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# Solution of Monkeypox Transmission Model using Picard Iterative Method

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ABSTRACT

Monkeypox, an emerging zoonotic disease, has demonstrated human-to-human transmission, which necessitates detailed analysis of its spread dynamics. Mathematical modeling is crucial for understanding these dynamics, but the reliability of numerical methods used to solve such models can vary. This paper applies the Picard Iterative Method (PIM) to a monkeypox transmission model represented by an eight-dimensional system of nonlinear ordinary differential equations. This study introduces a novel approach that applies the Picard Iterative Method to solve the monkeypox transmission model. While earlier studies have focused on both integer-order and fractional-order models, this study uniquely emphasizes the application of PIM in infectious disease modeling. A comparative analysis with the classical fourth-order Runge-Kutta (RK4) method is presented. The results suggest that PIM provides reliable short-term predictions of monkeypox dynamics, offering valuable insights into outbreak patterns, and enhancing public health response strategies through improved numerical modeling approaches.

## 1. INRODUCTION

Monkeypox, a zoonotic illness caused by the Monkeypox virus (MPXV), poses a global health risk due to its potential for human-to-human transmission. Previously found only in Central and West Africa, the virus has recently spread to non-endemic areas, particularly in North America and Europe (Bunge et al., 2022). To predict future outbreaks and guide public health initiatives, it is crucial to comprehend the mechanisms of monkeypox transmission (Yinka-Ogunleye et al., 2019). Since the first human case was documented in the Democratic Republic of the Congo in 1970, monkeypox has continued to be endemic in areas where there are substantial interactions between people and wildlife. The 2022 outbreak demonstrated the virus's

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ability to spread quickly, making the creation of predictive epidemiological models necessary for a more successful public health response.

The spread of monkeypox beyond endemic areas emphasises the importance of strong mathematical models for predicting transmission and guiding health measures. The Picard Iterative Method (PIM) is a foundational technique in the numerical analysis of differential equations. This approach, which was developed by French mathematician Emile Picard, is frequently used to solve initial value problems by consecutive approximations. In order to converge towards the actual solution, the procedure entails making an initial approximation of the answer and then repeatedly improving it (Burden & Faires, 2011). Although it is well-known for solving differential equations, the conventional PIM frequently encounters difficulties with convergence in extremely nonlinear systems. The differential equation is converted into its integral form using the PIM, where each iteration improves the approximation based on the one before it (Atkinson, 1991). In addition to offering useful information for controlling disease spread and assessing interventions, mathematical models are essential for characterising the dynamics of infectious disease transmission (Keeling & Rohani, 2008). Particularly for illnesses like monkeypox that have an incubation period, compartmental models, such as the Susceptible-Infectious-Recovered (SIR) and Susceptible-Exposed-Infectious-Recovered (SEIR) models, are frequently used to depict the stages of disease progression (Hethcote, 2000). Numerical approaches, such as the PIM, are crucial for estimating solutions to nonlinear equations.

Ramos (2009) illustrated the utilisation of PIM for nonlinear advection-reaction-diffusion equations. Likewise, Geiser (2016) utilised this approach to resolve multicomponent transport equations in plasma simulations. Both papers employ Banach's fixed-point theorem to demonstrate convergence. In comparison to existing iteration techniques for contraction mappings, a hybrid variant known as Picard-S iteration has been created for solving differential equations with retarded arguments, showing faster convergence (Gürsoy & Karakaya, 2014). Moreover, PIM has been effectively utilised to address linear and nonlinear optimum control issues with quadratic objective functionals (Akkouche & Aidene, 2020). By applying PIM to the resulting two-point boundary-value issue, the essential optimality conditions are derived using Pontryagin's minimum principle. The method's efficacy has been demonstrated by numerical examples and comparisons with alternative methodologies across many applications.

Aswhad (2024) emphasised the PIM adaptability in providing approximate or accurate solutions for both linear and nonlinear partial differential equations. For approximating fixed points of no expansive mappings in Banach spaces, a generalised variant known as the Picard-Mann iterative approach has been devised, exhibiting convergence and stability qualities (Shukla et al., 2022). The Legendre-Picard iteration method has demonstrated efficacy in resolving two-point nonlinear boundary value problems by combining PIM with shifted Legendre polynomials and Legendre-Gauss quadrature (Tafakkori--Bafghi et al., 2022). A convergence theorem for PIM has been established, creating a new class of iteration functions and offering precise beginning approximations for high-order convergence. For Halley's method of locating simple and multiple zeros of analytic functions, this theorem has been used to demonstrate local convergence (Ivanov, 2022).

While Kumar et al. (2024) used the PIM to solve time-space fractional partial differential equations, Witula et al. (2011) used it for two-phase Stefan problems. The approach is superior to more complex methods due to its ease of use and straightforward application to computer algebra systems (Kumar et al., 2024). However, sluggish convergence is a problem with the traditional PIM (Yao et al., 2021). Researchers have created better methods to deal with this, such as the Picard-Newton iterative approach for non-equilibrium radiation diffusion issues with time step control (Yue & Yuan, 2011). Furthermore, a relaxation-based acceleration strategy has been put out that combines second-order iterative and basic iterative approaches, greatly increasing convergence rates while maintaining the benefits of the traditional PIM (Yao et al., 2021). These developments have improved the effectiveness of resolving challenging issues in heat conduction and radiation hydrodynamics.

