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Research article

Analysis of Covid 19 disease with SIR model and Taylor matrix method

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Abstract: Covid 19 emerged in Wuhan, China in December 2019 has continued to spread by affecting the whole world. The pandemic has affected over 328 million people with more than 5 million deaths in over 200 countries which has severely disrupted the healthcare system and halted economies of the countries. The aim of this study is to discuss the numerical solution of the SIR model on the spread of Covid 19 by the Taylor matrix and collocation method for Turkey. Predicting COVID-19 through appropriate models can help us to understand the potential spread in the population so that appropriate action can be taken to prevent further transmission and prepare health systems for medical management of the disease. We deal with Susceptible–Infected–Recovered (SIR) model. One of the proposed model's improvements is to reflect the societal feedback on the disease and confinement features. We obtain the time dependent rate of transmission of the disease from susceptible $\beta(t)$ and the rate of recovery from infectious to recovered γ using Turkey epidemic data. We apply the Taylor matrix and collocation method to the SIR model with γ, $\beta(t)$ and Covid 19 data of Turkey from the date of the first case March 11, 2020 through July 3, 2021. Using this method, we focus on the evolution of the Covid 19 in Turkey. We also show the estimates with the help of graphics and Maple.

Keywords: SIR model; nonlinear differential equation systems; Taylor polynomials and series; Covid 19; collocation points
Mathematics Subject Classification: 34A34, 65H10, 92D25, 92D30

1. Introduction

Human beings have struggled with various epidemic and pandemic diseases and millions of people lost their lives due to these diseases. For this reason, many studies based on science have emerged. Epidemiology is a branch of science that deals with the investigations of the distribution of health-

related facts and their determinants in a particular population and the studies in the control of health-related problems [1]. In epidemiology, mathematical models are used to express the behaviour of a system. Mathematical modeling is the process of transferring real-life situations to the language of mathematics and expressing them mathematically. The product that emerges at the end of this process is called a mathematical model. Mathematical models are very important in terms of providing information about epidemics and allowing predictions to be made.

Many studies have been carried out by many scientists until today. The first example of the use of mathematical models in the prediction of the spread of infectious diseases belongs to A. G. McKendrick and W. O. Kermack in [2]. In the model called SIR, developed by Kermack and McKendrick, the stages of an infectious disease are modeled with simple differential equations [3, 4]. F. C. Hoppensteadt studied population dynamics using numerical methods in [5]. In [6], B. Shulgin et al. studied an SIR model with a vaccination rate. In [7], M. C. Schuette and H. W. Hethcote developed an age-structured epidemiologic-demographic model with vaccination for varicella and zoster. In [8], D. J. Dalej and J. Gani studied about epidemic modelling. In [9], M. Ianelli modeled the spreading of an epidemic, taking care of the age structure of the population. In [10], M. Rafei et al. considered problem of the spread of a non-fatal disease in a population which is assumed to have constant size over the period of the epidemic. In [11], S. Ahmetolan et al. discussed the determination of baseline reproduction number, average duration of infectious period and estimation of timing of peak of epidemic using early stage data. U. Nguemdjo et al. analyzed the evolution of Covid 19 in [12]. E. B. Postnikov tested the application of based on the existence of mathematically sequential reduction of the three-compartmental SIR model to the Verhulst equation with the parameters determined by the basic characteristic of epidemic process in [13]. N. R. Record and A. Pershing examined how a coupled system works using a model of viral infection SIR model in [14]. In [15], N. S. Barlow and S. J. Weinstein obtained an accurate closed-form solution to the SIR epidemic model through the use of asymptotic approximants. N. A. Kudryashov et al aimed to establish the exact relationships among S, I, R population variables, as well as to suggest a form for the exact solution of the SIR model in [16, 17]. In the literature, methods are used for approximate solutions of epidemic diseases and population dynamics. F. Shakeri and M. Dehghan presented the solution of a delay differential equation by means of a homotopy perturbation method in [18]. D. J. Evans and K. R. Raslan applied the adomian decomposition method to the DDE in [19]. F. Shakeri and M. Dehghan investigated the numerical solution of a delay differential equation, namely, the pantograph equation by means of the adomian decomposition method in [20]. In [21], A. Saadatmandi and M. Dehghan applied the variational iteration method to solve the generalized pantograph equation. F. Shakeri and M. Dehghan considered a system of two nonlinear integro-differential equations which arises in biology and implemented the variational iteration method for finding the solution of this system in [22]. F. S. Akinboro et al. investigated the application of differential transformation method and variational iteration method in finding the approximate solution of Epidemiology (SIR) model in [23].

