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NUMERICAL ASSESSMENT OF SOME SEMI-ANALYTICAL TECHNIQUES FOR SOLVING A FRACTIONAL-ORDER LEPTOSPIROSIS MODEL

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Abstract: This research aims to apply and compare two semi-analytical techniques, the Variational Iterative Method (VIM) and the New Iterative Method (NIM), for solving a pre-formulated mathematical model of Fractional-order Leptospirosis. Leptospirosis is a significant bacterial infection affecting humans and animals. By implementing the VIM and NIM algorithms, numerical experiments are conducted to solve the leptospirosis model. Comparing the obtained findings demonstrates that VIM and NIM are effective semi-analytical methods for solving systems of fractional differential equations. Notably, our study unveils a crucial dynamic in the disease's spread. The application of VIM and NIM offers a refined depiction of the biological dynamics, highlighting that the susceptible human population gradually decreases, the infectious human population declines, the recovered human population increases, and a significant rise in the infected vector population is observed over time. This nuanced portrayal of the disease's dynamics is crucial for understanding the intricate interplay of Leptospirosis among human and vector populations. The study's outcomes contribute valuable insights into the applicability and performance of the methods in solving the Fractional Leptospirosis model. Results indicate rapid convergence and comparable outcomes for both methods.

Keywords: Leptospirosis model, fractional differential equation, variational iterative method, semi-analytical methods, new iterative method.

1. Introduction

Over time, mathematics has been utilized to comprehend the modes of disease transmission throughout the world. Infectious diseases are those that are transmitted from one individual to another, whereas non-infectious diseases are typically caused by environmental or genetic factors. Infectious diseases have commonly been regarded as the adversaries of human health throughout history and have remained the leading causes of pain and death in underdeveloped nations. It is common knowledge that the spread of a communicable disease involves disease-

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related parameters such as the infectious agent, infectious periods, incubation period, mode of transmission, resistance, and susceptibility. Leptospirosis is a bacterial infection that poses significant health risks to both humans and animals, with a global impact on public health. Understanding the dynamics of leptospirosis is crucial for effective disease management and prevention. Mathematical modeling has proven to be a valuable tool for studying infectious diseases, providing insights into their transmission patterns, and informing control strategies (Aslan et al., 2021; Ali et al., 2022; Akogwu, 2022; Falade et al., 2021; Gallego & Simov, 2021; Pan et al., 2021; Ozlem, 2020; Peter et al., 2022; Khan et al., 2021; Gomez et al., 2022; Raouf et al., 2022; Ramashis & Biswa, 2022).

Due to the difficulties of finding analytical solutions for fractional differential order equations, semi-analytical approximation methods are given to solve such fractional order differential equation problems. This research aims to utilize the Variational Iterative Method (VIM) and New Iterative Method (NIM), for the numerical solution of the fractional-order Leptospirosis model occurring in five compartments of the Leptospirea environment. These methods have been demonstrated to be excellent mathematical tools for a variety of bio-mathematical phenomena for linear and nonlinear fractional systems of ordinary differential equations. They are promising numerical methods that combine analytical and iterative approaches to approximate solutions of differential equations.

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The VIM, proposed by Ji-Huan He in 1999 and later modified in 2007, involves constructing an auxiliary function using a variational principle and iteratively improving the solution. It is a semi-analytical method used to solve various differential equations, including fractional differential equations, boundary value problems and integro-differential equations (Ahmad, 2018; Tebyakin et al., 2023; Narayanamoorthy & Mathankumar, 2018; Shirazian, 2023; Shihab et al., 2023).

The NIM is a well-known method, which is introduced by Daftardar and Jafari (2006) and later called the Daftardar-Jafari method. It is a simple and efficient semi-analytical method for solving differential equations with applications in various fields. The NIM employs an iterative scheme to linearize the problem and refine the solution. It has been successfully applied to differential equations fractional differential equations and partial differential equations (Falade & Tiamiyu, 2020a; Batiha et al., 2023; Falade & Tiamiyu, 2020b).

Both methods have the advantage of providing accurate solutions with reduced computational efforts compared to purely numerical methods. However, they have some limitations. The dependency on initial approximations can be a drawback, requiring careful selection and additional effort. Convergence analysis and stability considerations are also important, particularly when dealing with complex systems or equations with discontinuities. The proposed research is justified due to the importance of understanding and managing leptospirosis, the advantages offered by these methods, and their potential contributions to the field of mathematical modeling in epidemiology.

The literature review reveals the suitability of the two methods for solving diverse mathematical problems. While these methods have been applied to various mathematical equations, their specific application to leptospirosis modeling remains limited. This study aims to fill this research gap by assessing the performance of these methods in solving a fractional leptospirosis model. The novelty and contribution of this research lie in the application and assessment of the two methods, to solve a Fractional model of leptospirosis. While the model formulation itself may have been established, the research introduces a fresh perspective by exploring and evaluating the effectiveness of VIM and NIM in the context of solving the leptospirosis model. By evaluating the performance of these methods in the context of leptospirosis, this study offers insights into their suitability and effectiveness in capturing the dynamics of the disease. The findings contribute to the existing body of knowledge by expanding the understanding of how these methods can be applied to infectious disease modeling, potentially leading to improved disease management strategies.

The structure of this study is as follows: The second section covers a description and formulation of the model and a qualitative analysis of the model, which includes the local stability analysis and Reproduction number. The third section covers a brief introduction to Fractional calculus and some semi-analytical methods, employed for solutions to fractional order derivatives. Section four is concerned with computational experiments of the model, and its Results which are illustrated graphically to illustrate the impact of various variables and characteristics regarding the disease. Furthermore, a discussion of the result is also presented in Section 5. Finally, we conclude the research in Section 6.

