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Solving Time-Space Fractional Biological Population Model by Homotopy Perturbation Method

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ABSTRACT

This article aims to study the time-space fractional biological population model which describe population densities in the various biological movements. To find an approximate solution for the time-space fractional population model, we employ the Homotopy Perturbation Method (homotopy perturbation method), a powerful analytical technique for solving nonlinear fractional differential equations. Also, we prove the convergence of the developed method. Fractional-order one-dimensional biological model for the spread of genes in a population and a two- dimensional biological population model with Verhulst law are studied. Traveling wave solutions are observed for both one and two-dimensional models. The obtained results confirms that the proposed time-space fractional model provides valuable dynamic behavior of biological populations in fractional environments. Analytical and numerical solutions of models are presented in the form of tables and graphs with the help of SageMath programming..

Keywords: Fractional order biological population model, Homotopy perturbation method, Convergence, Fractional Calculus, SageMath, etc.

I. INTRODUCTION

Fractional differentiation and integrals are widely used to describe many physical as well as biological models. Various nonlinear facts are investigated in these models due to numerous applications found in plasma physics, nonlinear biological systems, acoustics etc[6, 9, 13, 15]. Finding the exact solutions of such models is a tedious task. Therefore, researchers follow the tools like numerical methods or series solution methods [3, 7, 8].

In recent years, various methods are in use for approximate solution estimation such as the Adomian decomposition method, Inverse scattering method, Homotopy perturbation method, He's semi-inverse method, Hirota's bilinear method, Tanh method, Laplace decomposition algorithm, Differential transform method, Fractional homotopy analysis transform method, Variational iteration method, etc.

The homotopy perturbation method for solving nonlinear initial and boundary value problems is developed by He. This method compacts the appropriate technique to obtain analytic or approximate solutions to a wide class of differential equations[**?**].

Motions and migrations of biological populations are distributed uniformly in their respective environments. This phenomenon is influenced by specific mechanochemical processes, such as environmental variations, population densities, overcrowding levels, and the motion of the surrounding fluid or air. These processes give rise to partial differential equations that govern molecular diffusion, convection, attraction, as well as the spatial spread of genes and diseases [2, 12, 10, 6, 1, 19]. In the 1930s, Kolmogorov, Petrovskii, and Piskunov introduced the equation [17],

$$\frac{\partial V}{\partial t} = D\frac{\partial^2 V}{\partial^2 x} + cV(1 - V) \qquad (1)$$

where $V(x, t)$ is the population density at x and time t, D is the diffusion coefficient, which indicates the movement or spread of the population, r is the intrinsic growth rate of the population, and $V(1 - V)$ is the logistic growth term with a carrying capacity of 1. Equation (1) is also known as the KPP equation. This equation de- scribes the logistic population growth with diffusion spreading across space. Furthermore, Fisher developed the Fisher-KPP equation [5]

$$\frac{\partial U}{\partial t} = D_1\frac{\partial^2 U}{\partial^2 x} + rU(1-U) \tag{2}$$

where $U(x, t)$ is the population density, D_1 is the diffusion coefficient, which represents the spatial movement of individuals, c is the growth rate, The term $U(1-U)$ represents logistic growth with a carrying capacity of 1. Equation (2) is the reaction-diffusion kind of model and it describe the spread of advantageous alleles through a population.

By incorporating fractional derivatives, biological population models adapt the ability to more accurately represent real-world phenomena than integer-order derivatives. Also, it enables the systems to exhibit anomalous diffusion, long-range spatial interactions, and memory effects. This article aims to obtain an approximate solution to time- space fractional biological population models for a better understanding of complex biological behaviors, such as memory and non-local effects, in population dynamics. Also, we demonstrate the effectiveness of the Homotopy Perturbation Method in solving these models, providing a more accurate and computationally efficient alternative to traditional methods.

II. BASIC PRELIMINARIES

In this section, we discuss some of the most common definitions related to fractional calculus.

Definition 1: The Riemann-Liouville fractional integral of a function f is defined as [11]

$$J^{\gamma}f(t) = \frac{1}{\Gamma(\gamma)}\int_0^t (t-\tau)^{\gamma-1}f(\tau)d\tau, \quad \text{for } 0<\gamma\le 1,$$

Definition 2: The Caputo fractional derivative of a function f is defined as [11]

$$D^{\beta}f(x) = \frac{1}{\Gamma(r-\beta)}\int_0^x (x-\tau)^{r-\beta-1}f^{(r)}(\tau)d\tau, \quad \text{for } r-1<\beta\le r$$

where $r = \lceil\beta\rceil$.

Remarks:

(i) $J^{\gamma}(t^s) = \frac{\Gamma(s+1)}{\Gamma(\gamma+s+1)}t^{\gamma+s}$ *for* $s>-1, \gamma\ge 0.$

(ii) $J^{\gamma}D^{\gamma}(f(x)) = f(x) - \sum_{k=0}^{r-1} f^{(k)}(0^+)\frac{x^k}{k!},\ x>0, \gamma\ge 0$

(iii) $J^{\gamma}J^{\beta}(f(t)) = J^{\gamma+\beta}(f(t)),$ *for* $\gamma, \beta\ge 0$

III. FRACTIONAL BIOLOGICAL POPULATION MODEL

The population density $V(x_1, x_2, \ldots, x_n, t)$ at a given time $t\ge 0$ and location $(x_1, x_2, \ldots, x_n)\in \mathbb{R}^n$ is governed by the following time-space fractional biological population model

$$D_t^{\alpha}(V) = D_0\Delta^{\beta}(V) + f(V), \tag{3}$$

where $0<\alpha\le 1,\ 1<\beta\le 2$, D_0 represents the dispersion rate, f provides the population supply, Δ^{β} is the fractional derivative (where $\Delta^{\beta} = D_x^{\beta}$ for one space dimension and $\Delta^{\beta} = (D_x^{\beta} + D_y^{\beta})$ for two space dimensions).

