

Computation of approximate solution to COVID-19 mathematical model

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Abstract

In this work, we investigate a modified population model of non-infected and infected (SI) compartments to predict the spread of the infectious disease COVID-19 in Pakistan. For Approximate solution, we use Laplace Adomian Decomposition Method (LADM). With the help of the said technique, we develop an algorithm to compute series type solution to the proposed problem. We compute few terms approximate solutions corresponding to different compartment. With the help of MATLAB, we also plot our approximate solutions for different compartment graphically.

Keywords: COVID-19; Compartmental model; Approximate solution; Laplace Adomian Decomposition Method.

1. Introduction

At present, COVID-19 is a contiguous and dreadful outbreak facing the entire world, which is considered to be spread in the world from a China city called Wuhan. In early January novel coronavirus was found in single patient and subsequently verified in 16 additional patients [4]. The virus is believed to have a zoonotic origin. Huanan Seafood Market, a live animal and seafood wholesale market in Wuhan, is considered as a primary source of this epidemic because about 55 percent of the first 425 confirmed cases were linked to the marketplace [5]. In the current century, after severe acute respiratory syndrome coronavirus (SARS-CoV) in 2002 that spread to 37 countries and the Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012 that spread to 27 countries, COVID-19 is the third zoonotic human coronavirus. Typical symptoms of COVID-19 infection include dry cough, fever, fatigue, breathing difficulty, and bilateral lung infiltration in severe cases, similar to those caused by SARS-CoV and MERS-CoV infections [6]. Non-respiratory symptoms such as nausea, vomiting, and diarrhea are also found in some people [7, 8].

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As per latest data approximately 0.6125 million persons have been deceased whereas, around 14 million have contracted the Corona virus across the globe [9]. However, majority of the infected persons have been recovered. The mortality and recovery rate have been varied from country to country; this is mainly due to the availability of the health systems and infrastructure in a particular country and enforcement of the precautionary measure taken and people adapting the prescribed protocols. Though many countries have taken measure to stop the spread of the disease, however, the disease outbreak took place right before the Spring Festival (i.e. the Lunar New Year), the most important holiday in China, and a huge population (several millions for the city of Wuhan alone, and hundreds of millions on a national scale) traveled during the month of January 2020, which makes fast and wide spread of the infection possible. As a result, countries opted for traveling ban by temporarily suspending the travel ban including air traffic and announced lock down in countries and cities to reduce the disease spread and safeguard precious human lives [1]. The history revealed that in such pandemic millions of persons lost lives around the world, however, the researchers and scientists are working hard to investigate cure or develop vaccine for the pandemic to control the spread and loss [4, 5, 6].

Several factors complicate the infection dynamics of COVID-19 and add challenges to control the disease. First, the origin of the infection is still uncertain. As the wholesale market place in Wuhan, is considered as a primary source of this epidemic but still majority of the infected individuals did not have any contact with said place. Still the infection has increased across the world so it is considered that the virus could be spread through the environmental reservoir [5]. Second, clinical evidence shows that the incubation period of this disease ranges from 2 to 14 days. During this period of time, infected individuals are capable of transmitting the disease to other people yet they may not develop any symptoms and may be unaware of their infection [12]. Third, as the virus is new so no antiviral drugs or vaccines are currently available.

To understand and investigate such pandemic like COVID-19 a Mathematical Modeling is one of major tool to be used. Using the concept of mathematical modeling was first used in 1927, later; various mathematical models have been created for different diseases. The researchers have investigated various aspects of the COVID-19 pandemic for instance the existence, stability, uniqueness, and approximate for detail see [2]. In other words, the mathematical models are useful for comprehending and recommending some strategies in order to control the disease spread and to take precautionary measure. Therefore, the Novel Corona Virus (COVID-19) has been studied through various models [25, 36]. This disease is extremely contagious, the countries around the world adapted the universal protocols to stop the spread from person to person which are social distancing, use of mask, use of sanitizer or frequently hand washing. Some authors have considered the immigration effects on the transmission dynamics of this disease.

In the current paper, we studied a modified population model of non-infected and infected (SI) compartments to predict the spread of the infectious disease COVID-19 in Pakistan. Since the infection is rapidly transmitting from one person to another, people would be advised to take necessary action such as wearing masks, strict isolation, large-scale quarantine, and advising the people to stay home to reduce the contact with the infected persons.

