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Numerical Investigation for Deterministic Hepatitis B Model using Adomian Decomposition Method

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Abstract- Numerical solutions are an essential approach to addressing dynamical system problems involving differential equations. This study focuses on solving a modified SITR model for the spread of Hepatitis B using the Adomian Decomposition Method (ADM) to obtain numerical solutions. The advantage of ADM lies in its efficiency and reliability in solving nonlinear problems without requiring linearization. The obtained solutions are presented as polynomial approximations for each compartment in the model. MAPLE software is employed as the primary instrument to implement ADM and perform numerical simulations. The analysis includes examining the behaviour of susceptible, infected, treated, and recovered populations over time. The implications of this study suggest that ADM-based numerical approaches can be a valuable tool for policymakers and health practitioners in predicting disease dynamics and supporting the development of effective intervention strategies for Hepatitis B.

1. Introduction

Globally, many infectious and deadly diseases affect human life, especially in developing countries, including Hepatitis (Endashaw & Mekonnen, 2022). Hepatitis is a disease caused by inflammation of the liver. This condition can be triggered by various factors such as the use of certain medications, autoimmune disorders, excessive alcohol consumption, and bacterial or viral infections. Among these causes, viral hepatitis is a contagious disease that specifically targets the liver and can lead to serious health complications, including death. Viral hepatitis is

attributed to five main hepatotropic viruses: Hepatitis A virus (HAV), Hepatitis B virus (HBV), Hepatitis C virus (HCV), Hepatitis D virus (HDV), and Hepatitis E virus (HEV). The mortality rate due to viral hepatitis infections has increased by 63% since 1990, making it the seventh leading cause of death worldwide (Belay et al., 2023). Moreover, this type of infection accounts for approximately 1.4 million deaths annually, largely due to chronic infections and liver cancer induced by hepatitis viruses. Of these deaths, around 47% are caused by Hepatitis B virus infections, according to the World Health Organisation in 2016. The transmission of Hepatitis B primarily occurs through sexual contact, vertical transmission from mother to child, shared use of contaminated needles, and exposure to infected blood (Abadi et al., 2021).

Given these facts, the spread of the Hepatitis B virus poses a significant public health challenge, particularly in understanding the transmission processes and disease dynamics within a population. To address this challenge, mathematical modelling can offer valuable insights into the potential spread of the disease. Mathematics plays a critical role in analysing disease transmission dynamics, which can be modelled as systems of equations or inequalities. These models represent the problem's behaviour based on a set of assumptions (Amar et al., 2025).

In recent years, mathematical models of infectious disease transmission have provided useful insights into the dynamics and control of infectious disease spread (Amar et al., 2025). Mathematical models of disease transmission dynamics are needed to provide better insights into disease behaviour, optimize the use of limited resources, and recommend infectious disease control approaches (Kotola & Mekonnen, 2022). Thus, they can suggest effective control and prevention measures and estimate the severity and potential scope of the epidemic disease (Belay et al., 2023). Mathematical models of disease spread are crucial for gaining better insights into disease behaviour. They can recommend steps to optimise the use of limited resources and combat infections (Wodajo et al., 2023).

Numerous studies have employed mathematical models to describe the spread of infectious diseases (Abadi et al., 2021; Alalhareth et al., 2023; Aldila et al., 2020; Attaullah & Sohaib, 2020; Nisardi et al., 2024). Several previous studies have addressed related topics. Abadi (2021) investigated a mathematical model of measles that incorporates vaccination and hospitalisation. The study utilised measles data from Jakarta, Indonesia, in 2017. The simulation results indicated that hospitalising measles patients in Jakarta enhances the effectiveness of the city's vaccination program. This finding provides useful insights for policymakers to give greater attention to hospitalising measles-infected individuals. In addition, the study by Alalhareth et al. (2023) focused on the transmission dynamics of leptospirosis using a fractional-order model. The simulations were carried out to examine both symptomatic and asymptomatic effects of leptospirosis worldwide, demonstrating the disease's actual behaviour. These results are expected to contribute to a better understanding of leptospirosis outbreaks under environmental influences and to inform future prediction and control strategies. Furthermore, Aldila et al. (2020) developed a mathematical model of COVID-19 that incorporated social distancing and rapid assessment, focusing on incidence data from Jakarta. The findings from these studies are expected to provide a theoretical framework for understanding the transmission dynamics of specific diseases, thereby informing epidemiological decision-making.

