EUROPEAN JOURNAL OF PURE AND APPLIED MATHEMATICS
2025, Vol. 18, Issue 1, Article Number 5529
ISSN 1307-5543 – ejpam.com
Published by New York Business Global

Using the Modified Decomposition Method Associated with Mohand Transforms for a Numerical Simulation of the Mathematical Model for Breast Cancer

Mohamed M. Khader[1,*], Ali H. Tedjani[1]

[1] *Department of Mathematics and Statistics, College of Science, Imam Mohammad Ibn Saud Islamic University (IMSIU), Riyadh, Saudi Arabia*

Abstract. We know that mathematical modeling is an important tool for understanding the dynamics of breast cancer (BC) development, spread and reduce new therapeutic approaches. So, in the current article, we have investigated the analytical solution of the mathematical model for BC by using the modified Adomian decomposition method (MADM). The MADM is based on the integral transform (Mohand transform) with the Adomian decomposition procedure. The MADM provides a series of solutions that converge quickly to the exact solution for the proposed problem. The convergence of this method is discussed. Through this work, a numerical simulation was presented to solve the mathematical model under study with several values of the approximation order, rate of the estrogen source, and effectiveness of anti-cancer drugs, to understand the extent of their effect on the numerical solution and then on the nature and dynamics of the system, and to provide some recommendations to reduce the impact of this malignant tumor. In addition, we presented a comparison between the solution generated by the proposed technique and that numerical solution by utilizing the Runge-Kutta method (RK4M). Finally, the proposed method can also be extended to solving other models in the applied sciences.

2020 Mathematics Subject Classifications: 34A12, 41A30, 26C10, 47H10, 65N20

Key Words and Phrases: Breast cancer, Modified Adomian decomposition method, Mohand transform, RK4M

1. Introduction

Breast cancer is described and defined as a disease condition resulting from the uncontrolled proliferation of cells within the breast tissue. Through many data provided by the WHO on the global burden of cancer, we find that BC has the highest prevalence rate when compared to other forms of cancer [6]. Globally, through surveys conducted by the WHO, which ranked breast cancer in 2004 as the second most common form of cancer, we find that it represents a major potential threat to women, as it affects approximately 8-9

*Corresponding author.
DOI: https://doi.org/10.29020/nybg.ejpam.v18i1.5529

Email addresses: mmkhader@imamu.edu.sa (M. M. Khader), Ahtedjani@imamu.edu.sa (A. H. Tedjani)

percent of women worldwide [1]. Despite all these studies and numerous investigations, the exact cause of breast cancer is still uncertain. It was also directly responsible for the deaths of 685,000 people in 2020, out of 2.3 million women affected, as indicated by the diagnosis of 7.8 million women during the previous five-year period ([1], [23]). Breast cancer is the most common in women after puberty and its incidence increases with age [1]. Based on all of the above considerations, we emphasize the need for a comprehensive understanding of the epidemiology of breast cancer and its effects on women's health, as it is of utmost importance in developing effective preventive and therapeutic approaches worldwide [10].

Mathematical modeling plays an important and pivotal role in understanding and studying cancer tumors in general and breast cancer, the focus of our study here in this research paper in particular, because it is used to describe and simulate the growth and behavior of tumors, in addition to how they interact with the surrounding tissues and the immune system as well ([2], [12], [13]). These models help researchers and clinicians gain insights into the fundamental mechanisms of tumor growth, predict treatment outcomes, and then provide suggestions and recommendations for improving therapeutic strategies ([3], [4], [20]). Finally, there are several mathematical models used in cancer research among them, Growth models, Pharmacokinetic models, Spatial models, Immune response models, and Evolutionary models. For more focus concerning these types of models with their definitions, properties, and uses see [17].

These mathematical models are often represented as a system of differential equations, which are calibrated and validated with the help of some experimental data. Through real solutions or numerical simulations of these equations, we can gain valuable insights into tumor behavior, its response to treatment, and the effectiveness of different therapeutic interventions. One of the most important and prominent of these models for breast cancer is the one in which the mathematical model is divided into four aspects represented by: the number of normal cells, number of cancer cells, immune response class, and estrogen compartment. From this standpoint, we find that these mathematical systems are a powerful tool for predicting some hypotheses, guiding experimental design, and assisting in clinical decision-making in cancer research and treatment. Finally, extreme caution must be exercised when interpreting the recommendations and predictions obtained from the numerical processing and solutions of these mathematical models, even though they are simplifications of a complex biological reality.

It is worth noting a few crucial points regarding the MT. Firstly, this method provides the solution in terms of easily computable components, making it highly practical for real-world applications. The solutions obtained using the MT exhibit rapid convergence, which is beneficial for solving physical problems accurately. The numerical results obtained from this approach have shown excellent agreement with their respective exact solutions, further validating its effectiveness. Secondly, the methods employed in this study were applied directly, without resorting to linearization, perturbation, or restrictive assumptions. This direct approach demonstrates the broad applicability of the MT in solving various linear and nonlinear problems encountered in applied science [21]. This transform is coupled with the analytical homotopy perturbation method, and applied to solve the Newell-White-

Segel equation [18], the nonlinear Pantograph delay differential equations [14].

