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Reduced Differential Transform Method for Solving The SEIR Epidemic Model

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Abstract This paper explores a model of nonlinear ODEs that describes the mechanism of COVID-19, a highly infectious virus. Our goal is to understand the complex behavior of this COVID-19 model, particularly how the virus spreads within a population. To manage the pandemic, measures such as social distancing, isolation, and travel restrictions have been commonly recommended. The analysis here uses the SEIR model, which divides the population into four groups: those who are susceptible (S), exposed but not yet infectious (E), actively infectious (I), and those who have recovered (R). This model framework, known as SEIR, is widely applicable to many human infectious diseases.

To examine the numerical results of our COVID-19 model, we apply the Reduced Differential Transformation Method (RDTM). This technique offers an efficient, iterative approach to approximate solutions using a Taylor series, reducing computational complexity. It's a versatile method, well-suited for many nonlinear problems in physical modeling, which makes it an ideal choice for analyzing the dynamics of COVID-19.

1 Introduction

COVID-19, short for "Coronavirus Disease 2019," is caused by the novel coronavirus SARS-CoV-2. It emerged in late 2019 in the city of Wuhan, Hubei Province, China, and quickly spread globally, leading to a pandemic declared by the World Health Organization (WHO) on March 11, 2020. The virus primarily spreads through respiratory droplets when an infected person coughs, sneezes, or talks. It can also spread by touching surfaces contaminated with the virus and then touching the face. The most common symptoms include fever, cough, and difficulty breathing, though the virus can cause a wide range of symptoms, from mild to severe, and may lead to complications such as pneumonia, acute respiratory distress syndrome (ARDS), and multi-organ failure, particularly in older adults and those with underlying health conditions [1, 2]. Mathematical models have been indispensable tools in the battle against COVID-19, offering insights into the dynamics of disease transmission, the effectiveness of interventions, and the strain on healthcare systems. Epidemiological models like the Susceptible-Exposed-Infectious-Recovered (SEIR) has provided valuable frameworks for understanding how the virus spreads through populations and assessing the impact of control measures [3, 4]. SEIR models, based on the Susceptible-Exposed-Infectious-Removed framework, have been instrumental in understanding the transmission dynamics of COVID-19. These models divide the population into compartments representing individuals who are susceptible (S), exposed (E), infectious (I), and removed (R), where "removed" includes individuals who have recovered from the infection or died. The SEIR model tracks the flow of individuals between these compartments over time through a system of differential equations, allowing researchers to simulate how the virus spreads within a population and evaluate the impact of interventions. The SEIR model can represent many human infectious diseases [5, 6, 7]. In this work, we focus on examining and solving the model of nonlinear ordinary differential equations (ODEs) that characterizes the most prevalent and lethal coronavirus (COVID-19). The reduced differential transformation method is used to analyze the related numerical results of a mathematical model based on the four nonlinear ODEs.The reduced differential transforms technique is an iterative procedure for obtaining a Taylor series solution of differential equations. This method reduces the size of computational work and easily applicable to many nonlinear physical problems. The present manuscript is managed into different sections.

- In Section 2, reduced differential transform method is introduced.
- In Section 3, The details of SEIR Model is provided.
- Section 4 is related to Implementation of reduced differential transform method (RDTM) for the SEIR Model.
- In Section 5, conclusion of the proposed work is provided.

2 REDUCED DIFFERENTIAL TRANSFORM METHOD

The differential transform method involves transforming a given differential equation into a set of algebraic equations, which are then solved iteratively to obtain an approximate solution. The process involves transforming derivatives into finite differences through Taylor series expansions and then solving the resulting algebraic equations. The reduced differential transform method is a modification of DTM that simplifies the calculation process by reducing the number of terms in the series representation. This reduction can make the method more efficient and computationally tractable, especially for complex differential equations. Via Table 1, basic properties of the reduced differential transform are provided. Considered $u(x,t)$ as a function of two variable and let it can be represented as a product of two single-variable functions, i.e., $u(x,t) = f(x)g(t)$. Based on characteristics of 1D differential transform, function $u(x,t)$ can be notified as follows:

$$u(x,t) = (\sum_{i=0}^{\infty} F(i)x^i)(\sum_{j=0}^{\infty} G(j)t^j) = (\sum_{k=0}^{\infty} U_k(x)t^k). \tag{2.1}$$

where $U_k(x)$ is called t-dimensional spectrum function of u(x,t) [8, 9, 10].