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A popular technique for resolving differential equations by converting them into integral forms is the PIM. Under certain circumstances, such as when the function satisfies the Lipschitz condition, it guarantees convergence. This requirement ensures that, scaled by a constant, the difference in function outputs is proportionate to the difference in inputs. If this condition is satisfied, the method's iterative procedure, as long as the initial guess is close enough to the real solution, converges to a unique solution throughout the course of the iterations (Butcher, 2016). With careful examination of the operator's properties, the approach can be modified for some nonlinear situations and is especially useful for linear differential equations. Even in complicated systems, its versatility makes it a dependable and effective instrument for arriving at precise solutions (Evans, 2022).

The purpose of this study is to evaluate the PIM dependability and look into its convergence characteristics using a monkeypox transmission model. The study also aims to compare the outcomes produced by the traditional Fourth Order Runge-Kutta method (RK4) with those achieved using the PIM. Evaluations of the convergence for the PIM and graphical representations of the answers for both methods will be part of a comparative analysis. The results are likely to shed light on the PIM aptitude for accurately modelling infectious diseases such as monkeypox.

## 2. MATHEMATICAL PRELIMINARIES

This section defines all words related to the parameters and variables involved, the modification of the original problem, and the numerical method used to derive the numerical solution. The PIM is the approach that is recommended. To obtain the results, this approach was applied in terms of accuracy, computational simplification, and dependency.

### 2.1 Monkeypox Transmission Model

To explore monkeypox outbreaks in the United States, consider a nonlinear mathematical model proposed in Peter et al. (2022) consisting of the population sizes of humans and rodents. The human population $N_h$ is divided into five different classes, namely, susceptible class $S_h$, exposed class $E_h$, infected class $I_h$, isolation class $Q_h$, and recovery class $R_h$. The population of rodents $N_r$ is divided into three classes, namely susceptible class $S_r$, exposed class $E_r$, and infected class $I_r$. The model is given as follows:

$$\frac{dS_h}{dt} = \Lambda_h - \left(\frac{\beta_1 I_r + \beta_2 I_h}{N_h}\right) S_h - \mu_h S_h + \phi Q_h \tag{1}$$

$$\frac{dE_h}{dt} = \left(\frac{\beta_1 I_r + \beta_2 I_h}{N_h}\right) S_h - \left(\alpha_1 + \alpha_2 + \mu_h\right) E_h \tag{2}$$

$$\frac{dI_h}{dt} = \alpha_1 E_h - \left(\mu_h + \delta_h + \varrho\right) I_h \tag{3}$$

$$\frac{dQ_h}{dt} = \alpha_2 E_h - \left(\phi + \tau + \mu_h + \delta_h\right) Q_h \tag{4}$$

$$\frac{dR_h}{dt} = \varrho I_h + \tau Q_h - \mu_h R_h \tag{5}$$

$$\frac{dS_r}{dt} = \Lambda_r - \frac{\beta_3 S_r I_r}{N_r} - \mu_r S_r \tag{6}$$

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$$\frac{dE_r}{dt} = \frac{\beta_3 S_r I_r}{N_r} - \left(\mu_r + \alpha_3\right) E_r \tag{7}$$

$$\frac{dI_r}{dt} = \alpha_3 E_r - \left(\mu_r + \delta_r\right) I_r \tag{8}$$

where the recruitment rates of humans and rodents are represented by $\Lambda_h$ and $\Lambda_r$ respectively. The contact rate between rodents and humans is denoted as $\beta_1$, while $\beta_2$ and $\beta_3$ represent the contact rates between humans and between rodents, respectively. The transmission rate of humans from the exposed to the infectious class is given by $\alpha_1$, whereas $\alpha_2$ represents the rate at which suspected cases are identified, and $\alpha_3$ denotes the transmission rate of rodents from the exposed to the infectious class. The proportion of humans not detected after diagnosis is indicated by $\phi$. The rate of transmission from the isolation class to the recovered class is expressed as $\tau$, and the recovery rate is represented by $\varrho$. The natural death rates of humans and rodents are described by $\mu_h$ and $\mu_r$, respectively, while the disease-induced death rates for humans and rodents are indicated by $\delta_h$ and $\delta_r$, respectively.

### 2.2 Picard Iterative Method

The PIM, a classical approach to solving nonlinear and differential equations, is rooted in fixed-point iteration principles. This approach, created by Emile Picard, uses a mapping function iteratively to approximate solutions until subsequent iterations converge to a satisfactory degree of accuracy (Braun & Golubitsky, 1993). This method guarantees the iteration sequence's convergence and works especially well for continuous and well-behaved functions (Zill et al., 1997).

In general, the PIM converts a differential equation into an integral equation, thereby establishing the groundwork for iterative approximations. Starting with an initial approximation $u_0(x)$, each successive approximation $u_{n+1}(x)$ is computed by substituting $u_n(x)$, in order to ensure stability and convergence, this iterative procedure keeps updating the solution until the difference between iterations drops below a predetermined tolerance level (Braun & Golubitsky, 1993; Butcher, 2016).

For a differential equation of the form:

$$\frac{dS_h}{dt} = \Lambda_h - \left(\frac{\beta_1 I_r + \beta_2 I_h}{N_h}\right) S_h - \mu_h S_h + \phi Q_h \tag{9}$$

With initial condition $S_h(t_0) = S_0$, the Picard iteration is expressed as:

$$S_{h(n+1)}(t) = S_{h(0)}(t) + \int \left( \Lambda_h - \frac{\beta_1 I_{r(n)}(t) + \beta_2 I_{h(n)}(t)}{N_h} S_{h(n)}(t) - \mu_h S_{h(n)}(t) - \phi Q_{h(n)}(t) \right) dt \tag{10}$$

The success of this approach depends on the function $f(x,u)$ satisfying certain Lipschitz continuity conditions, ensuring that the Picard sequence $u_n$ converges to a unique solution as $n \to \infty$. (Bartle & Sherbert, 2000).