The biological model for the spread of genes is primarily based on the principles of genetics and evolution. We study the time-space fractional biological population model for the spread of genes. This model is a foundational concept in population genetics and provides insights into how genetic variations are distributed and evolve over generations in a simplified population [16, 18, 14]. We examine the following time-space fractional biological population model

$$D_t^{\alpha}(V) = D_0D_x^{\beta}(V) + cV(1-V), \tag{4}$$

where $V(x, t)$ represents the density or frequency of the advantageous allele, D_0 is the diffusion coefficient for the spatial spreading of the allele, c is a is the growth rate of the allele and $0<\alpha\le 1,\ 1<\beta\le 2$.

Furthermore, we study a two-dimensional biological population model with the Verhulst law, which also known as the logistic growth model [20, 4].

We consider the two-dimensional biological population model

$$D_t^{\alpha}(V) = D_0\left(D_x^{\beta}(V) + D_y^{\beta}(V)\right) + V(1-\lambda V), \tag{5}$$

where V is a population density, D_0 is the diffusion coefficient, which determines how the population spreads spatially, $\frac{1}{\lambda}$ is the maximum capacity of the space and $0<\alpha\le 1,\ 1<\beta\le 2$.

IV. THE FRACTIONAL HOMOTOPY PERTURBATION METHOD

In this section we exploare the time-space fractional Homotopy Perturbation Method. This method is chosen for solving the time-space fractional biological population model due to its ability to handle non-linear and fractional differential equations efficiently. Homotopy perturbation method is iterative in nature, which ensures convergence of the solution and its computational efficiency makes it a practical choice for complex models, offering a reliable analytical approximation without the need for intensive numerical methods. Consider the following time-space fractional biological population model,

$$D^{\alpha}_{t}(V) = D_0\Delta^{\beta}(V) + f(V), \tag{6}$$

where $0 < \alpha \leq 1,\ 1 < \beta \leq 2$. In order to solve problem (6), we define $H(v, p) : \mathbb{R} \times [0, 1] \to \mathbb{R}$ as follows

$$H(v, p) = D^{\alpha}_{t} v - D^{\alpha}_{t} V_0 + p\left(D^{\alpha}_{t} V_0 - D_0\Delta^{\beta}(v) - f(v)\right) = 0 \tag{7}$$

with initial approximation V_0. Now, we assume that the solution to time-space fractional biological population model as follows

$$v = \sum_{n=0}^{\infty} p^n v_n \tag{8}$$

Equation (7) becomes

$$D^{\alpha}_{t}\left(\sum_{n=0}^{\infty} p^n v_n\right) - D^{\alpha}_{t} V_0 + p\left(D^{\alpha}_{t} v_0 - D_0\Delta^{\beta}\left(\sum_{n=0}^{\infty} p^n v_n\right) - f\left(\sum_{n=0}^{\infty} p^n v_n\right)\right) = 0 \tag{9}$$

In most of the cases, term $f(V)$ is non-linear. Hence, by applying the Maclaurin expansion to $f\left(\sum_{i=0}^{\infty} v_i p^i\right)$ concerning p, we get

$$\begin{aligned} f\left(\sum_{i=0} v_i p^i\right) &= \sum_{n=0}^{\infty} \left(\frac{1}{n!}\frac{\partial^n}{\partial p^n} f\left(\sum_{i=0} v_i p^i\right)\right)_{p=0} p^n \\ &= \sum_{n=0}^{\infty} \left(\frac{1}{n!}\frac{\partial^n}{\partial p^n} f\left(\sum_{i=0} v_i p^i\right)\right)_{p=0} p^n \\ &= \sum_{n=0}^{\infty} H_n(v_0, v_1, v_2, \ldots, v_n) p^n \end{aligned} \tag{10}$$

where H_n are given by

$$H_n = \frac{1}{n!}\frac{\partial^n}{\partial p^n} f\left(\sum_{i=0} v_i p^i\right)_{p=0}$$

Equation (9), becomes

$$D^{\alpha}_{t}\left(\sum_{n=0} p^n v_n\right) - D^{\alpha} V_0 + p\left(D^{\alpha}_{t} v_0 - D_0\Delta^{\beta}\left(\sum_{n=0} p^n v_n\right) - \sum_{n=0} H_n p^n\right) = 0$$

By setting equal terms to like powers, we derive the values of $v_0, v_1, v_2, \ldots$.

$$\begin{aligned} v_0 &= V_0 \\ v_1 &= -J^{\alpha}_{t}\left(D^{\alpha}_{t} v_0 - D_0\Delta^{\beta}(v_0) - H_0\right) \\ v_2 &= -J^{\alpha}_{t}\left(-D_0\Delta^{\beta}(v_1) - H_1\right) \\ v_3 &= -J^{\alpha}_{t}\left(-D_0\Delta^{\beta}(v_2) - H_2\right) \\ &\ \ . \end{aligned}$$

Therefore, to obtain an approximate solution for equation (6), we can simply substitute $p = 1$ into equation (8), resulting in the following

$$V = \lim_{p \to 1} v = \sum_{n=0}^{\infty} v_n$$

V. CONVERGENCE

The convergence of the homotopy perturbation method is an important aspect of its effectiveness in solving nonlinear differential equations. The convergence of this method can be proved using the Banach spaces. By constructing a sequence of approximations to the solution of a nonlinear problem and by deforming it into a linear problem through a homotopy parameter, an then applying the Banach Fixed Point Theorem or Contraction Mapping Theorem ensures the convergence of the homotopy perturbation method. This allows the sequence of approximations to converge to the exact solution in a well-defined Banach space, ensuring the sequence converges as the homotopy parameter progresses from 0 to 1. Following theorems proves the convergences of the method.