In additon, There are also more recent contributions such as part-time SIR model and full-time SIR model that clarify the importance of initial conditions and provide "semi-analytical" solutions [24, 25]. In the present works, authors use the semi-time model, which means, that results are invalid at negative times.

In this study, the SIR model was used in order to observe the Covid 19 and to make predictions about its spread. The aim of this study is to apply the Taylor matrix and collocation method [26, 27], which

is used for differential equations and differential equation systems in the literature, for SIR model with Covid 19 data of Turkey. We develop a method to determine the time dependent rate of transmission of the disease from susceptible $\beta(t)$, the rate of recovery from infectious to recovered γ and the series truncated limit to give the best approach.

2. Method

In this study, we deal with the SIR model for modeling the total number of cases of Covid 19. We use the Taylor matrix and collocation method using Maple program to obtain the numerical solutions for this model.

2.1. SIR model for Covid 19

The SIR model which was introduced by W. O. Kermack has played an important role in mathematical epidemiology. In the model, a population is divided into three groups:
• Susceptible individuals $(S) = S(t)$: Represent individuals that were not contaminated by Covid 19 at time t
• Infected individuals $(I) = I(t)$: Represent individuals infected by Covid 19 at time t
• Recovered individuals $(R) = R(t)$: Represent individuals that have recovered and death from Covid 19 at time t.

There are some important assumptions for the simple SIR Model. The outbreak is short-lived. $N \gg 1$ is the total size of the population. The total population is large and closed, and its size remains. No natural birth or natural death occurs. Hence, the population N is constant over time. For any time t, $N = S(t) + I(t) + R(t)$ and $N' = S'(t) + I'(t) + R'(t) = 0$. The number of individuals in each compartment must be integer, but if the population size N is sufficiently large, it is possible to treat S and I as continuous variables. Initially, in the absence of infection we have $I + R = 0$ and $S \approx N$, i.e., $S/N \approx 1$ and we assume that the whole population is susceptible. The SIR model for Covid 19 spread is presented in the form of a chart as (2.1).

$$\underset{(S)}{\text{Susceptible}} \xrightarrow{\beta(t)} \underset{(I)}{\text{Infected}} \xrightarrow{\gamma} \underset{(R)}{\text{Recovered}} \tag{2.1}$$

$\beta(t)$: The time dependent rate of transmission of the disease from susceptible,

γ : The rate of recovery from infected to recovered.

We assume that the carriers leave the class infected (I) at a constant γ rate and enter directly to the class recovered (R). The motion line of the model is as follows.

$$(\text{S}) \xrightarrow{\beta(t)SI} (\text{I}) \xrightarrow{\gamma I} (\text{R})$$

SIR model considered that everyone in the population has an equal probability of getting infected. The SIR model can be mathematically represented as follows.

$$\begin{aligned} S'(t) &= -\beta(t)\,S(t)\,I(t) \\ I'(t) &= \beta(t)S(t)I(t) - \gamma I(t) \\ R'(t) &= \gamma I(t) \end{aligned} \tag{2.2}$$

subject to initial conditions $S(t_0)>0$, $I(t_0)>0$ and $R(t_0)\geq 0$. Since all-time SIR model means that the quantities S, I, R do not get negative for negative times (the past), initial condition $R(0) = 0$ is incompatible with the all-time SIR model, but only compatible with the semi-time SIR model. We have three differential equations for three categories of people within the population. Susceptible are those who are not infected and not immune. Infective are those who are infected and can transmit the disease. Recovered are those who have been infected, have recovered, have died from disease and are permanently immune. So, the number of susceptible is going to decrease according to the number of contacts between the infectives and the susceptibles. We assume that $\beta(t)$ is an exponential function, i.e., $\beta(t) = \beta_0 e^{-\alpha t}$. This conjecture will be verified by fitting data. We can calculate the function β using the least squares. We define the new infected in the unit of time with $i_n(t)=\beta(t)I(t)$, then we have $\beta(t)=i_n(t)/I(t)$.

