EURASIAN JOURNAL OF MATHEMATICAL AND COMPUTER APPLICATIONS
ISSN 2306–6172
Volume 12, Issue 4 (2024) 54 – 66

MATHEMATICAL ANALYSIS OF MONKEYPOX VIRUS USING THE DAFTARDAR-JAFARI ITERATIVE APPROACH

Jeeva N., Dharmalingam K.M.

Abstract Monkeypox is an emerging zoonotic disease, similar to smallpox, causing fever, rash, and swollen lymph nodes, transmitted through contact with infected animals, humans, or materials. In this paper, we focus on the new mathematical model of the monkeypox virus, which builds upon the epidemiological framework that categorized as susceptible $S(t)$, asymptomatic infected cases $E(t)$, infected $I(t)$, infected individuals who are hospitalized $Q(t)$, and recovered $R(t)$ populations. To deal with the system of nonlinear differential equations and to produce a semi-analytical solution for the monkeypox virus model, Daftardar-Jafari method (DJM) was used. The DJM approach provided highly accurate approximate solutions compared to numerical simulations, demonstrating its efficiency and accuracy. The DJM's iterative approach allows for the continuous development of solutions to differential equations that capture disease dynamics, offering insights into the complex interactions among individuals in a population and the progression of infectious diseases. Furthermore, by varying model parameters, we explored their impact on the various compartments, gaining valuable insights into the behavior of the model under different conditions. This analysis is essential for understanding how changes in transmission rates, recovery rates, and other factors influence the monkeypox virus's overall dynamics, ultimately informing better public health strategies and disease management practices.

Key words: Monkeypox virus, Mathematical modeling, Daftardar-Jafari method (DJM), Semi-analytical solution, Numerical simulation.

AMS Mathematics Subject Classification: 34A45, 65L05, 92-08.

DOI: 10.32523/2306-6172-2024-12-4-54-66

1 Introduction

Monkeypox is a zoonotic viral disease caused by the monkeypox virus, part of the Orthopoxvirus genus. It shares clinical similarities with smallpox, presenting with fever, vesicular-pustular rash, and lymphadenopathy, but typically exhibits lower morbidity and mortality rates. Transmission occurs through direct contact with bodily fluids or lesions of infected animals or humans, as well as contaminated fomites [8]. The disease is a significant public health concern due to its potential for human-to-human transmission and sporadic outbreaks outside endemic regions in Central and West Africa. The rising incidence of monkeypox has led to its classification as a global emergency, highlighting the need for thorough investigation of its public health implications and pandemic potential. This underscores the necessity for international funding to enhance case detection and surveillance, which are crucial for understanding the evolving epidemiology of this resurgent disease [3]. Recent outbreaks have revealed complex transmission routes, including zoonotic transmission via contact with infected animals like rodents and non-human primates, and human-to-human transmission through respiratory

droplets, bodily fluids, and contaminated fomites. The increase in infections outside endemic regions indicates changes in virus ecology and human behavior, necessitating updated public health strategies and international cooperation for effective control [15, 18]. Asymptomatic infections play a critical role in transmission, complicating containment efforts. Combatting monkeypox benefits from the cross-protection of existing smallpox vaccines and the development of new antiviral therapies and vaccines. Recent outbreaks in Nigeria (2019-2020) and subsequent cases in the United States and the United Kingdom underscore the urgent need for global preparedness, enhanced diagnostics, better healthcare infrastructure in endemic areas, and increased public awareness [19, 23, 28].

Statistical modeling is a fundamental aspect of modern data analysis, allowing us to draw conclusions about a population using sample data. Essentially, statistical modeling involves creating mathematical equations that illustrate the relationships between different variables. These models can range from simple linear regression, which shows a direct relationship between two variables, to more complex models like generalized nonlinear models and mixed-effects models that handle various types of data and relationships [6, 14, 16, 29]. Recent mathematical models of monkeypox virus transmission provide significant insights into understanding its spread and potential control measures. Usman and Adamu (2017) include treatment and vaccination strategies, highlighting their impact on virus dynamics. Lasisi et al. (2020) explore demographic factors and transmission rates, while Somma et al. (2019) focus on optimal control strategies to reduce infection rates. Additionally, Peter et al. (2023) present a detailed mathematical approach to understanding transmission dynamics, aiding in formulating effective interventions [13, 17, 24, 31]. A recent study used a continuous mathematical model with differential equations to investigate the spread of the monkeypox virus, focusing on the local and global stability of the model's equilibrium points [9]. Analytical solutions in epidemiology play a crucial role in understanding the behavior of infectious diseases and developing effective intervention strategies. By solving differential equations that model disease transmission dynamics, researchers can derive explicit formulas for key quantities such as infection rates, peak times, and equilibrium states. Several semi-analytical methods have been utilized to tackle complex mathematical problems. Recent advances in semi-analytical methods such as the Differential Transform Method (DTM), Adomian Decomposition Method (ADM), Homotopy Perturbation Method (HPM), Laplace Adomian Decomposition Method (LADM), Taylor Series Method (TSM), and Variation Iteration Method (VIM) offer deeper insights into disease dynamics and intervention strategies. These solutions help in predicting the spread of diseases, evaluating the impact of different control measures like vaccination and quarantine, and optimizing resource allocation during outbreaks. Analytical solutions provide a clear understanding of how various parameters influence the disease's progression and the population's response [1, 7, 10, 11, 12, 25, 27, 32]. Over time, numerous analytical methods have been developed, including the Daftardar-Jafari method, known for its efficiency in solving complex differential equations accurately. The Daftardar-Jafari method stands out as a powerful tool for obtaining precise solutions in various mathematical models and systems [4].

