



Abundant exact closed-form solutions and solitonic structures for the double-chain deoxyribonucleic acid (DNA) model

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Abstract

In this work, the abundant exact closed-form solutions and dynamics of solitons for the double-chain deoxyribonucleic acid (DNA) model is obtained by utilizing the generalized exponential rational function (GERF) method. Deoxyribonucleic acid (DNA) retains the genetic information that creatures need to live and reproduce themselves. We obtained several novel exact soliton and exponential rational functional solutions in the shapes of dynamics of solitons like multi-solitons, breather-type solitons, abundant elastic interactions between multi-solitons, and nonlinear waves, oscillating multi-solitons, and Lump solitons. These derived solutions were never reported in the literature. The dynamical structures of some exact solitons are exhibited graphically by assigning suitable values to the free parameters via 3D figures. The generated solutions can be more useful and help to explain the internal interactions of the double-chain DNA model. The symbolic computational work and the obtained solutions show that the present proposed GERF method is effective, robust, and straightforward. Moreover, these types of higher-order NLEEs can be solved using the current technique.

Keywords Double-chain DNA model · GERF method · Exact solutions · Solitons

1 Introduction

Deoxyribonucleic acid, or DNA, is the central information storage system in every cell. It is an extremely large linear molecule that contains genetic instructions that make each specie unique in the form of a sequence of its constituent elements, that is, the nucleotides. The dynamics of DNA molecules is one of the most interesting problems in the field of modern biophysics as it is related to the basis of life. DNA is double stranded, that is, it is made up of two complementary chains or strands. These two chains run opposite to each other and connected by hydrogen bonds, and therefore known as anti-parallel chains. The word “deoxyribo” in

DNA describes the sugar and the “nucleic acid” refers to the phosphate molecules.

The study of qualitative and quantitative dynamics of mathematical modeling became an important research topic in the field of mathematical biology and applied mathematics. In the literature, many methods have been developed and extensively used by many researchers to solve these mathematical models. For instance, (G'/G) -expansion method [1], the reproducing kernel Hilbert space method [2], the Laplace homotopy perturbation method [3], Lie symmetry method [4–9], the sine-Gordon expansion method [10], GERF method [8, 11], and other mathematical techniques [12–19].

The dynamics of the DNA model have been analyzed by many mathematicians and biologists [20–24]. It has been observed that modeling of DNA system is very complicated because of its characteristic multiplicity and the chaoticity which is relevant for genome evolution [25]. Watson and Crick [26] described different structure for the salt of deoxyribose nucleic acid and then double helix structure of DNA has become an interesting topic in the field of biology and applied mathematics. Englander et al. [27] demonstrated the existence of open states in DNA system and double helices by hydrogen exchange measurements. They proved the

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