2. Model formulation

The total human population is divided into two compartments: that are non-infected and infected. We considered that the infected individuals have fully developed disease symptoms and can infect others. We introduce the mathematical model to describe the transmission dynamics of the COVID-19 epidemic [36] as:

$$\begin{cases} \frac{d}{dt}S(t) = \alpha - k(1 - \alpha)S(t)I(t) - \alpha k\beta S(t)I(t) - \delta S(t), \\ \frac{d}{dt}I(t) = k(1 - \alpha)S(t)I(t) + \alpha k\beta S(t)I(t) - \frac{1}{\gamma}I(t) - \delta I(t), \\ S(0) = S_0, I(0) = I_0. \end{cases} \quad (2.1)$$

Parameters of the model under consideration are explained as follows: initial value of non-infected class S_0 , initial value of infected class I_0 , the constant of recruitment is represented by the symbol α while the letter α denotes the rate of isolating the people. Similarly the symbol β represents the protective measure rate. The removal rate of infection is denoted by the letter δ , the symbol γ represents the natural death rate. Similarly the total infection rate is denoted by the symbols k .

3. Background Materials

In this portion, we provide some definitions from [1, 3].

Definition 3.1. Laplace transform of function $f(t)$ for $t > 0$ and integral over 0 to ∞ . can be define as

$$\mathcal{L}f(t) = F(s) = \int_0^{\infty} \exp(-st)f(t)dt.$$

It is generally an integral transform that takes function $f(t)$ and converts it into another function $F(s)$ in new parameter s .

Definition 3.2. Adomian decomposition method define the solution by a series given by

$$U = \sum_{k=0}^{\infty} U_k,$$

and replacing the nonlinear term by the given series

$$Q_u = \sum_{n=0}^{\infty} A_n,$$

where A_n is Adomian polynomial and is computed as

$$A_n = \frac{1}{\Gamma(n+1)} \left[\frac{d^n}{d\lambda^n} \left(\sum_{k=0}^n \lambda^k S_k \right) \left(\sum_{k=0}^n \lambda^k I_k \right) \right]_{\lambda=0}.$$

Although the Adomian's goal is to find a method unify linear and non-linear, ordinary or partial differential equations for solving initial and boundary value problem, in our paper we shall deal only (ODE). The Adomian decomposition Method (ADM) involves separating the equation under the investigation into linear and non-linear portions.

4. Main Work

Here we are going to discuss the approximate solution of the proposed model using LADM. To compute the required approximate solution, using Laplace transform on both sides of (2.1), we have

$$\begin{cases} \mathcal{L}\left[\frac{d}{dt}S(t)\right] = \mathcal{L}\left[a - k(1-\alpha)S(t)I(t) - \alpha k\beta S(t)I(t) - \delta S(t)\right], \\ \mathcal{L}\left[\frac{d}{dt}I(t)\right] = \mathcal{L}\left[k(1-\alpha)S(t)I(t) + \alpha k\beta S(t)I(t) - \frac{1}{\gamma}I(t) - \delta I(t)\right], \\ \mathcal{L}[S(t)] = \frac{S(0)}{s} + \frac{1}{s}\mathcal{L}\left[a - k(1-\alpha)S(t)I(t) - \alpha k\beta S(t)I(t) - \delta S(t)\right], \\ \mathcal{L}[I(t)] = \frac{I(0)}{s} + \frac{1}{s}\mathcal{L}\left[k(1-\alpha)S(t)I(t) + \alpha k\beta S(t)I(t) - \frac{1}{\gamma}I(t) - \delta I(t)\right]. \end{cases} \quad (4.1)$$

Now assuming the solution in the series form as

$$S(t) = \sum_{q=0}^{\infty} S_q(t), \quad I(t) = \sum_{q=0}^{\infty} I_q(t). \quad (4.2)$$

Further expressing the nonlinear terms $S(t)I(t)$ by using decomposition method

$$S(t)I(t) = \sum_{q=0}^{\infty} A_q(S, I), \quad (4.3)$$

where the "Adomian polynomial" $A_q(S, I)$ can be defined as

$$A_q(S, I) = \frac{1}{q!} \frac{d^q}{d\lambda^q} \left[\sum_{j=0}^q \lambda^j S_j(t) \sum_{j=0}^q \lambda^j I_j(t) \right] \Big|_{\lambda=0}.$$

