Mathematical Analysis and Numerical Solution of a Boundary Value Problem for the Covid-19 SIR Model

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Abstract: - This paper extends the work presented at IX. International Istanbul Scientific Research Congress held on May, 14-15, 2022, Istanbul/Türkiye. In that Congress the Authors narrowly focused on the numerical solutions of a boundary value problem for the Covid-19 SIR model appearing in literature. In this study this boundary value problem is solved numerically for all cases and also the stability analysis of the equilibrium points of the model is presented. The basic reproduction number R_0 is obtained and the importance of this number for the stability and the instability of the equilibrium points is emphasized. Numerical solutions are obtained using bvp4c, a boundary value problem solver in MATLAB and the results are presented in figures.

Key-Words: - Covid-19, Stability Analysis, Mathematical Modelling, MATLAB, Boundary Value Problem, Mathematical Analysis.

Received: April 9, 2023. Revised: December 17, 2023. Accepted: February 12, 2024. Published: April 3, 2024.

1 Introduction

The Covid-19 disease, which first appeared in China in December 2019 and spread all over the world in a short time, has taken its place among the epidemics, which has significantly affected life globally. Explaining the effects of this epidemic with mathematical models, as in other epidemics that have radically changed the life of humanity, has an important place in the literature.

Understanding past outbreaks can help us better prepare for future ones. Communicable diseases such as plague, malaria, smallpox, cholera, measles, tuberculosis, AIDS and flu, which are transmitted from animals, soil, water or human to human, have affected social life throughout history, causing demographic, social and economic problems. The answer to the question of how we will deal with future outbreaks can be obtained by examining past outbreaks, [1].

Mathematical models are very important in analyzing the spread and control of infectious diseases, [2], [3], [4], [5], [6], [7], [8], [9], [10]. Various mathematical models were used to be able to comment on these diseases and examine infectious diseases. In the SIR model, the society is divided into three groups, [11].

The well-known compartment model, consisting of susceptible, infected and recovered compartments, abbreviated as the SIR model, has been commonly used in infectious disease spread simulations for more than half a century although the mathematical model is very simple, [12].

Susceptible individuals have never been infected and therefore can catch the disease. Individuals who are infected can spread the disease, also individuals in the recovered state are assumed to be immune for life, [13].

Epidemiologically SIR model is used to determine the causes of diseases and health problems, to eliminate the natural development of diseases, to determine the health levels of the population, to investigate the change in time and when compared with other societies, to evaluate the results of clinical research, to evaluate the effectiveness of health services, and to determine the risks of encountering certain health problems of individuals in the population, [14].

2 The Model

The SIR model, [10], uses the system of ordinary differential equations

$$\frac{dS}{dt} = -\alpha SI \tag{1}$$

$$\frac{dI}{dt} = \alpha SI - \beta I \tag{2}$$

$$\frac{dR}{dt} = \beta I \tag{3}$$

where S, I and R mean the susceptible, infectious, and removed populations, respectively, and the parameter α is the transmission rate and β is the recovery rate (or in other words, the duration of infection $D = 1/\beta$). In the SIR model, for example, a person could change his or her condition from susceptible to infected with a ratio α, then to removed with a ratio β. Removed persons will never become susceptible. From eqs. (1)-(3) we have:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{4}$$

which means that $\mathrm{S(t) + I(t) + R(t) = const.}$ This is the total population size, and we denote it by N. At the time t=0 we assume $S(0) = S_0 = N - I_0$, $I(0) = I_0$ and $R(0) = 0$. From eqs. (1) and (2) we get:

$$\frac{dI}{dS} = \frac{\alpha SI - \beta I}{-\alpha SI}, \tag{5}$$

which yields that:

$$\frac{dI}{dS} = -1 + \frac{\beta}{\alpha S} \tag{6}$$

Integrating both sides we get:

$$I = -S + \frac{\beta}{\alpha}\ln(S) + C, \tag{7}$$

where C is an arbitrary constant. Using initial conditions we have:

$$C = I_0 + S_0 - \frac{\beta}{\alpha}\ln(S_0). \tag{8}$$

If eq. (8) is substituted in eq. (7) we get:

$$I = N - S + \frac{\beta}{\alpha}\ln\left(\frac{S}{S_0}\right). \tag{9}$$

Similarly, from eqs.(1) and (3) we obtain:

$$\frac{dS}{dR} = -\frac{\alpha}{\beta}S, \tag{10}$$

whose solution is:

$$S = S_0\, e^{-\frac{\alpha}{\beta}R}. \tag{11}$$

3 Stability Analysis of the Equilibrium Points of the Model

In this section [15], we find the equilibrium points of the model by considering that the model has two different set of equilibrium points, namely the disease-free equilibrium points and the disease-present equilibrium points.