This study investigates numerical methods for solving a mathematical model of Hepatitis B transmission using the Adomian Decomposition Method (ADM). ADM is a powerful method for solving systems of differential equations. One of its main advantages is the ability to handle nonlinear problems directly without requiring linearization, perturbation techniques, complex computations, or other transformations (Makinde, 2007). The ADM method offers rapidly converging series solutions, which enable the derivation of accurate analytical solutions for the model (Aguegboh et al., 2021). Furthermore, by comparing the exact solution with the numerical solution obtained using ADM, a very small error was found, demonstrating that the ADM method is efficient at obtaining numerical solutions (Guo, 2019; Maturi & Malaikah, 2021). Given these advantages, this study applies ADM to obtain a numerical solution for the Hepatitis B transmission model.

2. Methods

The model employed in this study is the SITR model for the spread of Hepatitis B, as proposed by Putriani & Nisardi (2024). This model consists of four compartments: Susceptible (S), Infected (I), Treatment (T), and Recovered (R). The system of differential equations that describes the model is given in Equation 1.

$$\begin{aligned}\frac{dS}{dt} &= \mu N - \frac{\beta(1-\varepsilon)SI}{N} - (\varepsilon+\mu)S \\ \frac{dI}{dt} &= \frac{\beta(1-\varepsilon)SI}{N} - (\alpha+\eta+\delta+\mu)I \\ \frac{dT}{dt} &= \alpha I - (\gamma+\delta+\mu)T \\ \frac{dR}{dt} &= \eta I + \varepsilon S + \gamma T - \mu R\end{aligned} \tag{1}$$

System (1) can be normalised to yield dimensionless equations. This is done by introducing the following dimensionless variables:

$$w = \frac{S}{N}; x = \frac{I}{N}; y = \frac{T}{N}; z = \frac{R}{N}$$

By substituting these into the system, we obtain the normalised differential equations:

$$\begin{aligned}\frac{dw}{dt} &= \mu - \beta(1-\varepsilon)wx - (\varepsilon+\mu)w \\ \frac{dx}{dt} &= \beta(1-\varepsilon)wx - (\alpha+\eta+\delta+\mu)x \\ \frac{dy}{dt} &= \alpha x - (\gamma+\delta+\mu)y \\ \frac{dz}{dt} &= \eta x + \varepsilon w + \gamma y - \mu z\end{aligned} \tag{2}$$

3. Results and Discussion

Given the normalised SITR model (2):

$$\frac{dw}{dt} = \mu - \beta(1-\varepsilon)wx - (\varepsilon+\mu)w$$

$$\frac{dx}{dt} = \beta(1-\varepsilon)wx - (\alpha+\eta+\delta+\mu)x$$

$$\frac{dy}{dt} = \alpha x - (\gamma+\delta+\mu)y$$

$$\frac{dz}{dt} = \eta x + \varepsilon w + \gamma y - \mu z$$

With initial conditions:

$$w(0) = w_0, x(0) = x_0, y(0) = y_0, z(0) = z_0$$

Let $L = \frac{d}{dt}$, The system becomes:

$$\begin{aligned}L_w &= \mu - \beta(1-\varepsilon)wx - (\varepsilon+\mu)w \\ L_x &= \beta(1-\varepsilon)wx - (\alpha+\eta+\delta+\mu)x \\ L_y &= \alpha x - (\gamma+\delta+\mu)y \\ L_z &= \eta x + \varepsilon w + \gamma y - \mu z\end{aligned} \tag{3}$$