### 2.3 Numerical Implementation

In this study, monkeypox modelling is solved using PIM. This method offers a stable and effective way to discover an approximate solution for the monkeypox model by building a series of sequential approximations. The correctional iteration formula for this specific model is formulated as follows:

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$$S_{h(n+1)}(t) = S_h(0)(t) + \int \left( \Lambda_h - \frac{\beta_1 I_r(n)(t) + \beta_2 I_h(n)(t)}{N_h} S_h(n)(t) - \mu_h S_h(n)(t) + \phi Q_h(n)(t) \right) dt \tag{11}$$

$$E_{h(n+1)}(t) = E_h(0)(t) + \int \left( \frac{\beta_1 I_r(n)(t) + \beta_2 I_h(n)(t)}{N_h} S_h(n)(t) - \left(\alpha_1 + \alpha_2 + \mu_h\right) E_h(n)(t) \right) dt \tag{12}$$

$$I_{h(n+1)}(t) = I_h(0)(t) + \int \left( \alpha_1 E_h(n)(t) - \left(\mu_h + \delta_h + \varrho\right) I_h(n)(t) \right) dt \tag{13}$$

$$Q_{h(n+1)}(t) = Q_h(0)(t) + \int \left( \alpha_1 E_h(n)(t) - \left(\phi + \tau + \mu_h + \delta_h\right) Q_h(n)(t) \right) dt \tag{14}$$

$$R_{h(n+1)}(t) = R_h(0)(t) + \int \left( \varrho I_h(n)(t) + \tau Q_h(n)(t) - \mu_h R_h(n)(t) \right) dt \tag{15}$$

$$S_{r(n+1)}(t) = S_r(0)(t) + \int \left( \Lambda_r - \frac{\beta_3 S_r(n)(t) I_r(n)(t)}{N_r} - \mu_r S_r(n)(t) \right) dt \tag{16}$$

$$E_{r(n+1)}(t) = E_r(0)(t) + \int \left( \frac{\beta_3 S_r(n)(t) I_r(n)(t)}{N_r} - \left(\mu_r + \alpha_3\right) E_r(n)(t) \right) dt \tag{17}$$

$$I_{r(n+1)}(t) = I_r(0)(t) + \int \left( \alpha_3 E_r(n)(t) - \left(\mu_r + \delta_r\right) I_r(n)(t) \right) dt \tag{18}$$

### 2.4 Convergence of the Picard Iterative Method

This section explains how the PIM can converge to the actual solution of an initial value problem. It focuses on three main aspects. First, the Existence and Uniqueness Theorem confirms that a unique solution exists. Next, the Boundedness of Iterates shows that the sequence produced by the method stays within a certain range. Finally, the Contraction Mapping ensures that the iteration moves closer to the true solution with each step.

#### 2.4.1 Existence and Uniqueness Theorem

The PIM, introduced as a foundational approach for solving ordinary differential equations (ODEs), is based mostly on repeated approximations to arrive at a solution. According to Gutermuth (2013), the approach iteratively builds a series of functions that, under certain assumptions about continuity and differentiability, converge to the differential equation's true solution.

One of the pioneering analyses of the convergence properties of this method was conducted by Richards in 1931. Richards' work provided substantial insights into the conditions under which the PIM is guaranteed to converge, focusing on the requirements for the function defining the differential equation to be Lipschitz continuous. In this study, Richards outlined that the convergence of the Picard iterations to the true solution depends on the existence of a Lipschitz constant $L$ for the function $f(x, y)$, with respect to $y$, in the differential equation of the form:

$$y' = f(x, y) \tag{19}$$

Richards (1931) analysis highlighted the importance of ensuring that $f$ meets the Lipschitz condition, which can be stated as follows:

$$\left| f\left(x, y_1\right) - f\left(x, y_2\right) \right| \leq L \left| y_1 - y_2 \right| \tag{20}$$

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for all $y_1, y_2$ in the domain of $f$. This constraint implies that the function does not vary too steeply with respect to $y$, allowing the successive approximations to converge linearly to the actual solution of the differential equation within a specified interval. Richards (1931) demonstrated that, under this condition, the iterative sequence produced by the PIM converges at a rate dependent on *L* and the initial values chosen for the sequence.

### 2.4.2 Boundedness of Iterates

Let

$$M = max\left\{\left|S_{h(0)}\right|,\left|E_{h(0)}\right|,\left|I_{h(0)}\right|,\left|Q_{h(0)}\right|,\left|R_{h(0)}\right|,\left|S_{r(0)}\right|,\left|E_{r(0)}\right|,\left|I_{r(0)}\right|\right\} \tag{21}$$

and suppose $S_h, E_h, I_h, Q_h, R_h, S_r, E_r, I_r$ remain bounded in a domain $[0, t]$.

