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Exact Solutions for Space-time Fractional Peyrard-Bishop-Dauxois Model of DNA Dynamics by Using the Unified Method

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ABSTRACT. In this study, we investigated the space-time fractional order Peyrard–Bishop–Dauxois model using the unified method to derive exact analytical traveling wave solutions. By incorporating fractional derivatives, the model effectively captures memory effects and nonlocal interactions intrinsic to DNA dynamics, providing a refined representation of processes such as DNA denaturation. Notably, our analysis led to the discovery of soliton solutions, along with novel hyperbolic, trigonometric, and rational forms. These results not only deepen our understanding of the complex nonlinear behavior inherent in biological systems but also underscore the robustness and versatility of the unified method in addressing intricate fractional differential equations. The findings of this study provide a foundation for the further refinement of mathematical models and the exploration of more sophisticated fractional dynamics in molecular biology.

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1. INTRODUCTION

Since ancient times, humans have endeavored to understand, interpret, and harness natural phenomena for various applications. This ongoing pursuit has driven extensive scientific efforts to develop mathematical models that systematically describe complex interactions within diverse systems. These models are formulated through equations that account for multiple variables and their interrelations, leading to their classification in the literature and the development of specialized solution methods. Consequently, mathematical modeling has emerged as a fundamental tool across numerous disciplines, including engineering, economics, and health sciences, facilitating a deeper understanding of intricate real-world phenomena. Each of these models is expressed with a differential equation. For example; in biology, in the detection of mutations that occur as a result of disruption in the structure of DNA, in the field of engineering; in measuring how many intensity earthquakes any structure will withstand, in the field of health; to calculate the rate of spread of a disease, the amount of antibodies produced in the body of a person infected with the disease, the differential equations we mentioned are used [6].

One of the classes of differential equations mentioned above is non-linear partial differential equations (NLPDE). NLPDE are mathematical equations involving derivatives of multivariable functions and non-linear terms and has a wide range of uses in many different areas. Some important application areas of NLPDEs: NLPDEs are widely

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used to model physical phenomena. For example, heat transfer, wave motion and fluid dynamics are expressed by such equations [7]. NLPDEs are used in the study of population dynamics, modelling of biological processes and ecosystem interactions [14]. It is also used in the reconstruction processes of images in medical imaging techniques (e.g. MRI) [17]. In summary, non-linear partial differential equations represent a significant instrument in scientific research, employed for the analysis and simulation of complex systems across a wide range of disciplines, including the natural sciences and medicine.

However, many processes in nature are too complex to be expressed in integers or occur momentarily at different speeds. Therefore, nonlinear fractional partial differential equations (NLFPDE) is needed to provide more flexibility and general validity to this situation and studies have shifted to this area. That is, NLFPDEs often provide a better representation of real-world problems. In addition, NLFPDEs, which are a more general form compared to classical integer order differential equations, are equations whose derivatives are defined in fractional order instead of integer order [20]. Such equations have important applications in various fields. Here are some of the applications of fractional order nonlinear partial differential equations: It is used to study the behaviour of chaotic or highly variable systems, fractional order derivatives are used to study how materials change or deform with time, for example the behaviour of viscoelastic materials. It can be used in control theory to better describe the dynamics of systems. In particular, situations where the response of systems is slow or uncertain can be analysed with such models. Mathematical models play a crucial role in describing complex physical, biological, and engineering phenomena. These models often involve differential equations that account for the dynamic interactions between various factors. The formulation and analysis of such equations enable researchers to gain deeper insights into the underlying mechanisms governing these systems. Developing efficient and accurate solution techniques for these equations is essential for advancing scientific understanding and practical applications. Consequently, numerous studies have been conducted to explore exact and approximate solutions using diverse mathematical approaches. Recently, many researchers have reported on these solutions using various methods. For soliton solutions, such as the inverse scattering transform method [18], Hirota's method [16], Painleve analysis method [2], bilinear approach method [4], the differential transformation method [8,21], the finite difference method [24], the homogeneous balance method [28], the (G'/G)-expansion method [10, 26, 31], the homotopy analysis method [5], the sinc-collocation method [29], the exponential function method [9, 15], the generalized Kudryashov method [12, 23, 25], the unifed method [13] etc.

