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Dynamical Characteristics and Approximate Technique to Solve the Model of Nonlinear Biological Reactions

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ABSTRACT

In this paper, we present a rigorous mathematical analysis of the nonlinear Michaelis-Menten biochemical reaction model, formulated as a system of non-dimensional coupled nonlinear ordinary differential equations (ODEs). Using the classical theory of ordinary differential equations, comparison principles, and Lyapunov's direct method, fundamental qualitative properties of the model, such as existence, uniqueness, non-negativity, boundedness, and local and global asymptotic stability of solutions, are established. The Elzaki Transform Homotopy Perturbation Method (ETHPM) is used to obtain an accurate approximate analytical solution, and its accuracy is studied by direct comparison with the fourth-order Runge-Kutta (RK4) method and error analysis. Numerical simulations confirm the temporal dynamics of biochemical systems and validate the efficiency and accuracy of the proposed semi-analytical approach. The results indicate that the Elzaki transform decomposition framework provides a computationally efficient, linearization-free, and highly accurate tool for analyzing nonlinear biochemical reaction models with wider applicability to a broad class of nonlinear problems arising in mathematical biology and applied science.

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1. INTRODUCTION

Mathematical modelling has become an important tool for understanding the dynamics of biochemical reaction systems. ODE models offer a rigorous framework for describing enzyme-substrate interactions, reaction kinetics, and temporal evolution of biochemical processes [1]. Enzyme kinetics constitutes a fundamental pillar of mathematical

biology, providing a quantitative framework for understanding the catalytic mechanisms underlying metabolic processes. The Michaelis–Menten model was first proposed by Michaelis and Menten in 1913 [2].

The dimensionless form of the Michaelis–Menten system is obtained by using a standard quasi-steady-state approximation and nondimensionalization procedure [3], and it simplifies the governing equations to a two-dimensional autonomous system with the dimensionless substrate concentration x(t) and intermediate complex concentration y(t). This reduction considerably simplifies the mathematical analysis while retaining the essential qualitative behavior of the full four-dimensional system[4]. The resulting system, described by the three dimensionless parameters α, β, and γ, is known not to have an exact closed-form solution for general values of the parameters; therefore, we resort to qualitative analysis and approximate approaches[5].

Several analytical and semi-analytical methods have been employed for related nonlinear biochemical and biological ODE systems. Sen [6] studied the transient behavior of biochemical reactions with the Adomian Decomposition Method (ADM). ADM is systematic but requires calculation of Adomian polynomials at each iteration, which becomes algebraically tedious for higher orders. Khader [7] used the Picard–Padé method, which is a rational approximation method that gives satisfactory accuracy but may fail outside a small convergence radius[8]. Laplace transform-based decomposition methods transform the ODE system into an algebraic form, but they have problems with strongly nonlinear terms and require evaluating the inverse Laplace transform at each step[9]. The classical Homotopy Perturbation Method (HPM) is powerful, but its use without an integral transform results in perturbation series whose convergence is sensitive to the choice of the homotopy parameter [10]. The Elzaki transform, introduced by Elzaki and extended later, overcomes this limitation by embedding the integral transform directly in the decomposition framework, thus improving the convergence behavior and computational efficiency [11].

The paper has the following specific contributions relative to all the previous works cited above: (i) it provides the first complete qualitative analysis of the dimensionless Michaelis–Menten model, which includes an existence-uniqueness proof based on Picard–Lindelöf, rigorous positivity and boundedness, local stability by means of the Routh-Hurwitz criterion, and global stability with the aid of an explicit Lyapunov function; (ii) it employs the Elzaki Transform Decomposition Method (ETDM), which combines the Elzaki transform with the decomposition series, to obtain a closed-form series solution without linearization or any restrictive assumptions on the parameters; and (iii) it provides a fully quantitative numerical validation, including tables of absolute error, residual error, convergence with respect to the number of terms, and CPU time, which are missing from all previous treatments of this model. The paper is analytical in nature, and numerical validation is used as a rigorous benchmark.

The remaining part of this paper is organized as follows. Section 2 describes the mathematical model, governing equations, dimensionless formulation, and parameters. Section 3 describes the main concepts of the Elzaki Transform Decomposition Method (ETDM). In Section 4, we prove the basic qualitative properties of the model, such as existence and uniqueness of solutions, positivity, and boundedness. Section 5 is devoted to the local and global stability analyses and sensitivity analyses. In Section 6, the approximate analytical solution of the proposed biochemical reaction model is obtained via the ETDM. Section 7 presents the numerical results, comparisons with the fourth-order Runge-Kutta (RK4) method, and a discussion on the accuracy and convergence of the proposed approach. Finally, Section 8 concludes the paper and points out the main findings and possible directions for future research.