For the analytical solution to the given problem, we have put into practice a recently created methodology. The MADM, which uses the Mohand transform (MT) in place of the Adomian decomposition method, is the process ([24], [25]). The sequence of obtained approximate solutions by using the MADM converges to the exact solution. By solving the resulting nonlinear system of ODEs, the application and validity of this method are verified. Tables and charting are utilized to compare the acquired results. The application of the MT approach in conjunction with the MADM to derive the approximate solution of the suggested model is another novel feature of this research. When the models are the same, the validation processes compare the outcomes directly to the models that have been constructed.

The paper is organized as follows: In Section 2, we give the formulation of the proposed model. Section 3 presents the procedure solution by giving the basic concepts of the Mohand transform, and implementing the modified Adomian decomposition method. Section 4 introduces the numerical simulation of the proposed model. Finally, Section 5 gives the conclusions and remarks.

2. Formulation of the model

As mentioned above, the mathematical modeling of the BC or any other biological phenomena has been an important tool for understanding the dynamic behavior of tumor growth in the treatment process and solving epidemiological problems. This is evident from the studies previously done in ([5], [11], [15]). Despite the large number of studies, none of the proposed mathematical models included a diet (ketogenic diet). Therefore, Oak et al. developed the model in [16], to include some of the control parameters such as the immune booster, ketogenic diet, and anticancer drug, to confirm that there is an interaction between cells due to the mutation in the tumor cell DNA ([7], [27]).

We study the following form of breast cancer ([22], [26]):

$$\begin{aligned}
\dot{\psi}_1(t) &= \psi_1(t)\lambda_1\left(p_1 - \beta_1\psi_1(t) - \alpha_1\,\psi_2(t)\right) - (1-p)\theta_1\,\psi_1(t)\psi_4(t),\\
\dot{\psi}_2(t) &= \psi_2(t)\lambda_2(p_2 d - \beta_2\psi_2(t) - \alpha_2\psi_3(t)) - \kappa\psi_2(t) + (1-p)\theta_1\psi_1(t)\psi_2(t)\psi_4(t),\\
\dot{\psi}_3(t) &= \sigma\rho + \psi_3(t)\lambda_1(p_3 - \beta_3 - \alpha_3\psi_2(t)) - (1-p)\theta_2\psi_3(t)\psi_4(t),\\
\dot{\psi}_4(t) &= \alpha_4\psi_4(t) + \varrho(1-p),
\end{aligned} \tag{1}$$

the corresponding initial conditions of this model are given as follows:

$$\psi_1(0) = \hat{\psi}_1^0, \qquad \psi_2(0) = \hat{\psi}_2^0, \qquad \psi_3(0) = \hat{\psi}_3^0, \qquad \psi_4(0) = \hat{\psi}_4^0. \tag{2}$$

The description of the meaning of the included parameters ($\in \mathbb{R}^+$) of the system (1), will be given in Table 1 ([11], [16]).

The stability analysis, equilibrium points, existence, and uniqueness, of the system under consideration are given in detail in [26].

Table 1: The description of the included parameters of the system (1).

Symbol	Description
$\psi_1(t)$	Normal cell population
$\psi_2(t)$	Luminal type tumor cells
$\psi_3(t)$	Class of immune response
$\psi_4(t)$	Estrogen compartment
λ_1	Growth rate of ψ_1
λ_2	Growth rate of ψ_2
p_i	Carrying capacity of ψ_i, $i = 1, 2, 3$
$(1-p)$	Effectiveness of anti-cancer drugs
κ	Result of the tumor starvation nutrients during the ketogenic diet
ϱ	Process of constantly replenishing excess estrogen
α_1	Inhibition rate of $\psi_1(t)$
α_2	Rate of the effectiveness of the immune system to the tumor cells
α_3	Rate of interaction between $\psi_2(t)$ and $\psi_3(t)$
α_4	Rate at which estrogen is being washed out from the body
θ_1	Tumor formation rate resulting from DNA mutation caused by the presence of excess estrogen
θ_2	Immune suppression rate
β_i	Logistic rate of ψ_i, $i = 1, 2, 3$
d	Ketogenic diet
σ	Source rate of immune response fully infused in the body daily

3. Numerical implementation

3.1. Basic concepts on the Mohand transform

The MT has some useful properties, including linearity, convolution, differentiation, and inversion, which make it a powerful tool in signal processing and other areas. It also has some connections with other well-known transforms, such as the Laplace transform and Mellin transform. We introduce some key definitions and introductory ideas for the MT in this subsection.

Definition 1. *[18]*

We examine functions in set $\mathbb{A}$ that are defined using the Mohand transform, which applies to exponential order functions:

$$\mathbb{A} = \Big\{ f(t) \, : \, \exists \, \Upsilon, \sigma_1, \sigma_2 > 0 \;\; |f(t)| < \Upsilon \, e^{\frac{|t|}{\sigma_j}}, \quad t \in (-1)^j \times [0, \infty) \Big\},$$

σ_1 and σ_2 may be infinite or finite given a function in the set $\mathbb{A}$, but the constant Υ must have a finite value.

