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A study of Covid 19 disease mathematical model via wavelets

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Abstract. In this study, we propose an effective numerical algorithm to study the Covid-19 epidemic model that is in the form of a system of the coupled ordinary differential equation. This algorithm includes the collocation method and truncated Laguerre wavelet. Here, we reduce the system of a differential equation into a set of algebraic equations which are having unknown Laguerre wavelet coefficients. Moreover, the modeling of the spreading of a Covid-19 disease in a population is numerically solved by the present method.

Keywords: Wavelets, collocation method, mathematical model.

2000 MSC: 65T60 42C15 93C15.

1. Introduction

Since the first reports of novel pneumonia (COVID-19) in Wuhan, Hubei province, China [1], there has been considerable discussion on the origin of the causative virus, SARS-CoV-2 also referred to as HCoV-19. Infections with SARS-CoV-2 are now wide. The spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has already taken on pandemic proportions, affecting over 100 countries in a matter of weeks. A study in Italy the patients who died, 42.2% were aged 80–89 years, 32.4% were aged 70–79 years, 8.4% were aged 60–69 years, and 2.8% were aged 50–59 years, those aged >90 years made up 14.1% [2]. The potential risk factors of older age, high SOFA score Wuhan Pulmonary Hospital December 2019, Wuhan, China was carried out and found out those increasing odds of in-hospital death associated with older age [3]. Because of the COVID-19 world health emergency, various governments suggested the WHO to have an **"*Immunity Passport*"** or **"*risk-free certificate*"** to provide work or travel permits. However no evidence that people who have recovered from COVID-19 and have antibodies are protected from a second infection.

Mathematical model of severe SARS-CoV-2 to assess the potential for sustained human-to-human transmission with four datasets from within and outside of Wuhan was addressed between December 2019, and February 2020 [4]. In another stochastic transmission model, parameterized to the COVID-19 outbreak. The model used to quantify the potential effectiveness of contact tracing and isolation of cases at controlling a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)-like pathogen. This could lead to having the success of controlling outbreaks using isolation and contact tracing and quantified the weekly maximum number of cases traced to measure the feasibility of public health effort [5]. In Wuhan, China, a novel and alarmingly contagious primary atypical (viral) pneumonia broke out in December 2019. It has since been identified as a zoonotic coronavirus, similar to SARS coronavirus and MERS coronavirus and named COVID-19. As of 8 February 2020, 33 738 confirmed cases and 811 deaths have been reported in China.

A review on the basic reproduction number $\left[\frac{\beta}{\gamma} = R_0\right]$ of the COVID-19 virus. R0 is an indication of the transmissibility of a virus, representing the average number of new infections generated by an infectious person in a naïve population. For $\left[\frac{\beta}{\gamma} = R_0 > 1\right]$, the number infected is likely to increase, and for $\left[\frac{\beta}{\gamma} = R_0 < 1\right]$, the transmission is likely to die out. The basic reproduction number is a central concept in infectious disease epidemiology, indicating the risk of an infectious agent concerning epidemic spread [6].

To examine how changes in population mixing have affected outbreak progression in Wuhan, we used synthetic location-specific contact patterns in Wuhan and adapted these in the presence of school closures, extended workplace closures, and a reduction in mixing in the general community. Using these matrices and the latest estimates of the epidemiological parameters of the Wuhan outbreak, the simulated the ongoing trajectory of an outbreak in Wuhan using an age-structured susceptible-exposed-infected-removed (SEIR) model for several physical distancing measures. The latest estimates of epidemic parameters from a transmission model to data on local and internationally exported cases from Wuhan in an age-structured epidemic framework and investigated the age distribution of cases. The simulated lifting of the control measures by allowing people to return to work in a phased-in way and looked at the effects of returning to work at different stages of the underlying outbreak (at the beginning of March or April) [7].

In real-time, estimates of the case fatality ratio (CFR) and infection fatality ratio (IFR) can be biased upwards by under-reporting of cases and downwards by failure to account for the delay from confirmation to death. Collecting detailed epidemiological information from a closed population such as the quarantined Diamond Princess Cruise ship in Japan can produce a more comprehensive description of asymptomatic and symptomatic cases and their subsequent outcomes. We aimed to estimate the IFR and CFR of coronavirus disease (COVID-19) in China, using data from passengers of the Diamond Princess while correcting for delays between confirmation and death and for the age structure of the population [8].