2. MATHEMATICAL MODEL

2.1 Reaction Scheme

The classical enzyme-catalyzed reaction mechanism is the Michaelis–Menten reaction mechanism [12] in **Equation 1**.

$$E + S \underset{k_{-1}}{\overset{k_1}{\rightleftharpoons}} ES \overset{k_2}{\rightarrow} E + P \qquad (1)$$

where E, S, ES, and P denote the free enzyme, substrate, enzyme–substrate complex, and reaction product, respectively. The positive constants k_1, k_{-1}, and k_2 represent the association, dissociation, and catalytic rate constants.

2.2 Governing Equations

Applying the law of mass action to the reaction scheme yields the following nonlinear system of ordinary differential equations [13]. In **Equations from 2 to 5**.

$$\frac{dS}{dt} = -k_1 ES + k_{-1} ES, \quad (2)$$

$$\frac{dE}{dt} = -k_1 ES + (k_{-1} + k_2) ES, \quad (3)$$

$$\frac{dES}{dt} = k_1 ES - (k_{-1} + k_2) ES, \quad (4)$$

$$\frac{dP}{dt} = k_2 ES, \quad (5)$$

with initial conditions

$$S(0) = S_0, \quad E(0) = E_0, \quad ES(0) = 0, \quad P(0) = 0.$$

2.3 Dimensionless Formulation

To simplify the mathematical analysis and reduce the number of governing parameters, the dimensional model is transformed into a dimensionless form. Following the standard nondimensionalization procedure for the Michaelis–Menten reaction model[14], the dimensionless variables are introduced as in **Equation 6**.

$$x = \frac{S}{S_0}, \qquad y = \frac{ES}{E_0}, \qquad \tau = k_1 S_0 t \quad (6)$$

where (S_0) and (E_0) denote the initial substrate and enzyme concentrations, respectively. The corresponding dimensionless parameters are defined by **Equation 7**.

$$\alpha = \frac{k_{-1}}{k_1 S_0}, \qquad \beta = \frac{k_{-1} + k_2}{k_1 S_0}, \qquad \gamma = \frac{E_0}{S_0} \quad (7)$$

Substituting these variables into the governing equations and omitting the dimensionless time variable (τ) for simplicity, the nonlinear biochemical reaction model is reduced to the following autonomous system in **Equations 8a and 8b**

$$\frac{dx}{dt} = -x + \beta y - \alpha y + xy \quad (8a)$$

$$\frac{dy}{dt} = \frac{1}{\gamma}(x - \beta y - xy) \quad (8b)$$

subject to the initial conditions

$$x(0) = 1, \qquad y(0) = 0$$

The reduced dimensionless system retains the essential dynamical behavior of the original Michaelis–Menten enzyme kinetics but dramatically simplifies the mathematical formulation. Hence, it offers a convenient framework for qualitative analysis, stability investigation, and development of accurate approximate analytical and numerical solutions.

2.4 Parameter List

All parameters appearing in system (7) are defined in **Table 1.**

Table 1. Parameter definitions for the dimensionless system (7). Physical conditions require β > α > 0 and γ > 0.

Parameter	Definition	Expression	Biological meaning
A	Dimensionless dissociation ratio	$k_{-1} / (k_1 S_0)$	Scaled reverse rate constant

B	Dimensionless Michaelis parameter	$(k_{-1} + k_2) / (k_1 S_0)$	Combined scaled unbinding rate
Γ	Enzyme-to-substrate ratio	E_0 / S_0	Relative enzyme availability
x(t)	Dimensionless substrate concentration	$S(t) / S_0$	Fraction of initial substrate remaining
y(t)	Dimensionless complex concentration	$ES(t) / E_0$	Fraction of enzyme bound to substrate

3. FUNDAMENTAL CONCEPTS OF THE ELZAKI DECOMPOSITION METHOD

To understand the fundamental concept of EDM [15], we study the specific form of nonlinear inhomogeneous ODEs with initial conditions, such as **Equation 9**.

$$Lu + Ru + Nu = g(t), \;\; u(0) = a \tag{9}$$

where L refers to the first-order derivative, R is a linear differential operator, N stands for the nonlinear terms, and g(t) is the source term. Applying the Elzaki transform to both sides of **Equation 10**.

$$E[Lu] + E[Ru] + E[Nu] = E[g(t)] \tag{10}$$

Using the Elzaki transform differentiation with the initial conditions of **Equation 11**, we obtain

$$E[u(t)] = au^2 + u\{E[g(t)] - E[Ru] - E[Nu]\} \tag{11}$$

Applying the inverse Elzaki transform to both sides of **Equation 12**.