For all $n$:

$$\left|S_{h(n+1)}(t)\right| \le \left|S_0\right| + \int_0^t \left(\Lambda_h - \frac{\beta_1 I_{r(n)}(t) + \beta_2 I_{h(n)}(t)}{N_h} S_{h(n)}(t) - \mu_h S_{h(n)}(t) + \phi Q_{h(n)}(t)\right) dt \tag{22}$$

Since $S_h(t), E_h(t), I_h(t), Q_h(t), R_h(t), S_r(t), E_r(t), I_r(t)$ are continuous and bounded on $[0, t]$, and $\beta, \Lambda, \phi$ are constant, the sequences $S_{h(n)}, E_{h(n)}, I_{h(n)}, Q_{h(n)}, R_{h(n)}, S_{r(n)}, E_{r(n)}, I_{r(n)}$ remain bounded for all $n$.

### 2.4.3 Contraction Mapping

Let:

$$\Delta S_{h(n)}(t) = S_{h(n+1)}(t) - S_{h(n)}(t) \tag{23}$$

For $\Delta S_{h(n)}(t)$:

$$\left|\Delta S_{h(n+1)}(t)\right| = \left| \begin{array}{l} \displaystyle\int_0^t \left(\Lambda_h - \frac{\beta_1 I_{r(n)}(t) + \beta_2 I_{h(n)}(t)}{N_h} S_{h(n)}(t) - \mu_h S_{h(n)}(t) + \phi Q_{h(n)}\right) \\ \displaystyle -\left(\Lambda_h - \frac{\beta_1 I_{r(n-1)}(t) + \beta_2 I_{h(n-1)}(t)}{N_h} S_{h(n-1)}(t) - \mu_h S_{h(n-1)}(t) + \phi Q_{h(n-1)}(t)\right) dt \end{array} \right| \tag{24}$$

Split the equation in (24) into components based on $n$ and $(n-1)$:

$$\Delta S_{h(n+1)} = \int_0^t \left(S_{h(n)} - S_{h(n-1)}\right) \mathrm{d}t \tag{25}$$

where:

$$S_{h(n)} = \Lambda_h - \frac{\beta_1 I_{r(n)}(t) + \beta_2 I_{h(n)}(t)}{N_h} S_{h(n)}(t) - \mu_h S_{h(n)}(t) + \phi Q_{h(n)}(t) \tag{26}$$

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Using the Lipschitz property:

Identify terms like $\left|S_{hn}(t) - S_{h(n-1)}(t)\right|$ that can be bounded. For example:

$$\left|\frac{\beta_1 I_{r(n)}(t)+\beta_2 I_{h(n)}(t)}{N_h}S_{h(n)}(t) - \frac{\beta_1 I_{r(n-1)}(t)+\beta_2 I_{h(n-1)}(t)}{N_h}S_{h(n-1)}(t)\right| \tag{27}$$

This difference will involve bounds for $\left|I_{rn}(t) - I_{r(n-1)}(t)\right|$, $\left|I_{hn}(t) - I_{h(n-1)}(t)\right|$, and $\left|S_{hn}(t) - S_{h(n-1)}(t)\right|$, each multiplied by their respective coefficients.

Using Lipschitz continuity assumptions for functions $I_r(t), I_h(t), S_h(t), Q_h(t)$:

Assume:

$$\left|f_{(n)}(t) - f_{(n-1)}(t)\right| \le L\left|S_{h(n)}(t) - S_{h(n-1)}(t)\right| \tag{28}$$

where $L$ is a Lipschitz constant.

The range in (28) then becomes:

$$\left|\Delta S_{h(n+1)}(t)\right| \le \int_0^t \left(L\left|\Delta S_{h(n)}(t)\right| + L\left|\Delta S_{h(n-1)}(t)\right|\right)\mathrm{d}t \tag{29}$$

Thus:

$$\left|\Delta S_{h(n+1)}(t)\right| \le \beta\int_0^t \left(\left|\Delta S_{h(n)}(t)\right| + \left|\Delta S_{h(n-1)}(t)\right|\right)\mathrm{d}t \tag{30}$$

Applying Gronwall's inequality:

$$\Delta_{n+1} \le \Delta_0 e^{Ct} \tag{31}$$

As $n \to \infty$, $\Delta_n \to 0$, proving the convergence of the sequence.

For the uniqueness theorem, assume the two solutions $S_{h1}, E_{h1}, I_{h1}, Q_{h1}, R_{h1}, S_{r1}, E_{r1}, I_{r1}$ and $S_{h2}, E_{h2}, I_{h2}, Q_{h2}, R_{h2}, S_{r2}, E_{r2}, I_{r2}$.

Their difference satisfies:

$$\left|S_{h1}(t) - S_{h2}(t)\right| \le \int_0^t \left|\beta\left(S_{h1}E_{h1} - S_{h2}E_{h2}\right)\right|\mathrm{d}t \tag{32}$$

Using the same Lipschitz bounds as above and applying Gronwall's inequality:

$$\left|S_{h1}(t) - S_{h2}(t)\right| = 0 \qquad |E_{h1}(t) - E_{h2}(t)| = 0 \qquad |I_{h1}(t) - I_{h2}(t)| = 0$$

$$|Q_{h1}(t) - Q_{h2}(t)| = 0 \qquad |R_{h1}(t) - R_{h2}(t)| = 0$$

$$|S_{r1}(t) - S_{r2}(t)| = 0 \qquad |E_{r1}(t) - E_{r2}(t)| = 0 \qquad |I_{r1}(t) - I_{r2}(t)| = 0$$

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## 3. RESULTS AND DISCUSSION

This section presents the results obtained from applying the PIM to the monkeypox transmission model. It includes convergence analysis, numerical simulations using real data, and comparisons with the RK4 method. The findings demonstrate the accuracy and efficiency of PIM, especially in early-stage predictions, and highlight its strengths and limitations when modeling both human and rodent populations.

