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Numerical Approximation of the SEIR Epidemic Model Using the Variational iteration Orthogonal Collocation method and Mamadu-Njoseh Polynomials

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Abstract: In this paper, we proposed the numerical method called the variational iteration orthogonal collocation method (VIOCM), for the approximate solution of the deadly Corona virus model using Mamadu-Njoseh polynomials as basis functions. The proposed method is an elegant mixture of the variational iteration method (VIM) and the orthogonal collocation method (OCM). It was observed that the proposed method converges rapidly to the exact solution even as N increases. This suggests that the use of orthogonal polynomials as trial functions for the SEIR model is indeed an effective approximant as it produces the analytic solution at just few iterations. Resulting numerical evidences were compared with the standard variational iteration method as available in literature. All computational frameworks were executed with MAPLE software.

Keywords: Orthogonal collocation; Variational iteration method; Mamadu-Njoseh polynomials; differential equations; Corona Virus; SEIR model.

1. Introduction

Coronavirus disease, COVID-19, otherwise known as severe acute respiratory syndrome coronavirus 2, SARS-CoV-2, is a global threat to public health [1]. In 2019, Wuhan, China was identified as the epicentre of the SARS-CoV-2 outbreak [2-3]. The world health organisation (WHO) has declared COVID-19 a pandemic on March 11th, 2020 and has recorded over five hundred thousand disease-induced deaths globally since the disease outbreak [4]. COVID-19 has brought great challenges and hardship to the lives of millions of people and could have a far reaching and negative impact on the global economy if effective control measures are not put in place. SARS-CoV-2 is a communicable disease and attacks the lower respiratory system and causes damage to the heart, liver, kidney, gastrointestinal system and central nervous system, and this could result to multiple organ failure [5-9].

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Mathematical models have been used by scholars to study the transmission pattern and control strategies of COVID-19 and also for calculating the basic reproduction numbers [10-15]. SEIR models which are based on the division of the population under study into the susceptible, exposed, infectious and recovered compartments, have been used to simulate the effects of SARS-CoV-2 and forecast the COVID-19 outbreak [16-18]. The author [17] extended the model presented by [18] for the control of SARS to the control of COVID-19. The study ascertained the effectiveness of public health education, quarantine and isolation in reducing the COVID-19 infection and the time taken to achieve that. Pontryagin's maximum principle has been employed in the optimal control of many infectious diseases including COVID-19 [17, 19]. Also, the author [17] reveals that optimal control is the generalisation of the optimization theory's classical calculus of variation which has to do with minimizing the cost functional, obtaining the Hamiltonian of the control model and applying the Pontryagin's maximum principle. It is clear from the foregoing that there are existing deterministic models for the analysis and control of the SARS-CoV-2, which can be solved either analytically or numerically. However, existing analytic methods such as, the Elzaki transform method, Laplace transform method, d-expansion method etc, requires complex mathematical configurations such as linearization, perturbation, quasi-linearization, and weak assumptions, which is often time consuming and challenging to undertake [20-28].

Over the years, numerical techniques have been explored for seeking the approximate solution of many mathematical models that exist in science and technology. This is due to the unfavourable situations encounters in executing most of the analytics methods. Basic unique characteristic of numerical methods lies in their ability to approximate the analytic solution of the model in a convergent series solution. Population existing numerical methods for solving many real-life problems can be seen in [29-36] and the references therein.

In this paper, we proposed an efficient and reliable numerical procedure called the " variational iteration orthogonal collocation method (VIOCM)" for the numerical approximation of SEIR (COVID-19) model. The proposed method is an elegant mixture of the variational iteration method (VIM) and the orthogonal collocation method (OCM) employing the Mamadu-Njoseh orthogonal polynomials as basis functions in the approximation of the analytic solution of the SEIR model [37–38].

The standard variational iteration method (VIM) was first proposed by He [39]. The VIM in recent years has been explored by many researchers to solve both linear and nonlinear problems due to its simplicity of application, less computational time, and rapid rate of convergence. The method involves the construction of correction functional for the existing problem, the use of variational theory and restricted variables [40]. The method is also independent of small parameter variation in the differential equation and present its solution as a sequence of series solution.

The use of orthogonal polynomials for the solution of differential equations was first uncovered in the 1930s [41]. An equation in a given closed interval possess a collocation solution in a given collocation space if it satisfies the cardinality of the dimension of that collocation space. However, it

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is an orthogonal collocation if the set of collocation points is at the zeros of orthogonal collocation [42].

Since the outbreak of the novel coronavirus, many numerical schemes have been put forward by different researchers worldwide to study, analyze and find a solution for the Coronavirus model [26, 43-44]. However, the adoption of orthogonal polynomials as trial functions for seeking the approximate solution of the Coronavirus model has not been explored. Therefore, it is the aim of this article to seek the approximate solution of the SEIR (COVID-19) model using the Mamadu-Njoseh polynomials as basis functions via the proposed method VIOCM. The choice of these polynomials is the fact that their existence is new and possess same rate of convergence as that of Chebyshev orthogonal polynomials [45-47].