$$u(t) = a + E^{-1}[u\{E[g(t)] - E[Ru] - E[Nu]\}] \tag{12}$$

The solution is expressed as the infinite series **in Equation 13**.

$$u(t) = \sum_{n=0}^{\infty} u_n(t), \tag{13}$$

and the nonlinear term may be decomposed as in **Equation 14**.

$$Nu(t) = \sum_{n=0}^{\infty} A_n, \tag{14}$$

where $A_n$are Adomian polynomials of $u_0, u_1, u_2, \cdots$ and we can calculate them as in **Equations 15 and 16**.

$$A_n = \frac{1}{n!}\frac{d^n}{d\lambda^n}\left[N\left(\sum_{i=0}^{\infty} \lambda^i u_i(t)\right)\right]_{\lambda=0}, \quad n = 0,1,2,\ldots. \tag{15}$$

$$\sum_{n=0}^{\infty} u_n(t) = B(t) - E^{-1}\left[uE[R\sum_{n=0}^{\infty} u_n(t) + \sum_{n=0}^{\infty} A_n]\right], \tag{16}$$

where B(t) is the term that results from the starting condition and the source term. Equating the terms of identical order yields the recursive scheme to compare both sides; we obtain:

$$u_0(t) = B(t) \tag{17}$$

$$u_1(t) = -E^{-1}\left[uE[Ru_0(t) + A_0]\right] \tag{18}$$

$$u_2(t) = -E^{-1}\left[uE[Ru_1(t) + A_1]\right] \tag{19}$$

$$u_{n+1}(t) = -E^{-1}\left[uE[Ru_n(t) + A_n]\right] \quad (20)$$

The series form of the desirable solutions, u_0, u_1, u_2 may be computed from the general **Equations from 17 to 20**.

4. EXISTENCE, UNIQUENESS, POSITIVITY, AND BOUNDEDNESS

4.1 Existence and Uniqueness

Theorem 4.1 (Existence and Uniqueness of Solutions) is shown in Equations 21 and 22.

$$Let[D = [0,\infty)^2 = \{(x,y) \in \mathbb{R}^2 : x \geq 0,\ y \geq 0\}]$$

and define $F: D \to \mathbb{R}^2 by$

$$F(x,y) = \begin{pmatrix} -x + \beta - \alpha y + xy \\ \frac{1}{\gamma}(x - \beta y - xy) \end{pmatrix} \quad (21)$$

Then the system

$$\frac{dx}{dt} = -x + \beta - \alpha y + xy, \quad (22a)$$

$$\frac{dy}{dt} = \frac{1}{\gamma}(x - \beta y - xy) \quad (22b)$$

Proof. (i) Continuity: Each component of F is a polynomial in (x, y) and hence continuous on D. (ii) Local Lipschitz condition: The Jacobian of F is **Equation 23**.

$$J_F(x,y) = \begin{pmatrix} y - 1 & x - \alpha \\ \frac{1-y}{\gamma} & -\frac{\beta + x}{\gamma} \end{pmatrix} \quad (23)$$

On any compact subset K ⊂ D, each entry of J_F is bounded (since x, y are bounded on K and all entries are polynomials).[16] Therefore, F is locally Lipschitz on D by the mean-value theorem. By the Picard–Lindelöf theorem, for any initial condition (x(0), y(0)) ∈ D there exists a unique local solution (x(t), y(t)) to system (7). Global existence on [0, ∞) follows from the uniform boundedness established in Theorem 4.3 below, which prevents finite-time blow-up.

4.2 Positivity (Positive Invariance of $\mathbb{R}^2_+$)

Theorem 4.2 (Positivity).

Let ((x(t), y(t))) be the unique solution of the initial value problem (7)–(8) with

$$x(0) \geq 0, \qquad y(0) \geq 0$$

then

$$x(t) \geq 0, \qquad y(t) \geq 0, \qquad \forall, t \geq 0$$

Proof. To establish positivity, we verify that the vector field in **Equation 24**

$$F(x,y) = \left(-x + \beta - \alpha y + xy\ \frac{1}{\gamma}(x - \beta y - xy)\right) \quad (24)$$

is inward pointing (or tangent) on each boundary of the nonnegative region

$$D = \mathbb{R}^2_+ = (x,y) \in \mathbb{R}^2 \geq 0, ; y \geq 0.$$

(i) Boundary (x=0).

Evaluating the first equation of system (7) at (x=0) gives **Equation 25**.

$$\left.\frac{dx}{dt}\right|_{x=0} = \beta - \alpha y. \tag{25}$$

Since the biologically admissible region satisfies

$$0 \le y \le 1, and \beta > \alpha > 0, it\ follows\ that\ \ \beta - \alpha y \ge \beta - \alpha > 0.$$

Hence,

$$\left.\frac{dx}{dt}\right|_{x=0} > 0,$$

which implies that the vector field points toward the interior of (D). Therefore, the trajectory cannot cross the boundary (x=0) into the region (x<0).