The primary aim of this paper is to address the monkeypox virus model by applying the Daftardar-Jafari Method (DJM). The study seeks to analyze the model thoroughly and provide insights into effective prevention measures. By leveraging DJM, the paper aims to derive accurate solutions and evaluate the model's stability, ultimately contributing to better disease control strategies and understanding the dynamics of monkeypox virus transmission. The paper is structured as follows: Section 2 details the DJM methodology. Section 3 introduces the mathematical model of the monkeypox virus using system of nonlinear differential

equations. Section 4 presents the semi-analytical solution of the monkeypox virus model using DJM. Section 5 discusses the findings, and Section 6 provides the conclusion of the paper.

2 Daftardar-Jafari method (DJM)

The Daftardar-Jafari method (DJM) is a powerful iterative technique for solving nonlinear differential and functional equations. Introduced by Daftardar-Gejji and Jafari in 2006, this method has proven effective in addressing various mathematical and physical problems. It is particularly useful for efficiently solving nonlinear issues and provides convergent approximations. The DJM employs a systematic iterative process that separates the problem into linear and nonlinear operators, facilitating the approximation of solutions without requiring stringent assumptions. Theoretical analyses of the DJM's convergence and stability underscore its value as a tool for accurately solving complex mathematical and physical problems [2, 22, 26, 30].

Let us examine the nonlinear equation [4, 5]

$$\mathcal{W} = g + L[\mathcal{W}] + N[\mathcal{W}] \tag{1}$$

where $\mathcal{W}$ is a function of x, $L[\mathcal{W}]$ is linear, and $N[\mathcal{W}]$ is a nonlinear term. The series solution for this equation is provided as follows:

$$\mathcal{W} = \sum_{n=0}^{\infty} \mathcal{W}_n$$

Since L is a linear operator, we can express

$$L(\sum_{n=0}^{\infty} \mathcal{W}_n) = \sum_{n=0}^{\infty} L(\mathcal{W}_n)$$

Now, we will define the nonlinear terms

$$G_0 = N(\mathcal{W}_0), \quad G_i = N(\sum_{i=0}^{n} \mathcal{W}_i) - N(\sum_{i=0}^{n-1} \mathcal{W}_i)$$

Thus $N(w)$ is decomposed as:

$$N(\sum_{i=0}^{\infty} \mathcal{W}_i) = \underbrace{N(\mathcal{W}_0)}_{G_0} + \underbrace{N(\mathcal{W}_0 + \mathcal{W}_1) - N(\mathcal{W}_0)}_{G_1} + \underbrace{N(\mathcal{W}_0 + \mathcal{W}_1 + \mathcal{W}_2) - N(\mathcal{W}_0 + \mathcal{W}_1)}_{G_2} + \dots$$

The recursive relation for the components of $\mathcal{W}(x)$ can be described as follows:

$$\mathcal{W}_0 = g, \mathcal{W}_1 = L(\mathcal{W}_0) + G_0, \dots, \mathcal{W}_{i+1} = L(\mathcal{W}_i) + G_k \tag{2}$$

Thus,

$$\sum_{n=0}^{\infty} \mathcal{W}_n = g + L(\sum_{n=0}^{\infty} \mathcal{W}_n) + N(\sum_{n=0}^{\infty} \mathcal{W}_n) \tag{3}$$

It is evident from the equation that $\sum_{n=0}^{\infty} \mathcal{W}_n$ serves as a solution to equation (1), where $\mathcal{W}_i$, $i = 0, 1, 2, \dots$, are determined by algorithm (2). The term n_i is used to approximate the solution of (3), which can be expressed as $\mathcal{W} = \sum_{i=0}^{n-1} \mathcal{W}_i$.

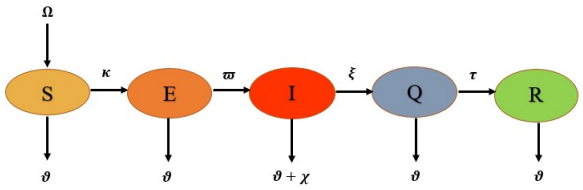


Figure 1: Flow chart of monkeypox virus transmission model.

The application of DJM is predominantly observed in addressing nonlinear scenarios such as thin film flow, solving fractional PDEs, and dealing with boundary value problems. There are limited research papers utilizing DJM for solving system of nonlinear equations in epidemiology [20, 21]. This study uniquely employs DJM approach for the monkeypox model, showcasing its versatility and potential in the system of nonlinear equations of the epidemic modeling and analysis.

3 Governing system of equations

In this section, we examine the monkeypox virus model developed by Imane Smouni et al [9]. The model classifies the population within the monkeypox virus into five groups: susceptible individuals at risk of acquiring the monkeypox virus $S(t)$, asymptomatic infected cases $E(t)$, symptomatic carriers of the virus $I(t)$, infected individuals who are hospitalized $Q(t)$, and those who have recovered $R(t)$. The sum of all compartments determines the overall size of the population, $N(t)$: $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$. The system of equations for the monkeypox virus model is represented by equations (4):

$$\begin{aligned}
\frac{dS}{dt} &= \Omega - \kappa SE - \vartheta S \\
\frac{dE}{dt} &= \kappa SE - (\varpi + \vartheta)E \\
\frac{dI}{dt} &= \varpi E - (\xi + \vartheta + \chi)I \\
\frac{dQ}{dt} &= \xi I - (\tau + \vartheta)Q \\
\frac{dR}{dt} &= \tau Q - \vartheta R
\end{aligned} \tag{4}$$

Initial conditions:

$$S(0) = m_1, \;\; E(0) = m_2, \;\; I(0) = m_3, \;\; Q(0) = m_4, \;\; R(0) = m_5 \tag{5}$$

The birth rate is represented by Ω. The contact rate with asymptomatic infected individuals is given by η. Natural mortality is represented by ϑ. Asymptomatic infected individuals progress to symptomatic cases and become virus carriers at a rate indicated by ϖ. Infected individuals are hospitalized at a rate of ξ. Disease-related mortality occurs at a rate of χ. Individuals who have received hospital treatment are considered at a rate of τ. The parameter κ is determined by $\kappa = \frac{\eta}{N}$, where N is the total number of population. Figure 1 presents the flow chart of the monkeypox virus model. The numerical values for the parameters are: $\Omega = 1500$, $\vartheta = 0.04$, $\eta = 0.5$, $\varpi = 0.09$, $\xi = 0.05$, $\chi = 0.5$, $\tau = 0.05$, $N = 26000$.