2. Materials and Methods

2.1 Orthogonal polynomials

Let [45 – 46]

$$\int_{-1}^{1} w(x)\,\varphi_n(x)\varphi_m(x)\,dx = \begin{cases} 0, & n \neq m \\ 1, & n = m \end{cases}, \qquad (1)$$

where $w(x)$ is a positive and continuous weight function on $[-1,1]$ such that the moment

$$\mu = \int_{-1}^{1} w(x)\,x^n\,dx, \quad n = 0,1,2,\ldots \qquad (2)$$

exists. Then the inner product of $\varphi_n(x)$ and $\varphi_m(x)$ denoted as $\langle \varphi_n(x),\ \varphi_m(x)\rangle$ is orthogonal if

$$\langle \varphi_m(x), \varphi_n(x)\rangle = 0, \quad m \neq n, \qquad x \in [-1,1] \qquad (3)$$

2.1.1 Mamadu-Njoseh Polynomials, $\boldsymbol{\varphi_n(x)}$

These are orthogonal polynomials constructed via the weight function $w(x) = 1 + x^2,\ x \in [-1,1]$ using the following properties [45]:

i. $\varphi_n(x) = \sum_{i=0}^{n} a_i x^i$

ii. $\langle \varphi_n(x),\ \varphi_m(x)\rangle = 0,\ m \neq n,\ x \in [-1,1]$

iii. $\varphi_n(1) = 1.$

Thus, the first seven Mamadu-Njoseh polynomials are given as follows:

$\varphi_0(x) = 1$

$\varphi_1(x) = x$

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$$\varphi_2(x) = \frac{1}{3}(5x^2 - 2)$$

$$\varphi_3(x) = \frac{1}{5}(14x^3 - 9x)$$

$$\varphi_4(x) = \frac{1}{648}(333 - 2898x^2 + 3213x^4)$$

$$\varphi_5(x) = \frac{1}{136}(325x - 1410x^3 + 1221x^5)$$

$$\varphi_6(x) = \frac{1}{1064}(-460 + 8685x^2 - 24750x^4 + 17589x^6)$$

The graphs of these polynomials (up to n = 5) are shown below:

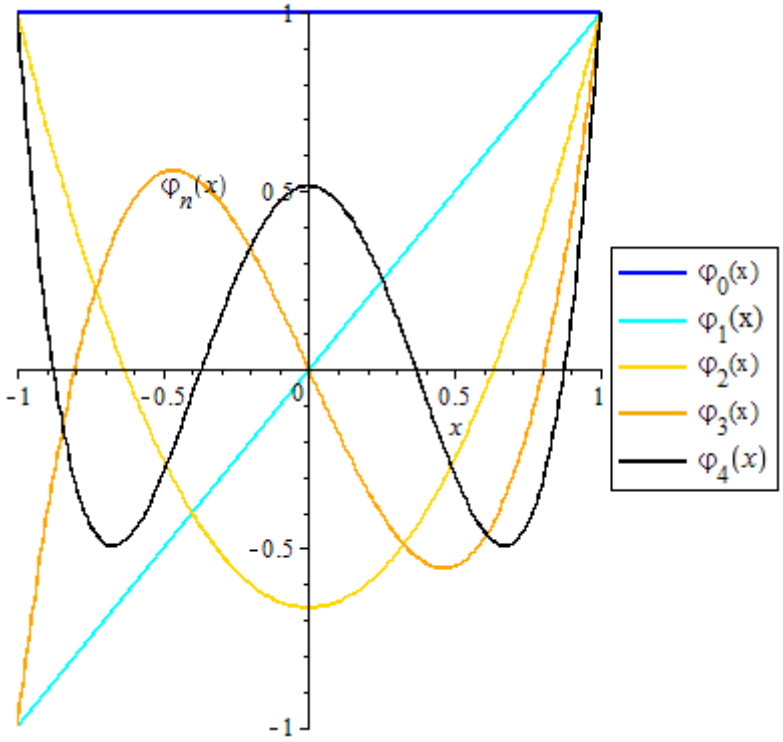

Figure 1: Mamadu-Njoseh Polynomials

2.2 SEIR Model

In epidemiology, the model is defined via the non-linear systems of differential equations below [37 – 38]

$$\left.\begin{aligned} \dot{S}(t) + aS(t)I(t) &= 0 \\ \dot{E}(t) - aS(t)I(t) + bE(t) &= 0 \\ \dot{I}(t) - bE(t) + cI(t) &= 0 \\ \dot{R}(t) - cI(t) &= 0 \end{aligned}\right\} \qquad (4)$$

where individuals of the population that are susceptible, exposed, infectious and recovered are denoted by S, E, I and R respectively. Also, a, b and c are positive constants.