In this study, we focus on the Peyrard-Bishop-Dauxois (PBD) model, an advanced extension of the Peyrard-Bishop (PB) model, which serves as a fundamental mathematical and physical framework for investigating the structural and dynamic properties of DNA. Originally introduced by Peyrard and Bishop in 1989 [3], this model has been instrumental in understanding DNA denaturation, a critical biological process in which the double-stranded structure of DNA separates into single strands under the influence of thermal fluctuations or external forces.

The Peyrard-Bishop model primarily describes the interactions between base pairs through nonlinear potentials, which account for the anharmonic nature of the hydrogen bonds between complementary bases. However, a significant refinement was introduced by Dauxois, leading to the development of the Peyrard-Bishop-Dauxois (PBD) model. This extended model incorporates nonlocal stacking interactions between adjacent base pairs, improving the accuracy of DNA denaturation predictions by including the role of cooperative effects [27]. The introduction of the PBD model has facilitated a deeper understanding of the double-helix structure of DNA, particularly by enabling the modeling of fluctuations and deformations in a more realistic manner. Mathematically, the inclusion of these interactions leads to fractional-order differential equations, which more accurately capture the complex dynamical behavior of DNA strands.

Our primary objective in this study is to determine soliton solutions to the biological population model described by the PBD framework. Solitons, defined as wave solutions that maintain their coherence under specific conditions, play a crucial role in nonlinear dynamics. These localized waves, which are solutions to partial differential equations (PDEs), are particularly significant in the context of nonlinear systems, including DNA models. The solitonic nature of solutions is of paramount importance, as solitons exhibit unique physical and mathematical properties. Unlike dispersive waves that dissipate over time, solitons retain their shape while propagating at a constant velocity. Furthermore, when interacting with other solitons, they emerge unchanged apart from a possible phase shift, demonstrating particlelike behavior [22]. From a mathematical perspective, the soliton solutions of the PBD model provide critical insights into the energy transport mechanisms and stability of DNA structures. These solutions offer an analytical approach to exploring the nonlinear effects governing base pair dynamics and the thermally induced transitions leading to DNA denaturation. The study of solitons within the PBD framework not only advances our theoretical understanding of DNA mechanics but also has potential applications in biophysics, genetic engineering, and molecular biology.

It is an irrefutable conclusion that solitary wave solutions play a substantial role in the interpretation of the physical properties of mathematical models that describe DNA dynamics. The ability of solitons to maintain their form and energy while traversing the nonlinear landscape of DNA molecular interactions underscores their importance in both theoretical and applied scientific contexts. The employment of sophisticated mathematical techniques to obtain and analyse soliton solutions is intended to enhance the comprehension of DNA stability, denaturation, and the fundamental principles governing nucleic acid behaviour.

This study is structured as follows: Section 2 provides a concise introduction to the theoretical framework and fundamental properties of the beta fractional derivative. In Section 3, an overview of the unified method is presented, highlighting its effectiveness in solving fractional-order partial differential equations. Section 4 demonstrates the application of the unified method to derive precise analytical solutions for specific fractional partial differential equations. Finally, the conclusion offers a comprehensive discussion of the obtained results and suggests possible directions for future research.

2. Preliminaries

Analytical solutions for nonlinear fractional differential equations (NFDEs) incorporating beta derivatives play a critical role in advancing mathematical modeling of complex systems. A defining feature of beta derivatives, which significantly enhances their utility in fractional calculus, is their adherence to the fractional chain rule a property essential for rigorous analysis of NFDEs. In order to establish a foundation for subsequent discussions, a concise overview of the beta derivative operator and its fundamental mathematical properties is now provided.