In the least-squares approach, the objective function requires to be minimized. The objective is based upon adjusting the parameters for a model function to fit a data set in a best possible way. A simple data set consist of n points (x_h, y_h), where x_h shows an independent variable and y_h stands for a dependent variable whose value is computed using observation. The model function possesses the form $g(x, p)$, where m adjustable parameters are kept in the vector p. The goal is to notice the parameters for the model that fit the data in a best possible way. Such a fit of a model to a data point is measured by its residual, defined as the difference between the real available value of the dependent variable and the value predicted by the model:

$$r_h = y_h - g(x_h, p) \tag{2.3}$$

The least-squares method obtains the optimal parameter values by minimizing the sum of squared residuals as shown below [28]:

$$G = \sum_{h=1}^{m} (r_h)^2 = \sum_{h=1}^{m} (y_h - g(x_h, p))^2 \tag{2.4}$$

This mathematical model works on a few assumptions. SIR model considered that everyone in the population has an equal probability of getting infected and model reliability depends on the quality of data, it is assumed that the data available on the open platform is correct. It is difficult to predict the future of the pandemic as an infected individual cannot be reinfected and government future steps to control the pandemic is always uncertain like weekly lockdown, or partial opening in the future and due to uncertainty in the future actions by authorities. Because of these uncertainties and assumptions, this work has concentrated on the analysis of the evolution of the infection.

2.2. Method of solution For SIR model

Our aim in this section, the nonlinear differential equation systems defined as Eq (2.2) is where the time dependent rate of transmission of the disease from susceptible $\beta(t)$, the rate of recovery from infectious to recovered γ,

$$S(t) = \sum_{n=0}^{M} S_n t^n, \qquad S_n = \frac{S^{(n)}(0)}{n!}, \qquad n = 0, 1, 2, ...M, \qquad 0 \leq t \leq b \tag{2.5}$$

$$I(t) = \sum_{n=0}^{M} I_n t^n, \qquad I_n = \frac{I^{(n)}(0)}{n!}, \qquad n = 0, 1, 2, ...M, \qquad 0 \leq t \leq b \tag{2.6}$$

$$R(t) = \sum_{n=0}^{M} R_n t^n, \qquad R_n = \frac{R^{(n)}(0)}{n!}, \qquad n = 0, 1, 2, ...M, \qquad 0 \le t \le b \tag{2.7}$$

with the initial condition Nth order to obtain the numerical solution in terms of truncated Taylor series forms. We consider the approximate solution $S(t)$, $I(t)$, $R(t)$ and their derivative defined by truncated Taylor series (2.5)–(2.7). If we write (2.5)–(2.7) in the matrix form, we obtain

$$S(t) = T(t) S \tag{2.8}$$

$$I(t) = T(t) I \tag{2.9}$$

$$R(t) = T(t) R \tag{2.10}$$

where

$$T(t) = \begin{bmatrix} 1 & t & t^2 & \cdots & t^M \end{bmatrix}_{1\times(M+1)}$$

$$S = \begin{bmatrix} S_0 \\ S_1 \\ \vdots \\ S_M \end{bmatrix}_{(M+1)\times 1}$$

$$I = \begin{bmatrix} I_0 \\ I_1 \\ \vdots \\ I_M \end{bmatrix}_{(M+1)\times 1}$$

$$R = \begin{bmatrix} R_0 \\ R_1 \\ \vdots \\ R_M \end{bmatrix}_{(M+1)\times 1}.$$

Also when we write (2.5)–(2.7) derivative in the matrix form, we have

$$S'(t) = T(t) BS \tag{2.11}$$

$$I'(t) = T(t) BI \tag{2.12}$$

$$R'(t) = T(t) BR \tag{2.13}$$

where

$$B = \begin{bmatrix} 0 & 1 & 0 & \cdots & 0 \\ 0 & 0 & 2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & M \\ 0 & 0 & 0 & \cdots & 0 \end{bmatrix}_{(M+1)\times(M+1)}.$$