The novel 2019 coronavirus, SARS-CoV-2 (COVID-19), emerged towards the end of 2019 in the city of Wuhan in the province of Hubei in the People's Republic of China, and it has spread to the entire world very fast and in a very short time. This study aimed to investigate the course of the pandemic by mathematical modeling based on the information that the time-dependent change (spreading) rate of the H number of individuals who have caught a contagious disease is proportional to the multiplication of the numbers of those who have caught the disease and those who have not. According to the results of the mathematical modeling in our study, in the case that sufficient precautions are not taken, or precautions are reduced, the course of the pandemic may show a very fast change in the negative direction. For this reason, every precaution, individual or social, will be significant in terms of the course of the COVID-19 pandemic [9].

The outbreak of novel coronavirus-caused pneumonia (COVID-19) in Wuhan has attracted worldwide attention. Here, we propose a generalized SEIR model to analyze this epidemic. Based on the public data of the National Health Commission of China from Jan. 20th to Feb. 9th, 2020, we reliably estimate key epidemic parameters and make predictions on the inflection point and possible ending time for 5 different regions. According to optimistic estimation, the epidemics in Beijing and Shanghai will end soon within two weeks, while for most of China, including the majority of cities in Hubei province, the success of anti-epidemic will be no later than the middle of March. The situation in Wuhan is still very severe, at least based on public data until Feb. 15th. We expect it will end up at the beginning of April. Moreover, by inverse inference, we find the outbreak of COVID-19 in Mainland, Hubei province and Wuhan all can be dated back to the end of December 2019, and the doubling time is around two days at the early stage.

Wavelets are special functions in a limited domain that is, a wave function instead of oscillating forever it drops to zero. Recently, we have facing different kinds of wavelets which are depending on two parameters such as, n is dilation parameter and k is the translation parameter [10]. The theory and application of wavelets is a comparatively young branch in signal processing and mathematical field. It has been applied in engineering disciplines, such as signal analysis, time-frequency analysis, and engineering mathematics [11-17].

In this study, we proposed a new algorithm to obtain numerical solutions for the system of ordinary differential equations with different constraints. it is very important to obtain numerical solutions for the system of nonlinear ordinary differential equations in many different fields of science and engineering such as chemical physics, fluid mechanics, solid-state physics, plasma physics, and plasma waves. Most realistic systems of ordinary differential equations do not have exact solutions, therefore, we need numerical techniques [18]. Consider the system of an ordinary differential equation is of the form [16]:

$$y_{p_1}^{d}(x) = f(x, y_1^{n_1}, y_2^{n_2}, \dots, y_p^{n_p}) \tag{1.1}$$

Where, $d \geq n_i \in \{0\} UN, p_1 \; and \; i = 1, \dots, p, p$ is any natural number, d and n_i represents the order of the derivatives. Corresponding initial conditions are as follows,

$$y_{p_1}^{d_1}(a_1) = b_j, \;\; j, d_1 = 0,1, \dots, d-1, \tag{1.2}$$

Or boundary conditions (only for a system having second-order differential equations) are of the form,

$$y_{p_1}(a_2) = b_j, \;\; y_{p_1}(a_3) = c_j \tag{1.3}$$

Where b_j and c_j are constant. Many mathematicians already contributed some methods towards the solution of the system of ordinary differential equations they are as follows, Adomian decomposition method [19], operational matrix method with Chebyshev polynomials [20], Modification of Adomian Decomposition

Method [21], Approximation Algorithm [22], Modified Differential Transform Method [23], Matrix free method [24], Block hybrid second derivative method [25], Continuous block backward differentiation formula [26], homotopy perturbation method [27] and Laplace Adomian Decomposition Method [28].

The motivation of this article is to illustrate the present algorithm in solving the Covid-19 epidemic model. The proposed algorithm is useful for obtaining numerical solutions of the system of both linear and nonlinear differential equations. Especially, this algorithm yields an exact solution for a system of ordinary differential equations which are having solutions as a polynomial of finite degree. The obtained results are compared with the exact solution and the Adomian decomposition method (ADM).

The organization of the rest of the paper is as follows. In section 2, Preliminaries of Laguerre wavelets are discussed. Covid-19 epidemic SIR model is generated in section 3. Section 4 contains a description of the proposed technique and applications of the proposed method is implemented in section 5. Finally, conclusions are drawn in section 6.