4 Semi-analytical solution of monkeypox virus model using DJM

In this section, we will utilize the DJM approach for analyzing the transmission of the monkeypox virus. To apply the DJM and derive an approximate solution for the problem, we perform integration on both sides of equation (4) considering the initial condition (5), leading to:

$$\begin{aligned} S(t) &= m_1 + \Omega t + \int_0^t (-\kappa SE - \vartheta S)ds \\ E(t) &= m_2 + \int_0^t (\kappa SE - (\varpi + \vartheta)E)ds \\ I(t) &= m_3 + \int_0^t (\vartheta E - (\xi + \vartheta + \chi)I)ds \\ Q(t) &= m_4 + \int_0^t (\xi I - (\tau + \vartheta)Q)ds \\ R(t) &= m_5 + \int_0^t (\tau Q - \vartheta R)ds \end{aligned} \tag{6}$$

The general expression of the nonlinear terms in the system of equation (6) under the DJM approach can be described as:

$$\begin{aligned} \overline{S_{n+1}}(t) &= \int_0^t N_1(\sum_{i=0}^{n} \overline{S_i}(s))ds - \int_0^t N_1(\sum_{i=0}^{n-1} \overline{S_i}(s))ds \\ \overline{E_{n+1}}(t) &= \int_0^t N_2(\sum_{i=0}^{n} \overline{E_i}(s))ds - \int_0^t N_2(\sum_{i=0}^{n-1} \overline{E_i}(s))ds \\ \overline{I_{n+1}}(t) &= \int_0^t N_3(\sum_{i=0}^{n} \overline{I_i}(s))ds - \int_0^t N_3(\sum_{i=0}^{n-1} \overline{I_i}(s))ds \\ \overline{Q_{n+1}}(t) &= \int_0^t N_4(\sum_{i=0}^{n} \overline{Q_i}(s))ds - \int_0^t N_4(\sum_{i=0}^{n-1} \overline{Q_i}(s))ds \\ \overline{R_{n+1}}(t) &= \int_0^t N_5(\sum_{i=0}^{n} \overline{R_i}(s))ds - \int_0^t N_5(\sum_{i=0}^{n-1} \overline{R_i}(s))ds \end{aligned} \tag{7}$$

The series solution $\mathcal{W}_{DJM} = \sum_{n=0}^{\infty} \mathcal{W}_n$ for equation (7) can be determined by aggregating the individual components $\mathcal{W}_i$ obtained through the DJM method.
Thus, by employing this approach, we obtain the initial iteration:

$$S_0 = m_1 + \Omega t, \;\; E_0 = m_2, \;\; I_0 = m_3, \;\; Q_0 = m_4, \;\; R_0 = m_5 \tag{8}$$

To simplify and brevity, we provide only the series up to the first iteration, as follows:

$$\begin{aligned} S_1 &= m_1 - (\kappa m_2 m_1 + \vartheta m_1 - \Omega)\, t - \left(\frac{1}{2}\kappa m_2 \Omega + \frac{1}{2}\vartheta\Omega\right) t^2 \\ E_1 &= m_2 + (\kappa m_2 m_1 - (\varpi + \vartheta)m_2)\, t + \frac{1}{2}\kappa m_2 \Omega t^2 \\ I_1 &= m_3 + (\varpi m_2 - (\xi + \vartheta + \chi)m_3)t \\ Q_1 &= m_4 + (\xi m_3 - (\tau + \vartheta)m_4)t \\ R_1 &= m_5 + (\tau m_4 - m_5\vartheta)t \end{aligned} \tag{9}$$

The solution presented above corresponds to $\mathcal{W}_{DJM1}$. By utilizing MAPLE, we were able to calculate a fifth-iteration denoted as $\mathcal{W}_{DJM5}$. Additionally, it is feasible to derive higher-order

solutions until convergence is achieved.
Thus, the semi-analytical solution for the monkeypox virus up to the sixth order, obtained using the DJM approach (8), (9), and incorporating the parameter values along with the initial conditions: $S(0) = 10000$, $E(0) = 8000$, $I(0) = 5000$, $Q(0) = 2000$, $R(0) = 1000$, has been accurately determined as follows:

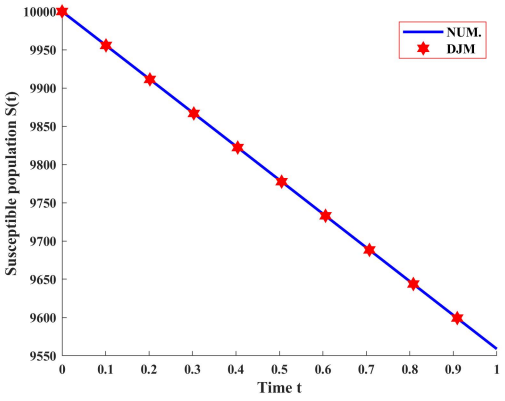
$$\begin{aligned} S(t) &= 10000 - 438.461538t - 5.43195269t^2 + 2.918579878t^3 + 0.1205366936t^4 \\ &\quad -0.01797235373t^5 - 0.001707434408t^6, \qquad (10) \\ E(t) &= 8000 + 498.4615384t - 18.19881654t^2 - 2.057538460t^3 + 0.05543258262t^4 \\ &\quad +0.02862180753t^5 + 0.002675231404t^6, \qquad (11) \\ I(t) &= 5000 - 2230.00t + 680.280769t^2 - 134.3345157t^3 + 19.76804645t^4 \\ &\quad +0.07839762261t^5 + 0.001476523403t^6, \qquad (12) \\ Q(t) &= 2000 + 70.00t - 58.90000000t^2 + 13.10501281t^3 - 1.974044235t^4 \\ &\quad -0.007338154300t^5 - 0.00008874544836t^6, \qquad (13) \\ R(t) &= 1000 + 60.00t + 0.5500000000t^2 - 0.9890000001t^3 + 0.1737026601t^4 \\ &\quad -0.02113006365t^5 - 0.00006403590122t^6. \qquad (14) \end{aligned}$$

5 Discussion of Results

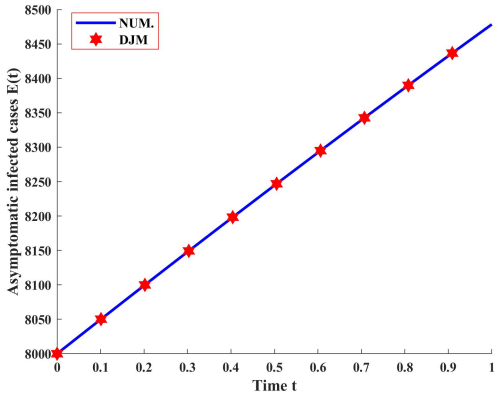
A new approach, Daftardar-Jafari method (DJM), was used to tackle the system of nonlinear differential equations present in the monkeypox virus model. The semi-analytical solutions for the populations S, E, I, Q, and R are expressed in equations (10)-(14), representing the approach's outcomes. Utilizing the *ode*45 solver within a MATLAB program, the system described by equation (4) was numerically solved.

In Fig. 2a, the graph illustrates the comparison between equation (10) and numerical simulation for the susceptible monkeypox virus population, denoted as $S(t)$, over time. As susceptible monkeypox virus individuals come into contact with asymptomatic infected cases, they become exposed to the disease. It is evident from the data that there is a decrease in the count of susceptible monkeypox virus individuals as they transition to the exposed state. Fig. 2b depicts the comparison between equation (11) and numerical simulation for the population of asymptotically infected individuals of the monkeypox virus, represented as $E(t)$, over time. A substantial increase in the number of asymptotically infected population is observed. This increase is attributed to the progression of the virus towards symptomatic cases, transforming individuals into carriers of the virus who may then interact with infected monkeypox virus individuals.

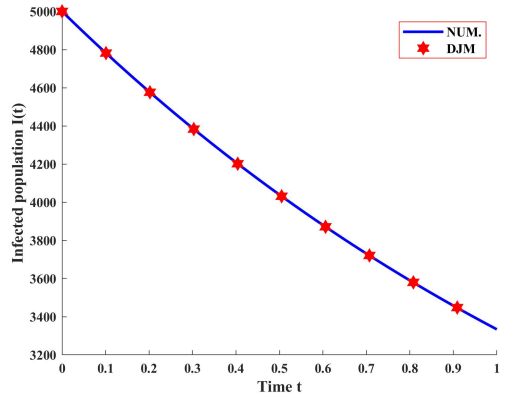
In Fig. 2c, the graph illustrates the comparison between equation (12) and numerical simulation for the population of symptomatic carriers or infected individuals of the monkeypox virus, denoted as $I(t)$, over time. A decline in the count of the infected monkeypox virus population is observed, attributed to infected individuals being promptly hospitalized. Fig. 2d demonstrates the comparison between equation (13) and numerical simulation for the infected individuals who are hospitalized, represented as $Q(t)$, over time. The population in the hospital compartment increases as infected individuals undergo the process of quarantine and treatment. In Fig. 2e, the graph illustrates the comparison between equation (14) and numerical simulation for the population of recovered individuals of the monkeypox virus, denoted as $R(t)$, over time. A noticeable increase in the count of recovered individuals from



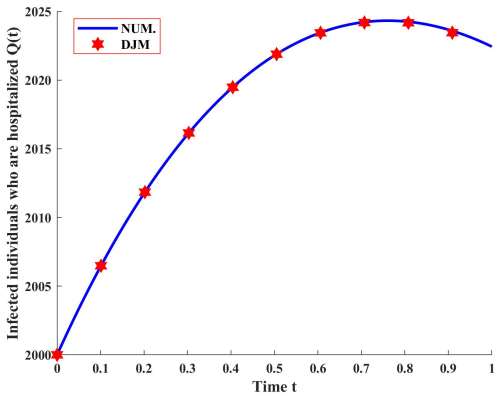
(a) Susceptible individuals $S(t)$.



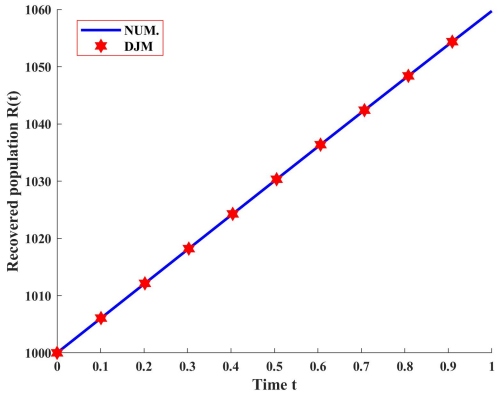
(b) Asymptomatic infected individuals $E(t)$.