Theorem 1. *The homotopy perturbation method used to solve time-space fractional biological population model*

$$D_t^{\alpha}(V) = D_0\Delta^{\beta}(V) + f(V),\ 0 < \alpha \leq 1,\ 1 < \beta \leq 2. \tag{11}$$

is similar to estimating sequence

$s_n = \sum_{i=1}^{n} v_n,\ s_0 = 0$ *where*

$$s_{n+1} = J_t^{\alpha}\left[D_0\Delta^{\beta}(s_n + v_0)\right] + J_t^{\alpha}\left[f_n(s_n + v_0)\right] - u_0,$$

and

$$f_n\left(\sum_{i=0}^{n} v_i\right) = \sum_{n=0}^{n} H_i, \quad n = 0, 1, 2, \ldots$$

Proof. We prove this theorem by a strong form of mathematical induction on n. For $n = 0$, we have;

$$\begin{aligned} s_1 &= J_t^{\alpha}\left[D_0\Delta^{\beta}(s_0 + v_0)\right] + J_t^{\alpha}\left[f_0(s_0 + v_0)\right] - u_0 \\ &= J_t^{\alpha}\left[D_0\Delta^{\beta}(v_0)\right] + J_t^{\alpha}[H_0] - u_0 = -J_t^{\alpha}\left[D_t^{\alpha}u_0 - D_0\Delta^{\beta}(v_0) - H_0\right] \end{aligned}$$

Therefore,

$$v_1 = -J_t^{\alpha}\left[D_t^{\alpha}u_0 - D_0\Delta^{\beta}(v_0) - H_0\right] \tag{12}$$

For $n = 2$, we have

$$\begin{aligned} s_2 &= J_t^{\alpha}\left[D_0\Delta^{\beta}(s_1 + v_0)\right] + J_t^{\alpha}\left[f_1(s_1 + v_0)\right] - u_0 \\ &= J_t^{\alpha}\left[D_0\Delta^{\beta}(v_1 + v_0)\right] + J_t^{\alpha}\left[f_1(v_1 + v_0)\right] - u_0 \\ &= J_t^{\alpha}\left[D_0\Delta^{\beta}(v_1) + D_0\Delta^{\beta}(v_0)\right] + J_t^{\alpha}\left[H_1 + H_0\right] - u_0 \\ &= -J_t^{\alpha}\left[-D_0\Delta^{\beta}(v_1) - H_1\right] - J_t^{\alpha}\left[D_t^{\alpha}(u_0) - D_0\Delta^{\beta}(v_0) - H_0\right] \\ &= -J_t^{\alpha}\left[-D_0\Delta^{\beta}(v_1) - H_1\right] + v_1 \end{aligned}$$

As $s_2 = v_1 + v_2$, we get $v_2 = -J_t^{\alpha}\left[-D_0\Delta^{\beta}(v_1) - H_1\right]$.

Now, assume that $v_{k+1} = -J_t^{\alpha}\left[-D_0\Delta^{\beta}(v_k + v_0) - H_k\right]$, for $k = 2, 3, \ldots, n-1$.

Consider

$$\begin{aligned} s_{n+1} &= J_t^{\alpha}\left[D_0\Delta^{\beta}(s_n + v_0)\right] + J_t^{\alpha}\left[f_n(s_n + v_0)\right] - u_0 \\ &= J_t^{\alpha}\left[D_0\Delta^{\beta}\left(\sum_{i=0}^{n} v_i\right)\right] + J_t^{\alpha}\left[\sum_{i=0}^{n} H_i\right] - u_0 \\ &= J_t^{\alpha}\left[D_0\left(\sum_{i=0}^{n} \Delta^{\beta} v_i\right)\right] + \left[\sum_{i=0}^{n} J_t^{\alpha} H_i\right] - u_0 \\ &= -J_t^{\alpha}\left[-D_0\Delta^{\beta}(v_n + v_0) - H_n\right] + v_n + v_{n-1} + \cdots + v_2 + v_1 + v_0 \end{aligned}$$

Therefore, we get

$$v_{n+1} = -J_t^{\alpha}\left[-D_0\Delta^{\beta}(v_n + v_0) - H_n\right]$$

Hence, the theorem is proved. □

Theorem 2. *Let B be a Banach space. Then*

(a) $\sum_{i=0}^{\infty} v_i$ *convergence to $s \in B$, if there exists $\mu \in [0, 1)$ such that*

$$\|v_n\| \leqslant \mu \|v_{n-1}\|, \quad \forall n \in \mathbb{N}$$

(b) $s = \sum_{n=1}^{\infty} v_n$*, holds in*

$$s = J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}[f_n(s+v_0)] - u_0$$

(c) Equation $s = J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}[f_n(s+v_0)] - u_0$ *is equivalent to*

$$D_t^{\alpha}(V) = D_0\Delta^{\beta}(V) + f(V) \tag{13}$$

Proof. (a) Consider

$$\left\|s_{n+1} - s_n\right\| = \left\|v_{n+1}\right\| \leqslant \mu\left\|v_n\right\| \leqslant \mu^2\left\|v_{n-1}\right\| \leqslant \cdots \leqslant \mu^{n+1}\left\|v_0\right\|.$$

Therefore, for $n, m \in \mathbb{N}, n \geqslant m$, we drive

$$\left\|s_n - s_m\right\| \leqslant \frac{\mu^{m+1}}{1-\mu}\left\|v_0\right\|.$$

So

$$\lim_{n,m\to\infty}\left\|s_n - s_m\right\| = 0.$$

Therefore, the sequence $\{s_n\}$ is a Cauchy sequence within the Banach space, and it converges, so

$$\exists s \in \mathrm{B},\ s.t \lim_{n\to\infty} s_n = \sum_{n=1}^{\infty} v_n = s.$$