Mahgoub and Mohand explained the Mohand transform in 2017 for the function $f(t)$ for $t \geq 0$. For a function $f(t)$, the Mohand transformation indicated by $\mathbb{M}(.)$ is defined as [24]:

$$\mathbb{M}\{f(t)\} = F(s) = s^2 \int_0^\infty f(t) e^{-st} dt, \qquad \sigma_1 \leq s \leq \sigma_2. \tag{3}$$

If the MT of $f(t)$ is $F(s)$ then $f(t)$ is known as the inverse of $F(s)$ which can be described by:

$$\mathbb{M}^{-1}\{F(s)\} = f(t), \qquad \mathbb{M}^{-1} \text{ is the inverse MT.} \tag{4}$$

Some properties of the MT [24]:
Linearity property for $\mathbb{M}\{.\}$: For arbitrary constants a_1, a_2, we have

$$\mathbb{M}\{a_1 f_1(t) + a_2 f_2(t)\} = a_1\mathbb{M}\{f_1(t)\} + a_2\mathbb{M}\{f_2(t)\}.$$

Change of scale property: If $\mathbb{M}\{f(t)\} = F(s)$, then $\mathbb{M}\{f(at)\} = aF\left(\frac{s}{a}\right)$.
Shifting property: $\mathbb{M}\{e^{at}f(t)\} = \frac{s^2}{(s-a)^2}F(s-a)$.
Convolution theorem for $\mathbb{M}\{.\}$: If $\mathbb{M}\{f_1(t)\} = F_1(s)$ and $\mathbb{M}\{f_2(t)\} = F_2(s)$, then

$$\mathbb{M}\left\{f_1(t) * f_2(t)\right\} = \frac{1}{s^2}F_1(s)F_2(s).$$

Mohand transforms of the derivatives of the function $f(t)$:

$$\mathbb{M}\left\{f^{(n)}(t)\right\} = s^n F(s) - s^{n+1}f(0) - s^n f'(0) - \ldots - s^2 f^{(n-1)}(0), \qquad n = 1, 2, 3, \ldots. \tag{5}$$

Mohand transforms for the power functions:

$$\mathbb{M}\left\{t^n\right\} = \begin{cases} \frac{n!}{s^{n-1}}, & n \in \mathbb{N}, \\ \frac{\Gamma(n+1)}{s^{n-1}}, & n > -1. \end{cases}$$

3.2. Implementation of the modified Adomian decomposition method

In this current subsection, we briefly explained the procedure of the newly adopted modified technique.

To implement the MADM for solving the proposed system (1)-(2), we will rewrite it in the following operator form:

$$\begin{aligned} \dot{\psi}_1(t) &= N_1(\psi_1, \psi_2, \psi_3, \psi_4), \\ \dot{\psi}_2(t) &= N_2(\psi_1, \psi_2, \psi_3, \psi_4), \\ \dot{\psi}_3(t) &= \sigma\rho + N_3(\psi_1, \psi_2, \psi_3, \psi_4), \\ \dot{\psi}_4(t) &= \varrho(1-p) + N_4(\psi_1, \psi_2, \psi_3, \psi_4), \end{aligned} \tag{6}$$

where the nonlinear operator functions $N_i(\psi_1, \psi_2, \psi_3, \psi_4),\ i = 1, 2, 3, 4$ are defined as follows:

$$\begin{aligned} N_1 &= \lambda_1\,\psi_1(t)(p_1 - \beta_1\psi_1(t) - \alpha_1\,\psi_2(t)) - (1-p)\theta_1\,\psi_1(t)\psi_4(t), \\ N_2 &= \lambda_2\,\psi_2(t)\,(p_2 d - \beta_2\psi_2(t) - \alpha_2\psi_3(t)) - \kappa\psi_2(t) + (1-p)\theta_1\psi_1(t)\psi_2(t)\psi_4(t), \\ N_3 &= \lambda_1\,\psi_3(t)(p_3 - \beta_3 - \alpha_3\psi_2(t)) - (1-p)\theta_2\psi_3(t)\psi_4(t), \\ N_4 &= -\alpha_4\,\psi_4(t). \end{aligned} \tag{7}$$

Take the MT of the system (6) as follows:

$$\begin{aligned}
s\,\Psi_1(s) - s^2\psi_1(0) &= \mathbb{M}\left[N_1(\psi_1,\psi_2,\psi_3,\psi_4)\right],\\
s\,\Psi_2(s) - s^2\psi_2(0) &= \mathbb{M}\left[N_2(\psi_1,\psi_2,\psi_3,\psi_4)\right],\\
s\,\Psi_3(s) - s^2\psi_3(0) &= \sigma\rho\,s + \mathbb{M}\left[N_3(\psi_1,\psi_2,\psi_3,\psi_4)\right],\\
s\,\Psi_4(s) - s^2\psi_4(0) &= \varrho(1-p)\,s + \mathbb{M}\left[N_4(\psi_1,\psi_2,\psi_3,\psi_4)\right].
\end{aligned} \tag{8}$$

By using the initial conditions (2), we can solve the above algebraic system as follows:

$$\begin{aligned}
\Psi_1(s) &= \hat{\psi}_1^0\,s + \frac{1}{s}\mathbb{M}\left[N_1(\psi_1,\psi_2,\psi_3,\psi_4)\right],\\
\Psi_2(s) &= \hat{\psi}_2^0\,s + \frac{1}{s}\mathbb{M}\left[N_2(\psi_1,\psi_2,\psi_3,\psi_4)\right],\\
\Psi_3(s) &= \hat{\psi}_3^0\,s + \sigma\rho\, + \frac{1}{s}\mathbb{M}\left[N_3(\psi_1,\psi_2,\psi_3,\psi_4)\right],\\
\Psi_4(s) &= \hat{\psi}_4^0\,s + \varrho(1-p) + \frac{1}{s}\mathbb{M}\left[N_4(\psi_1,\psi_2,\psi_3,\psi_4)\right].
\end{aligned} \tag{9}$$