(c) Infected individuals $I(t)$.

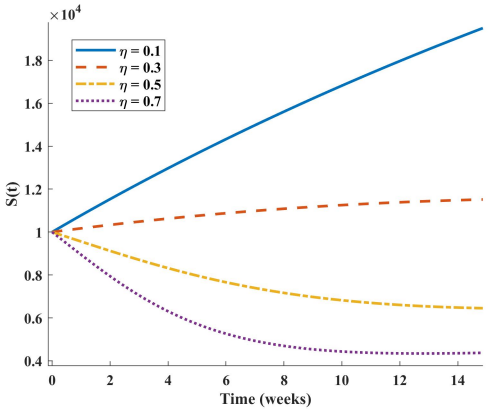


(d) Hospitalized individuals $Q(t)$.

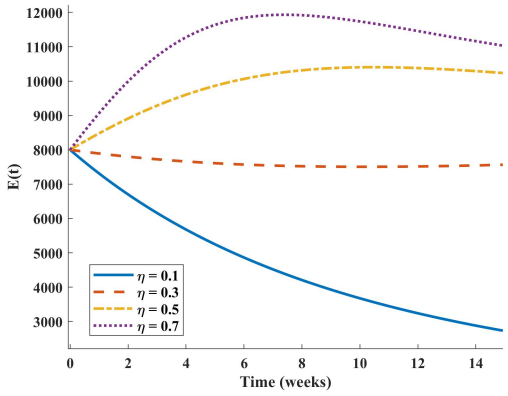


(e) Recovered individuals $R(t)$.

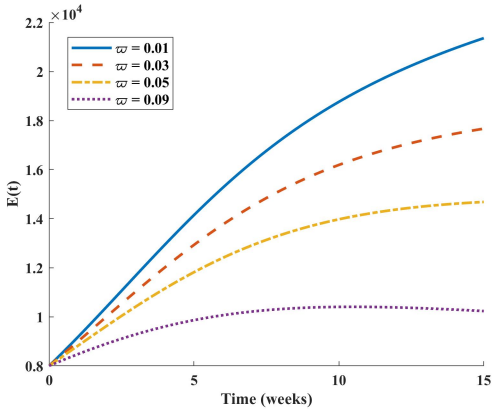
Figure 2: Graphical representation of monkeypox virus using the DJM and numerical simulations.



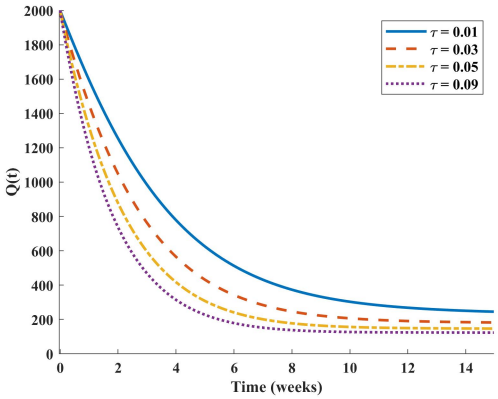
(a) Effects of varying η on $S(t)$.



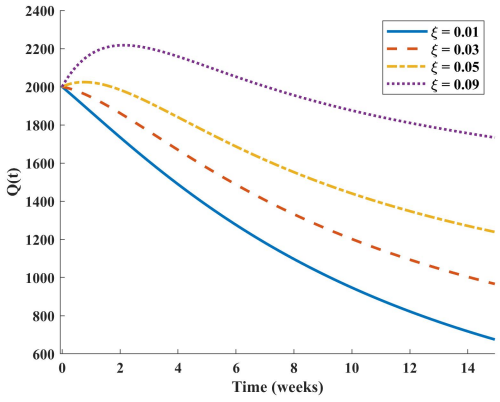
(b) Effects of varying η on $E(t)$.



(c) Effects of varying ϖ on $E(t)$.

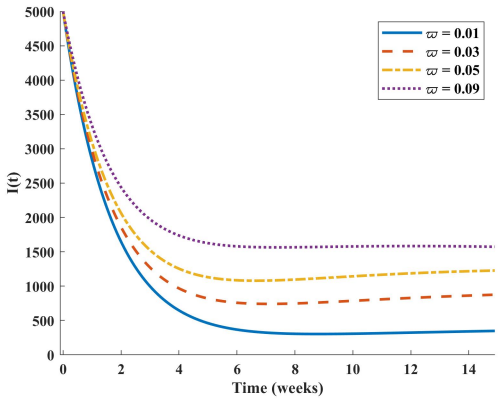


(d) Effects of varying τ on $Q(t)$.

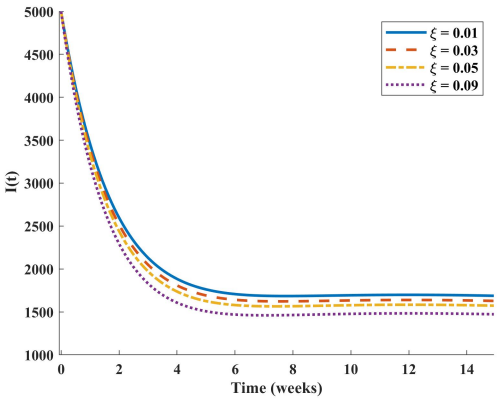


(e) Effects of varying ξ on $Q(t)$.

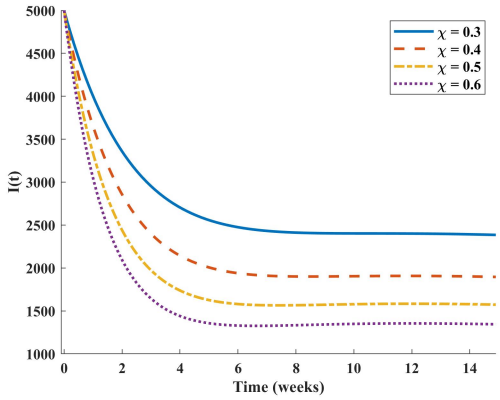
Figure 3: Effects of varying parameters on the susceptible, exposed and hospitalized compartments.