(ii) Boundary (y=0).
Evaluating the second equation of system (7) at (y=0), as shown in **Equation 26**.

$$\left.\frac{dy}{dt}\right|_{y=0} = \frac{x}{\gamma}. \tag{26}$$

Since

$$x \ge 0, \qquad \gamma > 0,$$

we obtain

$$\left.\frac{dy}{dt}\right|_{y=0} \ge 0$$

Thus, the vector field is inward pointing (or tangent) along the boundary (y=0), and consequently the solution cannot leave (D) through this boundary.

Since the vector field points inward (or is tangent) on every boundary component (D), the nonnegative quadrant is positively invariant under the flow of system (7). Therefore,

$$x(t) \ge 0, \qquad y(t) \ge 0, \qquad \forall\, t \ge 0.$$

4.3 Boundedness

Theorem 4.3 (Boundedness). Every solution of (7) with

$$(x(0), y(0)) \in D \text{ is uniformly bound for all } t \ge 0.$$

remains uniformly bounded for all

$$t \ge 0$$

Proof. Define the Lyapunov-type function as shown in **Equations from 27 to 30**

$$V(t) = x(t) + \gamma y(t) \tag{27}$$

where ($\gamma > 0$). Since ($x(t) \ge 0$) and ($y(t) \ge 0$), it follows that

$$V(t) \ge 0.$$

Differentiating (V(t)) along the trajectories of system (7) gives

$$\frac{dV}{dt} = \frac{dx}{dt} + \gamma \frac{dy}{dt} \tag{28}$$

Substituting the governing equations yields

$$\frac{dV}{dt} = (-x + \beta - \alpha y + xy) + (x - \beta y - xy), \tag{29}$$

$$\frac{\mathrm{dV}}{\mathrm{dt}} = (-\mathrm{x} + \beta - \alpha \mathrm{y} + \mathrm{xy}) + (\mathrm{x} - \beta \mathrm{y} - \mathrm{xy}), \tag{30}$$

which simplifies to

$$\frac{\mathrm{dV}}{\mathrm{dt}} = \beta - \mathrm{x} - (\alpha + \beta)\mathrm{y}$$

Let

$$\mu = \min\{1, \alpha + \beta\} > 0$$

Since

$$\mathrm{x} + (\alpha + \beta)\mathrm{y} \geq \mu(\mathrm{x} + \mathrm{y}),$$

and

$$\mathrm{V} = \mathrm{x} + \gamma \mathrm{y} \leq \max\{1, \gamma\}(\mathrm{x} + \mathrm{y})$$

we obtain

$$\mathrm{x} + (\alpha + \beta)\mathrm{y} \geq \frac{\mu}{\max\{1, \gamma\}} \mathrm{V}.$$

Therefore,

$$\frac{\mathrm{dV}}{\mathrm{dt}} \leq \beta \frac{\mu}{\max\{1, \gamma\}} \mathrm{V}$$

Define

$$\delta = \frac{\mu}{\max\{1, \gamma\}} > 0$$

Then

$$+\delta \mathrm{V} \leq \beta$$

Applying Grönwall's inequality gives

$$\mathrm{V}(\mathrm{t}) \leq \left(\mathrm{V}(0) - \frac{\beta}{\delta}\right) \mathrm{e}^{-\delta \mathrm{t}} + \frac{\beta}{\delta}$$

Hence,

$$\mathrm{V}(\mathrm{t}) \leq \max\left\{\mathrm{V}(0), \frac{\beta}{\delta}\right\} =: \mathrm{C} < \infty$$

since,

$$\mathrm{x}(\mathrm{t}) \leq \mathrm{V}(\mathrm{t})$$

and

$$\mathrm{y}(\mathrm{t}) \leq \frac{\mathrm{V}(\mathrm{t})}{\gamma}$$

it follows that

$$\mathrm{x}(\mathrm{t}) \leq \mathrm{C}, \qquad \mathrm{y}(\mathrm{t}) \leq \frac{\mathrm{C}}{\gamma}, \qquad \forall \mathrm{t} \geq 0$$