Since R represents the number of the removed populations, it is enough to consider only the eqs. (1) and (2) to find the disease-free equilibrium points of the model. Therefore, it is easy to see that the disease-free equilibrium points of the system (1)-(2) are $E_{eq}^0 = (\mu, 0)$ for any real number μ.

We must consider the whole model consisting of eqs. (1)-(3) to find the disease-present equilibrium points which we call it $E_{eq}^* = (S^*, I^*, R^*)$.

If eq. (2) is set equal to zero we find $S^* = \frac{\beta}{\alpha}$ since $I^* \neq 0$. From eq. (9) one gets:

$$I^* = N - S^* + \frac{\beta}{\alpha}\ln\left(\frac{S^*}{S_0}\right). \tag{12}$$

Therefore, we obtain:

$$I^* = N + \frac{\beta}{\alpha}\left[\ln\left(\frac{\beta}{\alpha S_0}\right) - 1\right] \tag{13}$$

$$= \frac{\beta}{\alpha}\left(\underbrace{N\frac{\alpha}{\beta} + \ln\frac{\beta}{\alpha S_0}}_{R_0}\right) - \frac{\beta}{\alpha} \tag{14}$$

Let $R_0 = N\frac{\alpha}{\beta} + \ln\frac{\beta}{\alpha S_0}$ be the basic reproduction number (replicate number) that measures the average number of the new infected individuals generated by a single infected individual in a population of susceptible individuals. The value of R_0 will indicate whether the epidemic could occur or not.

As a result, the disease-present equilibrium points become

$$I^* = \frac{\beta}{\alpha}(R_0 - 1),\ S^* = \frac{\beta}{\alpha},\ R^* = -\frac{\beta}{\alpha}\ln\frac{\beta}{\alpha S_0}. \tag{15}$$

Since $\ln\frac{\beta}{\alpha S_0}$ must be < 0 one obtains $0 < \frac{\beta}{\alpha S_0} < 1$.

3.1 Local Stability Analysis of the Equilibria

Now we proceed to study the stability behavior of equilibria E_{eq}^0 and E_{eq}^*.

3.1.1 Local Stability Analysis of the Disease-Free Equilibrium

In this section, we analyze the local stability of the COVID-19 disease-free equilibrium. Computing the Jacobian matrix:

$$J(I,S) = \begin{pmatrix} -\alpha I & -\alpha S \\ \alpha I & \alpha S - \beta \end{pmatrix}, \quad (16)$$

at the disease-free equilibrium points E_{eq}^0, we get:

$$J\left(E_{eq}^0\right) = \begin{pmatrix} 0 & -\alpha\mu \\ 0 & \alpha\mu - \beta \end{pmatrix}. \quad (17)$$

The characteristic equation of this matrix becomes:

$$(-\lambda)(\alpha\mu - \beta - \lambda) = 0, \quad (18)$$

whose solutions are $\lambda_1 = 0$ and $\lambda_2 = \alpha\mu - \beta$. These are the eigenvalues of J. If $\alpha\mu < \beta$ we get $\lambda_1 = 0$ and $\lambda_2 < 0$, so that we have an attractive equilibrium line. Therefore, the equilibrium points are stable but not asymptotically.

If $\alpha\mu > \beta$ we obtain $\lambda_1 = 0$ and $\lambda_2 > 0$, so that we have a repulsive line of the equilibria, which means that the equilibrium points are unstable, [16].