By applying the inverse operator $L^{-1} = \int_0^t (.)\, dt$ to both sides in system (3):

$$\begin{aligned}L^{-1}L_w &= L^{-1}\mu - L^{-1}\beta(1-\varepsilon)wx - L^{-1}(\varepsilon+\mu)w \\ L^{-1}L_x &= L^{-1}\beta(1-\varepsilon)wx - L^{-1}(\alpha+\eta+\delta+\mu)x \\ L^{-1}L_y &= L^{-1}\alpha x - L^{-1}(\gamma+\delta+\mu)y \\ L^{-1}L_z &= L^{-1}\eta x + L^{-1}\varepsilon w + L^{-1}\gamma y - L^{-1}\mu z\end{aligned} \tag{4}$$

The Adomian Decomposition Method (ADM) decomposes the functions. w, x, y and z into an infinite series:

$$w(t) = \sum_0^\infty w_n,\ x(t) = \sum_0^\infty x_n,\ y(t) = \sum_0^\infty y,\ z(t) = \sum_0^\infty z_n, \tag{5}$$

For the nonlinear term: wx, it is decomposed as

$$wx = \sum_0^\infty A_n. \tag{6}$$

with

$$A_n = \sum_0^\infty x_k z_{n-k}$$

$k = 0,1,2, \dots, n.$

Furthermore, the Adomian polynomials A_n are given by:

$$A_0 = x_0 z_0$$
$$A_1 = x_0 z_1 + x_1 z_0$$
$$A_2 = x_0 z_2 + x_1 z_1 + + x_2 z_0$$
$$A_3 = x_0 z_3 + x_1 z_2 + + x_2 z_1 + x_3 z_0$$
$$\vdots$$

By substituting equation (5) and (6) into the system yields (4), we obtain:

$$w(t) - w(0) = L^{-1}\mu - L^{-1}\beta(1-\varepsilon)\sum_0^\infty A_n - L^{-1}(\varepsilon+\mu)\sum_0^\infty w_n$$
$$x(t) - x(0) = L^{-1}\beta(1-\varepsilon)\sum_0^\infty A_n - L^{-1}(\alpha+\eta+\delta+\mu)\sum_0^\infty x_n$$
$$y(t) - y(0) = L^{-1}\alpha\sum_0^\infty x_n - L^{-1}(\gamma+\delta+\mu)\sum_0^\infty y_n$$
$$z(t) - z(0) = L^{-1}\eta\sum_0^\infty x_n + L^{-1}\varepsilon\sum_0^\infty w_n + L^{-1}\gamma\sum_0^\infty y_n - L^{-1}\mu\sum_0^\infty z_n$$

or

$$\sum_0^\infty w_n - w(0) = L^{-1}\mu - L^{-1}\beta(1-\varepsilon)\sum_0^\infty A_n - L^{-1}(\varepsilon+\mu)\sum_0^\infty w_n$$
$$\sum_0^\infty x_n - x(0) = L^{-1}\beta(1-\varepsilon)\sum_0^\infty A_n - L^{-1}(\alpha+\eta+\delta+\mu)\sum_0^\infty x_n$$
$$\sum_0^\infty y_n - y(0) = L^{-1}\alpha\sum_0^\infty x_n - L^{-1}(\gamma+\delta+\mu)\sum_0^\infty y_n$$
$$\sum_0^\infty z_n - z(0) = L^{-1}\eta\sum_0^\infty x_n + L^{-1}\varepsilon\sum_0^\infty w_n + L^{-1}\gamma\sum_0^\infty y_n - L^{-1}\mu\sum_0^\infty z_n$$