Similarly, $S(t)I(t)$ which is the nonlinear term of Eq (2.2) can be defined by the relation

$$S(t) I(t) = T(t) T^*(t) \overline{S} \tag{2.14}$$

where

$$T^*(t) = \begin{bmatrix} T(t) & 0 & \cdots & 0 \\ 0 & T(t) & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & T(t) \end{bmatrix}_{(M+1)\times(M+1)^2}$$

$$\overline{S} = \begin{bmatrix} S_0 I \\ S_1 I \\ \vdots \\ S_n I \end{bmatrix}_{(M+1)^2\times 1}.$$

By substituting (2.8)–(2.14) into Eq (2.2), we obtain the matrix equation as:

$$T(t)BS + \beta(t)T(t)T^*(t)\overline{S} = 0 \tag{2.15}$$

$$[T(t)B + \gamma T(t)]I - \beta(t)T(t)T^*(t)\overline{S} = 0 \tag{2.16}$$

$$T(t)BR - \gamma T(t)I = 0. \tag{2.17}$$

Thus, the matrix representation of the logistic differential equation systems (2.15) and (2.16) becomes

$$D_1(t)S + H_1\overline{S} = 0 \tag{2.18}$$

$$D_2(t)I + H_2\overline{S} = 0 \tag{2.19}$$

where

$$\begin{aligned} D_1(t) &= T(t)B \\ H_1(t) &= \beta(t)T(t)T^*(t) \\ D_2(t) &= T(t)B + \gamma T(t) \\ H_2(t) &= -\beta(t)T(t)T^*(t). \end{aligned}$$

If we define

$$D(t) = \begin{bmatrix} D_1(t) & 0 \\ 0 & D_2(t) \end{bmatrix}_{2\times 2(M+1)}$$

$$H(t) = \begin{bmatrix} H_1(t) & 0 \\ 0 & H_2(t) \end{bmatrix}_{2\times 2(M+1)^2}$$

$$\overline{SI} = \begin{bmatrix} S \\ I \end{bmatrix}_{2(M+1)\times 1}$$

$$\overline{\overline{S}} = \begin{bmatrix} \overline{S} \\ \overline{S} \end{bmatrix}_{2(M+1)^2\times 1}$$

$$G(t) = \begin{bmatrix} 0 \\ 0 \end{bmatrix}_{2\times 1},$$

we obtain

$$D(t)\overline{SI} + H(t)\overline{\overline{S}} = G(t). \tag{2.20}$$

If the collocation points which are defined as

$$t_s = \frac{b}{M}s, \qquad s = 0, 1, ..., M \qquad 0 \le t \le b$$

substitute into Eq (2.20), we obtain

$$D\left(t_s\right)\overline{SI} + H\left(t_s\right)\overline{\overline{S}} = G\left(t_s\right) \tag{2.21}$$

or the matrix equation

$$\widetilde{D}\overline{\overline{SI}} + \widetilde{H}\widetilde{S} = \widetilde{G} \tag{2.22}$$

where

$$\widetilde{D} = \begin{bmatrix} D\left(t_0\right) & 0 & \cdots & 0 \\ 0 & D\left(t_1\right) & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & D\left(t_N\right) \end{bmatrix}_{2(M+1)\times 2(M+1)^2}$$

$$\overline{\overline{SI}} = \begin{bmatrix} SI \\ SI \\ \vdots \\ SI \end{bmatrix}_{2(M+1)^2\times 1}$$

$$\widetilde{H} = \begin{bmatrix} H\left(t_0\right) & 0 & \cdots & 0 \\ 0 & H\left(t_1\right) & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & H\left(t_N\right) \end{bmatrix}_{2(M+1)\times 2(M+1)^3}$$

$$\widetilde{S} = \begin{bmatrix} \overline{\overline{S}} \\ \overline{\overline{S}} \\ \vdots \\ \overline{\overline{S}} \end{bmatrix}_{2(M+1)^3\times 1}$$

$$\widetilde{G} = \begin{bmatrix} G(t_1) \\ G(t_2) \\ \vdots \\ G(t_N) \end{bmatrix}_{2(M+1)\times 1}.$$

When the matrix form of the conditions is written as

$$T\left(0\right)S = \lambda_1 \tag{2.23}$$

$$T\left(0\right)I = \lambda_2 \tag{2.24}$$

and replaces any two row of Eq (2.22), the new conditional matrix equation is obtained. Thus, the matrix equation of the system (2.2) turns into a nonlinear algebric system under the given initial conditions. This system consist of $2(M + 1)$ equations. Here, if we calculate the unknown coefficients and substitute in Eqs (2.5) and (2.6), we obtain Taylor polynomial solution for $S(t)$ and $I(t)$. Then, if we substitute the obtained $I(t)$ Taylor polynomial solution in Eq (2.7), we obtain Taylor polynomial solution for $R(t)$.