Definition 2.1. If function $u(x,t)$ is analytical and continuously differentiable w.r.t. t and x in computational domain, then let

$$U_k(x,t) = \frac{1}{k!}[\frac{\partial^k}{\partial x^k}u(x,t)]_{t=0}. \tag{2.2}$$

where t-dimensional spectrum function $U_k(x)$ is transformed function. In this article, $u(x,t)$ is regarded as the original function, while $U_k(x)$ spokes for transformed function.

Definition 2.2. Differential inverse transformed of $U_k(x)$ is defined as follows:

$$u(x,t) = \sum_{k=0}^{\infty} U_k(x)t^k, \tag{2.3}$$

On combining above two equations it can be written as follows:

$$u(x,t) = \sum_{k=0}^{\infty} \frac{1}{k!}[\frac{\partial^k}{\partial t^k}u(x,t)]_{t=0}t^k. \tag{2.4}$$

3 THE SEIR MODEL

The SEIR model is a compartmental epidemiological model used to simulate the spread of Infectious, and Removed (or recovered), which represent the different stages an individual can go through during the course of an infectious disease outbreak. It divides the population into four

Original Function	**Reduced Differential Transformed Function**
$R_D[u(x,y,z,t)v(x,y,z,t)]$	$U_k(x,y,z) \otimes V_k(x,y,z) = \sum_{r=0}^{k} U_r(x,y,z)V_{k-r}(x,y,z)$
$R_D[\alpha u(x,y,z,t) \pm \beta v(x,y,z,t)]$	$\alpha U_k(x,y,z,t) \pm \beta V_k(x,y,z,t)$
$R_D\left[\frac{\partial^n}{\partial t^n} u(x,y,z,t)\right]$	$(k+1)(k+2)\ldots(k+n)U_{k+n}(x,y,z)$
$R_D\left[\frac{\partial^{m+n+p+s}}{\partial x^m \partial y^n \partial z^p \partial t^s} u(x,y,z,t)\right]$	$\frac{(k+s)!}{k!} \frac{\partial^{m+n+p}}{\partial x^m \partial y^n \partial z^p} U_{k+s}(x,y,z)$
$R_D[x^m y^n z^p]$	$x^m y^n z^p, k = q$, else 0 otherwise
$R_D[\sin(\alpha x + \beta y + \gamma z + \omega t)]$	$\frac{\omega^k}{k!} \sin\left(\frac{\pi k}{2} + \alpha x + \beta y + \gamma z\right)$
$R_D[\cos(\alpha x + \beta y + \gamma z + \omega t)]$	$\frac{\omega^k}{k!} \cos\left(\frac{\pi k}{2} + \alpha x + \beta y + \gamma z\right)$
$R_D[u(x,t)v(x,t)]$	$\sum_{i=0}^{k} U_i(x)V_{k-i}(x)$
$R_D[u(x,t)v(x,t)w(x,t)]$	$\sum_{i=0}^{k} \sum_{j=0}^{i} U_j(x)V_{i-j}(x)W_{k-i}(x)$
$R_D\left[w(x,t) = \frac{\partial^n}{\partial x^n} u(x,t)\right]$	$W_k(x) = (k+1)(k+2)\ldots(k+n)U_{k+n}(x) = \frac{(k+n)!}{k!} U_{k+n}(x)$

Table 1. Properties of Reduced Differential Transform Method

distinct compartments: susceptible (S), exposed (E), infectious (I), and recovered (R). Individuals start in the susceptible compartment, meaning they are susceptible to the disease. When individuals are exposed to the infectious agent but are not yet infectious themselves, they move into the exposed compartment. From there, they transition to the infectious compartment, where they can transmit the disease to susceptible individuals. Finally, individuals either recover from the disease and move to the recovered compartment or, in some cases, may transition to other states such as hospitalization or death. The flow of individuals between these compartments is governed by a set of differential equations, typically based on parameters such as transmission rates, incubation periods, and recovery rates. By simulating the dynamics of an epidemic using the SEIR model, researchers can assess the potential impact of interventions such as vaccination, social distancing, or quarantine measures, aiding in the development of effective strategies to control and mitigate the spread of infectious diseases. The SEIR model, often used in epidemiology to understand the spread of infectious diseases, is represented by a system of differential equations as follows:

$$\frac{ds}{dt}(t) = -\beta s(t)i(t), \tag{3.1}$$

$$\frac{de}{dt}(t) = \beta s(t)i(t) - \alpha e(t), \tag{3.2}$$

$$\frac{di}{dt}(t) = \alpha e(t) - \gamma i(t), \tag{3.3}$$

$$\frac{dr}{dt}(t) = \gamma i(t). \tag{3.4}$$

α, β and γ are positive parameters and S, E, I, and R denote fractions of population which are susceptible, exposed, infectious, and recovered, respectively. In Table 2, different parameters are explained. For additional details regarding model, see [11, 12, 13, 14]. For some related study see [15, 16, 17]. Now, this is how new coronavirus, or COVID-19, is represented in SEIR model:

$$\frac{ds}{dt}(t) = -\frac{\beta s(t)}{N} I(t) - \frac{Z}{N} s(t) + (\rho_I + \rho_E) - \left(\frac{q_I}{N} + \frac{q_E}{N}\right) s(t) + \omega N(t) - \mu s(t), \tag{3.5}$$

$$\frac{de}{dt}(t) = \frac{\beta s(t)}{N} I(t) - \frac{Z}{N} s(t) - \alpha e(t) - \left(\frac{q_I}{N} + \frac{q_E}{N}\right) s(t) - \mu e(t) - \sigma e(t), \tag{3.6}$$

$$\frac{di}{dt}(t) = \alpha e(t) - \gamma i(t) - \left(\frac{q_I}{N} + \frac{q_E}{N}\right) i(t) - \mu i(t), \tag{3.7}$$

$$\frac{dr}{dt}(t) = \gamma i(t) - \mu r(t) + \sigma e(t). \tag{3.8}$$

With initial conditions:

$$s(0) = s_0,$$
$$e(0) = e_0,$$
$$i(0) = i_0,$$
$$r(0) = r_0.$$

Parameter	Definition
α	No. of exposed people over avg. latency period
β	Avg. no. of people infected by infectious person over avg. duration of infection
γ	No. of infected people over avg. duration of infection
μ	Death rate of people
ω	Birth rate parameter of people
σ	Cure rate of people
Z	Force of infection in baseline scenario
ρ_I	Avg. daily number of international inbound air passengers
ρ_E	Avg. daily number of domestic inbound air passengers
q_I	Avg. daily no. of international outbound air passengers
q_E	Avg. daily no. of domestic outbound travelers
s_0	No. of susceptible people at time $t = 0$
e_0	No. of asymptomatic and noninfectious people at time $t = 0$
i_0	No. of asymptomatic but infectious people at time $t = 0$
r_0	No. of recovered people at time $t = 0$
N	Total no. of Population, $N(t) = S(t) + E(t) + I(t) + R(t)$

Table 2. Parameters and initial conditions of SEIR model

4 IMPLEMENTATION OF REDUCED DIFFERENTIAL TRANSFORM METHOD

$$\begin{cases} \frac{ds}{dt}(t) = -\frac{\beta s(t)}{N} I(t) - \frac{Z}{N} s(t) + (\rho_I + \rho_E) - \left(\frac{q_I}{N} + \frac{q_E}{N}\right) s(t) + \omega N(t) - \mu s(t), \\ \frac{de}{dt}(t) = \frac{\beta s(t)}{N} I(t) - \frac{Z}{N} s(t) - \alpha e(t) - \left(\frac{q_I}{N} + \frac{q_E}{N}\right) s(t) - \mu e(t) - \sigma e(t), \\ \frac{di}{dt}(t) = \alpha e(t) - \gamma i(t) - \left(\frac{q_I}{N} + \frac{q_E}{N}\right) i(t) - \mu i(t), \\ \frac{dr}{dt}(t) = \gamma i(t) - \mu r(t) + \sigma e(t). \end{cases} \tag{4.1}$$