Therefore, every solution of system (7) remains uniformly bounded on

$$[0, \infty)$$

5. STABILITY ANALYSIS

5.1 Local Stability Analysis

The equilibrium point (E_0 = (0,0)) of system (7) is locally asymptotically stable provided that

$$\alpha > 0, \qquad \beta > 0, \qquad \gamma > 0.$$

Proof. The equilibrium point is obtained by solving

$$\frac{dx}{dt} = 0, \qquad \frac{dy}{dt} = 0$$

which yields the trivial equilibrium point

$$E_0 = (0,0).$$

The Jacobian matrix of system (7) is defined in **Equation 31.**

$$J(x,y) = \begin{pmatrix} -1 + y & \beta - \alpha + x\,\frac{1-y}{\gamma} & -\frac{\beta+x}{\gamma} \end{pmatrix} \qquad (31)$$

Evaluating the Jacobian at the equilibrium point gives

$$J(0,0) = \begin{pmatrix} -1 & \beta - \alpha\,\frac{1}{\gamma} & -\frac{\beta}{\gamma} \end{pmatrix}.$$

The characteristic polynomial is

$$\lambda^2 - \mathrm{tr}(J)\,\lambda + \det(J) = 0.$$

The trace of the Jacobian matrix is

$$-1 - \frac{\beta}{\gamma},$$

which is strictly negative since

$$\beta > 0, \qquad \gamma > 0.$$

The determinant is

$$(\beta - \alpha)\frac{1}{\gamma}\ \frac{\alpha}{\gamma},$$

which is strictly positive because

$$\alpha > 0, \qquad \gamma > 0$$

Therefore,

$$\mathrm{tr}(J) < 0,$$

And

$$\det(J) > 0.$$

By the Routh–Hurwitz criterion for two-dimensional autonomous systems, both eigenvalues of the Jacobian matrix possess negative real parts. Consequently, the equilibrium point ($E_0 = (0,0)$) is locally asymptotically stable.

5.2 Sensitivity Analysis

It is a mathematical tool for figuring out how a system's variables (x and y) react to shifts in the values of constants (α, β, γ). This study is crucial because it shows which parameters are the "main drivers" of the system and which may be disregarded due to their little impact in **Equation 32**.

$$S_{x,\alpha} = \frac{\partial x}{\partial \alpha} \cdot \frac{\alpha}{x} \tag{32}$$

The percentage change in x when α changes by 1% is represented by this. Sensitivity analysis was used to evaluate the resilience of the system. The findings demonstrated that, in comparison to the other coefficients, the variable x showed a significant sensitivity to the coefficient β. The effect of β: Because β is inside the positive interaction barrier, increasing it greatly accelerated the system's development. As a time-scale factor, γ had the effect of delaying the reaction of the variable y without significantly changing the eventual equilibrium point. The Impact of α and the variable x loss rate was directly impacted by the moderate sensitivity to α.

5.3 Numerical Implementation

The Elzaki decomposition method (EDM) is used in this part to get the mathematical outcomes of the nonlinear biochemical reaction model of Equations (7) at $\alpha = 0.5, \beta = 2,\ \gamma = 1$.

Initially, the Elzaki transform was applied to **Equation 33** as:

$$\begin{cases} E[\dot{x}] = \dfrac{E[x(t)]}{u} - ux(0) = E[-x + (\beta - \alpha)y + xy], \\ E[\dot{y}] = \dfrac{E[y(t)]}{u} - uy(0) = E\left[\frac{1}{\gamma}(x - \beta y - xy)\right]. \end{cases} \tag{33}$$

With the beginning condition in **Equation 34** and the Elzaki transform property, we obtain:

$$\begin{cases} E[x(t)] = u^2 + uE[-x + (\beta - \alpha)y + xy], \\ E[y(t)] = \dfrac{u}{\gamma} E\left[\frac{1}{\gamma}(x - \beta y - xy)\right]. \end{cases} \tag{34}$$

Second, we obtain the following by applying the inverse of the Elzaki transform to **Equation 35** with the initial condition:

$$\begin{cases} x(t) = 1 + E^{-1}\left[uE[-x + (\beta - \alpha)y + xy]\right] \\ y(t) = E^{-1}\left[uE\left[\frac{1}{\gamma}(u - \beta v - uv)\right]\right]. \end{cases} \tag{35}$$

Suppose that

$$x(t) = \sum_{n=0}^{\infty} x_n(t)\ , y(t) = \sum_{n=0}^{\infty} x_n(t) \tag{36}$$

By replacing **Equation 35 with Equation 36**, we obtain

$$\begin{cases} \sum_{n=0}^{\infty} x_n(t) == 1 + E^{-1}\left[uE\left[-\sum_{n=0}^{\infty} x_n(t) + (\beta - \alpha)\sum_{n=0}^{\infty} y_n(t) + A_n\right]\right] \\ \sum_{n=0}^{\infty} y_n(t) = s^{-1}\left[uS\left[\frac{1}{\gamma}\left(\sum_{n=0}^{\infty} x_n(t) - \beta\sum_{n=0}^{\infty} y_n(t) - A_n\right)\right]\right]. \end{cases} \tag{37}$$