3. Numerical application

In this section, we apply the Covid 19 data to the SIR model, which is received from Ministry of Health (Turkey). We obtain necessary results by analyzing the Taylor collocation method using Maple program.

3.1. Turkey and Covid 19

3.1.1. Susceptible (S)

The time dependent rate of transmission of the disease from susceptible $\beta(t)$ and the rate of recovery from infectious to recovered γ are solved using the method described in Section 2. We calculate epidemic parameters in Eq (2.2) as $\beta(t)$=$0.05472e^{(-0.00062t)}$ and we plot Figure 1 with maple program. Covid 19 infected individuals generally develop symptoms, including mild respiratory symptom and fever on an average of 5–6 days after infection. In our simulation, we set γ=1/15 and t is varied from 0 to 480 in suitable units. For visualizing purposes, $\beta(t)$ parameter is monitored and analyzed for better understanding of the infectious disease dynamics.

Initially, in the absence of infection we have $I+R = 0$ and $S \approx N$, i.e., $S/N \approx 1$ and we assume that the whole population to be susceptible. For modelling purpose, this study has considered $S_0 = 81.999.999$, and the number of initial cases as $I_0 = \frac{1}{81.999.999}$ and $R_0 = 0$. We plot the Figure 2 using these values with Maple program. We can see that up to $t = 480$, the rate of susceptible (S) gradually decreases.

3.1.2. Infected (I)

Similarly, we calculate the epidemic parameters in Eq (2.2) as $\beta(t)$=$0.05472e^{(-0.00062t)}$, $\gamma = \frac{1}{15}$ and t is varied from 0 to 480 in suitable units. And we assume that $S_0 = 81.999.999$, $I_0 = \frac{1}{81.999.999}$ and $R_0 = 0$. We plot the Figure 3 using these values with Maple program. We can see that up to 480, the rate of infected (I) gradually increases.

3.1.3. Recovered (R)

We calculate the epidemic parameters in Eq (2.2) as $\beta(t)$=$0.05472e^{(-0.00062t)}$, $\gamma = \frac{1}{15}$ and t is varied from 0 to 464 in suitable units. And we assume that $S_0 = 81.999.999$, $I_0 = \frac{1}{81.999.999}$ and $R_0 = 0$. We plot the Figure 4 using these values with Maple program. We can see that up to $t = 464$, the rate of recovered (R) gradually increases.