2. Preliminaries of Laguerre wavelet

Wavelets constitute a family of functions constructed from dilation and translation of a single function called mother wavelet. When the dilation parameter a and translation parameter b varies continuously, we have the following family of continuous wavelets:

$$\psi_{a,b}(x) = |a|^{-1/2}\psi(\tfrac{x-b}{a}), \forall\ a,b \in R, a \neq 0.$$

If we restrict the parameters a and b to discrete values as $a = a_0^{-k},\ b = nb_0a_0^{-k},\ a_0 > 1,\ b_0 > 0$. We have the following family of discrete wavelets

$$\psi_{k,n}(x) = |a|^{1/2}\psi(a_0^k x - nb_0), \forall a,b \in R, a \neq 0,$$

where $\psi_{k,n}$ form a wavelet basis for $L^2(R)$. In particular, when $a_0 = 2$ and $b_0 = 1$,then $\psi_{k,n}(x)$ forms an orthonormal basis. Laguerre wavelets are defined as:

$$\psi_{n,m}(x) = \begin{cases} \frac{2^{\frac{k}{2}}}{m!}L_m(2^k x - 2n + 1), & \frac{n-1}{2^{k-1}} \leq x < \frac{n}{2^{k-1}} \\ 0, & \text{otherwise} \end{cases} \tag{2.1}$$

where $m = 0,1,\dots,M-1$ and $n = 1,2,\dots,2^{k-1}$ where k is assumed any positive integer. Here $L_m(x)$ are Laguerre polynomials of degree m concerning weight function $W(x) = 1$ on the interval $[0,\infty)$ and satisfies the following recurrence formula $L_0(x) = 1, L_1(x) = 1 - x$,

$$L_{m+2}(x) = \frac{(2m+3-x)L_{m+1}(x) - (m+1)L_m(x)}{m+2} \quad where\ m = 0,1,2,\dots$$

3. Covid-19 epidemic SIR model

Let y_1 be the susceptible population, y_2 be the Infected population and y_3 represents a recovered population then the total population is $n = y_1 + y_2 + y_3$.

$$y_1' = -\beta y_1 y_2$$

$$y_2' = \beta y_1 y_2 - \gamma y_2$$

$$y_3' = \gamma y_2$$

Where β says that the rate of infection and γ represents the rate of recovery. β decreases as increasing the following factors such as border control, stay at home, observe hygiene and develop vaccines, γ increases as on better medicine.

$$\frac{dy_2}{dy_1} = \frac{\beta y_1 y_2 - \gamma y_2}{-\beta y_1 y_2} = -1 + \frac{\gamma}{\beta y_1}$$

$$y_1 + y_2 = \frac{\gamma}{\beta}\ln(y_1).$$

$$\frac{dy_2}{dx} = \beta y_1 y_2 - \gamma y_2$$

$$\frac{dy_2}{y_2} = (\beta y_1(x_0) - \gamma)dx$$

$$y_2 = e^{(\beta y_1(x_0)-\gamma)x}$$

The rate of infectives increases exponentially if $\frac{\beta}{\gamma} > 1$, and its decay exponentially if $\frac{\beta}{\gamma} < 1$.

$$\frac{dy_1}{dx} = -\beta y_1 y_2(x_0)$$

$$\frac{dy_1}{y_1} = -\beta y_2(x_0)dx$$

$$y_1 = e^{-\beta y_2(x_0)x}.$$

The rate of susceptible populations varies exponentially depends on the value of β.

$$\frac{dy_3}{dx} = \gamma y_2(x_0)$$

$$y_3 = \gamma y_2(x_0)x$$

The rate of recovery of the population always varies linearly depends on the value of γ.

4. Method of solution

Consider the system of ordinary differential equations of the form:

$$y_{p_1}^{d}(x) = f(x, y_1^{n_1}, y_2^{n_2}, \dots, y_p^{n_p}) \tag{4.1}$$

Where, $d \geq n_i \in \{0\}UN, p_1\ and\ i = 1, \dots, p, p$ is any natural number, d and n_i represents the order of the derivatives. Corresponding initial conditions are as follows,

$$y_{p_1}^{d_1}(a_1) = b_j,\ \ j, d_1 = 0,1, \dots, d-1, \tag{4.2}$$

Or boundary conditions (only for the system having second-order differential equations) are of the form,