Below is a systematic diagram for the various compartments of the SEIR model in the transmission among individuals in the populations.

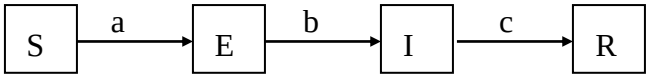

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Figure 2: SEIR transmission model

Interpretation of the SEIR model (CORONA VIRUS MODEL)

Below is a precise interpretation of the SEIR model arising from (4):

$$i. \quad \dot{S}(t) = \frac{a}{N_0} S(t) I(t) - \frac{k}{N_0} S(t) + (\beta_1 + \beta_2) - \frac{(\alpha_1 + \alpha_2)}{N_0} S(t) + g N_0(t) - \tau S(t) \qquad (5)$$

where:

$\dot{S}(t) \equiv \frac{dS(t)}{dt}$ = rate of change of susceptible individuals in the population.

$\frac{a}{N_0} S(t) I(t)$ = proportion of the population that is susceptible × average value of the population infected by a carrier (infectious individual) over the entire duration of infection × population infected by infectious individual.

$\frac{k}{N_0} S(t)$ = fraction of the population that is susceptible source of infectious animal.

$(\beta_1 + \beta_2$ = entrance of travellers.

$\frac{(\alpha_1 + \alpha_2)}{N_0} S(t)$ = proportion of population in percentage travelling out multiplying the population of susceptible persons.

$g N_0(t)$ = birth rate due to natural occurrence multiplying the entire population.

$\tau S(t)$ = rate of death occurrence of susceptible individual multiplying the average number of susceptible individuals.

$$ii. \quad \dot{E}(t) = \frac{a}{N_0} S(t) I(t) - \frac{k}{N_0} S(t) - bE(t) - \frac{(\alpha_1 + \alpha_2)}{N_0} E(t) - \tau E(t) - cE(t) \qquad (6)$$

where:

$\dot{E}(t) = \frac{dE(t)}{dt}$ = rate of change of exposed individuals in the population.

$bE(t) =$ average number of persons exposed over the latency period.

$\frac{(\alpha_1 + \alpha_2)}{N_0} E(t) =$ proportion of population in percentage travelling out multiplying the population of exposed persons.

$\tau E(t) =$ rate of death occurrence of exposed persons (individuals) multiplying the average number of exposed persons.

$cE(t) =$ therapy and testing rate multiplying the number of exposed individuals.

$$iii. \quad \dot{I}(t) = bE(t) - cI(t) - (\alpha_1 + \alpha_2) \frac{I(t)}{N_0} - \tau I(t) \qquad (7)$$

$$iii. \quad \dot{I}(t) = bE(t) - cI(t) - (\alpha_1 + \alpha_2) \frac{I(t)}{N_0} - \tau I(t) \qquad (7)$$

where:

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$I(t)$ = rate of change of infected persons in the population.

$bE(t)$ = average number of persons exposed over the latency period.

$c(t)$ = average number of infected persons in the duration of the infection.

$(\alpha_1 + \alpha_2)\frac{I(t)}{N_0}$ = proportion of the population in percentage travelling out multiplying the population of infected persons.

$\tau I(t)$ = rate of death of infected persons multiplying the average number of infected persons.

$$iv. \quad \dot{R}(t) = cI(t) - \tau R(t) + cE(t) \tag{8}$$

where:

$\dot{R}(t)$ = rate of change of recovered persons in the population.

$cI(t)$ = average number of infected persons in the duration of the infection.

$\tau R(t)$ = rate of death of infected persons multiplying the average number of recovered persons.

$cE(t)$ = therapy and testing rate multiplyinh the number of recovered individuals.

Thus, the systematic transmission of the various compartments of the novel coronavirus model (model) is now expressed by the following first order differential systems:

$$\left.\begin{aligned}
\dot{S}(t) &= \frac{a}{N_0}S(t)I(t) - \frac{K}{N_0}S(t) + (\beta_1 + \beta_2) - \frac{(\alpha_1 + \alpha_2)}{N_0}S(t) + gN_0(t) - \tau S(t) \\
\dot{E}(t) &= \frac{a}{N_0}S(t)I(t) - \frac{K}{N_0}S(t) - bE(t) - \frac{(\alpha_1 + \alpha_2)}{N_0}E(t) - \tau E(t) - \rho E(t) \\
\dot{I}(t) &= bE(t) - cI(t) - (\alpha_1 + \alpha_2)\frac{I(t)}{N_0} - \tau I(t) \\
\dot{R}(t) &= cI(t) - \tau R(t) + \rho E(t)
\end{aligned}\right\}, \tag{9}$$

subject to the following constraints:

$$S(0) = k_0, \quad E(0) = k_1, \quad I(0) = k_2, \quad R(0) = k_3 \tag{10}$$

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Table 1: Definition of Parameters

Parameter	Description
N_0	Entire population,
a	Average value of the population infected by an infectious individual over the entire duration of infection.
b	Average number of persons exposed over the latency period.
c	Average number of infected persons in the duration of the infection.
α_1	Daily number of international air inbound travellers.
α_2	Daily number of domestic air inbound travellers.
β_1	Daily number of international air outbound travellers.
β_2	Daily number of domestic air outbound travellers.
τ	Rate of death occurrence.
g	Birth rate occurrence due to natural occurrence.
k	Scenario of baseline force of infection.
ρ	Therapy and testing rate of the population.