### 3.1 Analysis of Numerical Method

The following criterion was used to evaluate the iterative method's convergence:

$$\in = \left| S_{h(n+1)}(t) - S_{h(n)}(t) \right|$$

where $t = 0.1$, this step size is chosen because smaller step sizes generally improve accuracy (Arefin et al., 2021). The iterative process was stopped when:

$$\in \leq 10^{-10}$$

Table 1. Convergence Error Analysis for the Modified Picard Iterative Method

| Number of Iteration | Convergence Value |
|---|---|
| 1 | 0.01409560 |
| 2 | 0.62046244 |
| 3 | 0.10652680 |
| 4 | 0.01001646 |
| 5 | 0.00066608 |
| 6 | 0.00003454 |
| 7 | $1.47338532 \times 10^{-5}$ |
| 8 | $5.34611703 \times 10^{-8}$ |
| 9 | $1.68954291 \times 10^{-9}$ |

The convergence values obtained by using the PIM on the monkeypox model are displayed in Table 1 above, indicating a methodical approach to the solution. The approach first demonstrates fast convergence, with the numbers sharply declining in the initial rounds. For instance, after the fourth iteration, the convergence value decreased from 0.10652680 in the second to 0.01001646. This rapid drop implies that the approach immediately reduces the initial error, bringing the solution closer to stability right away. The convergence values continue to drop as the iterations go on, although more slowly, indicating a slow but steady approach to the actual solution.

The convergence value reaches the order of $10^{-8}$ by the eighth iteration, indicating that the error value is tiny and that the solution is extremely close to a highly exact numerical answer. In order to guarantee a high enough degree of precision for this model, the needed tolerance $10^{-10}$ was chosen, and the convergence value further dropped to $10^{-9}$ in the ninth iteration. The PIM is configured to terminate upon the attainment of this threshold, and it achieves convergence within nine iterations. This demonstrates how well the method may achieve a high degree of accuracy with a very small number of iterations. Overall, the findings demonstrate how well the PIM works to solve the model equations repeatedly, lowering errors in the first phases quickly and gradually approaching an accurate solution in a manageable number of cycles.

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### 3.2 Numerical Simulation on Monkeypox Model

In this section, numerical simulations on the monkeypox model have been conducted. Firstly, the value of parameters, initial approximation and open data of Monkeypox in USA are adopted from Sayers (2024). Assume that the value for $N_h = 10051.00, S_h(0) = 10000, E_h(0) = 50\,,\ I_h(0) = 0.57, Q_h(0) = 0.43, R_h(0) = 0, N_h = 1110, S_r(0) = 1000, E_r(0) = 100, I_r(0) = 10$. Maple22 is used to compute the iteration of the Monkeypox model using the PIM.

Table 2. Parameter values for Monkeypox Transmission model simulation

| Parameter | Value | Description |
|---|---|---|
| $\Lambda_h$ | 0.34857 | Recruitment rates of human |
| $\Lambda_r$ | 0.60822 | Recruitment rates of rodent |
| $\mu_h$ | $\frac{1}{79*365}$ | Natural death rates of human |
| $\mu_r$ | $\frac{1}{5*365}$ | Natural death rates of rodent |
| $\alpha_1$ | 0.423890 | Transmission rate of humans from exposed to infectious class |
| $\alpha_2$ | 1.797575 | Rate of identification of suspected case |
| $\alpha_3$ | 0.025289 | Transmission rate of rodents from exposed to infectious class |
| $\beta_1$ | 0.011503 | Contact rate between rodent and human |
| $\beta_2$ | 0.747322 | Contact rate between human |
| $\beta_3$ | 0.321102 | Contact rate between rodent |
| $\delta_h$ | 0.015016 | Disease-induced death rates of human |
| $\delta_r$ | 0.000025 | Disease-induced death rates of rodent |
| $\varrho$ | 0.067689 | Recovery rate |
| $\phi$ | 1.575454 | Proportion of humans not detected after diagnosis |
| $\tau$ | 0.999763 | Rate of transmission from isolation to recovered class |

Source: Sayers, 2024

### 3.3 Numerical Solution of the Monkeypox Transmission Model using Picard Iterative Method

All the parameter values in Table 2 are substituted into the equations of the Monkeypox model to obtain the following system for the first iteration:

$$S_{h1}(t) = 10000 + 0.1409560350t \tag{33}$$

$$E_{h1}(t) = 50 - 110.5367256t \tag{34}$$

$$I_{h1}(t) = 0.57 + 21.14733838t \tag{35}$$

$$Q_{h1}(t) = 0.43 + 88.76493490t \tag{36}$$

$$R_{h1}(t) = 0.4684808200t \tag{37}$$

$$S_{r1}(t) = 1000 - 2.832536016t \tag{38}$$

$$E_{r1}(t) = 100 + 0.3091162900t \tag{39}$$

$$I_{r1}(t) = 10 + 2.523170548t \tag{40}$$

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For the second iteration, the system becomes:

$$S_{h2}(t) = 10000 + 0.1409560350\,t + 62.04625101t^2 - 0.00007401393346t^3 \quad (41)$$

$$E_{h2}(t) = 50 - 110.5367256t + 130.6549326t^2 + 0.00007401393346t^3 \quad (42)$$

$$I_{h2}(t) = 0.57 + 21.14733838t - 24.30256831t^2 \quad (43)$$

$$Q_{h2}(t) = 0.43 + 88.76493490t - 214.3114982t^2 \quad (44)$$

$$R_{h2}(t) = 0.4684808200t + 45.08766178t^2 \quad (45)$$

$$S_{r2}(t) = 1000 - 2.832536016t - 0.3600797193t^2 + 0.0006891612094t^3 \quad (46)$$