or

$$\sum_0^\infty w_n = w(0) + L^{-1}\mu - L^{-1}\beta(1-\varepsilon)\sum_0^\infty A_n - L^{-1}(\varepsilon+\mu)\sum_0^\infty w_n$$
$$\sum_0^\infty x_n = x(0) + L^{-1}\beta(1-\varepsilon)\sum_0^\infty A_n - L^{-1}(\alpha+\eta+\delta+\mu)\sum_0^\infty x_n \quad (7)$$
$$\sum_0^\infty y_n = y(0) + L^{-1}\alpha\sum_0^\infty x_n - L^{-1}(\gamma+\delta+\mu)\sum_0^\infty y_n$$
$$\sum_0^\infty z_n = z(0) + L^{-1}\eta\sum_0^\infty x_n + L^{-1}\varepsilon\sum_0^\infty w_n + L^{-1}\gamma\sum_0^\infty y_n - L^{-1}\mu\sum_0^\infty z_n.$$

With initial values $w(0) = w_0, x(0) = x_0, y(0) = y_0$ and $z(0) = z_0$ In system (7) , we obtain

$$w_0 + w_1 + w_2 + \cdots = w(0) + L^{-1}\mu - L^{-1}\beta(1-\varepsilon)(A_0 + A_1 + A_2 + \cdots) - L^{-1}(\varepsilon+\mu)(w_0 + w_1 + w_2 + \cdots)$$
$$x_0 + x_1 + x_2 + \cdots = x(0) + L^{-1}\beta(1-\varepsilon)(A_0 + A_1 + A_2 + \cdots) - L^{-1}(\alpha+\eta+\delta+\mu)(x_0 + x_1 + x_2 + \cdots)$$
$$y_0 + y_1 + y_2 + \cdots = y(0) + L^{-1}\alpha(x_0 + x_1 + x_2 + \cdots) - L^{-1}(\gamma+\delta+\mu)(y_0 + y_1 + y_2 + \cdots)$$
$$z_0 + z_1 + z_2 + \cdots = z(0) + L^{-1}\eta(x_0 + x_1 + x_2 + \cdots) + L^{-1}\varepsilon(w_0 + w_1 + w_2 + \cdots) + L^{-1}\gamma(y_0 + y_1 + y_2 + \cdots) - L^{-1}\mu(z_0 + z_1 + z_2 + \cdots)$$

From the equations before, we can write it as:

$$w_0 = w(0) + L^{-1}\mu$$
$$w_1 = -L^{-1}\beta(1-\varepsilon)A_0 - L^{-1}(\varepsilon+\mu)w_0$$
$$w_2 = -L^{-1}\beta(1-\varepsilon)A_1 - L^{-1}(\varepsilon+\mu)w_1$$
$$\dots$$

Similarly

$$x_0 = x(0)$$
$$x_1 = L^{-1}\beta(1-\varepsilon)A_0 - L^{-1}(\alpha+\eta+\delta+\mu)x_0$$
$$x_2 = L^{-1}\beta(1-\varepsilon)A_1 - L^{-1}(\alpha+\eta+\delta+\mu)x_1$$
$$\dots$$
$$y_0 = y(0)$$
$$y_1 = L^{-1}\alpha x_0 - L^{-1}(\gamma+\delta+\mu)y_0$$
$$y_2 = L^{-1}\alpha x_1 - L^{-1}(\gamma+\delta+\mu)y_1$$
$$\dots$$

$$z_0 = z(0)$$
$$z_1 = +L^{-1}\eta x_0 + L^{-1}\varepsilon w_0 + L^{-1}\gamma y_0 - L^{-1}\mu z_0$$
$$z_2 = +L^{-1}\eta x_1 + L^{-1}\varepsilon w_1 + L^{-1}\gamma y_1 - L^{-1}\mu z_1$$

In general, the solution of the system is the sum of all iterations. The number of iterations can be chosen based on the required accuracy. For example, to approximate the solution up to the third iteration:

$$w(t) \approx W = w_0 + w_1 + w_2 + w_3$$
$$x(t) \approx X = x_0 + x_1 + x_2 + x_3$$
$$y(t) \approx Y = y_0 + y_1 + y_2 + y_3$$
$$z(t) \approx Z = z_0 + z_1 + z_2 + z_3$$

(a) Numerical Simulation

The numerical simulation is conducted using the parameter values shown in Table 1.