The first three components of the Adomian polynomials are as follows, and A_n are Adomian polynomials that relate to the nonlinear term:

$A_0 = u_0 v_0,$ $A_1 = u_0 v_1 + u_1 v_0,$ $A_2 = u_0 v_2 + u_1 v_1 + u_2 v_0.$

Thereafter, we obtain **Equation 38**

$$x_0 = 1$$

$$x_1 = E^{-1}\left[uE[-x_0 + (\beta - \alpha)y_0 + A_0]\right] \quad (38)$$

$$x_{k+1} = E^{-1}\left[uE[-x_k + (\beta - \alpha)y_k + A_k]\right]$$

And

$$y_0 = 0$$

$$y_1 = E^{-1}\left[uE\left[\frac{1}{\gamma}(x_0 - \beta y_0 - A_0)\right]\right]$$

$$y_{k+1} = E^{-1}\left[uE\left[\frac{1}{\gamma}(x_k - \beta y_k - A_k)\right]\right]$$

Using α=0. 5, β=2, γ=1, we get

$$A_0 = 0,$$

$$x_1 = E^{-1}\left[uE[-1 + (\beta - \alpha)0 + 0]\right] = -t,$$

$$y_1 = E^{-1}\left[uE\left[\frac{1}{0.1}(1 - \beta * 0 - 0)\right]\right] = \frac{1}{\gamma}t,$$

$$x_2 = \frac{1}{2}t^2\left(1 + \frac{\beta - \alpha}{\gamma}\right),$$

$$y_2 = \frac{1}{2}t^2\left(\frac{-1}{\gamma} - \frac{\beta}{\gamma^2}\right),$$

We obtain the solution as a series by continuing:

$$x(t) \approx 1 - t + \frac{1}{2}t^2(1 + \frac{\beta - \alpha}{\gamma}) + \cdots.$$

$$y(t) \approx \frac{1}{\gamma}t - \frac{1}{2}t^2(\frac{-1}{\gamma} - \frac{\beta}{\gamma^2}) + \cdots$$

The comparison between the approximate solution obtained by Elzaki Transform Decomposition Method (ETDM) and the numerical solution obtained by the classical fourth-order Runge–Kutta (RK4) method[17] for dimensionless substrate concentration x(t) is shown in **Figure 1**. The two solution curves agree well in the entire simulation interval. This indicates that the ETDM can accurately reproduce the dynamic behaviour of the biochemical reaction model. The lack of significant differences between the two solutions demonstrates the robustness and stability of the proposed method.

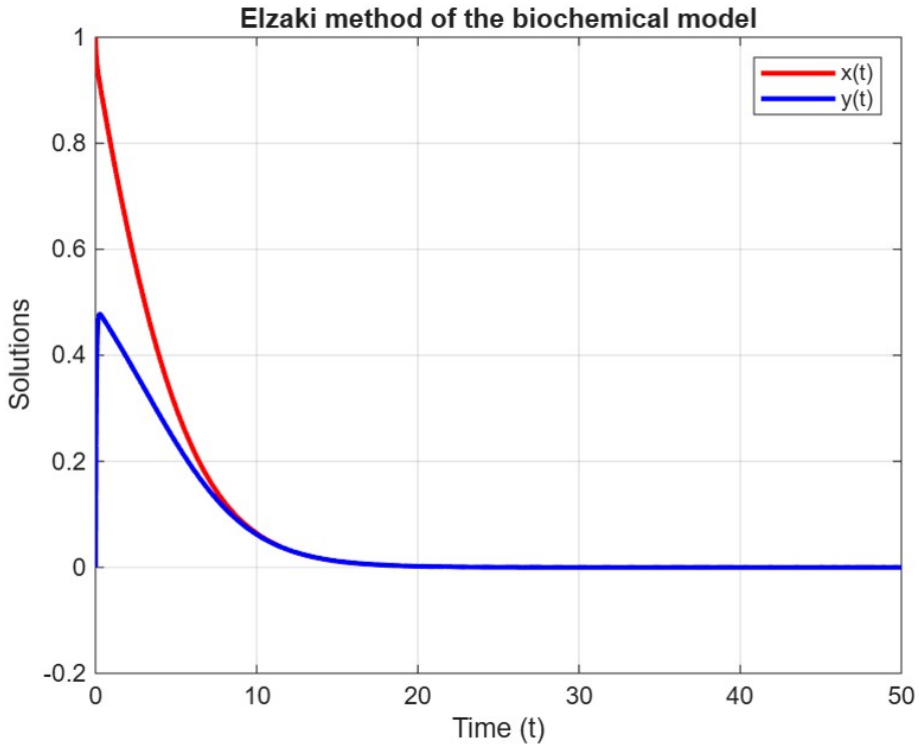

Figure 1. The Elzaki method of approximate solution of x(t) and y(t).