3.1.2 Local Stability Analysis of the Disease-Present Equilibrium

In this section, we analyze the local stability of the disease-present equilibrium. If we now use the disease-present equilibrium point in eq. (16) we get:

$$J\left(E_{eq}^*\right) = \begin{pmatrix} -\beta(R_0 - 1) & -\beta \\ \beta(R_0 - 1) & 0 \end{pmatrix}. \quad (19)$$

In this case the characteristic equation becomes:

$$\lambda^2 + \lambda\beta(R_0 - 1) + \beta^2(R_0 - 1) = 0. \quad (20)$$

According to the Routh Hurwitz stability criterion, if $R_0 > 1$ the equilibrium point is asymptotically stable and it is unstable if $R_0 \leq 1$, [16], [17], [18], [19], [20].

4 Solutions to the Boundary Value Problem for the SIR Model

In the following computations we take $N = 60.48x10^6, S_0 = 6.48x10^6,$ $R(30) = 2.5x10^3, \quad I(30) = 31x10^3, \quad R(0) = 0,$ $r_0 = 10, R_0 = 0, \beta = \frac{1}{5}, \ \alpha = r_0\beta/N.$

4.1 Susceptible Individuals

If we differentiate eq. (1) we get:

$$\frac{d^2S}{dt^2} = -\alpha\left(\frac{dS}{dt}I + S\frac{dI}{dt}\right). \quad (21)$$

Using eq. (2) one obtains:

$$\frac{d^2S}{dt^2} = -\alpha\left[\frac{dS}{dt}I + S(\alpha SI - \beta I)\right]. \quad (22)$$

From eq. (1) it is easy to see that:

$$S\frac{d^2S}{dt^2} = \left(\frac{dS}{dt}\right)^2 + S(\alpha S - \beta)\frac{dS}{dt}. \quad (23)$$

We now solve this ordinary differential equation (ODE) with the boundary conditions provided above to study the number of healthy individuals who may contract the disease in 30 days.

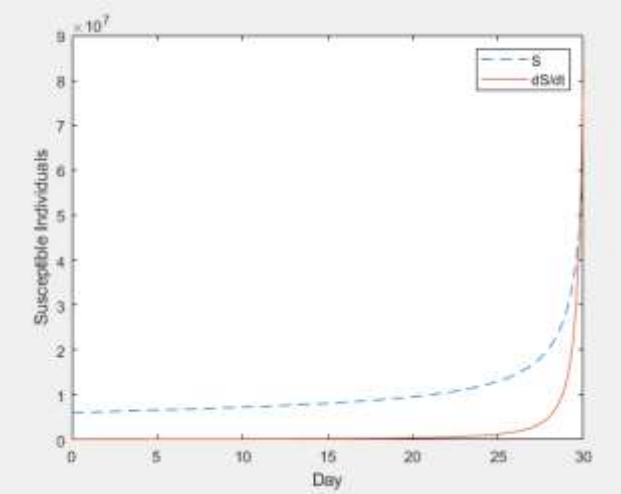

Fig. 1: Susceptible Individuals and the Change of Them in Time.

As seen in Figure 1, the dashed curve is the graph of susceptible individuals while the solid curve is the graph of the derivative of susceptible individuals over 30 days. While the number of the population that can get sick is small at the beginning, it increases over time and progresses to the entire population. The solid curve shows that the population that may be sick continues to increase over time and progress toward the entire population.

4.2 Infected Individuals

Similarly, if we differentiate eq. (2) we get:

$$\frac{d^2I}{dt^2} = -\alpha\left(\frac{dS}{dt}I + S\frac{dI}{dt}\right) - \beta\frac{dI}{dt}. \quad (24)$$

Using eq. (1) one obtains:

$$\frac{d^2I}{dt^2} = \alpha(-\beta SI)I + \alpha S\frac{dI}{dt} - \beta\frac{dI}{dt}, \quad (25)$$

and

$$I\frac{d^2I}{dt^2} = -\alpha\frac{dI}{dt}I^2 - \alpha\beta I^3 + \left(\frac{dI}{dt}\right)^2. \quad (26)$$

We now solve this ODE with the boundary conditions given above to study the number of infected individuals in 30 days.