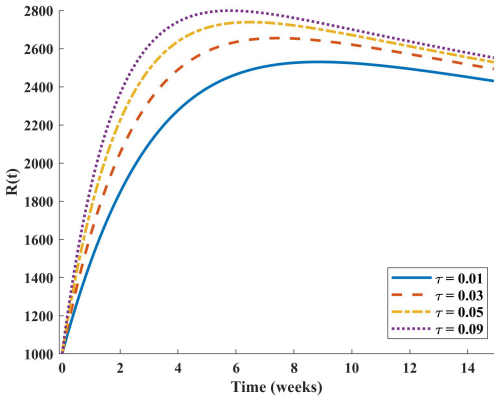
(a) Effects of varying ϖ on $I(t)$.



(b) Effects of varying ξ on $I(t)$.



(c) Effects of varying χ on $I(t)$.



(d) Effects of varying τ on $R(t)$.

Figure 4: Effects of varying parameters on the infected and recovered compartments.

the monkeypox virus is observed. This increase can be attributed to the infected and exposed populations undergoing treatment and quarantine, potentially resulting in improved progression rates by reducing the disease's contact rate.

In Fig. 3a, when fixing other parameters and increasing the contact rate with asymptomatic infected individuals η, the susceptible monkeypox virus population decreases. In Fig. 3b, when increasing the contact rate η, the asymptomatic infected individuals also increases. In Fig. 3c, when increasing the progress rate of symptomatic cases ϖ, the asymptomatic infected individuals decreases. In Fig. 3d, when increasing the hospitalized or quarantine rate ξ, the infected individuals who are hospitalized increases. In Fig. 3e, when increasing the treatment rate τ, the infected individuals who are hospitalized decreases. In Fig 4a, when increasing the progress rate of symptomatic cases ϖ, the infected monkeypox virus population increases. Similarly, In Fig. 4b and 4c, when increasing the monkeypox disease related mortality rate χ and hospitalized or quarantine rate ξ, the infected monkeypox virus population decreases. In Fig. 4d, when increasing the treatment rate τ, the recovered population is increased.

In Fig. 5a, the surface plot depicts the susceptible individuals of the monkeypox virus against the contact rate η and birth rate Ω at time $t = 0.5$. In Fig. 5b, the surface plot illustrates the asymptomatic infected individuals in relation to the progression rate of symptomatic cases ϖ and the contact rate η at time $t = 0.5$. Fig 5c shows the surface plot of

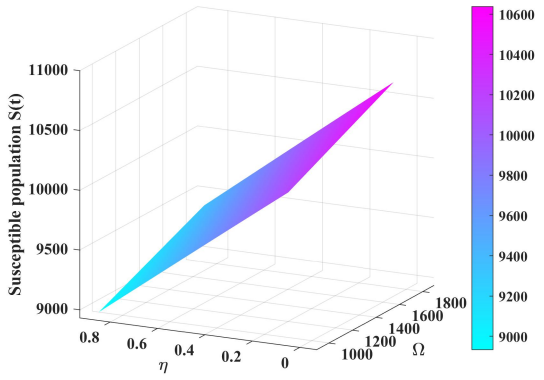
the infected individuals against the progression rate of symptomatic cases ϖ and the disease-related mortality rate χ at time $t = 0.5$. In Fig. 5d, the surface plot presents the infected individuals against the progression rate of symptomatic cases ϖ and the hospitalization or quarantine rate ξ at time $t = 0.5$. Fig. 5e depicts the surface plot of hospitalized infected individuals against the treatment rate τ and the hospitalization or quarantine rate ξ at time $t = 0.5$. Fig. 5f displays the surface plot of recovered individuals against the treatment rate τ and the natural mortality rate ϑ at time $t = 0.5$.

6 Conclusion

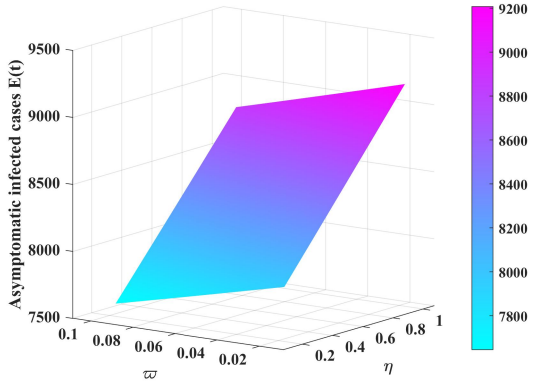
In this paper, we developed a semi-analytical expression for a system of nonlinear differential equations within the monkeypox virus model. We applied the Daftardar-Jafari method (DJM) method to evaluate the proposed model. DJM efficiently decomposes the original equation into linear, nonlinear, and functional components, that solves the system of equations iteratively, facilitating convergence of the solutions. A comparison of the analytical solutions with the numerical results showed a strong level of accuracy. The results presented in the Figs. demonstrate that the DJM approach excels in producing highly accurate computations. The DJM proves invaluable for analyzing the transmission dynamics of diseases, evaluating the effects of interventions, forecasting the progression of epidemics, and assessing strategies for disease control and prevention. Surface plots enhance the discussion by visually demonstrating the impact of various parameters on the monkeypox virus transmission model. The analysis highlights that, in addition to managing the contact rate of asymptomatic infected individuals, enhancing treatment efforts and implementing effective isolation measures are key strategies for controlling the spread of the monkeypox virus. Since the monkeypox virus does not have an exact vaccine, early detection and public health awareness campaigns become even more critical in preventing further outbreaks and mitigating transmission within communities. This method serves as a powerful computational tool in epidemiology, aiding in the study of disease spread patterns, the optimization of control measures, and the enhancement of our understanding of how infectious diseases propagate within populations.