(b) We have,

$$\begin{aligned}
\lim_{n\to\infty} s_{n+1} &= \lim_{n\to\infty}\left\{J_t^{\alpha}\left[D_0\Delta^{\beta}(s_n+v_0)\right] + J_t^{\alpha}\left[f_n(s_n+v_0)\right] - u_0\right\}\\
&= J_t^{\alpha}\left[D_0\Delta^{\beta}\left(\lim_{n\to\infty} s_n + v_0\right)\right] + J_t^{\alpha}\left[\lim_{n\to\infty}\left(f_n(s_n+v_0)\right)\right] - u_0\\
s &= J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}\left[\lim_{n\to\infty}\left(\sum_{i=0}^{n} H_i\right)\right] - u_0\\
&= J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}\left[\sum_{i=0}^{\infty} H_i\right] - u_0\\
&= J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}\left[f\left(\sum_{i=0}^{n} v_i\right)\right] - u_0\\
&= J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}[f(s+v_0)] - u_0
\end{aligned}$$

Equality

$$\sum_{i=0}^{\infty} H_i = f\left(\sum_{i=0}^{\infty} v_i\right)$$

can obtain by setting $p = 1$ in equation (10).

(c) Consider,

$$s = J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}[f(s+v_0)] - u_0$$

Rewrite as follows

$$s + u_0 = J_t^{\alpha}\left[D_0\Delta^{\beta}(s+v_0)\right] + J_t^{\alpha}[f(s+v_0)]$$

By applying the operator D_t^{α}, we derive

$$D_t^{\alpha}(s+V_0) = D_0\Delta^{\beta}(s+v_0) + f(s+v_0)$$

As $V_0 = v_0$, we obtain

$$D_t^{\alpha}(s+v_0) = D_0\Delta^{\beta}(s+v_0) + f(s+v_0)$$

By considering $V = s + v_0 = \sum_{n=0}^{\infty} v_i$, we get

$$D_t^{\alpha}(V) = D_0\Delta^{\beta}(V) + f(V)$$

This complete the proof. □

VI. NUMERICAL EXPERIMENTS

A. Time-space Fractional Biological Model for the Spread of Genes

Consider the following time-space fractional biological population model

$$D_t^{\alpha} V = D_0 D_x^{\beta} V + cV(1-V), \quad 0<\alpha\le 1, \ 1<\beta\le 2. \tag{14}$$

with $V(x,0) = \left(1+\exp\left(\sqrt{\frac{c}{6}}\,x\right)\right)^{-2}$. Moreover, we have the exact solution for $\alpha = 1, \ \beta = 2$ as follows

$$V(x,t) = \left(1+\exp\left(\sqrt{\frac{c}{6}}\,x - \frac{5c}{6}t\right)\right)^{-2} \tag{15}$$

To solve the problem,consider a mapping $H(v,p) : \mathbb{R}\times[0,1] \rightarrow \mathbb{R}$ as follows

$$H(v,p) = D_t^{\alpha} v - D_t^{\alpha} V_0 + p\left(D_t^{\alpha} V_0 - D_0 D_x^{\beta} v - f(v)\right) = 0 \tag{16}$$

with initial approximation $V_0 = \left(1+\exp\left(\sqrt{\frac{c}{6}}\,x\right)\right)^{-2}$. Suppose the solution is as follows

$$v = \sum_{n=0}^{\infty} p^n v_n \tag{17}$$

Equation (16) becomes

$$D_t^{\alpha}\left(\sum_{n=0}^{\infty} p^n v_n\right) - D_t^{\alpha} V_0 + p\left(D_t^{\alpha} v_0 - D_0 D_x^{\beta}\left(\sum_{n=0}^{\infty} p^n v_n\right) - f\left(\sum_{n=0}^{\infty} p^n v_n\right)\right) = 0$$

Equating like powers and solving the obtained system of equations, we obtain $v_0, \ v_1, \ v_2, \ldots$.

$$\begin{aligned}
v_0 &= V_0\\
v_1 &= -J_t^{\alpha}\left(-D_t^{\alpha} V_0 + D_0 D^{\beta_x} v_0 + c v_0 - c v_0^2\right)\\
v_2 &= -J^{\alpha}\left(D_0 D^{\beta_x} v_1 + c v_1 - 2c v_0 v_1\right)\\
v_3 &= -J^{\alpha}\left(D_0 D^{\beta_x} v_2 + c v_2 - 2c v_0 v_2 - c v_1^2\right)
\end{aligned}$$

.

Therefore, the approximate solution is

$$u = \lim_{p\to 1} v = \sum_{n=0}^{\infty} v_n$$

We estimate the above values using SageMath programmes as follows

```
u0=(1+exp(sqrt(c/6)*x))^(-2) v0=u0.taylor(x,0,40)
v1=-RLIT(D*CDS(v0,beta,0,x)+c*v0-c*v0^2,alpha,0,t) v2=-
RLIT(D*CDS(v1,beta,0,x)-2*v0*v1+c*v1,alpha,0,t)
v3=-RLIT(D*CDS(v2,beta,0,x)+c*v2-2*c*v0*v2-c*v1^2,alpha,0,t)
```

Particularly, the solution for $\alpha = 1,\ \beta = 2,\ D_0 = 1,\ c = 1$ is obtain as follows