Take the inverse MT of the system (9) as follows:

$$\begin{aligned}
\psi_1(t) &= \hat{\psi}_1^0 + \mathbb{M}^{-1}\left[\frac{1}{s}\mathbb{M}\left[N_1(\psi_1,\psi_2,\psi_3,\psi_4)\right]\right],\\
\psi_2(t) &= \hat{\psi}_2^0 + \mathbb{M}^{-1}\left[\frac{1}{s}\mathbb{M}\left[N_2(\psi_1,\psi_2,\psi_3,\psi_4)\right]\right],\\
\psi_3(t) &= \hat{\psi}_3^0 + \sigma\rho\,t + \mathbb{M}^{-1}\left[\frac{1}{s}\mathbb{M}\left[N_3(\psi_1,\psi_2,\psi_3,\psi_4)\right]\right],\\
\psi_4(t) &= \hat{\psi}_4^0 + \varrho(1-p)\,t + \mathbb{M}^{-1}\left[\frac{1}{s}\mathbb{M}\left[N_4(\psi_1,\psi_2,\psi_3,\psi_4)\right]\right].
\end{aligned} \tag{10}$$

Thus, the first initial components for the approximated solution of the given problem will be obtained as follows:

$$\psi_{1,0}(t) = \hat{\psi}_1^0, \qquad \psi_{2,0}(t) = \hat{\psi}_2^0, \qquad \psi_{3,0}(t) = \hat{\psi}_3^0 + \sigma\rho\,t, \qquad \psi_{4,0}(t) = \hat{\psi}_4^0 + \varrho(1-p)\,t, \tag{11}$$

then, the final iterative scheme for the other terms becomes as:

$$\psi_{k,m+1}(t) = \mathbb{M}^{-1}\left[\frac{1}{s}\mathbb{M}\left[N_k(\psi_1,\psi_2,\psi_3,\psi_4)\right]\right] = \mathbb{M}^{-1}\left[\frac{1}{s}\mathbb{M}\left[A_m^k\right]\right], \qquad k = 1,2,3,4. \tag{12}$$

The nonlinear terms $N_k(\psi_1,\psi_2,\psi_3,\psi_4)$, $k = 1,2,3,4$, are decomposed by using Adomian's polynomials defined as:

$$N_k(\psi_1,\psi_2,\psi_3,\psi_4) = \sum_{m=0}^{\infty} A_m^k, \qquad k = 1,2,3,4, \tag{13}$$

where,

$$A_m^k = \frac{1}{m!}\left[\frac{d^m}{d\lambda^m}\left[N_k\left(\sum_{b=0}^{\infty}\lambda^b\,\psi_{1,b}, \sum_{b=0}^{\infty}\lambda^b\psi_{2,b}, \sum_{b=0}^{\infty}\lambda^b\,\psi_{3,b}, \sum_{b=0}^{\infty}\lambda^b\,\psi_{4,b}\right)\right]\right]_{\lambda=0}, \quad m = 0, 1, \ldots. \tag{14}$$

In view of these formulae, we can compute the first Adomian's polynomials as follows:

$$\begin{aligned}
A_0^1 &= \lambda_1\,\psi_{1,0}(t)(p_1 - \beta_1\psi_{1,0}(t) - \alpha_1\,\psi_{2,0}(t)) - (1-p)\theta_1\,\psi_{1,0}(t)\psi_{4,0}(t)\\
&= \lambda_1\hat{\psi}_1^0\,(p_1 - \beta_1\,\hat{\psi}_1^0 - \alpha_1\,\hat{\psi}_2^0) - (1-p)\theta_1\,\hat{\psi}_1^0\hat{\psi}_4^0,\\
A_0^2 &= \lambda_2\,\psi_{2,0}(t)\,(p_2 d - \beta_2\psi_{2,0}(t) - \alpha_2\psi_{3,0}(t)) - \kappa\psi_{2,0}(t) + (1-p)\theta_1\psi_{1,0}(t)\psi_{2,0}(t)\psi_{4,0}(t)\\
&= \lambda_2\,\hat{\psi}_2^0\,(p_2 d - \beta_2\hat{\psi}_2^0 - \alpha_2\hat{\psi}_3^0) - \kappa\hat{\psi}_2^0 + (1-p)\theta_1\,\hat{\psi}_1^0\hat{\psi}_2^0\hat{\psi}_4^0,\\
A_0^3 &= \lambda_1\,\psi_{3,0}(t)(p_3 - \beta_3 - \alpha_3\psi_{2,0}(t)) - (1-p)\theta_2\psi_{3,0}(t)\psi_{4,0}(t)\\
&= \lambda_1\,\hat{\psi}_3^0\,(p_3 - \beta_3 - \alpha_3\hat{\psi}_2^0) - (1-p)\theta_2\,\hat{\psi}_3^0\hat{\psi}_4^0,\\
A_0^4 &= -\alpha_4\,\psi_{4,0}(t) = -\alpha_4\,\hat{\psi}_4^0.
\end{aligned} \tag{15}$$