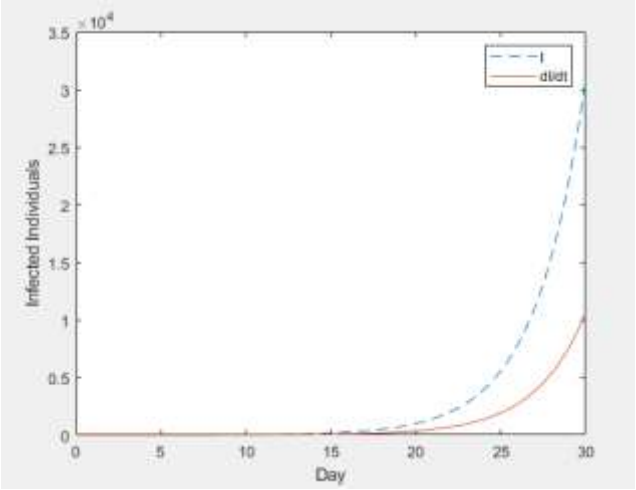

Fig. 2: Infected Individuals and the Change of Them in Time.

The dashed curve is the graph of infected individuals while the solid curve is the graph of the derivative of infected individuals over 30 days. Although the number of infected populations is small at the beginning, it increases over time. Also, the solid curve appears as evidence that the population that may become ill continues to increase over time. Figure 2 also shows us that the change in the number of infected individuals in society is proportional to the change in the number of infected individuals over time.

4.3 Removed Individuals

Recalling $S(t) + I(t) + R(t) = N$ and differentiating eq. (3) we get:

$$\frac{d^2R}{dt^2} = 0 - \beta\frac{dS}{dt} - \beta\frac{dR}{dt}. \quad (27)$$

From eq. (1) one obtains:

$$\frac{d^2R}{dt^2} = -\beta(-\alpha SI) - \beta\frac{dR}{dt}. \quad (28)$$

After some tedious work we come up with the differential equation

$$\frac{d^2R}{dt^2} = \left(\alpha S_0 \cdot e^{-\frac{\alpha}{\beta}R} - \beta\right)\frac{dR}{dt}. \quad (29)$$

We now obtain the solution of this ODE with the boundary conditions provided above to study the number of removed individuals in 30 days.

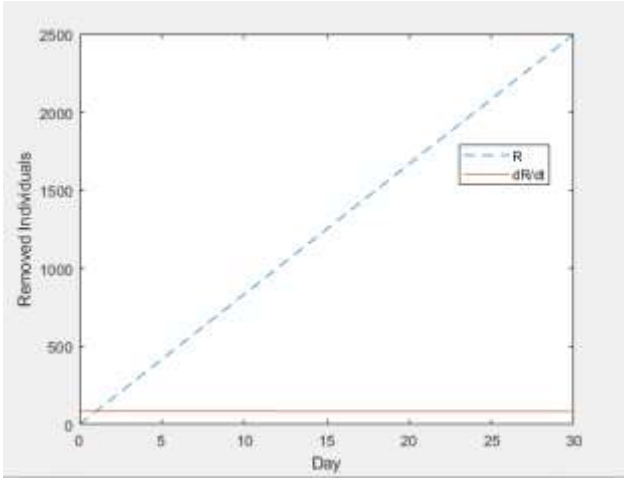

Fig. 3: Removed Individuals and The Change of Them in Time

The dashed curve is the graph of deceased individuals while the solid curve is the graph of the derivative of deceased individuals over 30 days. Although the number of individuals who died due to the epidemic is very low at the beginning, it continues to increase over time. Both curves continue linearly as they represent the number of dead individuals over time. According to Figure 3, a total of 2500 individuals died in the first 30 days. Therefore, an average of 83-84 people died daily. Indeed, Figure 3 reveals to us the whole reality regarding the number of changes in society. The daily number of dead individuals clearly expresses the number of changes in total deaths over time. Therefore, Figure 3 gives us descriptive information about all possible situations.

5 Discussion

In this paper we have shown numerically that as the virus infects individuals, the number of susceptible individuals decrease, while the number of individuals exposed to the virus increase. In this model, transitions from one group to another are unidirectional and there are no returns. In other words, an individual who has recovered will not be re-infected with the disease. Those who catch the virus interact with people who cannot be isolated and who do not have protection, and they transmit the disease to them, and the epidemic continues in this way. As the infected people regain their health or die, the number of individuals in the non-infectious group naturally increases.

In summary, among epidemiological models; the susceptible-infected-recovered (SIR) model, which says that infection provides permanent immunity, they have been used to describe diseases that spread where there is healing.