$$
\begin{aligned}
V(x,t) =& \left(\frac{5}{36}t^2 + \frac{4}{3}\right) + \left(\frac{5}{432}t^3 + \frac{1}{6}t\right)x + \left(\frac{1}{96}t^2 - \frac{1}{12}\right)x^2 + \left(-\frac{5}{10368}t^3 - \frac{1}{144}t\right)x^3 + \left(-\frac{1}{4608}t^2 + \frac{1}{576}\right)x^4 \\
&+ \left(\frac{1}{165888}t^3 + \frac{1}{11520}t\right)x^5 + \left(\frac{1}{552960}t^2 - \frac{1}{69120}\right)x^6 + \left(-\frac{1}{27869184}t^3 - \frac{1}{1935360}t\right)x^7 \\
&+ \left(-\frac{1}{123863040}t^2 + \frac{1}{15482880}\right)x^8 + \left(\frac{1}{8026324992}t^3 + \frac{1}{557383680}t\right)x^9 \\
&+ \left(\frac{1}{44590694400}t^2 - \frac{1}{5573836800}\right)x^{10} + \left(-\frac{1}{3531582996480}t^3 - \frac{1}{245248819200}t\right)x^{11} \\
&+ \left(-\frac{1}{23543886643200}t^2 + \frac{1}{2942985830400}\right)x^{12} + \left(\frac{1}{220370778980352 0}t^3 + \frac{1}{153035263180800}t\right)x^{13} \\
&+ \left(\frac{1}{17139949476249600}t^2 - \frac{1}{2142493684531200}\right)x^{14} \\
&+ \left(-\frac{1}{1851114543434956800}t^3 - \frac{1}{128549621071872000}t\right)x^{15} \\
&+ \left(-\frac{1}{1645435149719961600 0}t^2 + \frac{1}{205679393714995200 0}\right)x^{16} + \left(\frac{1}{20140126232572329984 00}t^3 \right.\\
&\left. + \frac{1}{139861987726196736000}t\right)x^{17} + \ldots
\end{aligned}
$$

The approximate solution of time-space fractional biological population model derived from the fractional homotopy perturbation method is compared with the exact solution in Table 1, demonstrating the method’s effectiveness. Figure 1 illustrates a comparison between the approximate solution and the exact solution of time-space fractional biological model for the given parameters $t = 0.1,\ c = 1,\ D_0 = 1$, within the range of $-6 \leq x \leq 6$. It is evident from the plot that the approximate solution closely aligns with the exact solution. Also, we observed that the allele gains dominance within the population as the wave progresses across the region. This implies that alleles spread through the population, moving towards fixation at specific locations. Furthermore, in Figure 2, we simulate an approximate solution that represents population density at fractional order $\alpha = 1,\ \beta = 2$, growth rate $c = 1$ and diffusivity coefficient $D_0 = 1$ and observe kink type traveling wave solution which shows population density decreases as time passes. In Figure 3, we conduct a simulation of population densities using fractional order parameters $\alpha = 1$ and $\beta = 2$, a growth rate of $c = 1$, and a diffusivity coefficient of $D_0 = 1$. Our findings

Table 1: **Absolute error for the parameters** $c = 0.01,\ D_0 = 1$

	Absolute error			
$x \rightarrow$ $t \downarrow$	0.0	0.1	0.2	0.3
0.1	6.45×10^{-4}	6.44×10^{-4}	6.43×10^{-4}	6.42×10^{-4}
0.2	1.33×10^{-3}	1.33×10^{-3}	1.32×10^{-3}	1.32×10^{-3}
0.3	2.06×10^{-3}	2.06×10^{-3}	2.05×10^{-3}	2.51×10^{-3}
0.4	2.83×10^{-3}	2.83×10^{-3}	2.82×10^{-3}	2.81×10^{-3}

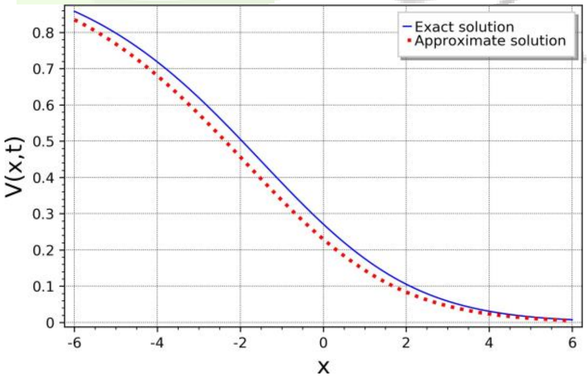

Figure 1: **Comparison of solutions**

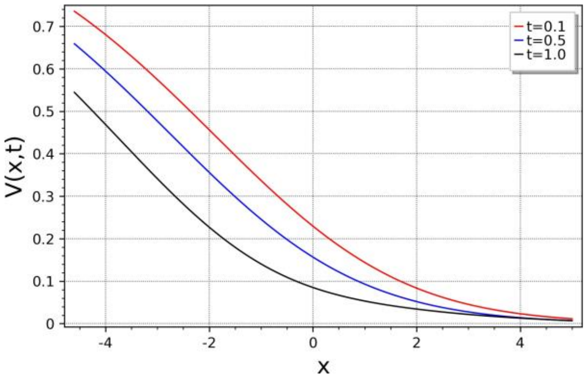

Figure 2: **Population desnsities at** $\alpha = 1, \beta = 2, c = 1$**, and** $D_0 = 1$

reveal that as time t progresses, the populations exhibit a continuous decrease while maintaining a constant shape and constant rate. After a brief initial period, the species either stabilizes or disappears entirely. In Figure 4, we

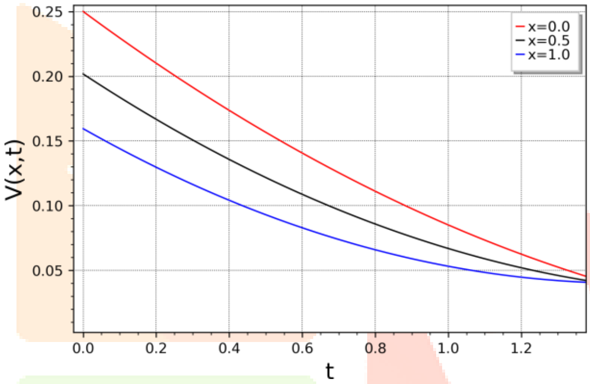

Figure 3: **Population densities at** $\alpha = 1, \beta = 2, c = 1$**, and** $D_0 = 1$

perform a simulation of population densities using fractional order parameters $\alpha = 1$ and $\beta = 2$, a diffusivity coefficient of $D_0 = 1$ at location $x = 0.5$, and varying values of the growth rate c. Our results indicate that as the growth rate c increases, the populations demonstrate a continuous rise while preserving a consistent shape and constant rate. In Figure 5, we conduct a simulation of population densities using fractional order parameters