2.3 Variational Iteration Method

As proposed by He [40], let us consider a generalised differential equation of the form

$$L\{u(x)\} + N\{u(x)\} = f(x) \qquad (11)$$

with some prescribed constraints, where $u(x)$ is the function of interest, L is a linear operator of the highest occurring derivative, N is a nonlinear operator and f is the source term.

The first call of the variational iteration method (VIM) is the construction of correction function for (11) as follows:

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$$u_{n+1}(x) = u_n(x) + \int_0^x \lambda(s)\left[L\{u_n(s)\} + \tilde{N}\{u_n(s)\}\right] \quad (12)$$

Where, $\lambda(s)$ is the general Lagrange multiplier which can be obtained via the variational theory, and $\tilde{N}\{u_n(s)\}$ is the restricted term.

2.3.1 Variational Iteration Orthogonal Collocation Method and Mamadu-Njoseh Polynomials

Let

$$S_n(t) = E_n(t) = I_n(t) = R_n(t) = \sum_{i=0}^{N} a_i \varphi_i(t), \quad (13)$$

be the approximate solution of the SEIR model with a_i's being constants to be determined.

By the variational iteration method, we construct a correction functional for the system of equations (9) as follows:

$$\begin{cases} S_{n+1}(t) = S_n(t) + \int_0^t \lambda_1(w)\left(\frac{dS_n}{dw}(w) + a\frac{\tilde{S}_n(w)}{N_0}\tilde{I}_n(w) + \frac{K}{N_0}\tilde{S}_n(w) - (\beta_1+\beta_2) + (\alpha_1+\alpha_2)\frac{\tilde{S}_n(w)}{N_0} + g\tilde{N}_0(w) - \tau\tilde{S}_n(w)\right)dw \\ E_{n+1}(t) = E_n(t) + \int_0^t \lambda_2(w)\left(\frac{dE_n}{dw}(w) - a\frac{\tilde{S}_n(w)}{N_0}\tilde{I}_n(w) - \frac{K}{N_0}\tilde{S}_n(w) + b\tilde{E}_n(w) + (\alpha_1+\alpha_2)\frac{\tilde{E}_n(w)}{N_0} + \rho\tilde{E}_n(w) + \tau\tilde{E}_n(w)\right)dw \\ I_{n+1}(t) = I_n(t) + \int_0^t \lambda_3(w)\left(\frac{dI_n}{dw}(w) - b\tilde{E}_n(w) + c\tilde{I}_n(w) + (\alpha_1+\alpha_2)\frac{\tilde{I}_n(w)}{N_0} + \tau\tilde{I}_n(w)\right)dw \\ R_{n+1}(t)(t) = R_n(t) + \int_0^t \lambda_4(w)\left(\frac{dR_n}{dw}(w) - c\tilde{I}_n(w) + \tau\tilde{R}_n(w) - \rho\tilde{E}_n(w)\right)dw \end{cases} \quad (14)$$

where $\lambda_i(w), i = 1(2)4$, are the general Lagrange multipliers, $n \geq 0$, and $\tilde{S}_n(w), \tilde{E}_n(w), \tilde{I}_n(w)$ and $\tilde{R}_n(w)$ are restricted.

To estimate the values of $\lambda_i(w), i = 1(2)4$, we take the variation δ on both sides of (14) as follows:

$$\begin{cases} \delta S_{n+1}(t) = \delta S_n(t) + \delta\int_0^t \lambda_1(w)\left(\frac{dS_n}{dw}(w) + a\frac{\tilde{S}_n(w)}{N_0}\tilde{I}_n(w) + \frac{K}{N_0}\tilde{S}_n(w) - (\beta_1+\beta_2) + (\alpha_1+\alpha_2)\frac{\tilde{S}_n(w)}{N_0} + g\tilde{N}_0(w) - \tau\tilde{S}_n(w)\right)dw = 0 \\ \delta E_{n+1}(t) = \delta E_n(t) + \delta\int_0^t \lambda_2(w)\left(\frac{dE_n}{dw}(w) - a\frac{\tilde{S}_n(w)}{N_0}\tilde{I}_n(w) - \frac{K}{N_0}\tilde{S}_n(w) + b\tilde{E}_n(w) + (\alpha_1+\alpha_2)\frac{\tilde{E}_n(w)}{N_0} + \rho\tilde{E}_n(w) + \tau\tilde{E}_n(w)\right)dw = 0 \\ \delta I_{n+1}(t) = \delta I_n(t) + \delta\int_0^t \lambda_3(w)\left(\frac{dI_n}{dw}(w) - b\tilde{E}_n(w) + c\tilde{I}_n(w) + (\alpha_1+\alpha_2)\frac{\tilde{I}_n(w)}{N_0} + \tau\tilde{I}_n(w)\right)dw = 0 \\ \delta R_{n+1}(t)(t) = \delta R_n(t) + \delta\int_0^t \lambda_4(w)\left(\frac{dR_n}{dw}(w) - c\tilde{I}_n(w) + \tau\tilde{R}_n(w) - \rho\tilde{E}_n(w)\right)dw = 0 \end{cases} \quad (15)$$

Solving the above equation (15) we obtain the values

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$$\lambda_1(w) = \lambda_2(w) = \lambda_3(w) = \lambda_4(w) = -1.$$

Thus, equation (14) becomes

$$\begin{cases} S_{n+1}(t) = S_n(t) - \int_0^t \left(\frac{dS_n}{dw}(w) + a\frac{S_n(w)}{N_0} I_n(w) + \frac{K}{N_0} S_n(w) - (\beta_1 + \beta_2) + (\alpha_1 + \alpha_2)\frac{S_n(w)}{N_0} + gN_0(w) - \tau S_n(w) \right) dw \\ E_{n+1}(t) = E_n(t) - \int_0^t \left(\frac{dE_n}{dw}(w) - a\frac{S_n(w)}{N_0} E_n(w) - \frac{K}{N_0} S_n(w) + bE_n(w) + (\alpha_1 + \alpha_2)\frac{E_n(w)}{N_0} + \rho E_n(w) + \tau E_n(w) \right) dw \\ I_{n+1}(t) = I_n(t) - \int_0^t \left(\frac{dI_n}{dw}(w) - bE_n(w) + cI_n(w) + (\alpha_1 + \alpha_2)\frac{I_n(w)}{N_0} + \tau I_n(w) \right) dw \\ R_{n+1}(t)(t) = R_n(t) - \int_0^t \left(\frac{dR_n}{dw}(w) - cI_n(w) + \tau R_n(w) - \rho E_n(w) \right) dw \end{cases} \quad (16)$$

To implement the iterative (16), we require an initial approximation to kick-off the iteration process which we shall obtain from using equation (10) and (14) as given below.

$$\begin{cases} S_0(t) = \sum_{i=0}^{N} a_i \varphi_i(t) - K_1 \\ E_0(t) = \sum_{i=0}^{N} a_i \varphi_i(t) - K_2 \\ I_0(t) = \sum_{i=0}^{N} a_i \varphi_i(t) - K_3 \\ R_0(t) = \sum_{i=0}^{N} a_i \varphi_i(t) - K_4 \end{cases} \quad (17)$$

Consequently, for $n \geq 0$, the required approximate solutions resulting from using (16) and (17) is thus given as the series solution

$$\begin{cases} S(t) = \sum_{i=0}^{N} S_i \\ E(t) = \sum_{i=0}^{N} E_i \\ I(t) = \sum_{i=0}^{N} I_i \\ R(t) = \sum_{i=0}^{N} I_i \end{cases} \quad (18)$$

where the values of $a_i's$ are computed via orthogonal collocation after linearization.

3. Results

Now, implementing the above iterative procedures for $n \geq 0$ with the aid of MAPLE software for $N = 3$ with the values $K_1 = 2500, K_2 = 1, K_3 = 1, K_4 = 0,$ we obtain the following approximations arising from equation (16) and (17) respectively:

Now, implementing the above iterative procedures for $n \geq 0$ with the aid of MAPLE software for $N = 3$ with the values $K_1 = 2500, K_2 = 1, K_3 = 1, K_4 = 0,$ we obtain the following approximations arising from equations (16) - (18) respectively:

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$$S(t) := 2a_0 + 20a_1 + 332a_2 + 5564a_3 - 5000 - \frac{a\beta\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t}{N_0} - \frac{K\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)t}{N_0} + \beta_1 t + \beta_E t - \left(\frac{\alpha_1}{N_0} + \frac{\alpha_E}{N_0}\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)t + gN_0 t - \tau\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)t$$

$$E(t) := 2a_0 + 20a_1 + 332a_2 + 5564a_3 - 2 + \frac{a\beta\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t}{N_0} + \frac{K\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)t}{N_0} - \left(b + \frac{\alpha_1}{N} + \frac{\alpha_E}{N} + \rho + \tau\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t$$

$$I(t) := 3a_0 + 30a_1 + 498a_2 + 8346a_3 - 3 + 2b\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t - 2\left(c + \frac{\alpha_1}{N_0} + \frac{\alpha_E}{N_0} + \tau\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t + b\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1 + \frac{a\beta\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t}{N_0} + \frac{K\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)t}{N_0} - \left(b + \frac{\alpha_1}{N} + \frac{\alpha_E}{N} + \rho + \tau\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t\right)t - \left(c + \frac{\alpha_1}{N_0} + \frac{\alpha_E}{N_0} + \tau\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1 + b\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t - \left(c + \frac{\alpha_1}{N_0} + \frac{\alpha_E}{N_0} + \tau\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t\right)t$$