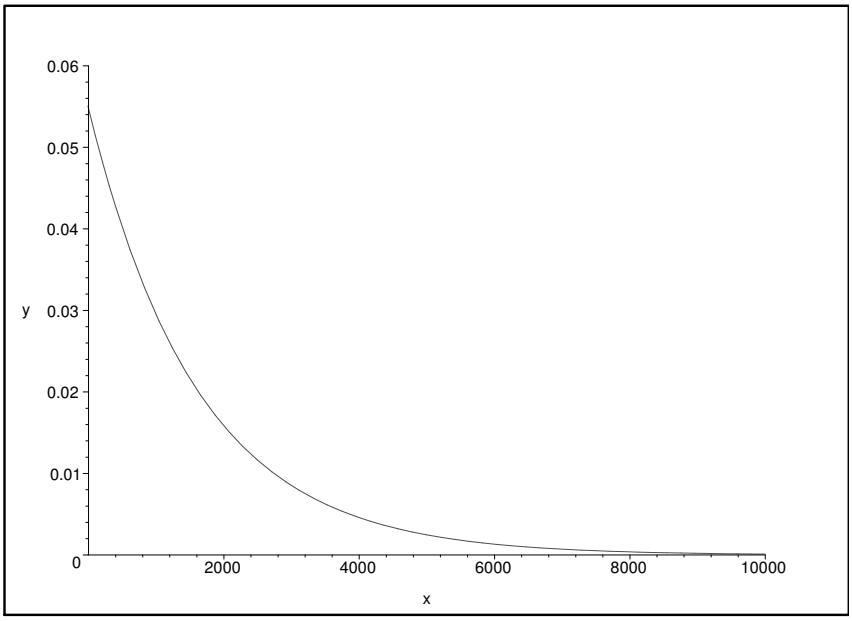

Figure 1. The time dependent decreasing rate of transmission of the disease from susceptible $\beta(t)$. (x-axis=days, y-axis=percentage of total population).

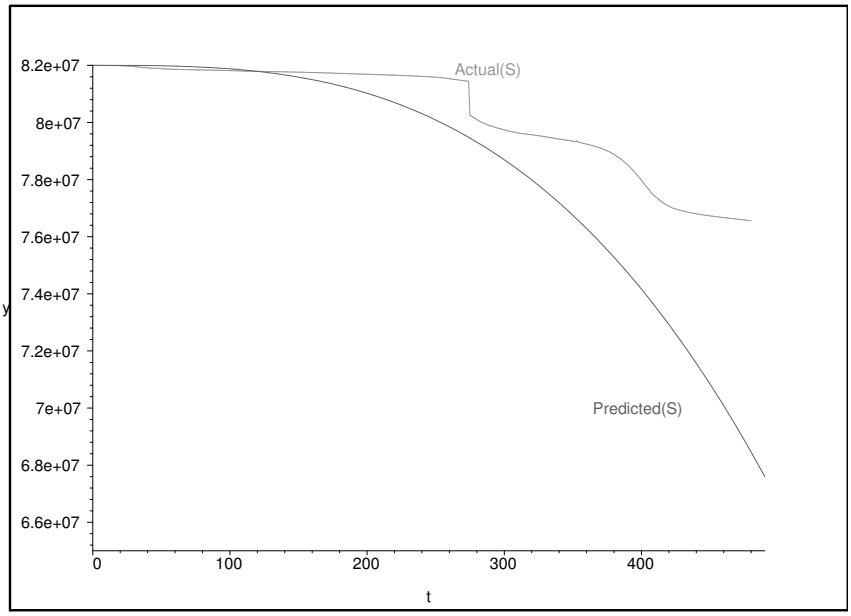

Figure 2. Time evolution of the number of Susceptible (S) is predicted by the SIR model with Taylor collocation method and actual Susceptible (S), which is number of people living in Turkey from the date of the first case March 11, 2020 through July 3, 2021 is obtained by Eq (2.2). The parameters are $\beta(t)$=0.05472$e^{(-0.00062t)}$ and γ=1/15. In addition, the number of susceptible (S) are solved for $M = 3$. (t-axis=days, y-axis=number of people).