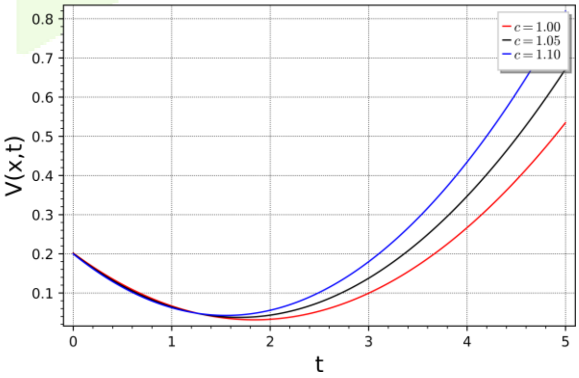

Figure 4: **Simulation of population densities with varying growth rates at** $\alpha = 1, \beta = 2, x = 0.5$**, and** $D_0 = 1$

$\alpha = 1$ and $\beta = 2$, a growth rate $c = 1$ at the designated location $x = 0.5$, and varied values of the diffusivity coefficient D_0. Our findings suggest that with an increase in the diffusivity coefficient D_0, the populations exhibit

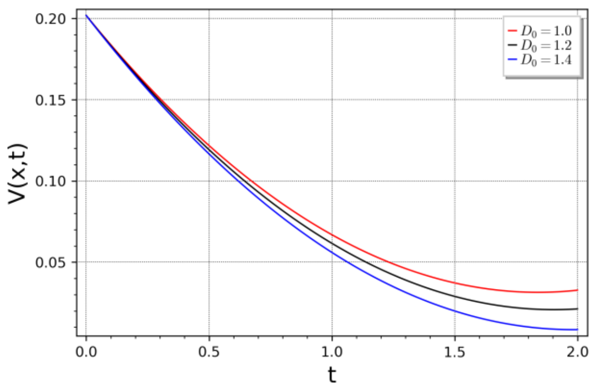

Figure 5: **Simulation of population densities**

a continuous decline while maintaining a consistent shape and constant rate. Figure 6 portrays the investigation of solution behavior for various fractional order values of α, β and observed that the population density rises as α, β decreases. Also, Figure 7 displays the plot of the approximate solution V for $\alpha = 0.95, \beta = 2, -1 \le t \le 1, -6 \le x \le 6, c = 1, D_0 = 1$. The graphical representation confirms that the proposed model exhibits a kink-type traveling wave solution.

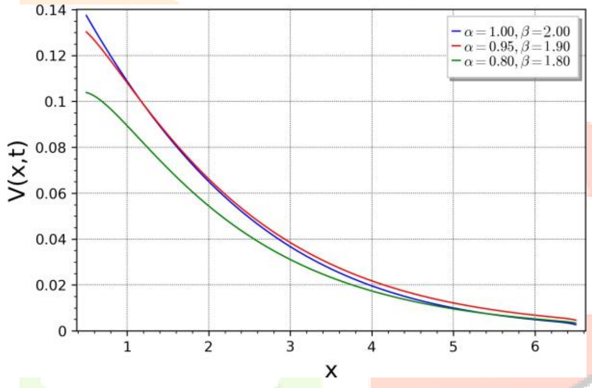

Figure 6: **Approximate solutions for** $t = 0.2, c = 1, D_0 = 1$

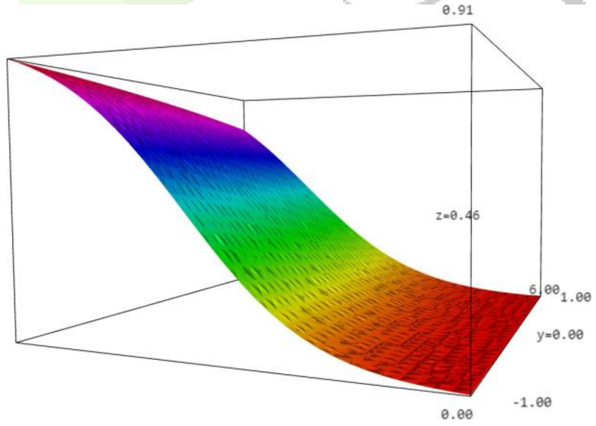

Figure 7: **Kink type travelling wave solution for** $\alpha = 0.95, \beta = 2, -1 \le t \le 1, -6 \le x \le 6, c = 1, D_0 = 1$

B. Time-space Fractional Biological Population Model in Two Dimensions

Consider the two dimensional time-space fractional biological population model as follows

$$D_t^{\alpha} V = D_0(D_x^{\beta} V + D_y^{\beta} V) + V(1 - \lambda V), \tag{18}$$

where $0 < \alpha \leq 1,\ 1 < \beta \leq 2$ and $V(x, 0) = \exp\left(\frac{1}{2}\sqrt{\frac{\lambda}{2}}(x + y)\right)$. Also, the exact solution when $\alpha = 1,\ \beta = 2$ is expressed as

$$V(x, t) = \exp\left[\frac{1}{2}\sqrt{\frac{\lambda}{2}}(x + y) + t\right] \tag{19}$$

We define a mapping $H(v, p) : \mathbb{R} \times [0, 1] \to \mathbb{R}$ as follows

$$H(v, p) = D_t^{\alpha} v - D_t^{\alpha} V_0 + p\left(D_t^{\alpha} V_0 - D_0 D_x^{\beta} v - D_0 D_y^{\beta} v - v(1 - \lambda v)\right) = 0 \tag{20}$$

with $V_0 = \left(1 + \exp\sqrt{\frac{c}{6}}\,x\right)^{-2}$.