With the initial conditions,

$$s(0) = s_0,$$
$$e(0) = e_0,$$
$$i(0) = i_0,$$
$$r(0) = r_0.$$

Introducing RDTM defined earlier equations can be expressed as follows:

$$\begin{cases} (k+1)(k+2)\ldots(k+n)S_{k+1} = -\frac{\beta}{N} \sum_{a=0}^{k} S_a I_{k-a} - \frac{Z}{N} S_k + (\rho_I + \rho_E)\delta(k) \\ -\left(\frac{q_I}{N} + \frac{q_E}{N}\right) S_k + \omega N_k - \mu S_k, \\ (k+1)(k+2)\ldots(k+n)E_{k+1} = \frac{\beta}{N} \sum_{a=0}^{k} S_a I_{k-a} - \frac{Z}{N} S_k + \alpha E_k \\ -\left(\frac{q_I}{N} + \frac{q_E}{N}\right) S_k - \mu E_k - \sigma E_k, \\ (k+1)(k+2)\ldots(k+n)I_{k+1} = \alpha E_k - \gamma I_k - \left(\frac{q_I}{N} + \frac{q_E}{N}\right) I_k - \mu I_k, \\ (k+1)(k+2)\ldots(k+n)R_{k+1} = \gamma I_k - \mu R_k + \sigma E_k. \end{cases} \tag{4.2}$$

Here n = 1 and for k = 0 in above equation we have first iterations as

$$\begin{cases} S_1 = -\frac{\beta}{N}\sum_{a=0}^{0} S_a I_{k-a} - \frac{Z}{N}S_0 + (\rho_I+\rho_E)\delta(0) - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_0 + \omega N_0 - \mu S_0, \\ E_1 = \frac{\beta}{N}\sum_{a=0}^{0} S_a I_{k-a} - \frac{Z}{N}S_0 + \alpha E_0 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_0 - \mu E_0 - \sigma E_0, \\ I_1 = \alpha E_0 - \gamma I_0 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)I_0 - \mu I_0, \\ R_1 = \gamma I_0 - \mu R_0 + \sigma E_0. \end{cases} \tag{4.3}$$

$$\begin{cases} S_1 = -\frac{\beta}{N}S_0 I_0 - \frac{Z}{N}S_0 + (\rho_I+\rho_E)\delta(0) - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_0 + \omega N_0 - \mu S_0, \\ E_1 = \frac{\beta}{N}S_0 I_0 - \frac{Z}{N}S_0 + \alpha E_0 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_0 - \mu E_0 - \sigma E_0, \\ I_1 = \alpha E_0 - \gamma I_0 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)I_0 - \mu I_0, \\ R_1 = \gamma I_0 - \mu R_0 + \sigma E_0. \end{cases} \tag{4.4}$$

The initial approximations and variables are given as follows:

$$S(0) = 2500, \quad E(0) = 1, \quad I(0) = 1, \quad R(0) = 0, \quad N = 2502.$$

The parameters are:

$$\beta = 0.8, \quad \alpha = 0.75, \quad \sigma = 0.1, \quad \gamma = 0.05, \quad \omega = \frac{0.009}{N}, \quad \mu = 0.01, \quad Z = 0.001.$$

$$\rho_I = 0.15, \quad \rho_E = 0.15, \quad q_I = 0.01, \quad q_E = 0.03.$$

$$\begin{cases} S_1 = -25.53132774, \\ E_1 = -0.059656274, \\ I_1 = 0.689984012, \\ R_1 = 0.15. \end{cases} \tag{4.5}$$

again n = 1 and for k = 1 in above equation we have second iterations as

$$\begin{cases} 2S_2 = -\frac{\beta}{N}\sum_{a=0}^{1} S_a I_{k-a} - \frac{Z}{N}S_1 + (\rho_I+\rho_E)\delta(1) - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_1 + \omega N_1 - \mu S_1, \\ 2E_2 = \frac{\beta}{N}\sum_{a=0}^{1} S_a I_{k-a} - \frac{Z}{N}S_1 + \alpha E_1 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_1 - \mu E_1 - \sigma E_1, \\ 2I_2 = \alpha E_1 - \gamma I_1 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)I_1 - \mu I_1, \\ 2R_2 = \gamma I_1 - \mu R_1 + \sigma E_1. \end{cases} \tag{4.6}$$