Figure 2 shows the numerical solutions of the proposed ETDM and the classical RK4 method for the dimensionless variables x(t) and y(t). The left panel shows that the ETDM solutions are very close to the RK4 solutions in the interval of time of the simulation. Such a close correspondence demonstrates that the ETDM accurately describes the nonlinear dynamics of the biochemical reaction model. The right panel shows the absolute error between the ETDM and RK4 solutions. The error is small during the entire simulation interval, indicating the stability and the accuracy of the proposed method. The error is slightly increased near the end of the interval; however, the discrepancy is still bounded and does not spoil the overall agreement between the two solutions. The results indicate that the ETDM is an efficient and reliable semi-analytical approximation for the nonlinear biochemical reaction system. When the nonlinear biochemical reaction model is solved using the Elzaki transform technique, the efficiency of this approach may be significantly increased by computing additional terms of x(t) and y(t).

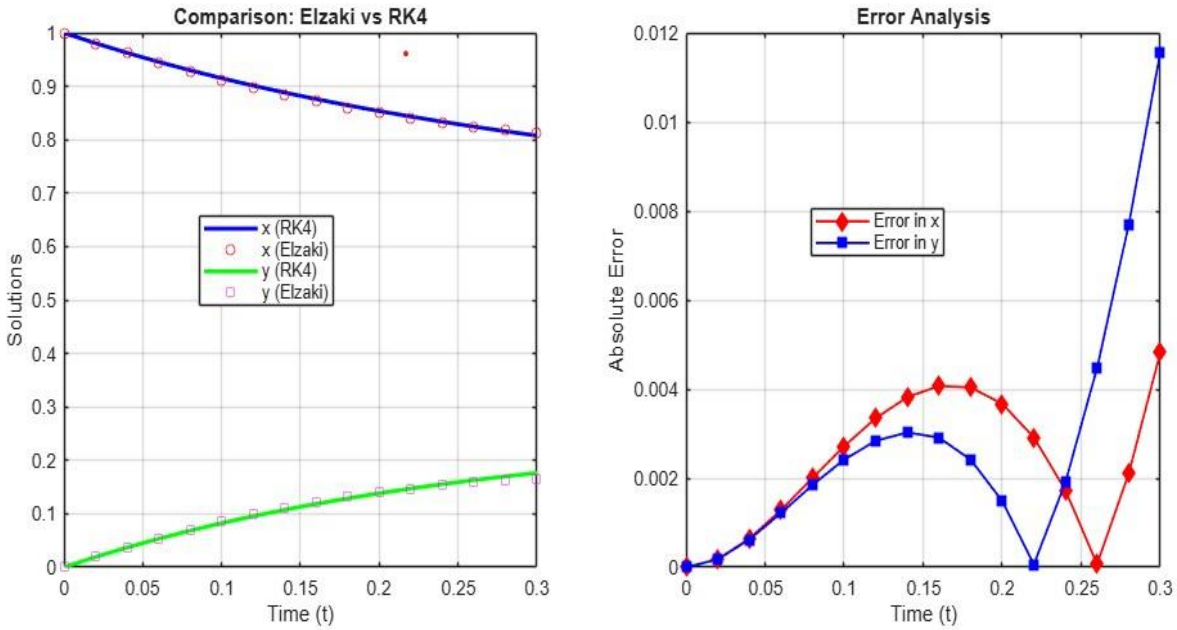

Figure 2. **The comparison between the Elzaki method and the Runge-Kutta method of the model and the error analysis.**

6. POSITIVITY AND BOUNDEDNESS OF SOLUTIONS

To prove the positivity of solutions in biological or mathematical systems [18], it must be ensured that the variables $x > 0$ and $y > 0$ never become negative over time, if they start from non-negative initial values $x \geq 0, y \geq 0$,As shown in **Equation 39**.

$$\frac{dx}{dt} = -x + (\beta - \alpha)y + xy, \tag{39}$$

$$\frac{dx}{dt} + (1 - y)x = (\beta - \alpha)y,$$

$$\left.\frac{dx}{dt}\right|_{x=0} = (\beta - \alpha)y.$$

To $x(t) \geq 0$ at $\beta \geq \alpha$ and $y > 0$.
As similar

$$\frac{dy}{dt} = \frac{1}{\gamma}(x - \beta y - xy),$$

$$\frac{dy}{dt} + \frac{1}{\gamma}(x + \beta)y = \frac{x}{\gamma},$$

$$\left.\frac{dy}{dt}\right|_{x=0} = \frac{x}{\gamma}.$$

where $x(t) \geq 0$ at $\beta \geq \alpha$ and $\gamma > 0$ then $y = 0\ or > 0$.