Suppose the solution is as follows

$$v = \sum_{n=0}^{\infty} p^n v_n \tag{21}$$

By substituting equation (21) into (20) and equating similar powers, we can obtain the values of $v_0, v_1, v_2, \ldots$.

$$v_0 = V_0$$

$$v_1 = -J^{\alpha}\left(-D_t^{\alpha} V_0 - D_0 D_x^{\beta} v_0 - D_0 D_y^{\beta} v_0 - v_0 + \lambda v_0^2\right)$$

$$v_2 = -J^{\alpha}\left(-D_t^{\alpha} V_0 - D_0 D_x^{\beta} v_0 - D_0 D_y^{\beta} v_0 - v_1 + 2\lambda v_0 v_1\right)$$

$$v_3 = -J_t^{\alpha}\left(-D^{\alpha} V_0 - D_0 D_x^{\beta} v_0 - D_0 D_y^{\beta} v_0 - v_2 + \lambda v_1^2 2\lambda v_0 v_2\right)$$

.

Consequently, we can derive the approximate solution as follows

$$u = \lim_{p \to 1} v = \sum_{n=0}^{\infty} v_n$$

With the provided initial approximation and the described algorithm, we compute the approximate solution of two-dimensional time-space fractional biological population model. We estimate the above values using SageMath programmes as follows

```
u0=exp((0.5*(sqrt(1/2))*(x+y))) v0=u0.taylor(x,0,10)
v1=-RLIT(-D0*CDSx(v0,beta,0,x)-D0*CDSy(v0,beta,0,x)-v0
+l*v0*v0,alpha,0,t)
v2=-RLIT(-D0*CDSx(v1,beta,0,x)-D0*CDSy(v1,beta,0,x)-v1
+2*l*v0*v1,alpha,0,t)
v3=-RLIT(-D0*CDSx(v2,beta,0,x)-D0*CDSy(v2,beta,0,x)-v2
+l*v1*v1+2*l*v0*v2,alpha,0,t)
```

By comparing it with the exact solution for the parameters $-30 \leq x \leq 30,\ t = 0.5,\ y = 1,\ \alpha = 1,\ \beta = 2$ in Figure 8, we observe a close resemblance between the approximate and exact solutions. Also, we observed that the population density increases because of some individuals may choose to disperse or migrate to areas with lower population density to avoid competition and find better resources. This can result in changes in the distribution of the population density over a space. Furthermore, when a population is initially introduced to a new environment with ample resources, we can observe a phase of rapid growth. This is characterized by an exponential increase in population size.

We further represent solutions of time-space fractional two dimensional biological population model in Figure 9 and noticed that the population densities increase with time-space fractional order. Also, in Figure 10, we simulate

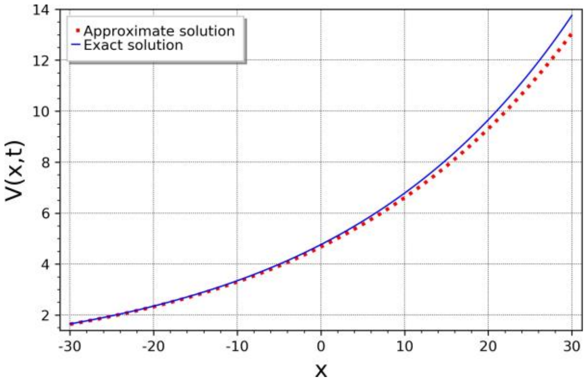

Figure 8: **Comparison of solutions**

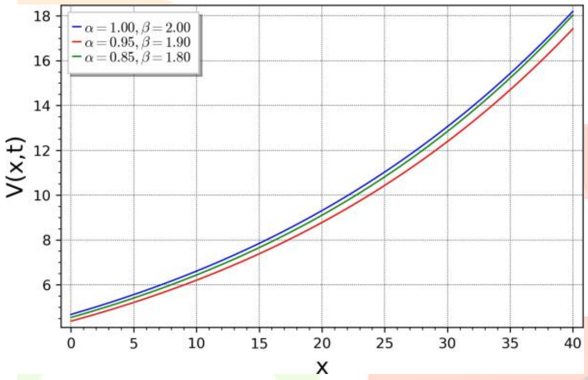

Figure 9: **Approximate solutions**

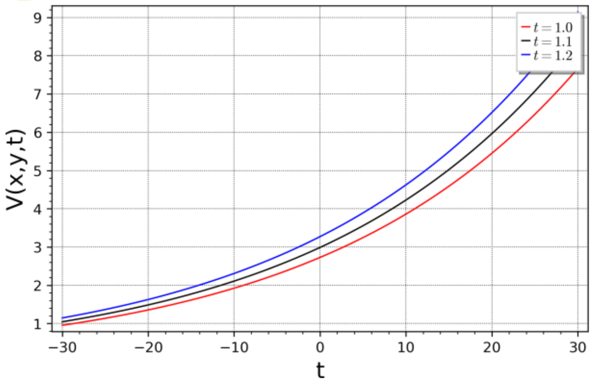

Figure 10: **Travelling wave solution for** $\alpha = 1, \beta = 2, -30 \le x \le 30, -30 \le y \le 30$

kink wave solution for two dimensional time-space fractional biological population model for the parameters $\alpha = 1, \beta = 2, -30 \le x \le 30, y = 1, c = 1, D_0 = 1$ and observe that wave marching in backward direction as time passes. Furthermore, Figure 11 displays the plot of the approximate solution V of time-space fractional biological population model for the parameters $\alpha = 0.9, \beta = 2, -30 \le x \le 30, -30 \le y \le 30, t = 0.5, c = 1, D_0 = 1$. The plot exhibits a kink-type traveling wave solution. Also, we observe that population density increase with constant speed and shape over the time period.