Definition 2.1. Let $\vartheta : \mathbb{R}^+ \cup \{0\} \to R$ and $\beta \in (0, 1]$ the beta derivative of $\vartheta(t)$ of order β has been described as follows:

$$(D_{\beta}\vartheta)(t) = \lim_{\varepsilon \to 0} \frac{\vartheta(t + \varepsilon t^{1-\beta}) - \vartheta(t)}{\varepsilon} \quad (t > 0).$$
(2.1)

Theorem 2.2. In accordance with the definition in Eq. (2.1), some important properties of beta derivative are as follows:

- $D_{\beta}(a\vartheta(t) + b\eta(t)) = aD_{\beta}\vartheta(t) + bD_{\beta}\eta(t)$, for all $a, b \in \mathbb{R}$,
- $D_{\beta}(t^n) = nt^{n-\beta}$ for all $n \in \mathbb{R}$,
- $D_{\beta}(\lambda) = 0$, for any constant λ ,

- $D_{\beta}(\vartheta(t)\eta(t)) = \vartheta(t)D_{\beta}\eta(t) + \eta(t)D_{\beta}\vartheta(t),$ $D_{\beta}(\frac{\vartheta(t)}{\eta(t)}) = \frac{\eta(t)D_{\beta}\vartheta(t) \vartheta(t)D_{\beta}\eta(t)}{\eta^{2}(t)},$ If, in addition, ϑ is differentiable, then $(D_{\beta}\vartheta)(t) = t^{1-\beta}\frac{d\vartheta}{dt},$

where ϑ and η two functions β differentiable and $\beta \in (0, 1]$ [1, 11].

3. Methodology

In this section, we outline the unified method for obtaining traveling wave solutions of NFDEs through the following steps. Consider an NFDE of the form

$$P(u, D_t^{\beta} u, D_x^{\beta} u, D_t^{2\beta} u, D_t^{\beta} D_x^{\beta} u, D_x^{2\beta} u...) = 0,$$
(3.1)

where u = u(x, t) is the unknown function, and P represents a polynomial in u and its various fractional derivatives, incorporating both the highest-order derivative and nonlinear terms. The fundamental steps of the unified method are described as follows:

Step 1: Define a compound variable ξ in terms of the real variables x and t using the following transformation:

$$u(x,t) = U(\xi), \quad \xi = \frac{1}{\Gamma(1+\beta)} x^{\beta} - \frac{k}{\Gamma(1+\beta)} t^{\beta}, \tag{3.2}$$

where *k* represents the wave velocity. The wave variable introduced in Eq. (3.2) transforms the original equation, Eq. (3.1), into the following ordinary differential equation (ODE):

$$Q(U, -kU', U', k^2U'', -kU'', U'', ...) = 0, (3.3)$$

where Q is a polynomial in U and its various derivatives. Here, the superscripts denote ordinary derivatives with respect to ξ . The resulting ODE is then integrated one or more times where possible, and for simplicity, the integration constant(s) are set to zero.

Step 2: The exact solution of Eq. (3.3) is expressed in the following form:

$$U(\xi) = a_0 + \sum_{i=1}^{m} \left[a_i \phi^i + b_i \phi^{-i} \right],$$
(3.4)

where $\phi(\xi) = \phi$ satisfies the Riccati differential equation

$$\phi'(\xi) = \phi^2(\xi) + \gamma.$$
(3.5)

Here, the $\phi' = \frac{d\phi}{d\xi}$ and *m* is a positive integer. The constants $a_i, b_i (i = 1, 2, 3, \dots, m), a_0$ and γ are to be determined. The general solution of Eq. (3.5) is given as follows:

Case 1: When $\gamma < 0$, the solutions of Eq. (3.5)

$$\phi(x) = \begin{cases} \frac{\sqrt{-(A^2 + B^2)\gamma - A\sqrt{-\gamma}\cosh(2\sqrt{-\gamma}(x+x_0))}}{A\sinh(2\sqrt{-\gamma}(x+x_0)) + B}, \\ \frac{-\sqrt{-(A^2 + B^2)\gamma - A\sqrt{-\gamma}\cosh(2\sqrt{-\gamma}(x+x_0))}}{A\sinh(2\sqrt{-\gamma}(x+x_0)) + B}, \\ \frac{-\sqrt{-\gamma} + (-2A\sqrt{-\gamma})}{A + \cosh(2\sqrt{-\gamma}(x+x_0)) - \sinh(2\sqrt{-\gamma}(x+x_0))}, \\ \frac{\sqrt{-\gamma} + 2A\sqrt{-\gamma}}{A + \cosh(2\sqrt{-\gamma}(x+x_0)) + \sinh(2\sqrt{-\gamma}(x+x_0))}. \end{cases}$$

Case 2: When $\gamma > 0$, the solutions of Eq. (3.5)

$$\phi(x) = \begin{cases} \frac{\sqrt{(A^2 - B^2)\gamma - A\sqrt{\gamma}\cos(2\sqrt{\gamma}(x+x_0))}}{A\sin(2\sqrt{\gamma}(x+x_0)) + B}, \\ \frac{-\sqrt{(A^2 - B^2)\gamma - A\sqrt{\gamma}\cos(2\sqrt{\gamma}(x+x_0))}}{A\sin(2\sqrt{\gamma}(x+x_0)) + B}, \\ \frac{i\sqrt{\gamma^2}(-2Ai\sqrt{\gamma})}{A+\cos(2\sqrt{\gamma}(x+x_0)) - i\sin(2\sqrt{\gamma}(x+x_0))}, \\ \frac{-i\sqrt{\gamma^2}+2Ai\sqrt{\gamma}}{A+\cos(2\sqrt{\gamma}(x+x_0)) + i\sin(2\sqrt{\gamma}(x+x_0))}. \end{cases}$$

Case 3: When $\gamma = 0$, the solution of Eq. (3.5)

$$\phi(x) = -\frac{1}{x + x_0}$$

where A and B are two real arbitrary constants, and x_0 is an arbitrary constant.

Step 3: Employing the homogeneous balance method outlined in Eq. (3.3) enables us to determine the positive integer values of *m* corresponding to the solution described in Eq. (3.4). By substituting the solution from Eq. (3.4) into equation Eq. (3.3) and incorporating the Riccati equation depicted in Eq.(3.5), we obtain a polynomial expression in terms of $\phi(\xi)$. This polynomial, upon equating coefficients of similar powers of $\phi(\xi)$ to zero, yields specific sets of algebraic equations.

Step 4: Upon substituting Eq. (3.4) into Eq.(3.3) alongside Eq. (3.5), a polynomial expression in terms of $\phi(\xi)$ is derived. Equating all coefficients of $\phi(\xi)$ to zero leads to a system of algebraic equations. By employing the Maple program, we can effectively solve this system to determine the values of parameters such as $a_0, a_i, b_i(i = 1, ..., m)$, and γ . Subsequently, upon substituting these values and Eq. (3.5) into Eq. (3.4), exact solutions for the reduced Eq. (3.3) can be obtained.

4. Application

The Peyrard–Bishop–Dauxois (PBD) model equation is analyzed to obtain exact traveling wave solutions using the unified method. The model is based on a Hamiltonian formulation that incorporates a Morse potential to describe the interactions between DNA base pairs. The Morse potential, which plays a crucial role in modelling the energy of these interactions, is mathematically expressed as:

$$W_s(V_p - \mu_q) = r \left| \exp(-u(V_p - \mu_q)) - 1 \right|^2.$$
(4.1)

Eq. (4.1), the term on the right-hand side represents the Morse potential, where u and r correspond to the width and depth of the potential well, respectively. These parameters characterize the strength and spatial extent of the interaction forces between adjacent nucleotides. The variables V_p , m_q represent the displacements of the nucleotides from their equilibrium positions, reflecting deviations in the DNA double-helix structure due to thermal or mechanical perturbations. This formulation provides a fundamental basis for understanding the nonlinear dynamics of DNA basepair motion [19]. The total energy of the system, incorporating both kinetic and potential contributions, is represented as follows, building upon the Hamiltonian formulation of the Peyrard–Bishop–Dauxois (PBD) model:

$$R(U) = \frac{1}{2n}v_p^2 + \frac{\sigma_1}{2}\Delta^2 V_p + \frac{\sigma_2}{4}\Delta^4 V_p + \tau \left(e^{-u\sqrt{2}V_p} - 1\right)^2.$$
(4.2)