$$E_{r2}(t) = 100 + 0.3091162900t + 0.3568624462t^2 - 0.0006891612094t^3 \quad (47)$$

$$I_{r2}(t) = 10 + 2.523170548t + 0.003185801695t^2 \quad (48)$$

For the third iteration, the system is:

$$S_{h3}(t) = 10000 + 0.1409560350t + 62.04625101t^2 - 106.5246562t^3 - 0.02437100065t^4 + 0.02242310668\,t^5 - 2.229010044 \times 10^{-8} t^6 \quad (49)$$

$$E_{h3}(t) = 50 - 110.5367256t + 130.6549326t^2 - 102.7719938t^3 + 0.02432989581t^4 - 0.02242310668t^5 + 2.229010044 \times 10^{-8} t^6 \quad (50)$$

$$I_{h3}(t) = 0.57 + 21.14733838t - 24.30256831t^2 + 19.13136870t^3 + 0.00007843441562t^4 \quad (51)$$

$$Q_{h3}(t) = 0.43 + 88.76493490t - 214.3114982t^2 + 263.3287292t^3 + 0.00003326139910t^4, \quad (52)$$

$$R_{h3}(t) = 0.4684808200t + 45.08766178t^2 - 71.96909553t^3 \quad (53)$$

$$S_{r3}(t) = 1000 - 2.832536016t - 0.3600797193t^2 + 0.0007949459768t^3 + 0.00006576584409t^4 - 3.423518282 \times 10^{-8} t^5 - 1.058542611 \times 10^{-10} t^6 \quad (54)$$

$$E_{r3}(t) = 100 + 0.3091162900t + 0.3568624462t^2 - 0.003802589815t^3 - 0.00061408794644t^4 + 3.423518282 \times 10^{-8} t^5 + 1.058542611 \times 10^{-10} t^6 \quad (55)$$

$$I_{r3}(t) = 10 + 2.523170548t + 0.003185801695t^2 + 0.003007623037t^3 - 0.000004357049455t^4 \quad (56)$$

...

The notation "..." indicates that the iterations continue following the same pattern. Due to space limitations, only the first three iterations are explicitly shown in this study. The iterative process continues up to the 10th iteration, progressively refining the approximations for each variable in the system.

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### 3.4 Analysis of Monkeypox Transmission Model

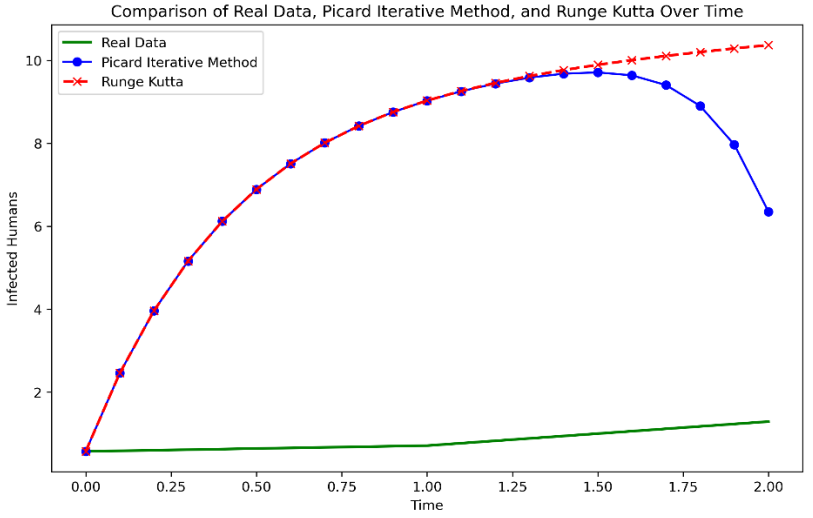


Fig. 1. Infected class human, $I_h$ over time, $t$

Fig. 1 illustrates a comparison between PIM, RK4 and the real data for infected human $I_h$ cases over time $t$. The real data values used were obtained from the article by Kumar et al (2023) and RK4 values shown are the results of using the built-in function in Maple. This graph depicts a characteristic infection trend, in which the count of infected individuals escalates sharply in the initial phase before it reaches a distinct peak, followed by a gradual decline. This pattern underscores the rapid spread of infection in the beginning, which can be attributed to a high transmission rate as susceptible individuals encounter already infected ones, accelerating the spread. In this numerical solution, the time step $t = 0.1$ is intentionally selected to be small due to the nature of the power series employed in the PIM. The approximation error might increase dramatically as the time step increases from the initial value, compromising the precision of the answer. By lowering this error, a smaller $t$ preserves the intricate dynamics of infection transmission while guaranteeing the accuracy of the numerical solution (Karimov et al., 2021).

In the early stages of infection dynamics, the PIM shows its dependability by closely following the RK4 Method trajectory and aligning well with the exact solution for time values less than 1. But when $t = 1$, while the RK4 technique still closely matches the exact solution, the PIM starts to diverge from both the RK4 the real data. This discrepancy implies that the PIM may become less accurate over longer time periods, although it is useful for making short-term predictions or for identifying the early phases of an outbreak. All things considered, the findings show that the PIM is reliable for roughly estimating the early dynamics of the monkeypox transmission model, offering important information on the disease's early course.