In view of the iteration formulae (12), we can compute the following first components of the approximate solution:

$$\begin{aligned}
\psi_{1,1}(t) &= \left(\lambda_1\hat{\psi}_1^0\,(p_1 - \beta_1\,\hat{\psi}_1^0 - \alpha_1\,\hat{\psi}_2^0) - (1-p)\theta_1\,\hat{\psi}_1^0\,\hat{\psi}_4^0\right)t,\\
\psi_{2,1}(t) &= \left(\lambda_2\,\hat{\psi}_2^0\,(p_2 d - \beta_2\hat{\psi}_2^0 - \alpha_2\hat{\psi}_3^0) - \kappa\hat{\psi}_2^0 + (1-p)\theta_1\,\hat{\psi}_1^0\hat{\psi}_2^0\hat{\psi}_4^0\right)t,\\
\psi_{3,1}(t) &= \left(\lambda_1\,\hat{\psi}_3^0\,(p_3 - \beta_3 - \alpha_3\hat{\psi}_2^0) - (1-p)\theta_2\,\hat{\psi}_3^0\hat{\psi}_4^0\right)t,\\
\psi_{4,1}(t) &= \left(-\alpha_4\,\hat{\psi}_4^0\right)t, \ldots.
\end{aligned} \tag{16}$$

Thus, the approximate solution is obtained by collecting m of the approximated terms as follows:

$$\psi_j(t) = \sum_{k=0}^{m-1}\psi_{j,k}(t), \qquad j = 1, 2, 3, 4. \tag{17}$$

4. Numerical simulation

We test the accuracy of the resulting numerical method by presenting numerical simulations on some cases in $[0, 3]$ for the proposed model (1). The behavior of $\psi_k(t)$, $k = 1, 2, 3, 4$ are presented in Figures 1-5 at different values of some parameters (m, ϱ, p).

We approach the system under study (1) with the following values for the parameters contained in it [8]:

$$\theta_1 = 0.2, \quad \theta_2 = 0.02, \quad \lambda_1 = 0.3, \quad \lambda_2 = 0.4, \quad d = 0.5, \quad \alpha_1 = 6\times10^{-8}, \quad \alpha_2 = 3\times10^{-7},$$

$$\alpha_3 = 1\times10^{-7}, \quad \alpha_4 = 0.97, \ \rho = 0.01, \ \kappa = 2, \quad \beta_1 = 0.15, \quad \beta_2 = 0.7, \quad \beta_3 = 0.1, \quad p = 0.5,$$
$$\sigma = 0.1, \quad p_1 = 0.1, \quad p_2 = 0.2, \quad p_3 = 0.3, \quad \varrho = 0.8.$$

With the initial conditions (I.Cs) $\psi_i(0) = 0.2$, $i = 1, 2, 3, 4$. Figures 1-5 show a numerical simulation of the system under investigation by applying the given procedure.

(i) Figure 1 gives the approximate solution for distinct values of the approximation order $m = 5, 10, 15$.

(ii) Figure 2 shows the approximate solution for distinct values of the estrogen source rate $\varrho = 0.8$, 1.4, 2.0, 2.6.

(iii) Figure 3 depicts the effect of p (= 0.25, 0.5, 0.75, 1.0) on the approximate solution.

(iv) Figure 4 presents a comparison between the solution generated by the obtained approach with that numerical solution by implementing the RK4M [9] with the same parameters and I.Cs.

(v) Figure 5 plots the residual error function (REF) [19] of the obtained approximate solution.

The behavior of the approximate solution is based on m, ϱ, p, as shown in Figures 1-3, respectively. From Figures 2 and 3, we can confirm that the behavior of the solution consists with of the natural effect of the parameters ϱ, and p, respectively. From Figures 4 and 5, we can point out that the proposed method has been well applied to solve the problem under study. Hence, we can verify that the expected behavior of the disease has been obtained, which means that we have provided a clear simulation of the proposed model that can be used by the relevant authorities to treat this deadly cancer.

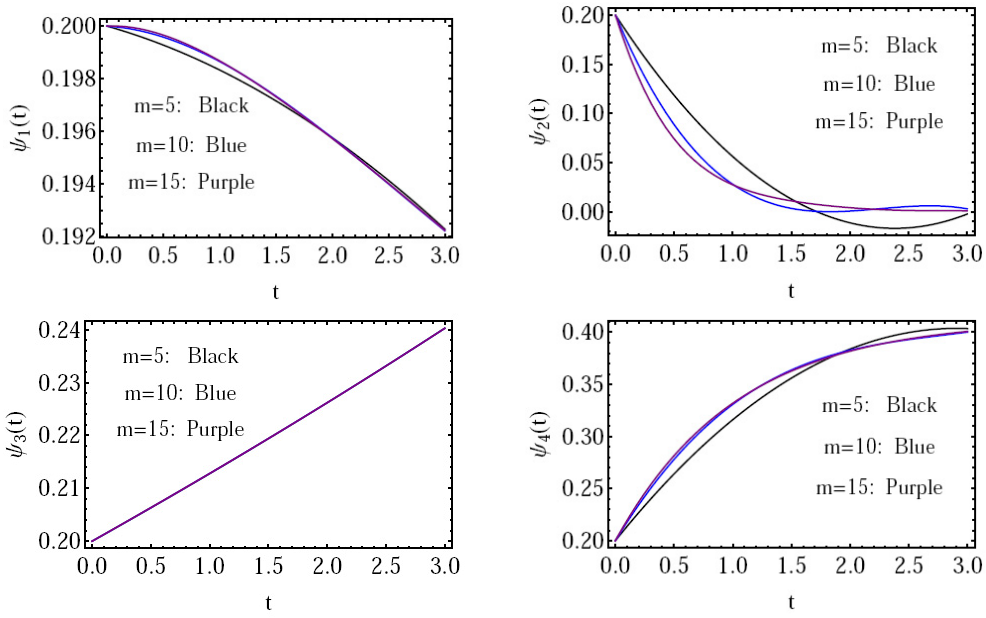

Figure 1. The approximate solution via various values of m.