In this expression, ϖ_1 and ϖ_2 represent the strengths of linear and nonlinear coupling, respectively, which characterize the interactions between adjacent base pairs in the DNA sequence. The term $v_p = n \frac{\partial V_p}{\partial t}$ denotes the momentum associated with the displacement V_p , where μ_q describes the deviation of a nucleotide from its equilibrium position. The higher-order derivative terms $\Delta^2 V_p$ account for the dispersive effects in the DNA chain, capturing both short-range and long-range interactions. The last term in the equation incorporates the nonlinear effects of hydrogen bond stretching between base pairs, governed by an exponential function that reflects the anharmonic nature of these interactions. This formulation is essential for deriving the nonlinear evolution equations that describe the dynamic behavior of DNA at the molecular level.

Eq. (4.2) constitutes the Hamiltonian governing the stretching dynamics of hydrogen bonds in DNA, pivotal for formulating the nonlinear evolution equations that describe the system's dynamical behavior. To derive the equation of motion for the displacement field U, the standard continuum approximation is applied to the discrete Hamiltonian framework. This procedure transforms the discrete lattice model into a continuum representation, yielding the nonlinear evolution equation for DNA base-pair dynamics:

$$U_{tt} - (\Phi_1 + 3\Phi_2(U_x)^2)U_{xx} - 2pre^{-pU}(e^{-pU} - 1) = 0,$$
(4.3)

where the coefficients $\Phi_1 = \frac{\varpi_1}{ns^2}$, $\Phi_2 = \frac{\varpi_2}{ns^4}$, correspond to the rescaled linear and nonlinear coupling strengths, respectively [19]. The parameter $r = \frac{\pi}{n}$, represents the effective Morse potential depth scaled by the nucleotide mass, while $p = \sqrt{2}u$ encodes the inverse width of the potential well. Here, *s* denotes the equilibrium inter-site distance between nucleotides along the DNA strand. The first two terms in the equation account for wave propagation modulated by nonlinear dispersion, where Φ_1 governs linear elasticity and Φ_2 introduces nonlinear coupling dependent on the strain U_x . The final term arises from the Morse potential's anharmonicity, capturing the asymmetric restoring forces due to hydrogen bond stretching. This integro-differential equation synthesizes the interplay of dispersive wave dynamics, nonlinear coupling, and substrate interactions, providing a continuum-level description of DNA's mechanical response to perturbations.

The fractional generalization of the classical Peyrard–Bishop–Dauxois (PBD) model, as articulated in Eq. (4.3), has been extended to incorporate non-integer order dynamics using the beta-derivative formalism, as explored in [30]. This fractional framework enables the modeling of anomalous transport phenomena and memory-dependent interactions inherent to complex biomolecular systems like DNA. In the present study, we investigate the following space-time fractional variant of the PBD model, formulated via the beta-derivative operator:

$$D_t^{2\beta}(U) - \left(\Phi_1 + 3\Phi_2(D_x^\beta(U))^2\right) D_x^{2\beta}(U) - 2pre^{-pU}(e^{-pU} - 1) = 0.$$
(4.4)

The fractional model PBD model is considered, as described by Eq. (4.1) and Eq. (4.4). To solve these nonlinear equations, the transformation $U(x, t) = v(\xi)$ is introduced, where

$$\xi = \frac{1}{\Gamma(1+\beta)} x^{\beta} - \frac{k}{\Gamma(1+\beta)} t^{\beta}.$$

By applying these transformations, Eq. (4.4) is reduced to the following ordinary differential equation (ODE):

$$k^{2}v'' - (\Phi_{1} + 3\Phi_{2}(v')^{2})v'' - 2pre^{-pv}(e^{-pv} - 1) = 0.$$
(4.5)

