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Analytical Simulation to Study the Behavior of Cancerous Tumors by Using Shehu Transformation-Akbari-Ganji's Method with the Padé Approximation

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Abstract: This paper presents an approximate analytical study of the dynamic model of the interaction between lymphocytes and tumor cells in the presence of cytokines. A new method that combines the Shehu transformation and Akbari-Ganji method with the Padé approximation was applied. The accuracy and high efficiency of this method were demonstrated by error tables and graphs. The study found that the rate and duration of treatment had a significant effect on preventing the growth of cancer cells and improving the function of cancer-fighting lymphocytes, confirming the importance of studying and determining the optimal concentrations of cytokines that contribute to inhibiting the growth of cancer cells and improving the function of lymphocytes in fighting cancer.

Keywords: Shehu transformation, Akbari -Ganji's method, Padé approximation, Tumors, Immunotherapy, Cytokine, Stability.

1. Introduction

Cancer is currently one of the most malignant and fatal diseases facing humans, and it is known that the currently available cancer treatments mainly use toxic chemicals and harmful radiation, which leads to dangerous side effects for patients. However, with the advancement of research and technology. Cancer treatments have recently undergone significant development to create a treatment that can rapidly dissolve a tumor without endangering nearby healthy tissue. Nani and Freedman investigated a general mathematical model of immunotherapy as a cancer treatment [1]. Sotolongo-Costa et al. [2] studied the behavior of tumors under unstable therapy using doses of cytokines. They discussed the model equations and hypotheses as well as general concepts of cancer immunotherapy. Tumor immune interactions were also researched by Banerjee and Sarkar [3]. To illustrate the immune system's basic defense mechanism, they divided the immune system into two subclasses: hunting cells (cytotoxic T lymphocytes) and the resting cells (T helper cells). Fukuhara et al. [4] discovered a new treatment for cancer using genetically modified viruses. Kumar et al. [5] studied the interactions between cancer cells and the immune architecture using a partial tumor model. Nave and Sigron presented a mathematical model for the treatment of melanoma with the BRAF/MEK inhibitor and anti-PD-1 [6]. Aljahdaly and Almushaity studied the immune response to a model of metastatic cancer with virotherapy [7]. In this paper, we will highlight the use of cytokines as a treatment for cancer. Cytokines are protein hormones that play a role in activating the immune system and enhancing its response to attack cancer cells [2]. What has just been discussed shows the importance of research in this field and its treatment using various simulation techniques. The

Akbari-Ganji method, initially pioneered by Ganji and Akbari, represents one of numerous analytical approaches that effectively address a wide range of ordinary and partial nonlinear differential equations [8]. Additionally, Pade's approximation, a numerical technique employed for function approximation by representing them as partial fractions, offers heightened precision and enhanced computational efficiency compared to alternative approximation methods. This method was originally introduced by Henri Padé in 1890 [9]. The Shehu transformation, established by Maitama and Zhao in 2019 [10], stands as an integral transformation renowned for its utility in solving both ordinary and partial differential equations, showcasing its versatility across various fields. To harness the full potential of integrative transformations and analytical methods, a synergistic approach has been increasingly explored in a multitude of investigations [11-16]. Building upon the insights from these prior studies, it becomes evident that numerical simulation serves as a cost-effective and time-efficient means to predict experimental outcomes. We are particularly interested in introducing enhancements to existing simulation methods to ensure the attainment of high-precision and dependable results. In our present study, we present a novel simulation method that arises from the fusion of contemporary and influential approximate analytical techniques. Specifically, we combine the Shehu transformation and the Akbari-Ganji method with the Padé approximation, herein referred to as SAGPM. The new method has been tested in solving the dynamic model of the interaction between lymphocytes and tumor cells in the presence of cytokines. In addition, we determined the extent of significant effect of the rate and duration of treatment on preventing the growth of cancer cells and improving the function of cancer-fighting lymphocytes. The application of the new approach showed the effectiveness and efficiency of the proposed strategy in terms of high accuracy and good convergence in comparison to other methods. The results also showed that treatment with doses of cytokines reduces tumor size and changes tumor behavior, which is consistent with the results of previous studies.