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$$R(t) := 3a_0 + 30a_1 + 498a_2 + 8346a_3 + 2c\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t - 2\tau\left(a_0 + 10a_1 + 166a_2 + 2782a_3\right)t + 2\rho\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t + c\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1 + b\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t - \left(c + \frac{\alpha_1}{N_0} + \frac{\alpha_E}{N_0} + \tau\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t\right)t - \tau\left(a_0 + 10a_1 + 166a_2 + 2782a_3 + c\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t - \tau\left(a_0 + 10a_1 + 166a_2 + 2782a_3\right)t + \rho\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t\right)t + \rho\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1 + \frac{a\beta\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t}{N_0} + \frac{K\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 2500\right)t}{N_0} - \left(b + \frac{\alpha_1}{N} + \frac{\alpha_E}{N} + \rho + \tau\right)\left(a_0 + 10a_1 + 166a_2 + 2782a_3 - 1\right)t\right)t$$

Using the assumed values,

$a = 0.8, b = 0.75, c = 0.05, K = 0.001, N_0 = 2502, \beta_1 = \beta_2 = 0.15, \alpha_1 = 0.01, \alpha_2 = 0.03, \rho = 0.1, \tau = 0.1$ and $g = 0.000003597122302$,

on the above equations and collocating orthogonally after linearization for the values of the unknowns $a_i's$, and substituting back into the (18) yields us the following approximations:

$$S(t) := 2500 - 25.53132774\cdot t - 0.143869926\cdot t^2 + 0.013851166\cdot t^3 + 0.00002273066243\cdot t^4 - 4.791588974\,10^{-7}\,t^5 + 4.31004739710^{-11}\,t^6$$

$$E(t) := 1 - 0.059656274\cdot t + 0.29733881\cdot t^2 - 0.09860941\cdot t^3 + 4.8381106310^{-4}\cdot t^4 - 4.79158897410^{-7}\cdot t^5 + 4.31004739710^{-11}\,t^6$$

$$I(t) := 1 + 0.689984012\cdot t - 0.043076138\cdot t^2 + 0.074410709\cdot t^3$$

$$R(t) := 0.15\cdot t + 0.013516786\cdot t^2 + 9.1483020810^{-3}\cdot t^3$$

3.2. Figures, Tables and Schemes

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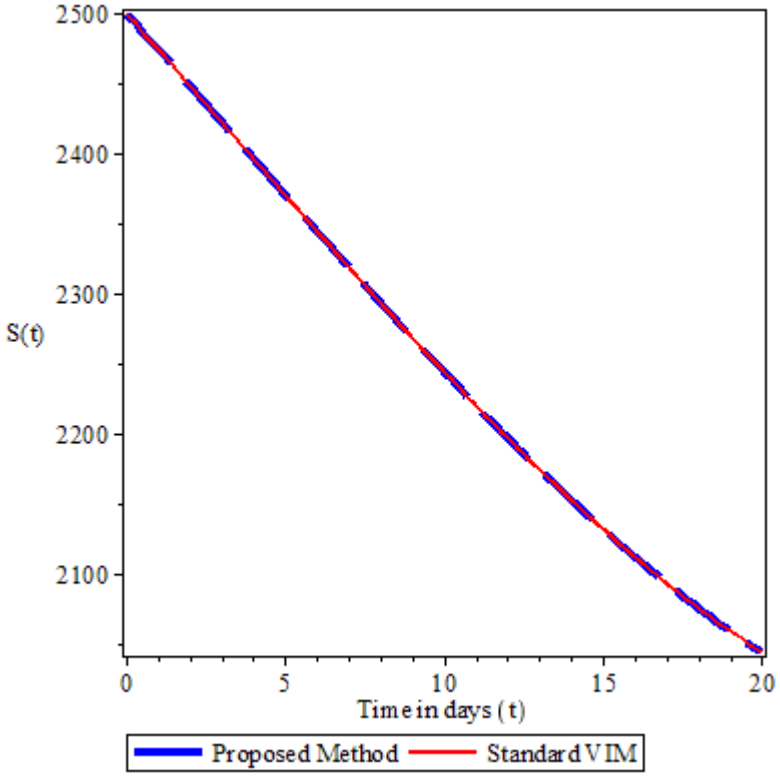

Figure 3: Comparison of the VIOCM and standard VIM of Susceptible individuals in the population against time (t).