$$y_{p_1}(a_2) = b_j,\ \ y_{p_1}(a_3) = c_j \tag{4.3}$$

Let assume that,

$$y_{p_1}(x) = \sum_{m=0}^{M-1} a_{1,m}^{p_1} \psi_{1,m}(x),\ \ M\ is\ any\ natural\ number \tag{4.4}$$

substitute (4.4) in (4.1) we get,

$$\sum_{m=0}^{M-1} a_{1,m}^{p_1} \psi_{1,m}^{d}(x) = f(x, \sum_{m=0}^{M-1} a_{1,m}^{1} \psi_{1,m}^{n_1}(x), \sum_{m=0}^{M-1} a_{1,m}^{2} \psi_{1,m}^{n_2}(x), \dots, \sum_{m=0}^{M-1} a_{1,m}^{p} \psi_{1,m}^{n_p}(x)) \tag{4.5}$$

Case I: If $d = 1$ then there should be p initial conditions. Now, collocate (4.5) by following collocation points. that is, $\{x_i\} = \{\frac{1}{2}(1 + cos(\frac{(i-1)\pi}{M}))\}$, $\forall i = 2,3, \dots, M$. Then we get $M - 1 \times p$ number of equations and there are p equations from (4.2). together we obtain a system of differential equations containing $M \times p$ number of equations. On solving this system we get the values of $M \times p$ unknown coefficients, substitute these coefficients in (4.4) which will yield the numerical solution of (4.1).

Case II: If $d = 2$ then there should be $d \times p$ boundary conditions. Now, collocate (4.5) by following collocation points. that is, $\{x_i\} = \{\frac{1}{2}(1 + cos(\frac{(i-1)\pi}{M-1}))\}$, $\forall i = 2,3, \dots, M-1$. Then we get $(M-2) \times p$ number of equations and there are $2 \times p$ equations from (4.3). together we obtain a system of differential equations containing $M \times p$ number of equations. On solving this system we get the values of $M \times p$ unknown coefficients, substitute these coefficients in (4.4) which will yield the numerical solution of (4.1).

5. Numerical Results

Example 1: Let us consider the linear problem[11],

$$y_1'' + xy_1 + xy_2 = 2 \tag{5.1}$$

$$y_2'' + 2xy_2 + 2xy_1 = -2 \tag{5.2}$$

with boundary conditions $y_1(0) = 0 = y_1(1)$ and $y_2(0) = 0 = y_2(1)$. The exact solutions of this problem are $y_1(x) = x^2 - x$ and $y_2(x) = x - x^2$. Solving this problem by the present method we obtain the exact solution itself.

Numerical implementation at $k = 1$, and $M = 3$:

Let assume,

$$y_1(x) = \sum_{m=0}^{2} a_{1,m}\psi_{1,m}(x) \tag{5.3}$$

$$y_2(x) = \sum_{m=0}^{2} b_{1,m}\psi_{1,m}(x) \tag{5.4}$$

Substitute above equations in (5.1) and (5.2) we get,

$$\sum_{m=0}^{2} a_{1,m}\psi_{1,m}''(x) + x\sum_{m=0}^{2} a_{1,m}\psi_{1,m}(x) + x\sum_{m=0}^{2} b_{1,m}\psi_{1,m}(x) = 2 \tag{5.5}$$

$$\sum_{m=0}^{2} b_{1,m}\psi_{1,m}''(x) + 2x\sum_{m=0}^{2} b_{1,m}\psi_{1,m}(x) + 2x\sum_{m=0}^{2} a_{1,m}\psi_{1,m}(x) = -2 \tag{5.6}$$

Now, collocate the above equations by points of the following sequence $\{x_i\} = \{\frac{1}{2}(1 + cos(\frac{(i-1)\pi}{2^{k-1}M-1}))\}$ $\forall i = 2,3,\dots,M-1$. If $M = 3$ then $x_2 = \frac{1}{2}$, collocate (5.5) and (5.6) at x_2 together with given boundary conditions, we get a system of equation containing six equations. Solving this system with suitable solvers we obtain unknown coefficients values as follows, $a_0 = \frac{-1}{6}$, $a_1 = 0$, $a_2 = \frac{\sqrt{5}}{30}$, $b_0 = \frac{1}{6}$, $b_1 = 0$, $b_2 = \frac{-\sqrt{5}}{30}$. On substituting these values in (5.3) and (5.4) will contribute exact solutions of example 1 as follows $y_1(x) = x^2 - x$ and $y_2(x) = x - x^2$. Fig. 1 represents Graphical interpretation between the numerical and exact solutions.

