I'(t)}{I_\ast} - \frac{I(t)}{I(t)} \right)
\]
\[
= \frac{e^{\alpha t}}{\gamma} \left( \frac{\gamma \beta S(t - \tau) I(t - \tau) e^{-\alpha t}}{I(t - \tau)} \right)
\]
\[
\leq \left[ \mu_1 + \mu_2 (1 - c(t)) + \alpha_1 + \alpha_2 c(t) + d \right] I(t)
\]
\[-\frac{e^{\phi t}}{\gamma} \left( \nu s(t - \tau) I(t - \tau)e^{-\sigma t} \right) \frac{P}{I(t)} + \frac{e^{\phi t}}{\gamma} [\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d]l \]
\[= \beta s(t - \tau) I(t - \tau) \frac{P}{I(t)} - \frac{[\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t}}{\gamma} I(t) \]
\[= \beta s(t - \tau) I(t - \tau) \frac{P}{I(t)} \]
\[-\beta s(t - \tau) I(t - \tau) \frac{P}{I(t)} = \frac{[\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t}}{\gamma} I(t) \]
\[= \frac{[\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t}}{\gamma} I(t) \]
\[\leq 0 \]  
\[\text{(11)}\]

and 
\[\frac{dl}{dt} = \beta s(t - \tau) I(t - \tau) \frac{P}{I(t)} \]
\[= \beta s(t - \tau) I(t - \tau) \frac{P}{I(t)} \]
\[-\beta s(t - \tau) I(t - \tau) \frac{P}{I(t)} + [\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t} I(t) \]
\[= [\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t} I(t) \]
\[\leq 0 \]  
\[\text{(12)}\]

If we consider together (10), (11) and (12) by using the relations 
\[b = \beta s(t - \tau) I(t - \tau) - ds(t - \tau) \]
\[= \frac{b s}{s(t - \tau)} + \beta s(t - \tau) I(t - \tau) + ds \]
\[+ \beta s(t - \tau) I(t - \tau) \frac{P}{I(t)} \]
\[-[\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t} I(t) \]
\[= [\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t} I(t) \]
\[= [\mu_1 + \mu_2(1 - c(t)) + \alpha_1 + \alpha_2c(t) + d] e^{\phi t} I(t) \]
\[\leq 0 \]  
\[\text{(13)}\]

Then the largest invariant set is contained by the set 
\[\{(S(t), I(t)) : \frac{dl}{dt} = 0\} \]
\[\text{(13)}\]

which consists only from the endemic equilibrium point \(P_.\) By LaSalle's Invariance Principle [10,12,13,14], all solutions of (6) tend to \(P_.\) and the endemic equilibrium point is global asymptotically stable on \(\Gamma_.\)  

3. Conclusion and some examples

The fact that any drug or vaccine, which has an exact effect in the struggle against to the COVID-19 pandemic caused of the new type of coronavirus, can not yet been found, has led to of all countries of the world to conduct a policy aimed that the number of individuals needed to hospitals don’t exceed the health care capacity. With this policy, the main purpose is to provide that the health care systems don’t collapse and so to save more time in combating with epidemic.

It is clear that the recovery rate and death rate are directly related to whether health care capacity is exceeded or not. In our model taking this fact into consideration, recovery rate and disease-induced death rate have been taken as variable according to status of the health care capacity with fixed lower bounds (\(\alpha_1\) and \(\mu_1\), respectively). Thus, it is anticipated that the disease-induced death rate will increase and the recovery rate will decrease while the level of availability to opportunities provided by health care system decreases.

Now we will present some simulations of our model with the parameters; \(b = 4000, \gamma = 0.75, \alpha_1 = 0.4, \alpha_2 = 0.4, d = \)
0.000015, δ = 0.005, μ₁ = 0.05, μ₂ = 0.05. τ = 10 and the function
\[ c(t) = \frac{400000}{400000 + I(t)} \]
in a population which has 100 million individuals.

As it can be seen that, \( c(t) = 1 \) for \( I(t) = 0 \). Also and \( c(t) \) decreases and tends to zero while \( I(t) \) increase.

We should be immediately state that although the mentioned parameters vary from day to day, it has been selected with an estimate based on the current data in worldwide.

Also the model (6) has been solved using the code “NDsolve” in the Wolfram Mathematica 12.1 with the initial conditions \( S(0) = 99999400 \), \( E(0) = 100 \), \( I(0) = 500 \) and \( R(0) = 0 \).

Firstly we give the following simulation which is a table that all countries of the world desire to encounter.

Indeed, the most important factor in the forming of this table is being small the effective contact rate \( \beta \). If \( \beta \) is not small enough, a dramatic increase in the number of infectious individuals will be inevitable, since the capacity of health care services will be exceeded. For example, if \( \beta \) increases by \( 0.17 \times 10^{-8} \) then the capacity of health care services will be exceeded and table in Fig. 1 will turn into table in Fig. 2(a).