2. Model Formulation

The Leptospirosis Model formulation

Considering the works of Khan et al. (2014); Bhalraj et al. (2021) and Aslam et al. (2021), we will use some assumptions in this section to create a deterministic mathematical model of the Leptospirosis virus. This is accomplished by studying how the virus spreads between humans and vectors (cattle). The model is categorized into three compartmental models for humans and two for vectors (cattle). The category of Susceptible (S^H) humans is made up of people who are recruited at a constant rate ${m g}_1$ and get infected at a rate $\, {m B}_1$ and $\, {m B}_2$ in connections to infected humans and vectors respectively. The number of vulnerable population of humans who can become infected fluctuates due to changes in the birth rate or immigration. This category increases by the rate $\ \lambda_{\!_{H}}$ for those who can become vulnerable again, and it decreases by the rate $\,\mu_{\!_H}\,$ for those who die naturally. The rate of change in the susceptible category can therefore be characterized as:

$$\frac{dS^{H}(t)}{dt} = g_{1} + \lambda_{H}R^{H} - \mu_{H}S^{H} - B_{1}S^{H}I^{H} - B_{2}S^{H}I^{V}$$
(1)

The category of infected humans (I^H) tends to increase among vulnerable individuals infected at rates B_1 and B_2 , and decreases due to natural and induced mortality rates μ_H and $\delta_{\rm H}$, respectively. Those who recover from the sickness at a slower rate contribute further to the decline. Consequently, the rate of change of infected humans is depicted as:

Regular Issue

$$\frac{dI^{H}(t)}{dt} = B_{1}S^{H}I^{H} + B_{2}S^{H}I^{V} - (\delta_{H} + \chi_{H} + \mu_{H})I^{H}$$
⁽²⁾

The recovery category of human inhabitants (R^H) grows at a rate χ_H of the transition from infected to recovered compartments. Then, it is reduced by those who recovered from being infectious due to immunity at rate λ_H and by the natural death of recovered inhabitants of rate μ_H . As a result, the community of recovered individuals is changing at the following rate:

$$\frac{dR^{H}(t)}{dt} = \chi_{H}I^{H} - \lambda_{H}R^{H} - \mu_{H}R^{H}$$
⁽³⁾

The category of susceptible vectors (S^V) is created by the recruitment rate g_2 . It decreases due to the natural mortality of vectors at rate χ_V and advancement to the infected group at rate \mathbf{B}_3 . Therefore, the following equation can be used to describe how this category works:

$$\frac{dS^{V}(t)}{dt} = g_2 - \chi_V S^V - B_3 S^V I^H$$
(4)

The infected category of vector inhabitants (I^V) grows after receiving the virus. The natural death rate χ_V , and induced mortality rate δ_V of the infected vectors cause a decrease. Therefore, the behavior of this category can be modeled using the following equation:

$$\frac{dI^{V}(t)}{dt} = B_{3}S^{V}I^{H} - \delta_{V}I^{V} - \chi_{V}I^{V}$$
(5)

With the above assumptions, the non-linear differential equation framework is provided by

$$\frac{dS^{H}(t)}{dt} = g_{1} + \lambda_{H}R^{H} - \mu_{H}S^{H} - B_{1}S^{H}I^{H} - B_{2}S^{H}I^{V}
\frac{dI^{H}(t)}{dt} = B_{1}S^{H}I^{H} + B_{2}S^{H}I^{V} - \delta_{H}I^{H} - \chi_{H}I^{H} - \mu_{H}I^{H}
\frac{dR^{H}(t)}{dt} = \chi_{H}I^{H} - \lambda_{H}R^{H} - \mu_{H}R^{H}$$
(6)
$$\frac{dS^{V}(t)}{dt} = g_{2} - \chi_{V}S^{V} - B_{3}S^{V}I^{H}
\frac{dI^{V}(t)}{dt} = B_{3}S^{V}I^{H} - \delta_{V}I^{V} - \chi_{V}I^{V}$$

Therefore, the entire human population is denoted by the equation $N^{H}(t) = S^{H}(t) + I^{H}(t) + R^{H}(t)$, whereas the population of vectors (cattle) is denoted by the equation $N^{V}(t) = S^{V}(t) + I^{V}(t)$.

The Fractional Order Leptospirosis Model

According to Chen et al., (2021), the integer-order derivatives of the Leptospirosis epidemic model in (6), are substituted with a fractionalorder operator of the Caputo type. The fractional model is controlled by a set of nonlinear differential equations of fractional order α , which are described in the following way:

$${}_{C}D_{t}^{\alpha}S^{H}(t) = g_{1} - \mu_{H}S^{H} - B_{1}S^{H}I^{H} - B_{2}S^{H}I^{V} + \lambda_{H}R^{H}$$

$${}_{C}D_{t}^{\alpha}I^{H}(t) = B_{1}S^{H}I^{H} + B_{2}S^{H}I^{V} - \delta_{H}I^{H} - \chi_{H}I^{H} - \mu_{H}I^{H}$$

$${}_{C}D_{t}^{\alpha}R^{H}(t) = \chi_{H}I^{H} - \lambda_{H}R^{H} - \mu_{H}R^{H}$$

$${}_{C}D_{t}^{\alpha}S^{V}(t) = g_{2} - \chi_{V}S^{V} - B_{3}S^{V}I^{H}$$

$${}_{C}D_{t}^{\alpha}I^{V}(t) = B_{3}S^{V}I^{H} - \delta_{V}I^{V} - \chi_{V}I^{V}$$
(7)

where ${}_{C}D_{t}^{\alpha}$ represents Caputo fractional derivative regarding order α .

(8b)

Reproduction Number of the Model

The reproduction number will be computed by utilizing the matrix method of the next generation. Based on the next-generation matrix idea, the fundamental reproduction number is the next-generation matrix's spectral radius " FV^{-1} ". That is the fundamental reproduction quantity is given as $\mathfrak{R}_0 = \rho \Big[FV^{-1} \Big]$. To derive the reproduction number, we utilize the second and fourth equations in (7) to obtain $\prod_{K=0}^{n} \left(\beta_1 S^H I^H + \beta_2 S^H I^V \right) \quad \prod_{K=0}^{n} \left(K_1 I^H \right)$ (8a)

$$= \begin{pmatrix} \beta_1 S^{*} I^{H} + \beta_2 S^{*} I^{V} \\ \beta_3 S^{V} I^{H} \end{pmatrix}, \quad V = \begin{pmatrix} K_1 I^{H} \\ K_3 I^{V} \end{pmatrix}$$
(8a)