Table 1. Parameter Values

Parameters	Values
$\boldsymbol{\mu}$	0.0004
$\boldsymbol{\beta}$	0.4286
$\boldsymbol{\varepsilon}$	0.0025
$\boldsymbol{\alpha}$	0.3
$\boldsymbol{\eta}$	0.0825
$\boldsymbol{\delta}$	0.25
$\boldsymbol{\gamma}$	0.005

Using the Adomian method, the initial values are:

$$w_0 = \frac{2000}{2709} + 0.00004t = 0.7382789 + 0.00004;$$
$$v_0 = \frac{110}{903} = 0.12181616;$$
$$x_0 = \frac{214}{2709} = 0.078996;$$
$$y_0 = \frac{55}{903} = 0.06090808$$

Using Maple software, the next iterations yield:
First iteration:

$$w_1 = -0.2133746824t - 0.00001158231229t^2$$
$$v_1 = -0.01803853281t + 0.000001566312292t^2$$
$$x_1 = 0.03592078258t$$
$$y_1 = 0.1849892950t + 0.0001t^2$$

Second iteration:

$$w_2 = 0.06606521058t^2 + 0.00003213971102t^3 - 2.013964345 \cdot 10^{-9}t^4 + 0.0004t$$
$$v_2 = -0.005684139559t^2 - 0.000009174168624t^3 + 2.013964345 \cdot 10^{-9}t^4$$
$$x_2 = -0.005695334025t^2 + 0.00004698936876t^3$$
$$y_2 = -0.05324527782t^2 - 0.0002898951547t^3$$

Third Iteration:

$$w_3 = -0.01901798745t^3 - 0.000005995499776t^4 + 1.867978694 \cdot 10^{-9}t^5 - 2.589555355 \cdot 10^{-13}t^6 - 0.0001158231229t^2 + 0.0004t$$
$$v_3 = 0.004665926109t^3 + 0.00001483440723t^4 - 2.139863881 \cdot 10^{-9}t^5 + 2.589555355 \cdot 10^{-13}t^6 + 0.000001566312292t^2$$
$$x_3 = -0.001660248729t^3 - 0.000002789372188t^4 + 6.041893035 \cdot 10^{-10}t^5$$
$$y_3 = 0.01650685043t^3 + 0.000008066348578t^4 - 5.026855005 \cdot 10^{-10}t^5 + 0.0001t^2$$

Hence, the total approximate solution is:

$$W = 0.7382798080 - 0.2121746824t + 0.06583356432t^2 - 0.01898584774t^3 - 0.000005997513741t^4 + 1.867978694 \cdot 10^{-9}t^5 - 2.589555355 \cdot 10^{-13}t^6$$
$$V = 0.1218161683 - 0.01803853281t - 0.005652813313t^2 + 0.004656751940t^3 + 0.000001485454687t^4 - 2.139863881 \cdot 10^{-9}t^5 + 2.589555355 \cdot 10^{-13}t^6$$
$$X = 0.07899593946 + 0.03592078258t - 0.005695334025t^2 - 0.001655549792t^3 - 0.000002789372188t^4 + 6.041893035 \cdot 10^{-10}t^5$$
$$Y = 0.06090808416 + 0.1849892950t - 0.05304527782t^2 + 0.01647786091t^3 + 0.000008066348578t^4 - 5.026855005 \cdot 10^{-10}t^5$$

Figure 1 illustrates the solution of the SITR model for Hepatitis B transmission using the Adomian Decomposition Method up to the third iteration. This solution is suitable for short-term time scales.