Multiplying Eq. (4.5) with v' and integrating with respect to x yields:

$$\frac{(k^2 - \Phi_1)}{2}(v')^2 - \frac{3}{4}\Phi_2(v')^4 + re^{-pv}(e^{-pv} - 2) + c = 0.$$

Here, c is the constant of integration. Using the transformation

$$F(x) = e^{-pv(\xi)}$$

we obtain the following nonlinear ODE:

$$\frac{(k^2 - \Phi_1)}{2p^2} F^2(F')^2 - \frac{3}{4p^4} \Phi_2(F')^4 + rF^5(F - 2) + cF^4 = 0.$$
(4.6)

The degree of the nonlinear term is balanced with the degree of the highest-order derivative in Eq. (4.6) using the homogeneous balance principle, which yields m = 2. Therefore, the proposed method suggests that the solution can be assumed in the following form:

$$F(\xi) = a_0 + a_1 \phi(\xi) + a_2 \phi^2(\xi) + b_1 \phi^{-1}(\xi) + b_2 \phi^{-2}(\xi).$$
(4.7)

By substituting the function $F(\xi)$ is substituted from Eq. (4.7) into Eq. (4.6), and simplifying using Eq. (3.5), we organize all terms such that each coefficient of $\phi^i(\xi)$ (i = 0, 1, ..., 24) equates to zero. This results in a system of equations, which can then be solved using mathematical software to deduce the solutions for k, a_0, a_i, b_i (i = 1, 2):

Set 1: In particular, the determined values for the constants are as follows: follows:

$$a_{0} = \gamma a_{2}, a_{1} = b_{1} = b_{2} = 0,$$

$$p = \pm \sqrt{\frac{\Phi_{1}a_{2} - k^{2}a_{2}}{12\gamma\Phi_{2}a_{2} - 12\Phi_{2}}}, r = \frac{k^{4} - 2k^{2}\Phi_{1} + (\Phi_{1})^{2}}{12\Phi_{2}(\gamma a_{2} - 1)^{2}},$$

$$c = -\frac{\gamma a_{2}\left(k^{4}\gamma a_{2} - 2k^{2}\gamma\Phi_{1}a_{2} - 2k^{4} + \gamma\Phi_{1}a_{2} + 4k^{2}\Phi_{1} - 2\Phi_{1}\right)}{12\Phi_{2}(\gamma a_{2} - 1)^{2}}.$$

Upon substituting these values into Eq. (4.7), the solution for Eq.(4.6) is obtained as:

(a) Hyperbolic function solutions (when $\gamma < 0$):

$$\begin{split} F_{11}(\xi) &= a_2\gamma - \frac{a_2(\sqrt{-(A^2 + B^2)\gamma} - A\sqrt{-\gamma}\cosh(2\sqrt{-\gamma}(x + x_0)))^2}{(A\sinh(2\sqrt{-\gamma}(x + x_0)) + B)^2},\\ F_{12}(\xi) &= a_2\gamma - \frac{a_2(-\sqrt{-(A^2 + B^2)\gamma} - A\sqrt{-\gamma}\cosh(2\sqrt{-\gamma}(x + x_0)))^2}{(A\sinh(2\sqrt{-\gamma}(x + x_0)) + B)^2},\\ F_{13}(\xi) &= a_2\gamma - \frac{a_2(-\sqrt{-\gamma} + (-2A\sqrt{-\gamma}))^2}{(A + \cosh(2\sqrt{-\gamma}(x + x_0)) - \sinh(2\sqrt{-\gamma}(x + x_0)))^2},\\ F_{14}(\xi) &= a_2\gamma - \frac{a_2(\sqrt{-\gamma} + 2A\sqrt{-\gamma})^2}{(A + \cosh(2\sqrt{-\gamma}(x + x_0)) + \sinh(2\sqrt{-\gamma}(x + x_0)))^2}. \end{split}$$