As time progresses, the rate of new infections decreases, culminating in an apex at approximately $t = 1.5$ following which a downward trend is observed. This subsequent reduction, which is frequently seen in epidemiological modelling as the illness moves closer to its saturation point, could be the result of recovery, isolation measures, or decreased transmission rates brought on by a decline in the number of susceptible people.

Because PIM offers an iterative solution framework for nonlinear differential equations which are commonly encountered in the field of epidemiological modeling it is useful to employ it in this context. The estimate of $I_h$ is gradually improved with each iteration, enabling a more accurate representation of the infection dynamics over time. This iterative improvement guarantees that the model appropriately

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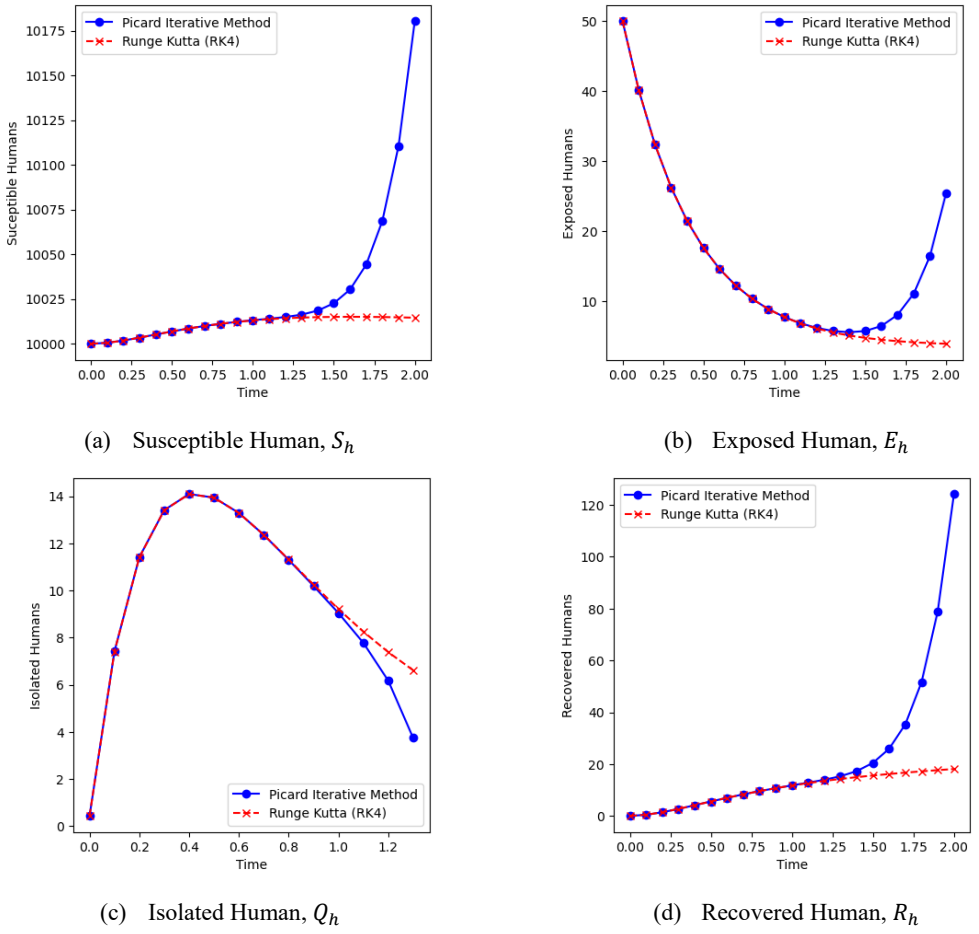
captures variations in the propagation of infections. It is clear from looking at this graph that the PIM can handle the complexity of disease spread patterns, such as those caused by monkeypox, by effectively capturing the complex dynamics of infection.

The solutions for the several compartments in the monkeypox model are shown in Fig. 2 and Fig. 3 below, which particularly show the dynamics of rodent and human populations in various classes. The susceptible human class, exposed human class, isolation class, recovery class, susceptible rodent class, exposed rodent class, and infected rodent class are the different components of the model that are represented by each graph. When taken as a whole, these graphs offer a thorough understanding of how each population compartment changes over time in response to human-rodent interactions and spread parameters. The graphs illustrate the variations in solution accuracy and behaviour across the model components by contrasting the RK4 Method with the PIM.




(a) Susceptible Human, $S_h$

(b) Exposed Human, $E_h$

(c) Isolated Human, $Q_h$

(d) Recovered Human, $R_h$

Fig. 2. Comparison of PIM and RK4 for the Monkeypox model (Human Class)

Fig. 2 (a) illustrates the comparison between PIM and RK4 method for the susceptible human population. Up to approximately $t = 1.25$, both methods yield comparable results, showing a gradual increase in the susceptible population. However, beyond $t = 1.25$, the PIM rises sharply, while the RK4 method remains stable. This significant divergence suggests potential convergence issues with the PIM over longer time intervals.