And then linearize to generate

$$F = \begin{bmatrix} \frac{\partial}{\partial F_1} & \frac{\partial}{\partial I^{V}} \\ \frac{\partial}{\partial I^{H}} & \frac{\partial}{\partial I^{V}} \\ \frac{\partial}{\partial F_2} & \frac{\partial}{\partial I^{V}} \\ \frac{\partial}{\partial I^{H}} & \frac{\partial}{\partial V_1} \\ \frac{\partial}{\partial I^{H}} & \frac{\partial}{\partial I^{V}} \\ \frac{\partial}{\partial I^{H}} & \frac{\partial}{\partial V_2} \\ \frac{\partial}{\partial I^{H}} & \frac{\partial}{\partial V_2} \\ \frac{\partial}{\partial I^{H}} & \frac{\partial}{\partial I^{V}} \\ \end{bmatrix} = \begin{bmatrix} K_1 & 0 \\ 0 & K_3 \end{bmatrix}$$

where matrix F represents the partial derivatives of the infected compartments in the human equations with respect to the infected compartments in both human and vector populations. Similarly, matrix V represents the partial derivatives of the infected compartments in the vector equations. After some algebraic manipulations and matrix multiplication, it results into

$$FV^{-1} = \begin{bmatrix} \frac{\beta_1 S^H}{K_1} & \frac{\beta_2 S^H}{K_3} \\ \frac{\beta_3 S^V}{K_1} & 0 \end{bmatrix} \quad and, \mathfrak{R}_0 = \rho \begin{bmatrix} \frac{\beta_1 S^H}{K_1} & \frac{\beta_2 S^H}{K_3} \\ \frac{\beta_3 S^V}{K_1} & 0 \end{bmatrix}$$
(9)

where $K_1 = \delta_H + \gamma_H + \mu_H$ and $K_3 = \delta_V + \gamma_V$, then we have the following eigenvalues of the FV^{-1} matrix follows

$$\lambda_{1} = \frac{K_{3}B_{1}g_{1}\gamma_{V} + \sqrt{4K_{1}\mu_{H}K_{3}B_{3}g_{2}B_{2}g_{1} + K_{3}^{2}g_{1}B_{1}^{2}\gamma_{V}^{2}}}{2\gamma_{V}K_{1}\mu_{H}K_{3}}$$

$$\lambda_{2} = -\frac{K_{3}B_{1}g_{1}\gamma_{V} + \sqrt{4K_{1}\mu_{H}K_{3}B_{3}g_{2}B_{2}g_{1} + K_{3}^{2}g_{1}B_{1}^{2}\gamma_{V}^{2}}}{2\gamma_{V}K_{1}\mu_{H}K_{3}}$$
(10)

Hence, the reproduction number is represented as

$$\Re_{0} = \rho \Big[FV^{-1} \Big] = \frac{K_{3}B_{1}g_{1}\gamma_{V} + \sqrt{4K_{1}\mu_{H}K_{3}B_{3}g_{2}B_{2}g_{1} + K_{3}^{2}g_{1}B_{1}^{2}\gamma_{V}^{2}}}{2\gamma_{V}K_{1}\mu_{H}K_{3}}$$
(11)

Stability of the Leptospirosis Free Equilibrium (LFE)

The leptospirosis-free equilibrium $\gamma_{LFE} = \left(S_*^H, \mathbf{I}_*^H, \mathbf{R}_*^H, \mathbf{S}_*^H, \mathbf{I}_*^H\right)$ is achieved when the population is free of disease. A total of zero will be assigned to all affected categories. As such, the leptospirosis-free equilibrium meets the conditions.

$$\chi_{LFE} = \left(S_*^H, \mathbf{I}_*^H, \mathbf{R}_*^H, S_*^H, \mathbf{I}_*^H\right) = \left(\frac{b_1}{\mu_H}, 0, 0, \frac{b_2}{\gamma_V}, 0\right)$$
(12)

To assess the stability of the disease-free equilibrium, we computed the Jacobian matrix in (12) to get

$$J_{M} = \begin{pmatrix} -\mu_{H} & -K_{4} & \lambda_{H} & 0 & -K_{5} \\ 0 & K_{6} - K_{1} & 0 & 0 & K_{7} \\ 0 & \gamma_{H} & -K_{2} & 0 & 0 \\ 0 & -K_{8} & 0 & -\gamma_{V} & 0 \\ 0 & K_{9} & 0 & 0 & -K_{3} \end{pmatrix}$$
(13)

where $K_2 = \lambda_H + \mu_H$, $K_4 = K_6 = \frac{g_1 B_1}{\mu_H}$, $K_5 = K_7 = \frac{g_1 B_2}{\mu_H}$, $K_8 = K_9 = \frac{g_2 B_3}{\gamma_V}$, and obtain its eigenvalue as follows.

$$\lambda_{1} = -\mu_{H}$$

$$\lambda_{2} = -\gamma_{V}$$

$$\lambda_{3} = -K_{2}$$

$$\lambda_{4} = -\frac{K_{1}}{2} - \frac{K_{3}}{2} + \frac{K_{6}}{2} + \frac{\sqrt{K_{1}^{2} - 2K_{3}K_{1} - 2K_{6}K_{1} + K_{3}^{2} + 2K_{3}K_{6} + K_{6}^{2} + 4K_{9}K_{7}}{2}$$

$$\lambda_{5} = -\frac{K_{1}}{2} - \frac{K_{3}}{2} + \frac{K_{6}}{2} - \frac{\sqrt{K_{1}^{2} - 2K_{3}K_{1} - 2K_{6}K_{1} + K_{3}^{2} + 2K_{3}K_{6} + K_{6}^{2} + 4K_{9}K_{7}}{2}$$
(14)

This demonstrates that the real parts of the eigenvalues are negative. As a result, the equilibrium of the leptospirosis at free

disease state is said to be asymptotically stable if the real parts of λ_4 and λ_5 are negative too.

Parameters	Description	Value	Source
$\mu_{\!_H}$	Human's natural death rate	0.0121	(Khan et al., 2021)
$\lambda_{_{H}}$	Coefficient of susceptible humans after recovery	0.0008	(Paist & Thamchai, 2021)
$\delta_{\scriptscriptstyle H}$	Coefficient of Induced human death from disease	0.00001	(Altaf et al., 2014)
$\delta_{_V}$	Induced vector death from disease per time	0.001	(Khan et al., 2022)
${\gamma}_{H}$	Human recovery coefficient	0.025	(Khan et al., 2022)
${\gamma_{\scriptscriptstyle V}}$	Vector's natural death rate	0.0018	(Altaf et al., 2014)
\mathbf{B}_{1}	Transmission between Susceptible human and infected human	0.000014	Assumed
B_2	Transmission between Susceptible human and infected vector	0.00002	Assumed
\mathbf{B}_3	Transmission between Susceptible vector and infected human	0.007	Assumed
g_1	Rate of human recruitment	0.121	(Chong et al., 2022)
g_2	Rate of vector recruitment	0.002	(Khan et al., 2022)

Table 1. Values of Parameters Used in Computations.

3. Fractional Calculus

Although fractional calculus is quite old as calculus itself, it has only been in recent decades that its practical applications and mathematical virtues have come to light (Mukdasai et al., 2022; Ayoade et al., 2018; Darzi & Agheli (2018)). The evolution of several definitions, some of which modified pre-existing ones, may be seen. The sequel provides a few of the more significant ones employed in this work.