Hence in view of (4.2) and (4.3), the system (4.1) becomes

$$\begin{cases} \mathcal{L}\left[\sum_{q=0}^{\infty} S_q(t)\right] = \frac{S(0)}{s} + \frac{1}{s}\mathcal{L}\left[a - \left(k(1-\alpha) + \alpha k\beta\right) \sum_{q=0}^{\infty} A_q(S, I) - \delta \sum_{q=0}^{\infty} S_q(t)\right] \\ \mathcal{L}\left[\sum_{q=0}^{\infty} I_q(t)\right] = \frac{I(0)}{s} + \frac{1}{s}\mathcal{L}\left[\left(k(1-\alpha) + \alpha k\beta\right) \sum_{q=0}^{\infty} A_q(S, I) - \frac{1}{\gamma} \sum_{q=0}^{\infty} I_q(t) - \delta \sum_{q=0}^{\infty} I_q(t)\right]. \quad q \geq 0 \end{cases} \quad (4.4)$$

From (4.4), we equate terms as

$$\left\{ \begin{array}{l} \mathcal{L}[S_0(t)] = \frac{S_0}{s} + \frac{1}{s} \mathcal{L}(\alpha), \quad \mathcal{L}[I_0(t)] = \frac{I_0}{s}, \\ \mathcal{L}[S_1(t)] = \frac{1}{s} \mathcal{L} \left[- \left(k(1-\alpha) + \alpha k \beta \right) A_0(S, I) - \delta S_0(t) \right], \\ \mathcal{L}[I_1(t)] = \frac{1}{s} \mathcal{L} \left[\left(k(1-\alpha) + \alpha k \beta \right) A_0(S, I) - \left(\frac{1}{\gamma} + \delta \right) I_0(t) \right], \\ \mathcal{L}[S_2(t)] = \frac{1}{s} \mathcal{L} \left[\left(-k(1-\alpha) - \alpha k \beta \right) A_1(S, I) - \delta S_1(t) \right], \\ \mathcal{L}[I_2(t)] = \frac{1}{s} \mathcal{L} \left[\left(k(1-\alpha) + \alpha k \beta \right) A_1(S, I) - \left(\frac{1}{\gamma} + \delta \right) I_1 \right], \\ \vdots \\ \mathcal{L}[S_{q+1}(t)] = \frac{1}{s} \mathcal{L} \left[\left(-k(1-\alpha) - \alpha k \beta \right) A_q(S, I) - \delta S_q(t) \right], \\ \mathcal{L}[I_{q+1}(t)] = \frac{1}{s} \mathcal{L} \left[\left(-k(1-\alpha) - \alpha k \beta \right) A_q(S, I) - \left(\frac{1}{\gamma} + \delta \right) I_q \right], \quad q \geq 0. \end{array} \right. \quad (4.5)$$

Now utilizing inverse Laplace transform in (4.5), we get few terms of series solution as

$$\begin{aligned} S_0(t) &= S_0 + \alpha t, \quad I_0(t) = I_0 \\ S_1(t) &= D_1 t, \quad \text{where } D_1 = \left(- (k(1-\alpha) + \alpha k \beta) S_0 I_0 - \delta S_0 \right) \\ I_1(t) &= D_2 t, \quad \text{where } D_2 = \left(\left(k(1-\alpha) + \alpha k \beta \right) S_0 I_0 - \left(\frac{1}{\gamma} + \delta \right) I_0 \right) \\ S_2(t) &= \left[(-k(1-\alpha) - \alpha k \beta) (I_0 D_1 + S_0 D_2) - \delta D_1 \right] \frac{t^2}{2!} \\ I_2(t) &= \left[(k(1-\alpha) + \alpha k \beta) (I_0 D_1 + S_0 D_2) - \left(\frac{1}{\gamma} + \delta \right) D_2 \right] \frac{t^2}{2!} \end{aligned} \quad (4.6)$$

and so on. In this way the other terms may be computed. Using these values, we get approximate solution from (4.6) in the form of infinite series as

$$\begin{aligned} S(t) &= S_0 + S_1 + S_2 + \dots \\ I(t) &= I_0 + I_1 + I_2 + \dots \end{aligned} \quad (4.7)$$