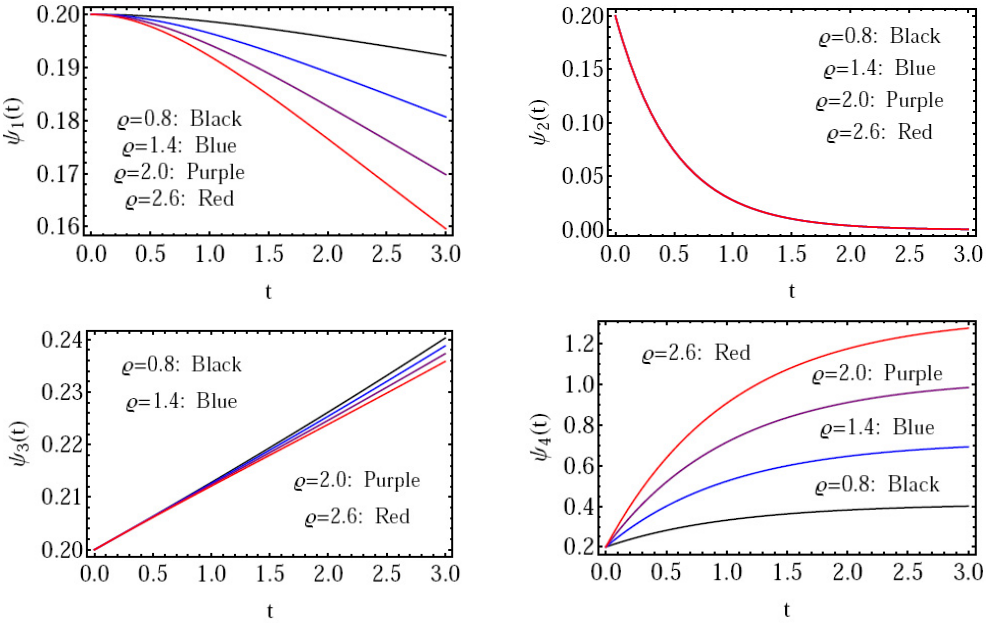

Figure 2. The approximate solution via various values of ϱ.

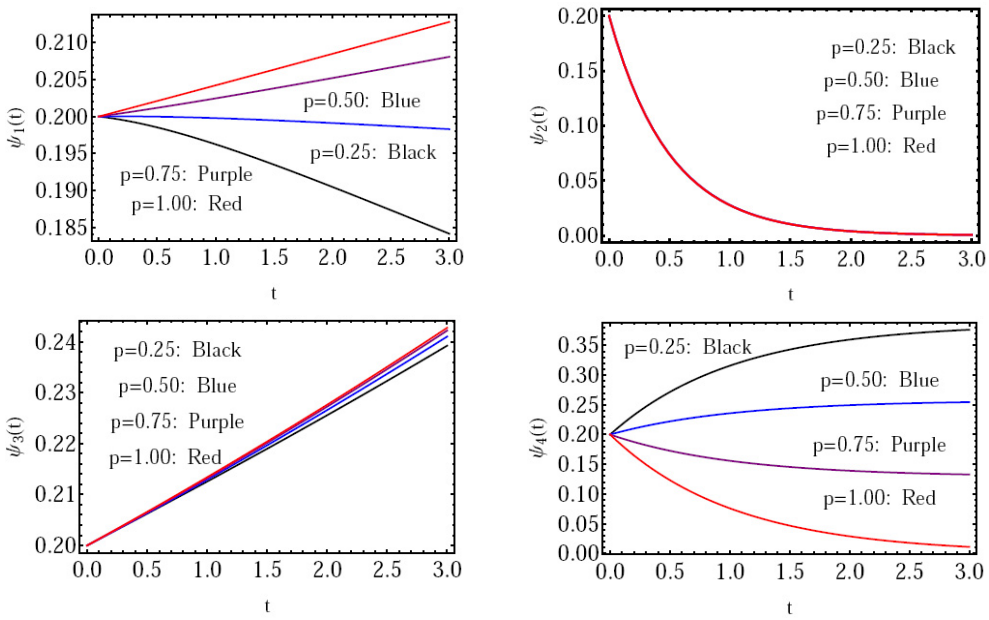

Figure 3. The approximate solution via various values of p.