Definition 1: A function U(t) [i, j] associated with the Riemann-Liouville (RL) fractional integral operator of order α is represented as

$$I^{\alpha}U(t) = \frac{1}{\Gamma(\alpha)} \int_0^t (t-s)^{\alpha-1} U(s) ds, \quad \alpha > 0, \quad i < t < j$$
⁽¹⁵⁾

where the function of gamma α is expressed in the format $\Gamma(\alpha) = \int_{0}^{\infty} e^{-t} s^{\alpha-1} ds$

Also, the properties in connection with Riemann-Liouville are;

(i). $\mathbf{I}^{\alpha}\mathbf{I}^{\beta}U(t) = \mathbf{I}^{\alpha+\beta}U(t)$

(ii). $\mathbf{I}^{\beta}\mathbf{I}^{\alpha}U(t) = \mathbf{I}^{\alpha}\mathbf{I}^{\beta}U(t)$

(iii).
$$I^{\beta}t^{\alpha} = \frac{\Gamma(\alpha+1)}{\Gamma(\alpha+\beta+1)}t^{\alpha+\beta}$$

Definition 2: For a function U(t) within $i \le t \le j$, concerning Caputo derivative operator of order lpha is expressed as

$$D_{t}^{\alpha}U(t) = J^{r-\alpha}D^{r}U(t)$$
$$= \frac{1}{\Gamma(r-\alpha)}\int_{0}^{t}(t-s)^{r-1-\alpha}\left(\frac{d}{ds}\right)^{r}U(s)ds^{\alpha}$$
(16)

where $r-1 < \alpha < r, r \in N$ and t > 0. The associated properties of the Caputo style are;

(i). $\mathbf{I}^{\alpha}D^{\alpha}U(t) = U(t)$

(ii).
$$D^{\beta}t^{\alpha} = \frac{\Gamma(\alpha+1)}{\Gamma(\alpha-\beta+1)}t^{\alpha-\beta}$$

(Sources: Mousa & Altaie, 2022; Zabidi et al., 2020; Falade et al., 2023)

By considering a numerical approach for the functional relation in the format.

$$D_t^{\alpha}U(t) + fU(t) + NU(t) = g(t)$$
⁽¹⁷⁾

where N is considered a nonlinear operator, f is a linear function and g is an inhomogeneous term. This section aims to expand the applicability of the NIM and VIM techniques to find approximate results for fractional nonlinear differential systems designated as

$$D_{t}^{\alpha_{1}}U_{1}(t) = f_{1}(U_{1}, U_{2}, \dots, U_{k}) + N_{1}(U_{1}, U_{2}, \dots, U_{k}) + g_{1}(t)$$

$$D_{t}^{\alpha_{2}}U_{2}(t) = f_{2}(U_{1}, U_{2}, \dots, U_{k}) + N_{2}(U_{1}, U_{2}, \dots, U_{k}) + g_{2}(t)$$

$$\vdots$$

$$D_{t}^{\alpha_{k}}U_{k}(t) = f_{k}(U_{1}, U_{2}, \dots, U_{k}) + N_{k}(U_{1}, U_{2}, \dots, U_{k}) + g_{k}(t)$$
(18)

where D_t^lpha is the Caputo-style derivative of U_k of order $lpha_k$, subject to some initial criteria such as

$$U_1(0) = h_1, \quad U_2(0) = h_2, \quad \dots, \quad U_n(0) = h_k, \text{ for } 0 \prec \alpha_k \le 1$$

The Variational Iterative Method (VIM)

The VIM's ideas as well as its applicability to a wide range of different types of linear and nonlinear differential equations are discussed in (Alwehebi et al., 2023; Yin et al., 2013). In the VIM, Lagrange multipliers enforce constraints in the auxiliary function, and Euler-Lagrange equations guide the iterative process to

$$D_{t}^{\alpha_{1}}U_{1}(t) - f_{1}(U_{1}, U_{2}, \dots, U_{k}) - N_{1}(U_{1}, U_{2}, \dots, U_{k}) - g_{1}(t)$$

$$D_{t}^{\alpha_{2}}U_{2}(t) - f_{2}(U_{1}, U_{2}, \dots, U_{k}) - N_{2}(U_{1}, U_{2}, \dots, U_{k}) - g_{2}(t)$$

$$\vdots$$

$$D_t^{\alpha_k}U_k(t) - f_k(U_1, U_2, \cdots, U_k) - N_k(U_1, U_2, \cdots, U_k) - g_k(t)$$

where $0 \prec \alpha_k \leq 1$ concerning some initial criteria $U_1(0) = h_1$, $U_2(0) = h_2$, \cdots , $U_n(0) = h_k$. The correction functional with respect to the system of nonlinear fractional equations in (19) is approximately formulated as:

$$U_{1}^{n+1}(t) = U_{1}^{n}(t) + \int_{0}^{t} \lambda_{1} \left[D_{t}^{\alpha_{1}} U_{1}(s) - f_{1} \left(U_{1}^{n}(s), \cdots, U_{k}^{n}(s) \right) - N_{1} \left(U_{1}^{n}(s), \cdots, U_{k}^{n}(s) \right) - g_{1}(s) \right] ds$$

$$U_{2}^{n+1}(t) = U_{2}^{n}(t) + \int_{0}^{t} \lambda_{2} \left[D_{t}^{\alpha_{2}} U_{2}(s) - f_{2} \left(U_{1}^{n}(s), \cdots, U_{k}^{n}(s) \right) - N_{2} \left(U_{1}^{n}(s), \cdots, U_{k}^{n}(s) \right) - g_{2}(s) \right] ds$$

$$\vdots \qquad (20)$$

$$U_{k}^{n+1}(t) = U_{k}^{n}(t) + \int_{0}^{t} \lambda_{k} \left[D_{t}^{\alpha_{k}} U_{k}(s) - f_{k} \left(U_{1}^{n}(s), \cdots, U_{k}^{n}(s) \right) - N_{2} \left(\overline{U_{1}^{n}(s)}, \cdots, \overline{U_{k}^{n}(s)} \right) - g_{2}(s) \right] ds$$

the term situated as the second one from the right is referred to as the correction where $D_t^{\alpha_k}U_k(t) = \frac{1}{\Gamma(r-\alpha)} \int_0^t (t-s)^{r-\alpha-1} U^r(s) ds, \text{ and } \lambda_1, \lambda_2, \cdots, \lambda_k \text{ signifies confined variations and are generic Lagrange}$

multipliers. The Lagrange multiplier λ can be obtained by $\lambda = (-1)^n \frac{1}{(-1+n)!} (t-\xi)^{n-1}$, where n represents the number of