(b) Trigonometric function solutions (when $\gamma > 0$):

$$\begin{split} F_{15}(\xi) &= a_2 \gamma - \frac{a_2 (\sqrt{(A^2 - B^2)\gamma} - A\sqrt{\gamma}\cos(2\sqrt{\gamma}(x + x_0)))^2}{(A\sin(2\sqrt{\gamma}(x + x_0)) + B)^2},\\ F_{16}(\xi) &= a_2 \gamma - \frac{a_2 (-\sqrt{(A^2 - B^2)\gamma} - A\sqrt{\gamma}\cos(2\sqrt{\gamma}(x + x_0)))^2}{(A\sin(2\sqrt{\gamma}(x + x_0)) + B)^2},\\ F_{17}(\xi) &= a_2 \gamma - \frac{a_2 (i\sqrt{\gamma} + (-2Ai\sqrt{\gamma}))^2}{(A + \cos(2\sqrt{\gamma}(x + x_0)) - i\sin(2\sqrt{\gamma}(x + x_0)))^2}, \end{split}$$

$$F_{18}(\xi) = a_2 \gamma - \frac{a_2 (-i\sqrt{\gamma} + 2Ai\sqrt{\gamma})^2}{(A + \cos(2\sqrt{\gamma}(x + x_0)) + i\sin(2\sqrt{\gamma}(x + x_0)))^2}.$$

(c) Rational function solutions (when $\gamma = 0$):

$$F_{19}(\xi) = a_2 \gamma - \frac{a_2}{(x+x_0)^2}.$$

Set 2:

$$a_{0} = \frac{b_{2}}{\gamma}, a_{1} = b_{1} = a_{2} = 0,$$

$$p = \pm \sqrt{\frac{k^{2}b_{2} - \Phi_{1}b_{2}}{12\gamma^{2}\Phi_{2} - 12\gamma\Phi_{2}b_{2}}}, r = \frac{\gamma^{2}\left(k^{4} - 2k^{2}\Phi_{1} + (\Phi_{1})^{2}\right)}{12\Phi_{2}\left(\gamma - b_{2}\right)^{2}},$$

$$c = \frac{b_{2}\left(2k^{4}\gamma - k^{4}b_{2} - 4k^{2}\gamma\Phi_{1} + 2k^{2}\Phi_{1}b_{2} + 2\gamma\Phi_{1} - \Phi_{1}b_{2}\right)}{12\Phi_{2}\left(\gamma - b_{2}\right)^{2}}.$$

Upon substituting these values into Eq.(4.7), the solution for Eq.(4.6) is obtained as:

(a) Hyperbolic function solutions (when $\gamma < 0$):

$$F_{21}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A\sinh(2\sqrt{-\gamma}(x+x_0))+B)^2}{(\sqrt{-(A^2+B^2)\gamma} - A\sqrt{-\gamma}\cosh(2\sqrt{-\gamma}(x+x_0)))^2}$$

$$F_{22}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A\sinh(2\sqrt{-\gamma}(x+x_0))+B)^2}{(-\sqrt{-(A^2+B^2)\gamma} - A\sqrt{-\gamma}\cosh(2\sqrt{-\gamma}(x+x_0)))^2}$$

$$F_{23}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A+\cosh(2\sqrt{-\gamma}(x+x_0))-\sinh(2\sqrt{-\gamma}(x+x_0)))^2}{(-\sqrt{-\gamma}+(-2A\sqrt{-\gamma}))^2}$$

$$F_{24}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A+\cosh(2\sqrt{-\gamma}(x+x_0))+\sinh(2\sqrt{-\gamma}(x+x_0)))^2}{(\sqrt{-\gamma}+2A\sqrt{-\gamma})^2}$$