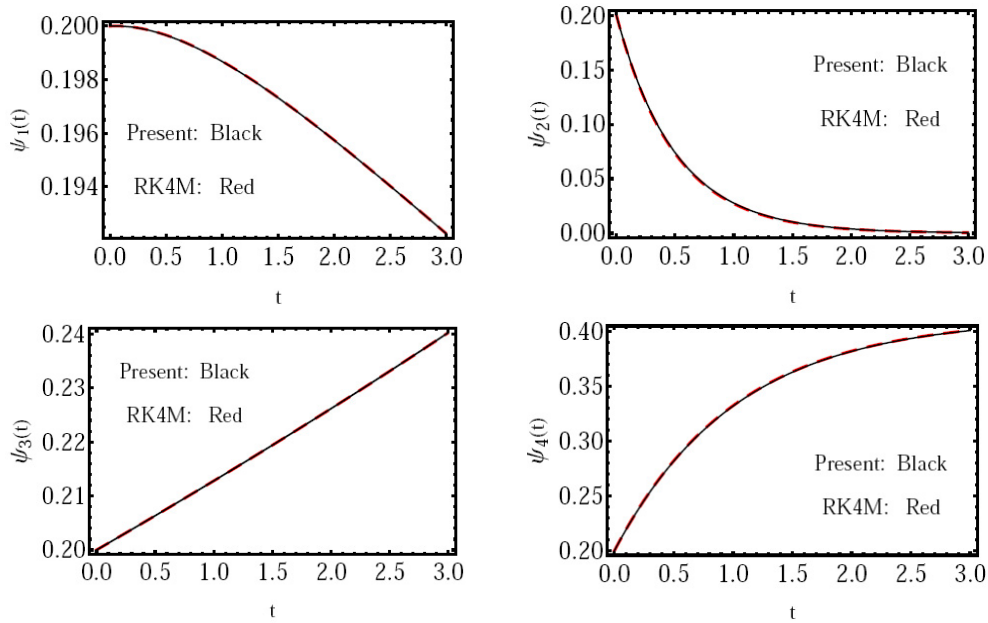

Figure 4. Comparison the solution obtained by the proposed method and RK4M.

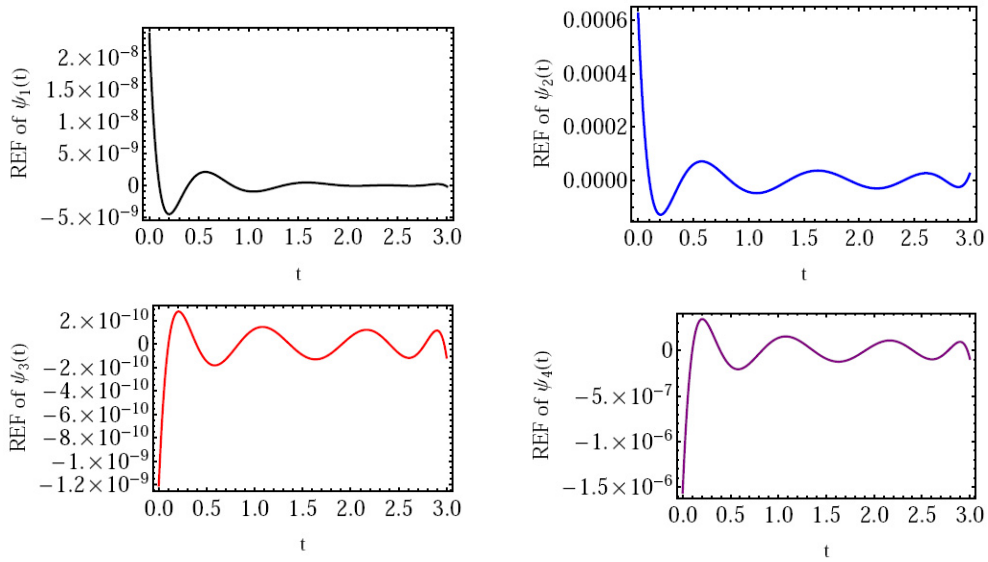

Figure 5. The REF of the obtained approximate solution.

5. Conclusions

We implemented an approximate method by using the modified Adomian decomposition method associated with Mohand transforms to solve and simulate the mathematical model for Breast Cancer. By means of this work, we used several values of the approximation order, estrogen source rate, and anti-cancer drug efficacy to obtain the approximate solution of the model under investigation. The obtained results were compared graphically with those obtained using the RK4 approach, from which we found a great deal of convergence between them. The accuracy of the resulting solutions can be increased by increasing m. From the obtained results, we can confirm that the proposed approach is surprisingly successful in simulating the BC model, as well as it demonstrating the accuracy and computational effectiveness of this method. Finally, the present study may contribute to providing more robust physical explanations for future theoretical and computational studies on the same topic.

References

[1] Breast cancer. Available online: `https://www.who.int/news-room/fact-sheets/detail/breast-cancer` (accessed on 15 July 2023).

[2] M. Adel, M. M. Khader, T. A. Assiri, and W. Kaleel. Numerical simulation for covid-19 model using a multidomain spectral relaxation technique. *Symmetry*, 15:1–12, 2023.

[3] M. M. Al-Shomrani and M. A. Abdelkawy. Numerical simulation for a fractional-

order differential system of a glioblastoma multiforme and immune system. *Adv. Differ. Equ.*, 2020:516, 2020.

[4] I. M. Batiha, A. Bataihah, A. Al-Nana, S. Alshorm, I. H. Jebril, and A. Zraiqat. A numerical scheme for dealing with fractional initial value problem. *Int. J. Innov. Comput. Inform. Control*, 19:763–774, 2023.

[5] A. d'Ornafrio, U. Ledzewicz, H. Maurer, and H. Schaettler. On optimal delivery of combination therapy for tumors. *Math. Biosci.*, 222:13–26, 2009.