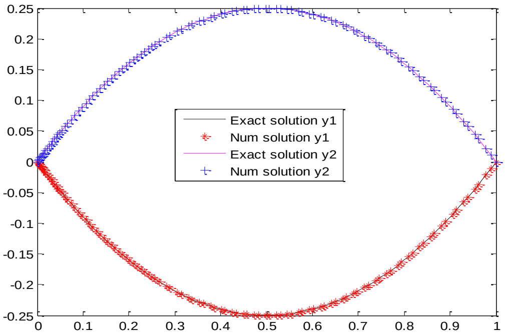

Fig. 1 Graphical comparison between the numerical and exact solutions

Example 2: Here, we consider the problem of spreading a COVID-19 disease in a population that is assumed to have constant size throughout the epidemic is considered in [16].

$$y_1' = -\beta y_1 y_2$$

$$y_2' = \beta y_1 y_2 - \gamma y_2$$

$$y_3' = \gamma y_2$$

with initial conditions $y_1(0) = k_1, y_2(0) = k_2, y_3(0) = k_3$. $y_1(x)$ represents susceptibles that are, those so far uninfected and therefore liable to infection, $y_2(x)$ represents infectives that are those who have to suffer from the disease and $y_3(x)$ represents an isolated population that is, who have recovered and are therefore immune. Here, all $y_1(x)$, $y_2(x)$ and $y_3(x)$ are a function of time x. We solve this model by assuming that there is a steady constant rate between susceptibles and infectives and that a constant proportion of these constant results in transmission.

Case 1: Numerical values for the following parameters are considered as:
$k_1 = 20$ denotes initial population of $y_1(x)$, who are susceptible. $k_2 = 15$ denotes initial population of $y_2(x)$, who are infective. $k_3 = 0$ denotes initial population of $y_3(x)$, who is immune. $\beta = 0.05$ denotes the Rate of change of susceptibles to infective population. $\gamma = 0.06$ denotes the Rate of change of infectives to the immune population. This system says that in the total population 20 members are susceptibles, 15are infective and there is no recovery.

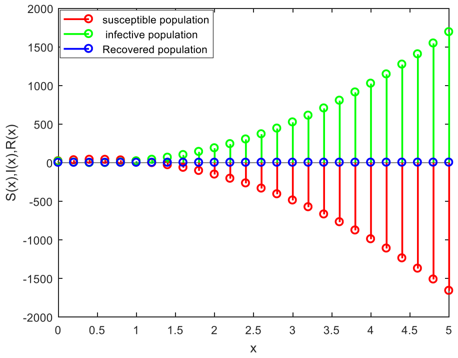

Fig. 2: Plot of the susceptible, infective, and recovered population for case 1.

Case II: Numerical values for the following parameters are considered:
$k_1 = 20$ denotes initial population of $y_1(x)$, who are susceptible. $k_2 = 15$ denotes initial population of $y_2(x)$, who are infective. $k_3 = 5$ denotes initial population of $y_3(x)$, who is immune. $\beta = 0.05$ denotes the Rate of change of susceptibles to infective population. $\gamma = 0.06$ denotes the Rate of change of infectives to the immune population. This system says that recovery begins.

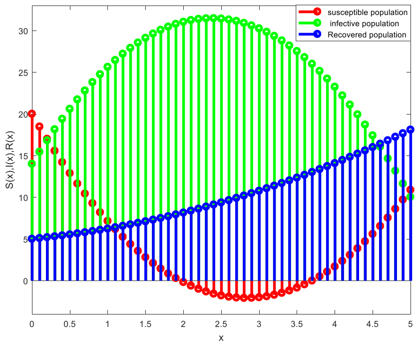

Fig. 3: Plot of the susceptible, infective, and recovered population for case 2.