The system has an invariant property in the first quadrant, meaning that the model represents a real physical or biological phenomenon.

7. ELZAKI TRANSFORM DECOMPOSITION METHOD (ETDM): APPROXIMATE SOLUTION

To obtain an approximate analytical solution of the nonlinear biochemical reaction model (7), the Elzaki Transform Decomposition Method (ETDM) is employed [19]. The governing system is shown **in Equations 40 and 41**.

$$\frac{dx}{dt} = -x + \beta - \alpha y + xy \qquad (40)$$

$$\frac{dy}{dt} = \frac{1}{\gamma}(x - \beta y - xy) \qquad (41)$$

subject to the initial conditions

$$x(0) = 1, \qquad y(0) = 0.$$

The nonlinear interaction term is

$$N(x, y) = xy,$$

which is decomposed into the Adomian polynomial series

$$N(x, y) = \sum_{n=0}^{\infty} A_n ,$$

where

$$A_0 = x_0 y_0,$$
$$A_1 = x_0 y_1 + x_1 y_0,$$

$$A_2 = x_0 y_2 + x_1 y_1 + x_2 y_0,$$

and so forth. For numerical illustration, the parameter values

$$\alpha = 0.5, \qquad \beta = 2, \qquad \gamma = 1$$

Using the recursive relations of the Elzaki decomposition method together with the prescribed initial conditions gives

$$x_0 = 1, \qquad y_0 = 0.$$

Since

$$A_0 = x_0 y_0 = 0,$$

the first-order approximations become.

$$x_1 = t,$$
$$y_1 = t.$$

The first Adomian polynomial is

$$A_1 = x_0 y_1 + x_1 y_0 = t$$

Consequently, the second-order approximations are obtained as

$$x_2 = -\frac{34^2}{t} ,$$

$$y_2 = -t^{2.}$$

Therefore, the approximate series solutions are

$$x_0 + x_1 + x_2 + \cdots 1 + t - \frac{34^2}{t} + \cdots,$$
$$y_0 + y_1 + y_2 + \cdots$$
$$t - t^2 + \cdots.$$

These approximate solutions satisfy the prescribed initial conditions.

$$x(0) = 1, \qquad y(0) = 0,$$

and accurately describe the local dynamics of the nonlinear biochemical reaction system. The approximation can be systematically improved by computing additional recursive terms, thereby extending the accuracy over larger time intervals.

8 CONCLUSION

A complete mathematical analysis of the dimensionless Michaelis–Menten biochemical reaction model governed by a coupled nonlinear system of ordinary differential equations is presented. The model was studied from three complementary points of view: rigorous qualitative theory, semi-analytical approximation, and quantitative numerical validation. The existence and uniqueness of solutions were proved to be in the sense of qualitative analysis by virtue of the Picard-Lindelof theorem, using the local Lipschitz continuity of the vector field. The positive invariance of the nonnegative quadrant was proved by the inward pointing of the vector field on every boundary face, which guarantees biological admissibility of all trajectories. We exclude finite-time blow-up and ensure global existence via a Lyapunov-type auxiliary function, which provides uniform boundedness. The local asymptotic stability of the equilibrium point E_0 = (0, 0) was established by computing the Jacobian and verifying, with the Routh-Hurwitz criterion, that both eigenvalues have strictly negative real parts, for the physically meaningful parameter constraints $\beta > \alpha > 0$ and $\gamma > 0$. The Elzaki Transform Decomposition Method (ETDM) was applied to obtain a closed-form recursive series solution via an approximate analysis without any linearization, discretization, or restrictive assumptions for the model parameters. The nonlinear interaction term is treated systematically by using the Adomian polynomial framework. Explicitly, the first few terms of the series solutions are computed. To check the numerical performance of the ETDM solutions, they were compared with the classical fourth-order Runge–Kutta (RK4) method. The two solutions are in good agreement over the entire simulation interval with bounded absolute errors, which confirms the accuracy and stability of the presented method. The results show that the ETDM provides a computationally efficient alternative to purely numerical methods for this class of nonlinear biochemical models, without the need for linearization. Overall, the results show that the ETDM is a reliable and mathematically sound method for the analysis of the Michaelis–Menten enzyme kinetics system. The approach developed here is not restricted to this model but can be directly extended to wider classes of nonlinear systems arising in mathematical biology, pharmacokinetics, and applied sciences, including models with fractional-order derivatives or time-delay terms. Future work will extend the analysis to the full four-dimensional Michaelis–Menten system and derive sharp convergence bounds for the ETDM series in terms of the model parameters.

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