[6] M. Fathoni, G. Gunardi, F. A. Kusumo, and S. H. Hutajulu. Mathematical model analysis of breast cancer stages with side effects on the heart in chemotherapy patients. In *Proceedings of the AIP Conference Proceedings*, Yogyakarta, Indonesia, 2019. AIP Publishing.

[7] M. A. Hajji and Q. Al-Mdallal. Numerical simulations of a delay model for immune system-tumor interaction. *Sultan Qaboos Univ. J. Sci.*, 23:19–31, 2018.

[8] M. A. Hammad, I. H. Jebril, S. Alshorm, I. M. Batiha, and N. A. Hammad. Numerical solution for a fractional-order mathematical model of immune-chemotherapeutic treatment for breast cancer using the modified fractional formula. *Int. J. Anal. Appl.*, 21:1–9, 2023.

[9] Y. F. Ibrahim, S. E. Abd El-Bar, M. M. Khader, and M. Adel. Studying and simulating the fractional covid-19 model using an efficient spectral collocation approach. *Fractal and Fractional*, 7:1–15, 2023.

[10] M. Idrees, A. S. Alnahdi, and M. B. Jeelani. Mathematical modeling of breast cancer based on the caputo-fabrizio fractal-fractional derivative. *Fractal Fract.*, 7:1–14, 2023.

[11] W. O. Kermarck and A. G. M. Kendrick. Contributions to the mathematical theory of epidemics. *Proc. R. Soc. Lond. Ser. A*, 115:700–721, 1927.

[12] M. M. Khader and M. Adel. Modeling and numerical simulation for covering the fractional covid-19 model using spectral collocation-optimization algorithms. *Fractal and Fractional*, 6:1–19, 2022.

[13] M. M. Khader, N. H. Sweilam, A. M. S. Mahdy, and N. K. A. Moniem. Numerical simulation for the fractional sirc model and influenza a. *Appl. Math. Inf. Sci.*, 8:1029–1036, 2014.

[14] C. D. Kumar and A. E. K. Pushpam. Mohand decomposition method for solving nonlinear pantograph delay differential equations. *Journal of Emerging Technologies and Innovative Research*, 6(2):264–267, 2019.

[15] C. Mufudza, S. Walter, and E. T. Chiyaka. Assessing the effects of estrogen on the dynamics of chemo-virotherapy cancer. *Comput. Math. Methods Med.*, 473572:1–15, 2012.

[16] S. I. Oke, M. B. Matadi, and S. S. Xulu. Optimal control analysis of a mathematical model for breast cancer. *Math. Comput. Appl.*, 21:1–16, 2018.

[17] F. Okose, M. T. Senel, and R. Habbireeh. Fractional-order mathematical modeling of cancer cells-cancer stem cells-immune system interaction with chemotherapy. *Math. Model. Numer. Simul. Appl.*, 1:67–83, 2021.

[18] O. O. Omotola, A. J. Temiatyo, A. A. Sufiat, and S. A. Ezekie. Application of mohand transforms coupled with homotopy perturbation method to solve newel-white-segel-

equation. *Annals of Mathematics and Computer Science*, 21:162–180, 2024.

[19] K. Parand and M. Delkhosh. Operational matrices to solve nonlinear volterra-fredholm integro-differential equations of multi-arbitrary order. *Gazi University Journal of Science*, 29:895–907, 2016.

[20] M. Abaid Ur Rehman, J. Ahmad, A. Hassan, J. Awrejcewicz, W. Pawlowski, H. Karamti, and F. M. Alharbi. The dynamics of a fractional-order mathematical model of cancer tumor disease. *Symmetry*, 14:1–15, 2022.

[21] R. Saadeh, A. Alshawabkeh, R. Khalil, M. A. Abdoon, N. E. Taha, and D. K. Almutairi. The mohanad transforms and their applications for solving systems of differential equations. *European Journal of Pure and Applied Mathematics*, 17(1):385–409, 2024.

[22] Z. Sabir, M. Munawar, M. A. Abdelkawy, M. A. Z. Raja, C. Ünlü, M. B. Jeelani, and A. S. Alnahdi. Numerical investigations of the fractional-order mathematical model underlying immune-chemotherapeutic treatment for breast cancer using the neural networks. *Fractal Fract.*, 6:1–16, 2022.

[23] C. E. De Santis, F. Bray, J. Ferlay, J. Lortet-Tieulent, B. O. Anderson, and A. Jemal. International variation in female breast cancer incidence and mortality rates. *Cancer Epidemiol Biomarkers Prev.*, 6:1495–1506, 2015.

[24] R. Shah, U. Farooq, H. Khan, D. Baleanu, P. Kumam, and M. Arif. Fractional view analysis of third-order kortewege-de vries equations, using a new analytical technique. *Frontiers in Physics*, 7:5–15, 2020.

[25] A. Sudhanshu, M. Rashmi, and K. Anuj. A comparative study of mohand and elzaki transforms. *Global Journal of Engineering Science and Researches*, 6:203–213, 2019.

[26] A. Yousef, F. Bozkurt, and T. Abdeljawad. Mathematical modeling of the immune-chemotherapeutic treatment of breast cancer under some control parameters. *Adva. Differ. Equs.*, 696:1–25, 2020.

[27] F. B. Yousef, A. Yousef, T. Abdeljawad, and A. Kalinli. Mathematical modeling of breast cancer in a mixed immune-chemotherapy treatment considering the effect of ketogenic diet. *Eur. Phys. J. Plus*, 135:1–23, 2020.