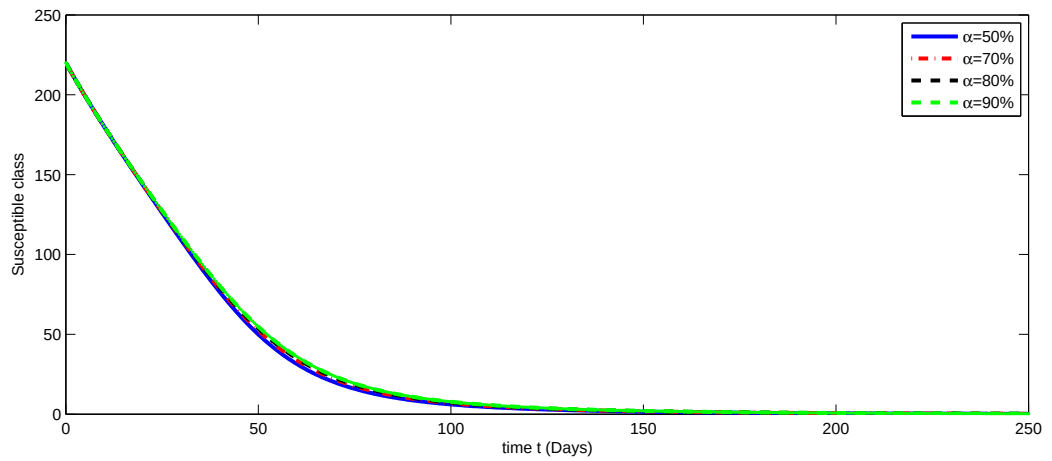
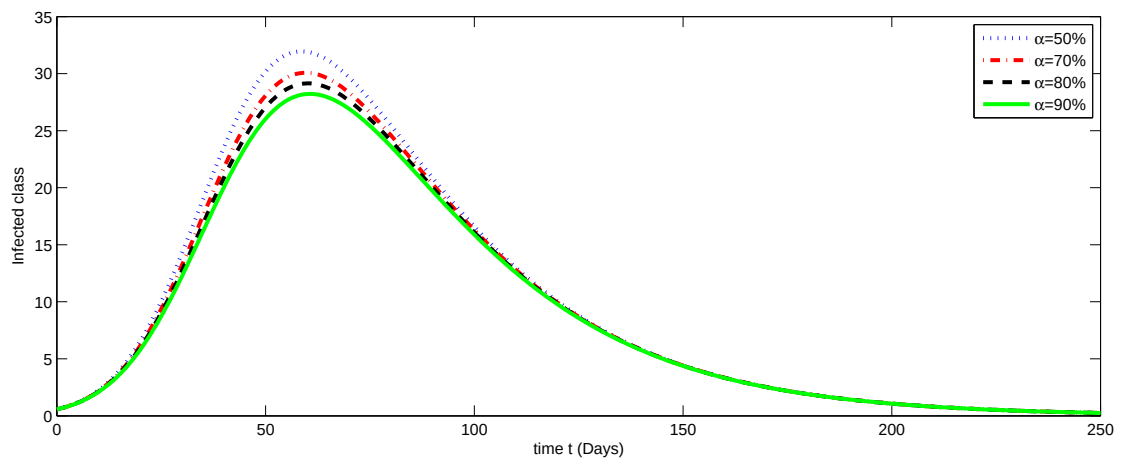
5. Graphical results and discussion

Here we give the table for numerical solution. Using the values given in table 1, we approximate the solution computed in (4.7) and present via graphs in Figure 1 and 2 respectively.

In Figure 1, non-infected plot at different values of α is given while in Figure 2, the corresponding plot of infected class is given. From Figure 1, we see that as susceptible population is decreasing which give rise to infection as shown in Figure 2. We notice that infection first increases but due to treatment procedure there is decreases in infected class as shown in Figure 2.

Parameters	Description of Parameters	Numerical value
S_0	Initial value of non-infected class	220 millions
I_0	Initial value of infected class	0.142 million
α	Recruitment rate	0.00009
k	Total infection rate	0.0009
α	Rate of isolating the people	50% ,70% ,80%
β	Protective measures rate	0.00078
γ	natural death rate	0.019
δ	removal rate of infection	100

Table 1: Parameters and description


Figure 1: Dynamics of non-infected class at different control values of α .

Figure 2: Dynamics of infected class at different control values of α .

6. Concluding Remarks

We have proposed a mathematical model to investigate on-going novel coronavirus pandemic by using LADM. The proposed model contains two compartments that are non-infected and infected. Our work is devoted to establish series type solutions to non-infected and infected (SI) compartments to predict the spread of the infectious disease COVID-19 in Pakistan. For the numerical solution of the proposed model, the Adomian decomposition and Laplace transform are used. We have computed the series solutions via LADM and have been presented the results graphically. From the graphs it is clear that due to increase in susceptible class increase in infection has occurred but if strict SOP's are follow and precautionary measures are taken then it will lead to decrease in infection.

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