Acknowledgement

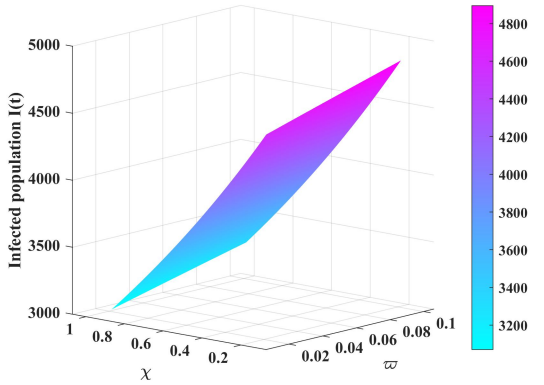
The authors would like to express their gratitude to Madura College for its continuous support and encouragement.



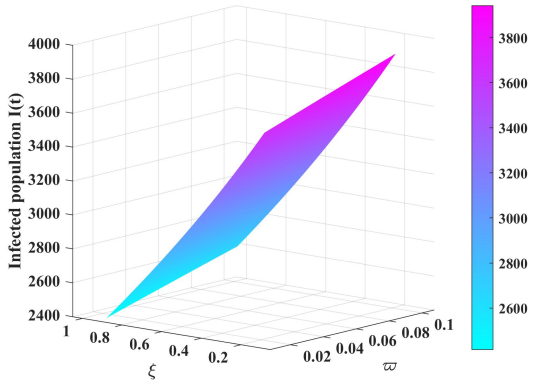
(a) Combined effects of η and Ω on $S(t)$.



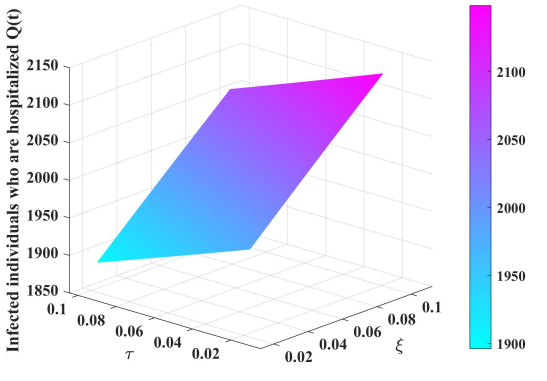
(b) Combined effects of ϖ and η on $E(t)$.



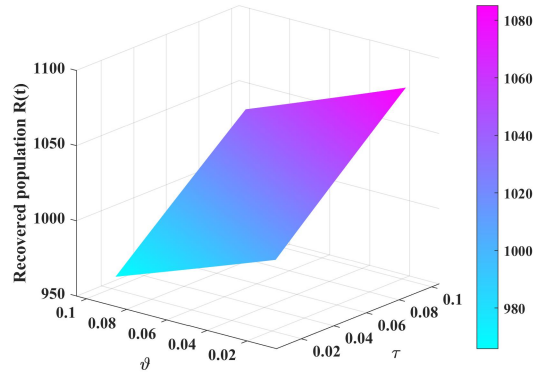
(c) Combined effects of χ and ϖ on $I(t)$.



(d) Combined effects of ξ and ϖ on $I(t)$.



(e) Combined effects of τ and ξ on $Q(t)$.



(f) Combined effects of ϑ and τ on $R(t)$.

Figure 5: Surface representation of different parameters in the monkeypox virus transmission model compartments.

References

[1] Adeniji, A.A., Mogbojuri, O.A., Kekana, M.C., Fadugba, S.E., *Numerical solution of rotavirus model using Runge-Kutta-Fehlberg method, differential transform method and Laplace Adomian decomposition method.* Alexandria Engineering Journal, 82 (2023), 323-329.

[2] AL-Jawary, M.A., Radhi, G.H., Ravnik, J., *Daftardar-Jafari method for solving nonlinear thin film flow problem*. Arab Journal of Basic and Applied Sciences, 25.1 (2018), 20-27.

[3] Bunge, E.M., Hoet, B., Chen, L., Lienert, F., et al., *The changing epidemiology of human monkeypox—A potential threat? A systematic review*. PLOS Neglected Tropical Diseases, 16 (2022).

[4] Daftardar-Gejji, V., Jafari, H., *An iterative method for solving nonlinear functional equations*. Journal of Mathematical Analysis and Applications, 316.2 (2006), 753-763.

[5] Daftardar-Gejji, V., Bhalekar, S., *Solving fractional boundary value problems with Dirichlet boundary conditions using a new iterative method*. Computers and Mathematics With Applications, 59.5 (2010), 1801-1809.

[6] Evirgen, F., Zkse, F., Yavuz, M., Zdemir, N., *Real data-based optimal control strategies for assessing the impact of the Omicron variant on heart attacks*. AIMS Biophysics and Bioengineering, 10.3 (2023), 218-239.

[7] Fadugba S.E., Kekana M.C., Jeeva N., Ibrahim I., *Development and implementation of innovative higher order inverse polynomial method for tackling physical models in epidemiology*. Journal of Mathematics and Computer Science, 36.4 (2025), 444-454.

[8] Giradkar, J., Khatib, M.N., *Human monkeypox: An emerging zoonosis*, Cureus, 2022.

[9] Imane, S., Mansouri, A.E., Khajji, B., Labzai, A., et al., *Mathematical modeling and analysis of a monkeypox model*. Communications in Mathematical Biology and Neuroscience, (2023).