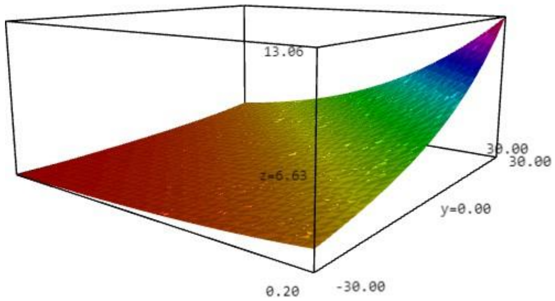

Figure 11: **Kink wave solution**

VII. CONCLUSION

We have successfully applied the fractional homotopy perturbation method to solve time-space fractional biological population models governing gene spread in species and two-dimensional time-space fractional biological population models with Verhulst's law. We estimate the error and observe a high level of accuracy and remarkable proximity between the approximate and exact solutions of the time-space fractional biological population models. In the gene spread model, we observed that the population density gains dominance within the population as the wave progresses across the region. This implies that genes spreads through the population, moving towards fixation at specific locations. We also observed that population density decreases over the time period as distance increases. Time-space fractional differentiation, Growth rate, and diffusivity coefficient also affects the population density over the time period. Also, in time-space fractional biological population model with Verhulst's law, we observed that the population density increase dues some individuals may choose to disperse or migrate to areas with lower population density to avoid competition and find better resources. This can result in changes in the distribution of the population density over a space. Furthermore, when a population is initially introduced to a new environment with ample resources, we can observe a phase of rapid growth. Also, we observe that population density increase with constant speed and shape over the time period. Furthermore, as the population approaches the carrying capacity of its environment, we notice that the growth rate begins to slow down.

The scope of this study in the future could focus on extending the method to multi-dimensional systems and incorporating stochastic effects to account for randomness in biological processes. Furthermore, one could incorporate higher-order fractional derivatives to capture more intricate memory and non-local effects, as well as apply homotopy perturbation method to more complex nonlinear reaction-diffusion models to better represent species interactions. Furthermore, validating the method through numerical simulations and real-world data, particularly in fields like epidemiology, multi-species ecosystem modeling, etc.

Bibliography

[1] A. A.M. Arafa, S. Z. Rida, and H. Mohamed. Homotopy analysis method for solving biological population model. *Communications in Theoretical Physics*, 56, 2011.

[2] Nourhane Attia, Ali Akgu¨l, Djamila Seba, and Abdelkader Nour. An efficient numerical technique for a biological population model of fractional order. *Chaos, Solitons and Fractals*, 141, 2020.

[3] Jafar Biazar, Zainab Ayati, and Hamideh Ebrahimi. Comparing Homotopy Perturbation Method and Adomian Decomposition Method. pages 80–86, Psalidi, Kos (Greece), 2008.

[4] Bernard Delmas. Pierre-franc¸ois verhulst et la loi logistique de la population. *Mathe´matiques et sciences humaines*, 2004.

[5] R. A. FISHER. The wave of advance of advantageous genes. *Annals of Eugenics*, 7, 1937.

[6] Hassan Khan, Rasool Shah, J. F. Go´mez-Aguilar, Shoaib, Dumitru Baleanu, and Poom Kumam. Travelling waves solution for fractional-order biological population model. *Mathematical Modelling of Natural Phenomena*, 16, 2021.

[7] Sharvari Kulkarni and Kalyanrao Takale. Application of adomian decomposition method for solving linear and nonlinear klein-gordon equations. *Int. Jr. of Engineering, Contemporary Mathematics and Sciences*, 1(2), 12 2015.

[8] Jian-Lin Li. Adomian's decomposition method and homotopy perturbation method in solving nonlinear equations. *Journal of Computational and Applied Mathematics*, 228(1):168–173, June 2009.

[9] Yuri Luchko. Fractional wave equation and damped waves. *Journal of Mathematical Physics*, 54(3):031505, March 2013.

[10] Kottakkaran Sooppy Nisar, Armando Ciancio, Khalid K. Ali, M. S. Osman, Carlo Cattani, Dumitru Baleanu, Asim Zafar, M. Raheel, and M. Azeem. On beta-time fractional biological population model with abundant solitary wave structures. *Alexandria Engineering Journal*, 61, 2022.

[11] Igor Podlubny. *Fractional differential equations : an introduction to fractional derivatives, fractional differ- ential equations, to methods of their solution and some of their applications*, volume 198. 1999.

[12] Amit Prakash and Rahul. Analysis and numerical simulation of fractional biological population model with singular and non-singular kernels. *Proceedings of the Institute of Mathematics and Mechanics*, 48, 2022.

[13] Arsen Pskhu and Sergo Rekhviashvili. Fractional Diffusion–Wave Equation with Application in Electrody- namics. *Mathematics*, 8(11), 2020.

[14] Leilei Qu, Qiuhui Pan, Xubin Gao, and Mingfeng He. Population dynamics of patients with bacterial resis- tance in hospital environment. *Computational and Mathematical Methods in Medicine*, 2016, 2016.

[15] Fathalla A. Rihan. Numerical Modeling of Fractional-Order Biological Systems. *Abstract and Applied Analysis*, 2013:1–11, 2013.

[16] Somnath Tagore and Rajat K. De. Simulating an infection growth model in certain healthy metabolic path- ways of homo sapiens for highlighting their role in type i diabetes mellitus using fire-spread strategy, feed- backs and sensitivities. *PLoS ONE*, 8, 2013.

[17] V. M. Tikhomirov. *A Study of the Diffusion Equation with Increase in the Amount of Substance, and its Application to a Biological Problem*. 1991.

[18] Ali Traore´. A theoretical assessment of the effects of vectors genetics on a host-vector disease. *Journal of Applied Mathematics and Computing*, 65, 2021.

[19] P. Veeresha and D. G. Prakasha. An efficient technique for two-dimensional fractional order biological population model. *International Journal of Modeling, Simulation, and Scientific Computing*, 11, 2020.

[20] R. Zwanzig. Generalized verhulst laws for population growth. *Proceedings of the National Academy of Sciences of the United States of America*, 70, 1973.