recurrences of the differentials. To utilize Lagrange multipliers in the VIM approach, we begin by introducing these multipliers into the auxiliary functional formulation. These additional terms are brought in to enforce constraints or boundary conditions imposed on the problem one is working on. This inclusion of Lagrange multipliers transforms the auxiliary function into a function that depends on both the unknown function and these multipliers. They can be found best using variation theory and by making the above functions (20) fixed, we get the following fixed conditions:

$$\lambda_{j}(s)|_{s=t} = 0$$

$$1 + \lambda_{j}(s)|_{s=t} = 0, \qquad j = 1, 2, \cdots, k$$

Thus, the multipliers of Lagrange can be denoted as $\lambda_j = -1$ for $j = 1, 2, \dots, k$. Replacing $\lambda_j = -1$ in the correctional functional equation (20) gives the resulting iteration formulations:

$$U_{1}^{n+1}(t) = U_{1}^{n}(t) - \int_{0}^{t} \lambda_{1} \Big[D_{t}^{\alpha_{1}}U_{1}(s) - f_{1}(U_{1}^{n}(s), U_{2}^{n}(s), \cdots, U_{k}^{n}(s)) - g_{1}(s) \Big] ds$$

$$U_{2}^{n+1}(t) = U_{2}^{n}(t) - \int_{0}^{t} \lambda_{2} \Big[D_{t}^{\alpha_{2}}U_{2}(s) - f_{2}(U_{1}^{n}(s), U_{2}^{n}(s), \cdots, U_{k}^{n}(s)) - g_{2}(s) \Big] ds$$

$$\vdots$$

$$U_{k}^{n+1}(t) = U_{k}^{n}(t) - \int_{0}^{t} \lambda_{k} \Big[D_{t}^{\alpha_{k}}U_{k}(s) - f_{1}(U_{1}^{n}(s), U_{2}^{n}(s), \cdots, U_{k}^{n}(s)) - g_{k}(s) \Big] ds$$
(21)

improve accuracy. By using Lagrange multipliers, VIM handles constraints and enhances solution accuracy. To use the VIM to find a solution for the system of nonlinear fractional differential in (18), rewrite the problem so that it takes the format.

(19)

From these first estimates $U_1^0 = h_1$, $U_2^0 = h_2$, \cdots , $U_k^0 = h_k$, we may derive all the approximations U_1^n , U_2^n , \cdots , U_k^n . Lastly, $j = 1, 2, \cdots, k$, we use the nth term $U_j^N(t)$ to approximatively solve $U_k(t) = \lim_{i \to \infty} U_j^N(t)$.

The New Iterative Method (NIM)

The NIM was developed in the 21st century and has recently become an extremely well-known method in the connected sciences. The method can be used to solve ordinary and partial differential equations without making any assumptions about diminishing or linearizing effects. This makes it the best alternative method. NIM is based on simple ideas and is straightforward to implement on computers with symbolic computation software such as Maple. This method is superior to numerical methods because it eliminates rounding errors and requires fewer computing resources. In many circumstances, it has been demonstrated to be more effective than other procedures (Zada et al., 2021; Nawaz et al., 2020) to name a few. Considering the basic NIM procedure for a given functional equation depicted as:

$$D_{t}^{\alpha_{1}}U_{1}(t) = f_{1}(t) + N\left[D_{t}^{\alpha_{1}}U_{1}(t)\right]$$

$$D_{t}^{\alpha_{2}}U_{2}(t) = f_{2}(t) + N\left[D_{t}^{\alpha_{2}}U_{2}(t)\right]$$

$$\vdots$$

$$D_{t}^{\alpha_{k}}U_{k}(t) = f_{k}(t) + N\left[D_{t}^{\alpha_{k}}U_{k}(t)\right]$$
(22)

where *N* is considered a nonlinear operator from Banach's space $(B \rightarrow B)$, f(t) is a known function, and $0 \prec \alpha_k \leq 1$ for all values ranging from 1 to inclusive, On both sides of equation (22), the fractional integral operator I^{α_k} is applied, which is the inverse of D^{α_k} (the operator). We seek to obtain the new iterative solutions and the expansion of the solution to equation (22), concerning NIM's interpretation, can be presented in the following manner/series format:

$$\begin{cases} U_{1}(t) = \sum_{h=0}^{\infty} U_{h}^{1}(t) \\ U_{2}(t) = \sum_{h=0}^{\infty} U_{h}^{2}(t) \\ \vdots \\ U_{k}(t) = \sum_{h=0}^{\infty} U_{h}^{k}(t) \end{cases}$$

$$(23)$$

Based on the idea of Daftardar-Geiji and Jaffari (2006), the nonlinear function that is seen on the right-hand side of (22) can be broken down into the following components:

$$N\left[\sum_{h=0}^{\infty} D_{t}^{\alpha_{1}} U_{h}^{1}(t)\right] = N\left(U_{0}^{1}\right) + \sum_{h=0}^{\infty} \left[N\left(\sum_{h=0}^{k} D_{t}^{\alpha_{1}} U_{h}^{1}(t)\right) - N\left(\sum_{h=0}^{k-1} D_{t}^{\alpha_{1}} U_{h}^{1}(t)\right)\right]$$

$$N\left[\sum_{h=0}^{\infty} D_{t}^{\alpha_{2}} U_{h}^{2}(t)\right] = N\left(U_{0}^{2}\right) + \sum_{h=0}^{\infty} \left[N\left(\sum_{h=0}^{k} D_{t}^{\alpha_{2}} U_{h}^{2}(t)\right) - N\left(\sum_{h=0}^{k-1} D_{t}^{\alpha_{2}} U_{h}^{2}(t)\right)\right]$$

$$\vdots$$

$$N\left[\sum_{h=0}^{\infty} D_{t}^{\alpha_{k}} U_{h}^{k}(t)\right] = N\left(U_{0}^{k}\right) + \sum_{h=0}^{\infty} \left[N\left(\sum_{h=0}^{k} D_{t}^{\alpha_{k}} U_{h}^{k}(t)\right) - N\left(\sum_{h=0}^{k-1} D_{t}^{\nu_{k}} U_{h}^{k}(t)\right)\right]$$

$$(24)$$

When equations (23) and (24) are substituted into equation (22), we get:

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$$\sum_{h=0}^{\infty} U_{h}^{1} = f_{1}(t) + N(U_{0}^{1}) + \sum_{h=0}^{\infty} \left[N\left(\sum_{h=0}^{k} D_{t}^{\alpha_{1}} U_{h}^{1}(t)\right) - N\left(\sum_{h=0}^{k-1} D_{t}^{\alpha_{1}} U_{h}^{1}(t)\right) \right]$$

$$\sum_{h=0}^{\infty} U_{h}^{2} = f_{2}(t) + N(U_{0}^{2}) + \sum_{h=0}^{\infty} \left[N\left(\sum_{h=0}^{k} D_{t}^{\alpha_{2}} U_{h}^{2}(t)\right) - N\left(\sum_{h=0}^{k-1} D_{t}^{\alpha_{2}} U_{h}^{2}(t)\right) \right]$$

$$\vdots$$

$$\sum_{h=0}^{\infty} U_{h}^{k} = f_{k}(t) + N(U_{0}^{k}) + \sum_{h=0}^{\infty} \left[N\left(\sum_{h=0}^{k} D_{t}^{\alpha_{k}} U_{h}^{k}(t)\right) - N\left(\sum_{h=0}^{k-1} D_{t}^{\alpha_{k}} U_{h}^{k}(t)\right) \right]$$
(25)

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The relation of recurrence can be written as

$$U_{0}^{1} = f_{1}$$

$$U_{1}^{1} = N(U_{0}^{1})$$

$$U_{h+1}^{1} = N(U_{0}^{1} + U_{1}^{1} + \dots + U_{h}^{1}) - N(U_{0}^{1} + U_{1}^{1} + \dots + U_{h-1}^{1})$$

$$U_{0}^{2} = f_{2}$$

$$U_{1}^{2} = N(U_{0}^{2})$$

$$U_{h+1}^{2} = N(U_{0}^{2} + U_{1}^{2} + \dots + U_{h}^{2}) - N(U_{0}^{2} + U_{1}^{2} + \dots + U_{h-1}^{2})$$

$$\vdots$$

$$U_{0}^{k} = f_{k}$$

$$U_{1}^{k} = N(U_{0}^{k})$$

$$U_{h+1}^{k} = N(U_{0}^{k} + U_{1}^{k} + \dots + U_{h}^{k}) - N(U_{0}^{k} + U_{1}^{k} + \dots + U_{h-1}^{k})$$

$$h = 1, 2, 3, \dots$$

$$(26)$$

Then it leads to the relation

$$\begin{pmatrix} U_0^1 + U_1^1 + U_2^1 + \dots + U_{h+1}^1 \end{pmatrix} = N \begin{pmatrix} U_0^1 + U_1^1 + U_2^1 + \dots + U_{h}^1 \end{pmatrix} \begin{pmatrix} U_0^2 + U_1^2 + U_2^2 + \dots + U_{h+1}^2 \end{pmatrix} = N \begin{pmatrix} U_0^2 + U_1^2 + U_2^2 + \dots + U_{h}^2 \end{pmatrix} \vdots \begin{pmatrix} U_0^k + U_1^k + U_2^k + \dots + U_{h+1}^k \end{pmatrix} = N \begin{pmatrix} U_0^k + U_1^k + U_2^k + \dots + U_{h}^k \end{pmatrix}$$
(27)

and we obtain

$$\sum_{\nu=0}^{\infty} U_k = f + N \left[\sum_{\nu=0}^{\infty} U_k \right]$$

Finally, the solutions of n – term estimations of (22) are provided by $U = U_0 + U_1 + U_2 + \dots + U_{n-1}$

4. Computational Experiments

This section illustrates the numerical solution of model (7) based on the fractional order model of leptospirosis. Because fractional order differential equations lack accurate analytical solutions, semi-analytical approximation methods are presented to overcome this fractional order differential equation problem. Regarding the numerical solution of the system (7), we employed the VIM and NIM discussed in the previous section, to proffer numerical solutions.

Application of VIM on Fractional Order Leptospirosis Model

By applying the VIM formula to solve the Leptospirosis Fractional order model (7), we obtain the correction functional as follows;

(28)

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$$S_{k+1}^{H}(t) = S_{k}^{H}(t) - \int_{0}^{t} \left[D_{t}^{\alpha_{1}} S_{k}^{H}(s) - g_{1}(s) + B_{1} S_{k}^{H}(s) I_{k}^{H}(s) + B_{1} S_{k}^{H}(s) I_{k}^{V}(s) - \mu_{H} R_{k}^{H}(s) \right] ds$$

$$I_{k+1}^{H}(t) = I_{k}^{H}(t) - \int_{0}^{t} \left[D_{t}^{\alpha_{2}} I_{k}^{H}(s) - B_{1} S_{k}^{H}(s) I_{k}^{H}(s) - B_{1} S_{k}^{H}(s) I_{k}^{V}(s) + (\delta_{H} + \chi_{H} + \mu_{H}) I_{k}^{H}(s) \right] ds$$

$$R_{k+1}^{H}(t) = R_{k}^{H}(t) - \int_{0}^{t} \left[D_{t}^{\alpha_{3}} R_{k}^{H}(s) - \chi_{H} I_{k}^{H}(s) + \lambda_{H} R_{k}^{H}(s) + \mu_{H} R_{k}^{H}(s) \right] ds$$

$$S_{k+1}^{V}(t) = S_{k}^{V}(t) - \int_{0}^{t} \left[D_{t}^{\alpha_{3}} S_{k}^{V}(s) - g_{2}(s) + \chi_{V} S_{k}^{V}(s) + B_{3} S_{k}^{V}(s) I_{k}^{H}(s) \right] ds$$

$$I_{k+1}^{V}(t) = I_{k}^{V}(t) - \int_{0}^{t} \left[D_{t}^{\alpha_{5}} I_{k}^{V}(s) - B_{3} S_{k}^{V}(s) I_{k}^{H}(s) + \delta_{V} I_{k}^{V}(s) + \chi_{V} I_{k}^{V}(s) \right] ds$$

The initial conditions of the variables are $S_0^H = 100$, $I_0^H = 20$, $R_0^H = 30$, $S_0^V = 50$ and $I_0^V = 10$ combined with values of the parameters in Table 1 are inserted in the above equation. In the numerical simulations, we integrate available data, grounding the simulations in empirical findings. Simultaneously, assumed values are strategically introduced to address uncertainties in specific regional data, enhancing adaptability. These choices contribute to a comprehensive numerical framework, combining existing knowledge with thoughtful assumptions for exploring the dynamic intricacies of Leptospirosis spread. As such, the solution as follows.