However, the SIR model does not have a latent stage (no exposed individual) and in this case is not suitable as a model for infectious exposure-progressed diseases such as COVID-19, [2].

6 Conclusion

In this study we have solved numerically a boundary value problem related to the Covid-19 SIR model over a period of time. By doing this we have observed the changes in the number of susceptible, infected and removed individuals and shown these changes in figures. Also, we have provided the stability analysis of the equilibrium points of the model and emphasized the importance of basic reproduction number R_0 (replicate number) for the stability and for the instability of the equilibrium points. We have seen that if $R_0 > 1$, there is an increase in the epidemic growth rate, if $R_0 < 1$ there is a decrease in the epidemic growth rate and if $R_0 = 1$ the epidemic growth rate is traveling at a constant speed.

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APPENDIX

MATLAB CODES

MATLAB Code to obtain the number of Susceptible Individuals

```
N = 60480000; % total population
r0 = 10; % breeding value
R0 = 0; % first population to recover
i_period = 5; % infectious period duration
beta = 1/i_period ;% recycling rate
alpha = r0*beta/N; % infection rate
ya(1) = 6048000;
yb(1) = 60446500;
f=@(x,y)[y(2);y(2)^2/y(1)+(alpha*y(1)-beta)*y(2)];
bc=@(ya,yb) [ya(1)-6048000;yb(1)-60446500];
%boundary conditions
xmesh= linspace (0,30,100); %create a network
solinit = bvpinit(xmesh, [1 0]); % first guess of the
solution
sol = bvp4c(f, bc, solinit); % run solver
figure;
plot(sol.x, sol.y(1,:), '--')
hold on;
plot(sol.x, sol.y(2,:), '-')
xlabel('Day');
ylabel('Susceptible Individuals S');
legend('S', 'dS/dt');
hold off;
```

MATLAB Code to obtain the number of Infected Individuals

```
N = 60480000; % total population
r0 = 10; % breeding value
R0 = 0; % first population to recover
i_period = 5; % infectious period duration
beta = 1/i_period ;% recycling rate
alpha = r0*beta/N; % infection rate
ya(1) = 1;
yb(1) = 31000;
f=@(x,y)[y(2);-alpha*y(2)*y(1)+y(2)^2/y(1)-
alpha*beta*y(1)^2];
bc=@(ya,yb) [ya(1)-1;yb(1)-31000]; % boundary
conditions
xmesh= linspace (0,30,200); % create a network
solinit = bvpinit(xmesh, [100 0]); % first guess of
the solution
sol = bvp4c(f, bc, solinit); % run solver
figure;
plot(sol.x, sol.y(1,:), '--')
hold on;
plot(sol.x, sol.y(2,:), '-')
xlabel('Day');
ylabel('Infected Individuals');
```

```
legend('I', 'dI/dt');
hold off;
```

MATLAB Code to obtain the number of Removed Individuals

```
N = 60480000; % total population
H0 = 6048000;
r0 = 10; % breeding value
R0 = 0; % first population to recover
i_period = 5; % infectious period duration
beta = 1/i_period ;% recycling rate
alpha = r0*beta/N; % infection rate
ya(1) = 0;
yb(1) = 2500;
f=@(x,y)[y(2);(alpha*H0*exp(-(alpha/beta)*y(1))-
beta)*y(2)];
bc=@(ya,yb) [ya(1);yb(1)-2500]; %boundary
conditions
xmesh = linspace (0,30,31); % create a network
solinit = bvpinit(xmesh, [1 0]); %% first guess of
the solution
sol = bvp4c(f, bc, solinit); % run solver
figure;
plot(sol.x, sol.y(1,:), '--')
hold on;
plot(sol.x, sol.y(2,:), '-')
xlabel('Day');
ylabel('Removed Individuals');
legend('R', 'dR/dt'); hold off;
```

Contribution of Individual Authors to the Creation of a Scientific Article (Ghostwriting Policy)

The authors equally contributed in the present research, at all stages from the formulation of the problem to the final findings and solution.

Sources of Funding for Research Presented in a Scientific Article or Scientific Article Itself

No funding was received for conducting this study.

Conflict of Interest

The authors have no conflicts of interest to declare.