Table 1. Numerical Comparison between the Adomian decomposition method [3] with the present method for Example 2 case III.

x	**Five terms approximation of y_1, its CPU time is 6.49 seconds**	**Present method numerical solution its CPU time is 5.49 seconds**
0.0	20.000000000000000	20.000000000000000
0.1	19.699578126371996	19.699578126359864
0.2	19.398425571303918	19.398425570548923
0.3	19.096713023320397	19.096713014983408
0.4	18.794612320125442	18.794612274799274
0.5	18.492296068742188	18.492295901675334
0.6	18.189937265652560	18.189936784339231
0.7	17.887708916936980	17.887707747739420
0.8	17.585783658414083	17.585781152859568
0.9	17.284333375780378	17.284328499145154
1	16.983528824749996	16.983520031505272

Case III: Numerical values for the following parameters are considered:
$k_1 = 20$ denotes initial population of $y_1(x)$, who are susceptible. $k_2 = 15$ denotes initial population of $y_2(x)$, who are infective. $k_3 = 10$ denotes initial population of $y_3(x)$, who is immune. $\beta = 0.01$ denotes the Rate of change of susceptibles to infective population. $\gamma = 0.02$ denotes the Rate of change of infectives to the immune population. On solving this system by the present method at a different value of M and compared with the Adomian decomposition method in [3].

Table 5. Numerical Comparison between the Adomian decomposition method [3] with the present method for Example 2 case III.

x	**Five terms approximation of y_2, its CPU time is 6.49 seconds**	**Present method numerical solution its CPU time is 5.49 seconds**
0.0	15.000000000000000	15.000000000000000
0.1	15.270151767739135	15.270151767750251
0.2	15.540493694892319	15.540493695580388
0.3	15.810854883914805	15.810854891481439
0.4	16.081063632394240	16.081063673364717
0.5	16.350947816046876	16.350947966422083
0.6	16.620335271713763	16.620335703005775
0.7	16.889054180356947	16.889055223041613
0.8	17.156933450055682	17.156935673000067
0.9	17.423803099002612	17.423807401460287
1	17.689494638499998	17.689502349312846

Table 3. Numerical Comparison between the Adomian decomposition method [3] with the present method for Example 2 case III.

x	**Five terms approximation of y_3, its CPU time is 6.49 seconds**	**Present method numerical solution its CPU time is 5.49 seconds**
0.0	10.000000000000000	10.000000000000000
0.1	10.030539859123818	10.030270105889885
0.2	10.062158872362208	10.061080733870691
0.3	10.094856190688018	10.092432093535155
0.4	10.128630958790655	10.124324051836005
0.5	10.163482311934377	10.156756131902572
0.6	10.199409372816543	10.189727512654985
0.7	10.236411248425934	10.223237029218968
0.8	10.274487026900992	10.257283174140374
0.9	10.313635774388130	10.291864099394566
1	10.353856531900002	10.326977619181893

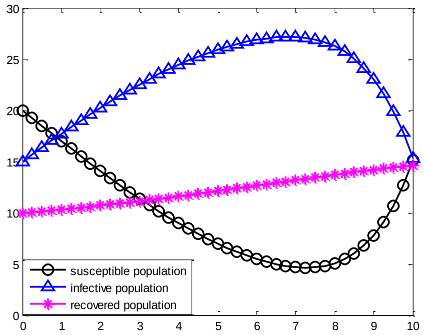

Fig. 4 The plot of the susceptible, infective, and recovered population at M = 9 for case 3.

Results and discussion

In the above section, we solved the Covid-19 epidemic model through the Laguerre wavelet method. Based on the observations on obtained results we analyze the data as follows:

In case I we nullified the rate of recovery, this follows that the susceptible rate goes on decreases as increasing the rate of infectives by maintaining the rate of recovery is constant as shown in fig 1. That is the rate of susceptible is inversely proportional to the rate of infectives depends on the rate of recovery. Since, $\frac{\beta}{\gamma} > 1$ therefore, y_2 is exponentially increase and never meets susceptible and infective curves. In case II the rate of recovery begins and it's increasing linearly after a certain time susceptible and infective curves meet, that is those curves again reach the starting point. In case III the rate of recovery is high therefore susceptible and infective curves meet rapidly towards initial points.

6. Conclusion

In this paper, we proposed a new algorithm to solve the system of the differential equation. The given system of the differential equation has been converted into an algebraic equation including unknown coefficients of Laguerre wavelet. The present algorithm provides exact solutions for the system of ODE which are having the polynomial solutions of finite degree is numerically proved by Example 1. Another example is given to demonstrate the effectiveness and accuracy of the present algorithm. Also, we discussed in each cases that how the rate of susceptible, infective, and recovery depends on each other.

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