[10] Jeeva N., Dharmalingam K.M., *Sensitivity analysis and semi-analytical solution for analyzing the dynamics of coffee berry disease*. Computer Research and Modeling, 16.3 (2024), 731-753.

[11] Jeeva N., Dharmalingam K.M., *Mathematical analysis of new SEIQR model via Laplace Adomian decomposition method*. Indian Journal of Natural Science, 15.83 (2024), 72148-72157.

[12] Jeeva N., Dharmalingam K.M., Fadugba S.E., Kekana M.C and Adeniji A.A., *Implementation of Laplace Adomian decomposition and differential transform methods for SARS-CoV-2 model*. Journal of applied mathematics and informatics, 42.4 (2024), 945-968.

[13] Lasisi, N.O., Akinwande, N.I., Oguntolu, F.A., *Development and exploration of a mathematical model for transmission of monkeypox disease in humans*. Mathematical Models in Engineering, 6.1 (2020), 23-33.

[14] Melese, A.S., Makinde, O.D., Obsu, L.L., *Mathematical modelling and analysis of coffee berry disease dynamics on a coffee farm*. Mathematical Biosciences and Engineering, 19.7 (2022), 7349-7373.

[15] Minhaj, F.S., Ogale, Y.P., Whitehill, F., Schultz, *Monkeypox outbreak—Nine states, May 2022*. American Journal of Transplantation, 22 (2022), 2104-2110.

[16] Oshinubi, K., Peter, O.J., Addai, E., Mwizerwa, E., et al., *Mathematical modelling of tuberculosis outbreak in an East African country incorporating vaccination and treatment*, Computation, 11.7 (2023), 143.

[17] Peter, O.J., Kumar, S., Kumari, N., Oguntolu, F.A., Oshinubi, K., Musa, R., *Transmission dynamics of monkeypox virus: A mathematical modelling approach*, Modeling Earth Systems and Environment, 8.3 (2022), 3423-3434.

[18] Precious, N.D., Agboola, P., Oluwatimilehin, O., Olakunle, *Re-emergence of monkeypox virus outbreak in Nigeria: Epidemic preparedness and response (Review-Commentary)*. Annals of Medicine and Surgery, 85 (2023), 3990-3996.

[19] Rizk, J.G., Lippi, G., Henry, B.M., Forthal, D.N., Rizk, Y., *Prevention and treatment of monkeypox*. Drugs, 82 (2022), 957-963.

[20] Sawsan Mohsin Abed, M.A. Al-Jawary, *Reliable Iterative Methods for Mathematical Model of COVID-19 Based on Data in Anhui, China*. Communications in Mathematical Biology and Neuroscience, (2020).

[21] Sawsan Mohsin Abed, M.A. Al-Jawary, *Reliable Iterative Methods for Mathematical Biology Model*, Communications in Mathematical Biology and Neuroscience, (2020).

[22] Shchigolev, V.K., *A simple analytic approximation of luminosity distance in FLRW cosmology using Daftardar-Jafari method*. Computer Science and Information Technology, 8.2 (2020), 43-49.

[23] Sklenovska, N., Van Ranst, M., *Emergence of monkeypox as the most important orthopoxvirus infection in humans*. Frontiers in Public Health, 6 (2018), 241.

[24] Somma, S.A., Akinwande, N.I., Chado, U.D., *A mathematical model of monkeypox virus transmission dynamics*. Ife Journal of Science, 21.1 (2019), 195.

[25] Suganya, G., Senthamarai, R., *Analytical approximation of a nonlinear model for pest control in coconut trees by the homotopy analysis method*. Communications in Nonlinear Science and Numerical Simulation, 14.5 (2022), 1093-1106.

[26] Taher, H.G., Ahmad, H., Singh, J., Kumar, D., Jassim, H.K., *Solving fractional PDEs by using Daftardar-Jafari method*. AIP Conference Proceedings, (2022).

[27] Thongmoon, M., Pusjuso, S., *The numerical solutions of differential transform method and the Laplace transform method for a system of differential equations*. Nonlinear Analysis: Hybrid Systems, 4.3 (2010), 425-431.

[28] Thornhill, J.P., Barkati, S., Walmsley, S., Rockstroh, J., et al., *Monkeypox virus infection in humans across 16 countries, April-June 2022*. New England Journal of Medicine, 387 (2022), 679-691.

[29] Tong, Z.-W., Lv, Y.-P., Din, R.U., Mahariq, I., Rahmat, G., *Global transmission dynamic of SIR model in the time of SARS-CoV-2*. Results in Physics, 25 (2021), 104253.

[30] Ullah, I., Khan, H., Rahim, M.T., *Numerical solutions of fifth and sixth order nonlinear boundary value problems by Daftardar-Jafari method*. Journal of Computational Engineering, 2014 (2014), 1-8.

[31] Usman, S., Isa Adamu, I., *Modeling the transmission dynamics of the monkeypox virus infection with treatment and vaccination interventions*. Science World Journal, 12.3 (2017), 20-25.

[32] Xu, J., Khan, H., Shah, R., Alderremy, A. A., Aly, S., Baleanu, D., *The analytical analysis of nonlinear fractional-order dynamical models*. AIMS Mathematics, 6.6 (2021), 6201-6219.

N. Jeeva,
The Madura College, PG and Research Department of Mathematics, Madurai, Tamil Nadu, India.
Email: jeevapirc2405@gmail.com.

K.M. Dharmalingam,
The Madura College, PG and Research Department of Mathematics, Madurai, Tamil Nadu, India.
Email: kmdharma6902@yahoo.in.

Received 28.07.2024, Revised 09.09.2024 Accepted 10.09.2024