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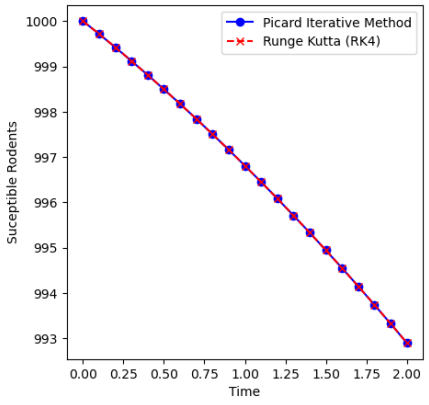
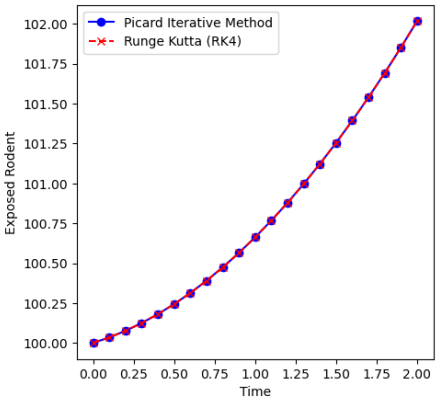
Next, Fig. 2 (b) provides a detailed comparison of PIM and RK4 method for the exposed human population over time. Initially, both methods align closely, showing a steady decline in the exposed population as time progresses. However, after approximately $t = 1.25$, the PIM begins to diverge significantly from the RK4 results. While the RK4 method stabilizes around a small number of exposed humans, the PIM starts to rise sharply after $t = 1.5$, indicating divergence. This behavior highlights potential limitations of the PIM in accurately modeling the exposed human population over extended time intervals, particularly regarding convergence and stability.

In Fig. 2 (c), the PIM and RK4 method are compared to model isolated human population patterns. Both approaches show good agreement starting from $t = 0$ to $t = 8$ with the number of solitary persons slowly growing and peaking at $t \approx 0.4$ to $t \approx 0.5$, stabilizing at about 14 individuals. Both techniques line closely until around $t = 1.0$ after the apex. Beyond $t \approx 1.0$, PIM a bit deviate from RK4 results. The PIM has a greater fall, especially after $t \approx 1.2$, compared to the RK4 method. The gap implies that the PIM may lose accuracy over longer time intervals, especially in the decreasing phase, indicating stability or convergence concerns.

Fig. 2 (d) shows the comparison between PIM and RK4 method in modelling the restored human population. During the initial phase, from $t = 0$ to about $t \approx 1.25$, both methods show a significant level of consistency, with the number of recovered people rising steadily and nearly matching. However, after $t \approx 1.25$, significant gap occurs between the two methods. The PIM demonstrates an exponential growth in the number of recovered individuals, with values rising drastically after $t \approx 1.5$ ultimately reaching 120 retrieved individuals at $t = 2.0$. Instead, the RK4 approach grows slowly and linearly, stabilizing at 17 recovered humans. In contrast, the RK4 technique predicts growth smoothly, consistently, and reliably, suggesting numerical stability. However, as time grows, the PIM becomes unstable and diverges due to numerical instability, convergence problems, or the problem's nonlinearity. While the RK4 approach better represents the recovery trend, the PIM rapid, unnatural exponential rise signals stability issues over longer time periods.




(a) Susceptible Rodent, $S_r$




(b) Exposed Rodent, $E_r$

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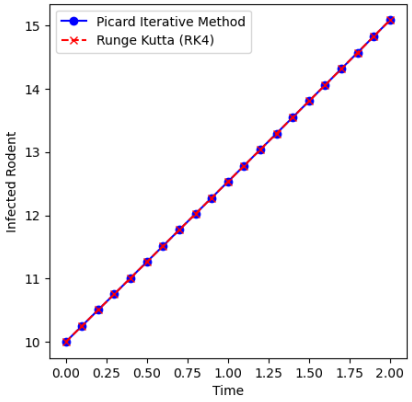


(c) Infected Rodent, $I_r$

Fig. 3. Comparison of PIM and RK4 for the Monkeypox model (Rodent Class)

Fig. 3 (a) presents a comparison of PIM and RK4 method for the susceptible rodent population in the monkeypox transmission model. Both methods show a gradual decline in the susceptible rodent population over time, starting from 1000 and decreasing to approximately 993 at $t = 2$. The close overlap between the PIM and the RK4 demonstrates that the PIM produces results that are highly consistent with the established RK4.Fig. 3 (b) provides an analysis of the exposed rodent population as modeled by PIM and RK4 method. Both methods depict a gradual increase in the exposed rodent population, starting from approximately 100 and rising to about 102 at $t = 2$. The results of the PIM closely align with those of the RK4 method show nearly identical trends.

Fig. 3 (c) explores the dynamics of the infected rodent population as solved by PIM and RK4 method. Both methods show a steady, near-linear increase in the infected rodent population over time, starting at 10 and reaching approximately 15 when $t = 2$. The results from both methods align almost perfectly, demonstrating the accuracy and reliability of the PIM in capturing the infection dynamics of the rodent population.

## 4. CONCLUSION

The PIM was successfully applied to the monkeypox transmission model in this work, and its effectiveness was contrasted with that of the RK4 method. The results show that, especially for short time intervals (e.g., $t \in [0,1]$), the PIM offers a dependable and accurate approximation for the monkeypox model. However, the approach starts to diverge after $t = 1$, which limits its usefulness for long-term forecasts. Despite this drawback, the PIM shows promise as an effective technique for resolving differential equations in disease modelling, particularly when short-term dynamics are the main focus.

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## 6. CONFLICT OF INTEREST STATEMENT

The authors declared that there is no conflict of interest in this paper.

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## 7. AUTHORS' CONTRIBUTIONS

Ahmad Bazli Khairuddin contributed to the development of the methodology. Mat Salim Selamat was responsible for reviewing and editing the manuscript, ensuring its quality and coherence. Nor Azizah M. Yacob provided valuable feedback through review and editing, contributing to the overall refinement of the work.

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