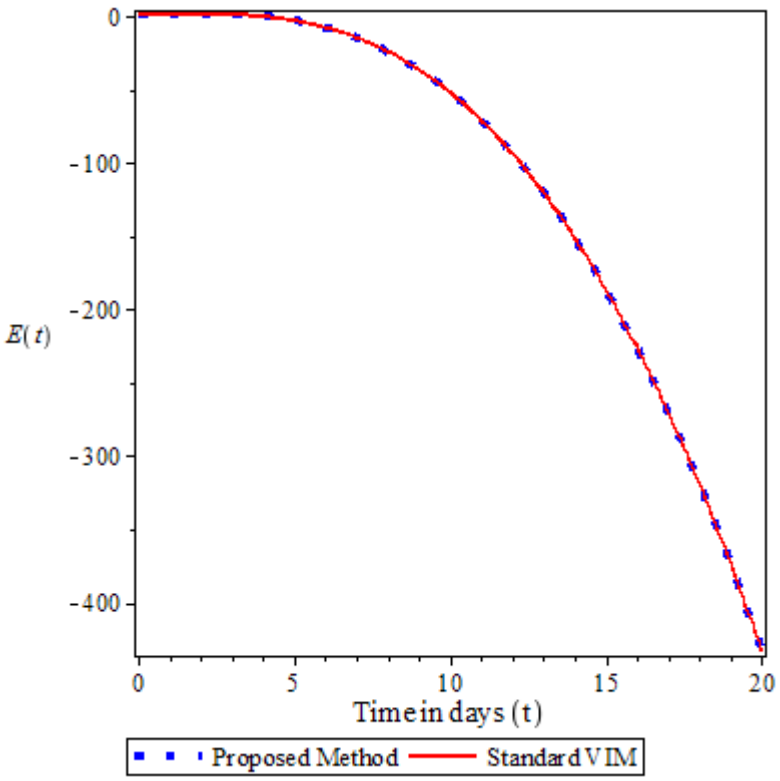

Figure 4: Comparison of the VIOCM and standard VIM of Exposed individuals in the population against time (t).

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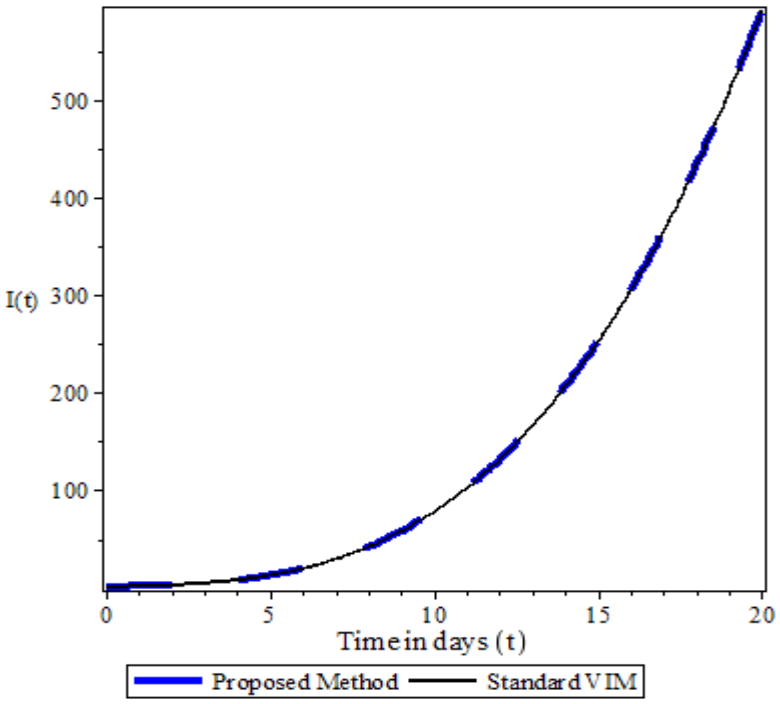

Figure 5: Comparison of the VIOCM and standard VIM of Infected individuals in the population against time (t).