$$\begin{cases} 2S_2 = -\frac{\beta}{N}(S_0 I_1 + S_1 I_0) - \frac{Z}{N}S_1 + (\rho_I+\rho_E)\delta(1) - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_1 + \omega N_1 - \mu S_1, \\ 2E_2 = \frac{\beta}{N}(S_0 I_1 + S_1 I_0) - \frac{Z}{N}S_1 + \alpha E_1 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_1 - \mu E_1 - \sigma E_1, \\ 2I_2 = \alpha E_1 - \gamma I_1 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)I_1 - \mu I_1, \\ 2R_2 = \gamma I_1 - \mu R_1 + \sigma E_1. \end{cases} \tag{4.7}$$

$$\begin{cases} S_2 = -0.143869927, \\ E_2 = 0.29733881, \\ I_2 = -0.043076138, \\ R_2 = 0.0135167866. \end{cases} \tag{4.8}$$

again n = 1 and for k = 2 in above equation we have third iterations as

$$\begin{cases} 3S_3 = -\frac{\beta}{N}\sum_{a=0}^{2} S_a I_{k-a} - \frac{Z}{N}S_2 + (\rho_I+\rho_E)\delta(2) - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_2 + \omega N_2 - \mu S_2, \\ 3E_3 = \frac{\beta}{N}\sum_{a=0}^{2} S_a I_{k-a} - \frac{Z}{N}S_2 + \alpha E_2 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)S_2 - \mu E_2 - \sigma E_2, \\ 3I_3 = \alpha E_2 - \gamma I_2 - \left(\frac{q_I}{N}+\frac{q_E}{N}\right)I_2 - \mu I_2, \\ 3R_3 = \gamma I_2 - \mu R_2 + \sigma E_2. \end{cases} \tag{4.9}$$

$$\begin{cases} 3S_3 = -\frac{\beta}{N}(S_0I_2 + S_1I_1 + S_2I_0) - \frac{Z}{N}S_2 + (\rho_I + \rho_E)\delta(2) - \left(\frac{q_I}{N} + \frac{q_E}{N}\right)S_2 + \omega N_2 - \mu S_2, \\ 3E_3 = \frac{\beta}{N}(S_0I_2 + S_1I_1 + S_2I_0) - \frac{Z}{N}S_2 + \alpha E_2 - \left(\frac{q_I}{N} + \frac{q_E}{N}\right)S_2 - \mu E_2 - \sigma E_2, \\ 3I_3 = \alpha E_2 - \gamma I_2 - \left(\frac{q_I}{N} + \frac{q_E}{N}\right)I_2 - \mu I_2, \\ 3R_3 = \gamma I_2 - \mu R_2 + \sigma E_2. \end{cases} \tag{4.10}$$

$$\begin{cases} S_3 = 0.0138516945, \\ E_3 = -0.098609411134, \\ I_3 = 0.075196454815, \\ R_3 = 0.00914830221. \end{cases} \tag{4.11}$$

Likewise, we can calculate more iterations. Then the transformed function can be rewritten as

$$u(x,t) = \sum_{k=0}^{\infty} U_k(x)t^{k\alpha} = \sum_{k=0}^{\infty} U_k(x)t^{k/\lambda}.$$

Then the series solution can be obtained as

$$s(t) = 2500 - 25.53132774t - 0.143869927t^2 + 0.0138516945t^3 + \dots$$

$$e(t) = 1 - 0.059656274t + 0.29733881t^2 - 0.098609411134t^3 + \dots$$

$$i(t) = 1 + 0.689984012t - 0.043076138t^2 + 0.075196454815t^3 + \dots$$

$$r(t) = 0.15t + 0.0135167866t^2 + 0.00914830221t^3 + \dots$$

5 Conclusion

A nonlinear system of ordinary differential equations (ODEs) that models the dynamics of the COVID-19 epidemic is the subject of this paper, and its analysis and solution are the primary points of emphasis. It is possible to illustrate the transmission of the disease by employing the SEIR model, which divides the population into four distinct categories: susceptible, exposed, infectious, and recovered. A computationally efficient and iterative strategy to obtaining numerical solutions is provided by the reduced differential transformation method, which is highlighted in this paper as being useful in solving nonlinear ordinary differential equations (ODEs). When it comes to solving a variety of nonlinear physical problems, such as the spread of infectious diseases like COVID-19, this strategy not only makes the computational effort easier to manage, but it also provides a useful tool for doing so. In addition, the research highlights the significance of public health measures like as social distancing, isolation, and travel limitations in the context of the pandemic-control efforts.

Conflict of Interest - Not applicable.
Data Availability Statement - All the data is provided in the manuscript.

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