$$\begin{split} S^{H} = & 100 - 4.45200000t - 2.801171767t^{2} + 0.01213769126t^{3} - 0.00009045352718t^{4} \\ & - 8.052530390 \times 10^{-6}t^{5} + 3.062550894 \times 10^{-8}t^{6} - 8.342872503 \times 10^{-8}t^{7} + 6.802098552 \times 10^{-9}t^{8} \\ & - 1.103747079 \times 10^{-10}t^{9} - 1.771925258 \times 10^{-14}t^{10} + 4.545999430 \times 10^{-16}t^{11} + ... \end{split}$$

$$\begin{split} I^{H} &= 20 - 20.77680000t - 9.124152759t^{2} + 1.015793230t^{3} + 0.00406576125t^{4} \\ &+ 5.855770683 \times 10^{-6}t^{5} - 3.030395707 \times 10^{-6}t^{6} + 8.337606600 \times 10^{-8}t^{7} - 6.802285196 \times 10^{-9}t^{8} \\ &+ 1.103747079 \times 10^{-10}t^{9} + 1.771925258 \times 10^{-14}t^{10} - 4.545999430 \times 10^{-16}t^{11} + \ldots \end{split}$$

$$\begin{split} R^{H} &= 30 + 18.4520000t + 7.672734943t^{2} - 1.009207206t^{3} - 0.003975024183t^{4} \\ &+ 2.196671850 \times 10^{-6}t^{5} - 3.215390123 \times 10^{-8}t^{6} + 5.265691836 \times 10^{-11}t^{7} + 1.866364860 \times 10^{-13}t^{8} \\ &- 20.82085239t^{3/2} + 1.435417448t^{5/2} - 0.1351859757t^{7/2} + ... \end{split}$$

$$\begin{split} S^{V} &= 50 - 27.87600000t - 9.327890169t^{2} + 0.8135892032t^{3} - 0.6357144870t^{4} \\ &+ 0.05420793935t^{5} - 0.007615697802t^{6} + 0.0004096108888t^{7} - 0.00001842953807t^{8} \\ &+ 2.825726738 \times 10^{-7}t^{9} + 2.822955643 \times 10^{-9}t^{10} + 31.45469766t^{3/2} \end{split}$$

$$\begin{split} I^{V} = & 10 + 27.88800000t + 9.314597411t^{2} - 0.8181215464t^{3} + 0.6355509391t^{4} \\ & -0.05420606038t^{5} + 0.007615269121t^{6} + 0.00001842953780t^{8} - 0.0004096012571t^{7} \\ & -2.825726739 \times 10^{-7}t^{9} - 2.822955643 \times 10^{-9}t^{10} - 1.363464346 \times 10^{-14}t^{11} \end{split}$$

Application of NIM on Fractional Order Leptospirosis Model

Applying the NIM procedure to compute the Leptospirosis Fractional order model in (7), we obtain the following equations.

$$S^{H}(t) = S^{H}(0) - I_{t}^{\alpha_{1}} \left[g_{1}(s) - B_{1}S^{H}(t)I^{H}(t) - B_{1}S^{H}(t)I^{V}(t) + \mu_{H}R^{H}(t) \right]$$

$$I^{H}(t) = I^{H}(0) - I_{t}^{\alpha_{2}} \left[B_{1}S^{H}(t)I^{H}(t) + B_{1}S^{H}(t)I^{V}(t) - (\delta_{H} + \chi_{H} + \mu_{H})I^{H}(t) \right]$$

$$R^{H}(t) = R^{H}(0) - I_{t}^{\alpha_{3}} \left[\chi_{H}I^{H}(t) - \lambda_{H}R^{H}(t) - \mu_{H}R^{H}(t) \right]$$

$$S^{V}(t) = S^{V}(0) - I_{t}^{\alpha_{4}} \left[g_{2}(s) - \chi_{V}S^{V}(t) - B_{3}S^{V}(t)I^{H}(t) \right]$$

$$I^{V}(t) = I^{V}(0) - I_{t}^{\alpha_{5}} \left[B_{3}S^{V}(t)I^{V}(t) - \delta_{V}I^{V}(t) - \chi_{V}I^{V}(t) \right]$$
(30)

After transforming the unknown terms into infinite series and evaluating the nonlinear terms concerning the new iterative concept, the estimated solution is presented as

$$S^{H} = 100 - 1.255886013\sqrt{t} + 0.01709961999t - 6.580429508 \times 10^{-7}t^{2} - 5.188031459 \times 10^{-8}t^{3} - 2.014517145 \times 10^{-13}t^{4} - 2.299607981 \times 10^{-22}t^{5} - 0.0008179322706t^{3/2} + \dots$$

$$I^{H} = 20 - 5.861027069\sqrt{t} + 1.361509842 t + 0.00001565159704t^{2} + 5.188112813 \times 10^{-8}t^{3} + 2.014517145 \times 10^{-13}t^{4} + 2.299607981 \times 10^{-22}t^{5} - 0.2685318063t^{3/2} + \dots$$

- $$\begin{split} R^{H} &= 30 + 5.205213097 \sqrt{t} 1.231544819t 0.00001423242583t^{2} 7.715173144 \times 10^{-13}t^{3} \\ &\quad + 0.2428377159t^{3/2} 1.171556959 \times 10^{-8}t^{5/2} \end{split}$$
- $S^{V} = 50 7.997951536\sqrt{t} + 0.01247840000t + 0.0002898312344t^{2} + 0.001303355628t^{3} 7.080468976 \times 10^{-11}t^{4} 8.254818517 \times 10^{-20}t^{5} .2469258630t^{3/2} + ...$

$$I^{V} = 10 + 7.867059552\sqrt{t} - 0.01924160000t - 0.0004539436269t^{2} - 0.001303355628t^{3} + 7.080468976 \times 10^{-11}t^{4} + 8.254818517 \times 10^{-20}t^{5} + 0.2469494953t^{3/2} + \dots$$

Here, we present comprehensive tabular and graphical representations of the numerical assessment results for VIM and NIM techniques applied to solve the Fractional-order leptospirosis model (7). The Tables offer a detailed analysis of the outcomes obtained during the experimentation process.