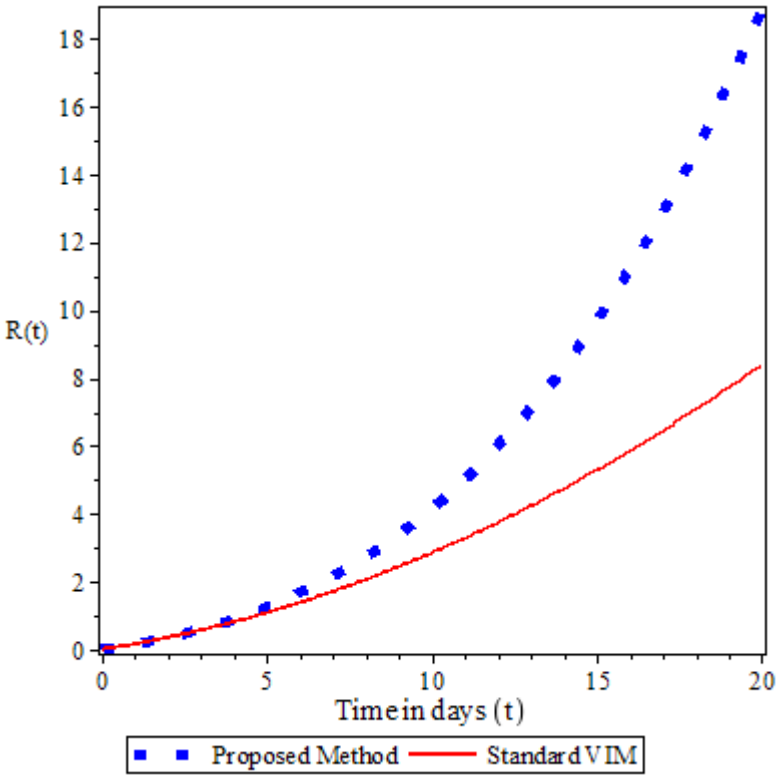

Figure 6: Comparison of the VIOCM and standard VIM of Recovered individuals in the population against time (t).

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Table 1: Percentage decline of susceptible individuals recorded against time in days (t).

Susceptible (%)	99.9	97.9	95.9	93.9	91.9	89.9	87.9	85.9	81.9	83.9	79.9
Time in days (t)	0	2	4	6	8	10	12	14	16	18	20

Table 2: Percentage of Exposed individuals recorded against time in days (t).

Exposed (%)	0	0	0	-0.4	-0.8	-2	-4	-6	-9	-13	-20
Time in days (t)	0	2	4	6	8	10	12	14	16	18	20

Table 3: Percentage increase of infected individuals recorded against time in days (t).

Infectious (%)	0	0	0.4	1.2	2	3.2	5.6	8	12	17.99	23.98
Time in days (t)	0	2	4	6	8	10	12	14	16	18	20

Table 4: Percentage of recovered individuals recorded against time in days (t).

Recovered (%)	0	0.008	0.04	0.07	0.1	0.2	0.24	0.32	0.41	0.56	0.74
Time in days (t)	0	2	4	6	8	10	12	14	16	18	20

4. Discussion

Haven implemented the proposed method for the numerical approximation of the SEIR Coronavirus model, the following observations are recorded:

i. There is decline of susceptible individuals in the population with a common difference of 2 as shown in **Figure 3**. For instance, at the initial time (in days), 99.9% of the population is susceptible to the COVID-19 disease. In time (in days) 20, 79.9% of the population is noticed to be susceptible to the disease. **Table 1** shows the percentage decline of susceptible individuals recorded against time in days (t).

The reason for such a decline could be as a result of the following factors: a properly functioning immune system, age factor, genetics factor, environmental factor, nutrition and by chance [48].

ii. Individuals were less exposed individuals to the COVID-19 disease in the first 20 days (in time) in the population as shown in **Figure 4**. **Table 2** shows the percentage of exposed individuals recorded against time in days (t).

iii. There is a rapid rate of infected individuals to the COVID-19 disease in the population as shown in **Figure 5**. **Table 3** shows the percentage increase of infected individuals recorded against time in days (t). This rapid increase is caused either by coming in contact with the infected host or through contaminated objects or surfaces [49] .

iv. Recovered individuals to the COVID-19 disease in the population is notable as shown in **Figure 6**.

Table 4 shows the percentage of recovered individuals recorded against time in days (t).

5. Conclusions

Since the outbreak of the deadly novel coronavirus (COVID-19) epidemic in Wuhan, China, many mathematical models have been proposed to study the various compartments of the SEIR in the transmission among individuals in the population. Consequently, the SEIR model has been solved either analytically or numerically by the emerging researchers since the outbreak. However, the use of orthogonal polynomials has never been adopted in the approximation of the analytic solution of the SEIR model. In this article, we have successfully implemented the use of orthogonal Mamadu-Njoseh polynomials via the proposed method which is the variational iteration orthogonal collocation method to seek the solution of the SEIR model. It was observed that the proposed method converges rapidly to the exact solution even as N increases. This suggests that the use of orthogonal polynomials as trial functions for the SEIR model is indeed an effective approximant as it produces the analytic solution at just few iterations. Resulting numerical evidences were compared with the standard variational iteration method as available in the literature [38] as shown in the **Figures 3 – 6**.

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Conflicts of Interest: Declaration of interests

☐ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

☐ The authors declare that there was no financial interests/personal relationships which may be considered as potential competing interests.

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