Also if it is taken as \( \beta = 1.75 \times 10^{-8} \) instead of \( \beta = 1.5 \times 10^{-8} \) then the table in Fig. 2(a) will turn into table in Fig. 2(b) and as a result of this, while the maximum number of infectious individuals does not exceed 1.1 million, it rises to 2 million. Moreover, the case that the number of infectious exceed the capacity of health care services takes place approximately 3 months earlier.

On the other hand, if \( c(t) \) is taken as constant function such as \( c(t) = 1 \) then \( R_0 \) is founded as 4.11671. But it is more realistic that \( R_0 \) is variable during the outbreak. If function \( c(t) \) is choosen as
\[ c(t) = \frac{400000}{400000 + I(t)} \]
which is inversely proportional with \( I(t) \), then the change of \( R_0 \) is as follow.

It can be seen obviously that variations of \( R_0 \) and function \( I \) (in Fig. 2(b)) are compatible.

Consequently, for COVID-19 that the transmission risk of infection is very high, at this stage, the reduction of the effective contact rate and thus the reduction of the number of secondary infections \( R_0 \) will only be possible with a serious isolation and a conscious society.

On the other hand, for this population, behaviours of all compartment belong to the model (6) can be seen in Fig. 4.

Further, for same representative population and same parameters, in below figure, the reader can see the effect of function \( c(t) \) on the number of infectious individuals with the selections \( c(t) = 1 \), \( c(t) = 1/2 \), \( c(t) = 1/4 \) and \( c(t) = 1/8 \). As can be seen on the Fig. 5, for the case of \( c(t) = 1 \) which is mean that all hospi-
tal opportunities can be used fully, both the number of infectious individuals is more less and has been spread out over time.

Additionally, for same representative population and same parameters, Fig. 6 reflects the effect of the number of hospital beds on the number of infectious individuals.

Now, with a view to increase motivation for the reader, let us evaluate the process in Italy, which is one of the countries that are most shockingly affected from the pandemic. Due to the death rates experienced, Italy has passed through China, the center of the pandemic, and became one of the countries with the highest number of deaths. According to the reports of WHO; in Italy, from Jan 29 to 16 June 2020, there have been 236989 confirmed cases of COVID-19 with 34345 deaths, although in China, from Jan 11 to 16 June 2020, there have been 84823 confirmed cases of COVID-19 with 4645 deaths, [15,16]. Also, globally, as of 16 June 2020, there have been 7890687 confirmed cases of COVID-19, including 433404 deaths, reported to WHO, [1].

It should be immediately noted that, generally, in non-isolated or non-quarantined compartmental mathematical models, the all of population $S$ is assumed to be in free circulation. Of course, as a result of increasing cases of COVID-19 the some social isolation measures has been taken by government or individuals. So the number of susceptibles in circulation into the social lives has decreased with this fact.

We will focus on effect of the capacity of health care services on the number of infectious individuals for Italy. Italy is the country having, approximately, population of 60 million hospital beds 200000, intensive care units (ICUs) 7500 and ventilator machines 5324 in 2020, [17].

The Fig. 7 shows the harmony between the results of the model (6) solved by using the code “NDSolve” in the Wolfram Mathematica 12.1 and real datas (confirmed cases) with dates in Italy. While the model is solved, the parameters have been choosen as $\beta = 3000$, $\beta = 1.9 \times 10^{-7}$, $\gamma = 0.9$, $\alpha_1 = 0.25$, $\alpha_2 = 0.55$, $d = 0.00001$, $\delta = 0.1$, $\mu_1 = 0.05$, $\mu_2 = 0.15$, $\tau = 12$ and the function $c(t)$ has been taken as $c(t) = 200000/(200000 + I(t))$ too.

On the other hand, ICUs provides intensive treatment medicine and plays extremely significant role as life support in the treatment of COVID-19 and all critical diseases. Datas obtained from the model in this study aiming to show effect of health care capacity in process about COVID-19, has been obtained for ICUs 3000, 7500 and 3000, respectively. The obtained results have been compared with the real data of Italy in Fig. 8.

Also, the machine of ventilator is another one of the most vital health care used as life saver in the treatment of COVID-19. It is noted that Italy has currently about 5324 ventilator devices, [17]. Fig. 9 shows course of number of infectious according to different scenarios about number of ventilators.
The number of beds per person is an important indicator of the health care system of a country. One of the main measures will be taken in reducing the spread of COVID disease is to be reduction of infectious individuals in society. This can be achieved by allowed that serious patients are benefit from health care adequately. Therefore, it is very important to increase of countries the number of hospital beds, the number of ICUs and the number of ventilator devices, especially in the struggling against pandemic diseases.

**Declaration of Competing Interest**

The author declares that she has no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

**CRediT authorship contribution statement**

**Sümeyye Çakan**: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Resources, Software, Visualization, Writing - original draft, Writing - review & editing.

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