(b) Trigonometric function solutions (when $\gamma > 0$):

$$F_{25}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A\sin(2\sqrt{\gamma}(x+x_0))+B)^2}{(\sqrt{(A^2 - B^2)\gamma} - A\sqrt{\gamma}\cos(2\sqrt{\gamma}(x+x_0)))^2}$$

$$F_{26}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A\sin(2\sqrt{\gamma}(x+x_0))+B)^2}{(-\sqrt{(A^2 - B^2)\gamma} - A\sqrt{\gamma}\cos(2\sqrt{\gamma}(x+x_0)))^2}$$

$$F_{27}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A+\cos(2\sqrt{\gamma}(x+x_0)) - i\sin(2\sqrt{\gamma}(x+x_0)))^2}{(i\sqrt{\gamma} + (-2Ai\sqrt{\gamma}))^2}$$

$$F_{28}(\xi) = \frac{b_2}{\gamma} - \frac{b_2(A+\cos(2\sqrt{\gamma}(x+x_0)) + i\sin(2\sqrt{\gamma}(x+x_0)))^2}{(-i\sqrt{\gamma} + 2Ai\sqrt{\gamma})^2}$$

(c) Rational function solutions (when $\gamma = 0$):

$$F_{29}(\xi) = \frac{b_2}{\gamma} - b_2(x+x_0)^2.$$

Set 3:

$$a_{0} = 2\gamma a_{2}, a_{1} = b_{1} = 0, b_{2} = \gamma^{2} a_{2}$$

$$p = \pm \sqrt{\frac{\Phi_{1}a_{2} - k^{2}a_{2}}{48\gamma\Phi_{2}a_{2} - 12\Phi_{2}}}, r = \frac{k^{4} - 2k^{2}\Phi_{1} + (\Phi_{1})^{2}}{12\Phi_{2}(4\gamma a_{2} - 1)^{2}}$$

$$c = \frac{-2\gamma a_{2} \left(2k^{4}\gamma a_{2} - 4k^{2}\gamma\Phi_{1}a_{2} - k^{4} + 2\gamma\Phi_{1}a_{2} + 2k^{2}\Phi_{1} - \Phi_{1}\right)}{3\Phi_{2}(4\gamma a_{2} - 1)^{2}}$$

Upon substituting these values into Eq. (4.7), the solution for Eq. (4.6) is obtained as:

$$q(\xi) = a_2 \left(2\gamma + \gamma^2 \phi^{-2}(\xi) + \phi^2(\xi) \right).$$

Set 3 has not been formulated with the intention of eliminating procedural redundancy. Its calculation can be performed in a manner analogous to that of Set 1 and Set 2.

5. CONCLUSION

In this study, we successfully derived analytical solutions for the space-time fractional order Peyrard–Bishop– Dauxois model using the unified method. The derivation of these exact traveling wave solutions, including novel hyperbolic forms, represents a significant advancement in our understanding of the nonlinear dynamics inherent in DNA structural transitions, such as denaturation. The transformation of complex fractional partial differential equations into more manageable ordinary differential equations with integer orders via a potent fractional complex transformation. This approach not only validated the efficacy of the unified method but also highlighted the PBD model's significance in capturing the complex behavior of biological systems.

The analytical results obtained herein provide profound insights into the underlying mechanisms of DNA dynamics, particularly by incorporating memory effects and nonlocal interactions through fractional derivatives. This enhanced modeling approach offers a more comprehensive framework for exploring the phenomena observed in molecular biology and reinforces the value of advanced mathematical techniques in elucidating complex biological processes.

Future research may extend this work by considering additional nonlinearities and parameter regimes within the space-time fractional framework. Furthermore, integrating numerical simulations and experimental validations will be crucial in refining the model's predictive capabilities and further substantiating the analytical findings. These efforts will not only broaden the scope of mathematical techniques available for tackling challenging biological problems but also contribute to a deeper understanding of nonlinear dynamics in a wide range of scientific disciplines. In conclusion, the present work not only reinforces the efficacy and reliability of the unified method in solving complex fractional differential equations but also opens new avenues for exploring the rich dynamics of nonlinear biological phenomena.

CONFLICTS OF INTEREST

The authors declare no conflict of interest in relation to the publication of this article.

AUTHORS CONTRIBUTION STATEMENT

The authors have reviewed and approved the final version of the manuscript for publication.

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