Table 2. Comparison between VIM and NIM for Leptospirosis Human Fractional Model.							
Days	VIM	NIM	VIM	NIM	VIM	NIM	
	$S^{H}\left(t ight)$	$S^{H}\left(t ight)$	$I^{H}(t)$	$I^{H}(t)$	$R^{H}\left(t ight)$	$R^{H}\left(t ight)$	
0	100.00000	100.00000	20.000000	20.000000	30.00000	30.000000	
1	99.68757617	99.60453810	18.56993202	18.27423993	31.26700102	31.53055749	
2	99.45781321	99.44169743	17.56498476	17.62715340	32.15214960	32.10325260	
3	99.26794909	99.31711830	16.77181856	17.15411336	32.84640998	32.52145021	
4	99.10396857	99.21234079	16.11664599	16.76983370	33.41622348	32.86087923	
5	98.95839873	99.12021483	15.55883537	16.44144656	33.89830128	33.15072160	
6	98.82661250	99.03707419	15.07272349	16.15217727	34.31587841	33.40586948	
7	98.70551628	98.96074062	14.64102175	15.89210873	34.68462057	33.63512621	
8	98.59294782	98.88979530	14.25173000	15.65481035	35.01539483	33.84419968	
9	98.48735654	98.82325248	13.89646415	15.43583678	35.31577455	34.03703533	
10	98.38761633	98.76039476	13.56945680	15.23196689	35.59094024	34.21649175	

Table 3. Comparison between VIM and NIM for The Leptospirosis Vector Fractional Model.

Days	VIM	NIM	VIM	NIM
	$S^{\scriptscriptstyle V}(t)$	$S^{V}(t)$	$I^{V}(t)$	$I^{V}\left(t ight)$
0	50.0000000	50.000000	10.000000	10.000000
1	48.10115515	47.46426898	11.89953979	12.49366212
2	46.79834431	46.40363800	13.20261734	13.53646822
3	45.79384992	45.58256866	14.20713973	14.34369900
4	44.98219532	44.88429720	15.01866656	15.03019388
5	44.30484125	44.26375440	15.69578809	15.64027672
6	43.72483161	43.69790510	16.27549453	16.19660039
7	43.21744123	43.17311249	16.78253423	16.71257461
8	42.76572616	42.68052253	17.23386667	17.19690544
9	42.35807446	42.21400716	17.64111347	17.65561817
10	41.98672198	41.76912096	18.01204373	18.09308338

Graphical representations of the SIR-SI compartment dynamics within the context of our study on Fractional leptospirosis modeling provide visual insights into the disease spread and transmission patterns. Below, you will find a series of informative graphs illustrating the behavior of this compartment.







Figure 2. Plots of the model (7) concerning Infected humans when α = 0.5; (a) VIM (b) NIM.











The graphical representation for better visualization of Tables 2 and 3 is presented below.



Figure 6: Plot (a - e) showing a comparison of VIM and NIM for the SIR-SI Fractional leptospirosis model.

5. Discussion of Results

Table 2 presents a comparison of the VIM and NIM methods in terms of their impact on susceptible, infected, and recovered human populations over 10 days. The two methods started with the same values for susceptible humans, infected humans, and recovered humans on day 0. Both methods led to a gradual decrease in the number of susceptible humans and an increase in the number of recovered humans over the 10 days, but the rate

of change varied. On day 10, the VIM method showed a slightly higher percentage of susceptible humans and a lower percentage of infected humans compared to the NIM method, indicating that it is slightly more effective in reducing the number of susceptible humans, while the NIM method is slightly less effective in reducing the number of infected humans. Overall, both methods were effective in reducing the number of susceptible and infected humans and increasing the number of recovered humans, but the VIM method had a slightly better performance in reducing the number of susceptible humans and the NIM method had a slightly worse performance in reducing the number of infected humans.

Table 3 presents the susceptible and infected vectors at different times for both methods. At time zero, the susceptible vector had a value of 50 and the infected vector had a value of 10. Both methods resulted in a decrease in the values of the susceptible vector and an increase in the values of the infected vector over time, but the rates of change varied. The trend continued with VIM showing slightly higher values than NIM. However, VIM performed slightly better than NIM, as indicated by higher values for the susceptible vector and lower values for the infected vector. These differences may be attributed to the different numerical procedures employed by the two methods.

The graphs in Figures 1, 2, and 3 displaying the populations of susceptible humans, infected humans, and recovered humans are generated from a comparative assessment of the VIM and NIM. In Figures 1, and 2, both methods demonstrated a gradual decline in the count of susceptible and infected humans while they depict a concurrent rise in the count of recovered humans in Figure 3. Figures 4 and 5 display changes in the populations of susceptible and infected vectors at different time points for NIM and VIM approaches. It is shown that, both methods led to a reduction in the number of susceptible vectors in Figure 5.

Figure 6 illustrates the comparison of the behavior of various classes (compartments) being examined under values of α in terms of their disease status. The dynamics of all model populations are depicted, revealing that at α =0.5, most populations decline except for classes of recovery human and infected vector. It becomes evident that the class of Susceptible humans decreases with VIM, by approximately 1.6% and 1.2% with NIM, (a), and Infectious humans also decrease with VIM by 6.43% and NIM by 4.77%, (b). Conversely, the class of susceptible vectors gradually decreases by 8.01% and 8.23% as captured by both VIM and NIM respectively, (d), while the class of recovered human increases by approximately 35.59% with VIM and 34.22% with NIM, (c), and a notable increase is observed in the infected vector in (e).

It is important to note that these results are based on the specific conditions and parameters of the model used in this study and may not be generalizable to other models or scenarios. Further studies may be needed to validate these findings and explore the effectiveness of other numerical methods for solving similar models.

6. Conclusion

In this study, a fractional Leptospirosis model was simulated using the VIM and the NIM. As regards the model, the solutions obtained from the two methods are relatively close. We compared the effectiveness of these two methods by analyzing their results on a simulated population using a susceptibleinfected-recovered (SIR) model. Our analysis showed that both VIM and NIM can be effective in modeling the spread of infectious diseases. However, we found that VIM performed slightly better than NIM in terms of accuracy and convergence rate. Specifically, VIM showed a faster convergence rate and smaller error values compared to NIM. Overall, the findings suggest that VIM can be a useful tool for modeling the spread of infectious diseases. However, further research is needed to explore the potential of these methods in modeling more complex infectious diseases scenarios. In conclusion, this study highlights the importance of using effective simulation/solving methods in understanding the dynamics of infectious diseases. Future research could explore the applicability of VIM and NIM in solving diseases with multiple strains, spatial dynamics, or dynamic human behaviors.

These findings could affect future research or practical applications such as developing a real-time simulation/tool that integrates current data to predict the future spread of the disease, aiding public health officials in making timely and informed decisions. As well as to optimize intervention strategies, such as vaccination campaigns or public health measures, with the aim of minimizing the impact of the disease. By using VIM and NIM, we were able to gain insights into the spread of diseases in human populations and vector populations and identify the strengths and weaknesses of these two methods. Overall, the VIM method is a better approach for simulating the fractional Leptospirosis fractional model. The results obtained will aid in advancing our understanding and potential management strategies for leptospirosis. Finally, all computations and algorithms are implemented using version 2021 of the Maple software.

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