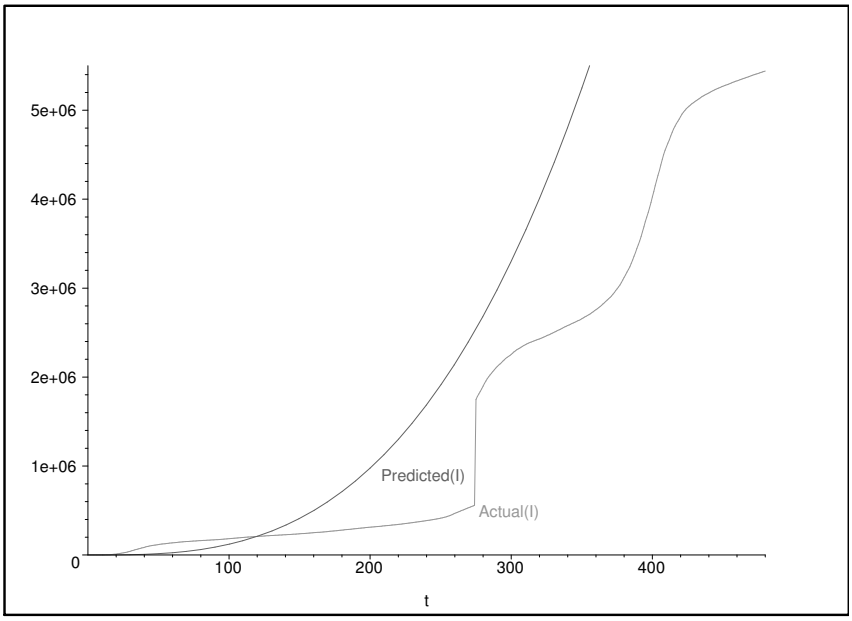

Figure 3. Time evolution of the number of Infected (I) is predicted by the SIR model with Taylor collocation method and actual Infected (I), which is number of infected people living in Turkey from the date of the first case March 11, 2020 through July 3, 2021 is obtained by Eq (2.2). The parameters are $\beta(t)$=0.05472$e^{(-0.00062t)}$ and γ=1/15. In addition, the number of infected (I) are solved for $M = 3$. (t-axis=days, y-axis=number of people).

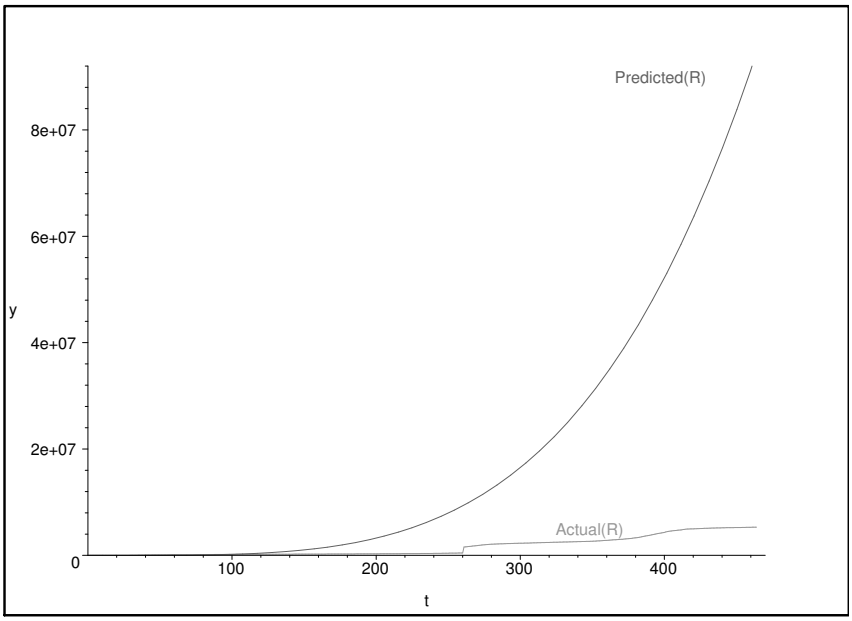

Figure 4. Time evolution of the number of Recovered (R) is predicted by the SIR model with Taylor collocation method and actual Recovered (R), which is number of recovered people living in Turkey from the date of the first case March 11, 2020 through July 3, 2021 is obtained by Eq (2.2). The parameters are $\beta(t)$=0.05472$e^{(-0.00062t)}$ and γ=1/15. In addition, the number of Recovered (R) are solved for $M = 3$. (t-axis=days, y-axis=number of people).

4. Conclusions

Studies on the modeling of epidemic diseases have gained considerable importance and popularity. The solutions of these models can be done much faster and more reliably with the development of computer technology. In this study, we investigated Covid 19 epidemic and made predictions about its spread. Applying data to the SIR model, we have tried to estimate the parameters that can be used to quantify the temporal evolution of Covid 19 in the country using Taylor matrix and collocation method. The number of susceptible (S), the number of infected (I) and the number of recovered (R) are solved for $M = 3$ in Figures 2–4, respectively. In addition, the accuracy of the solutions obtained can be checked by using Taylor matrix and collocation method which is increased when the large M is chosen. The results obtained can be recalculated and compared with the exact numerical solution of the SIR model in [15] and [24]. It is possible to make predictions for the occurences, progression and analysis of Covid 19 with this method. The SIR model of differential equations can be solved conveniently using a numerical solver for differential equations. This way the solution is not limited to small times. Also, this process is very useful as the results can be obtained easily with a computer program.

Conflict of interest

This work does not have any conflicts of interest.

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