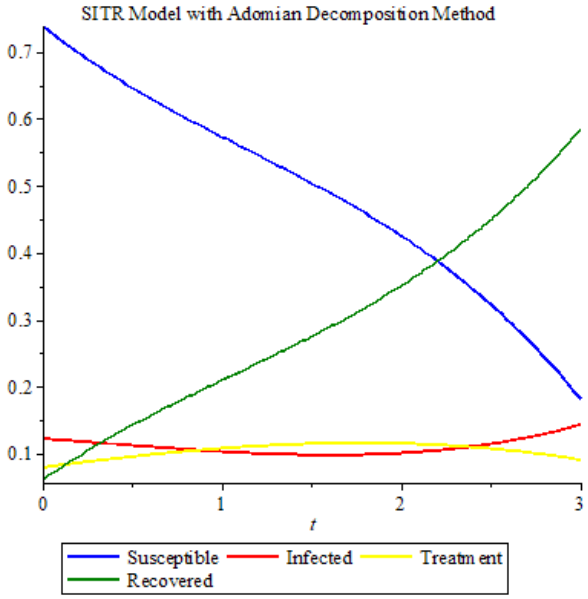

Figure 1. SITR Model with ADM

Figure 1 illustrates the behaviour of the solutions obtained using the Adomian Decomposition Method for each compartment in the model. Based on the simulation, the susceptible population experiences a considerable decline over the simulation interval. Meanwhile, the number of infected individuals initially decreases and then increases toward the end of the interval. The other two compartments, recovery and treatment, show significant increases and relatively small decreases, respectively.

The study conducted by Side et al. (2020) focused on the numerical simulation of an SIR model for Hepatitis B using the Homotopy Perturbation Method (HPM), and the results demonstrated a decrease in the susceptible population and an increase in the recovered population. Furthermore, the research by Harko & Mak (2020) focused on the numerical simulation of an SIR model using the Laplace Adomian Decomposition Method (LADM). Their findings indicated that truncating the series to only three terms already provides an accurate description of the numerical results for arbitrary parameter values within the model.

4. Conclusion

In this present work, we examined the dynamics of Hepatitis B transmission with a compartmental SITR model. This model was developed as a system of nonlinear differential equations, which was then reduced to a dimensionless system. Approximate analytical solutions for all compartments were obtained by applying the Adomian Decomposition Method (ADM) up to iteration three as follows.

$$W = 0.7382798080 - 0.2121746824t + 0.06583356432t^2 - 0.01898584774t^3 - 0.000005997513741t^4 + 1.867978694 \cdot 10^{-9}t^5 - 2.589555355 \cdot 10^{-13}t^6$$

$$V = 0.1218161683 - 0.01803853281t - 0.005652813313t^2 + 0.004656751940t^3 + 0.000001485454687t^4 - 2.139863881 \cdot 10^{-9}t^5 + 2.589555355 \cdot 10^{-13}t^6$$
$$X = 0.07899593946 + 0.03592078258t - 0.005695334025t^2 - 0.001655549792t^3 - 0.000002789372188t^4 + 6.041893035 \cdot 10^{-10}t^5$$
$$Y = 0.06090808416 + 0.1849892950t - 0.05304527782t^2 + 0.01647786091t^3 + 0.000008066348578t^4 - 5.026855005 \cdot 10^{-10}t^5$$

The results demonstrate that ADM is an effective and robust method for resolving nonlinear epidemic models, yielding a semi-analytic solution that represents the short-term dynamics of all system compartments. The numerical tests, supported by parameter values from the literature, indicate that the method can efficiently approximate the dynamic progression of susceptible, infected, treated, and recovered individuals over a short time period. The developed series solutions enable investigation of the dynamics of each population and provide insight into how effectively treatment and vaccination levels work, as reflected in parameters such as α and ε. Since ADM is well-suited for short-term approximation, alternative methods such as the Homotopy Analysis Method (HAM) or numerical solvers (e.g., Runge-Kutta) may be used for long-term behaviour analysis.

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