2. The SAGPM Algorithm

The core concept of the SAGPM is derived from the Shehu transformation method, the Akbari-Ganji method, and Padé's approximation algorithms, which are briefly outlined below:

2.1. Shehu transformation [10]

In 2019, Maitama and Zhao introduced the Shehu transformation method, serving as an extension of the Laplace and Sumudu integral transforms. This innovative transformation technique was applied to address differential equations.

The Shehu transformation is formulated within the context of the set B:

$$B = \left\{ f(x): \exists\, N, n_1, n_2 > 0, |f(x)| < N\, exp\left(\frac{|x|}{n_i}\right), if\ x \in\ (-1)^i \times [0,\infty) \right\},$$

defined as:

$$S[f(x)] = F(v,u) = \int_0^\infty exp(\tfrac{-vx}{u})\, f(x)\, dx$$

$$= lim_{a\to\infty} \int_0^a exp(\tfrac{-vx}{u})\, f(x)\, dx, \quad v > 0, u > 0. \tag{1}$$

The inverse Shehu transformation is expressed as:

$$S^{-1}[\, F(v,u)] = f(x), \text{ for } x \geq 0.$$

Equivalently

$$f(x) = S^{-1}[\, F(v,u)] = \frac{1}{2\pi i} \int_{a-i\infty}^{a+i\infty} \frac{1}{u} exp(\tfrac{vx}{u}) F(v,u)\, dv, \tag{2}$$

where v and u denote the variables of the Shehu transformation.

2.1.1. Shehu transformation of derivatives and some functions

If $S\{x(t)\} = X(v,u)$ then

1. $S\left\{\frac{dx}{dt}\right\} = \frac{v}{u}X(v,u) - x(0)$
2. $S\{x^{(n)}(t)\} = \frac{v^n}{u^n}X(v,u) - \sum_{k=0}^{n-1}\left(\frac{v}{u}\right)^{n-(k+1)} x^{(k)}$
3. $S\{t\} = \frac{v^2}{u^2}$
4. $S\left\{\frac{t^n}{n!}\right\} = \left(\frac{v}{n}\right)^{n+1}, \quad n = 0,1,2,\ldots$
5. $S\{\exp(at)\} = \frac{v}{u-av}$
6. $S\{\sin(t)\} = \frac{vu}{u^2-v^2}$
7. $S\{\cos(t)\} = \frac{vu}{u^2+v^2}$

2.2. Akbari-Ganji's method (AGM)

The AGM, developed by Akbari and Ganji, serves as a powerful computational methodology for effectively addressing a wide range of nonlinear differential equations. In this approach, the solution is approximated as a finite series, leading to the resolution of a sequence of algebraic problems [8].

To apply the AGM, the differential equation for a function $x(t)$ and its derivatives can be expressed as follows:

The nonlinear differential equation with m^{th}-order derivatives is represented as:

$$h_k = f(x,x',x'',\ldots,x^{(m)}) = 0, \quad x = x\ (t) \tag{3}$$

with boundary conditions:

$$x(t) = x_0, x'(t) = x_1, \ldots, x^{(m-1)}(t) = x_{m-1}, \ at\ t = 0 \tag{4a}$$

$$x(t) = x_{L_0}, x'(t) = x_{L_1}, \ldots, x^{(m-1)}(t) = x_{L_{m-1}}, \ at\ t = L \tag{4b}$$

Now, let's assume the solution for the differential equation (3) as follows:

$$x(t) = \sum_{i=0}^{n} a_i\ t^i. \tag{5}$$

Eq. (5) can be solved with a high degree of accuracy by including more terms in the series. If the series (5) has (n) terms, there will be (n) unknown coefficients to determine, thus allowing the solution to be found for the differential equation (3). Boundary conditions (4a) and (4b) are applied to Eq. (5) as follows:

We can calculate the following at $t = 0$.

$$\begin{cases} x(0) = a_0 = x_0 \\ x'(0) = a_1 = x_1 \\ x''(0) = a_2 = x_2 \\ \vdots \end{cases} \tag{6}$$

when $t = L$

$$\begin{cases} x(L) = a_0 + a_1 L + ... + a_n L^n = x_{L_0} \\ x'(L) = a_1 + 2a_2 L + ... + n a_n L^{n-1} = x_{L_1} \\ x''(L) = 2a_2 + 6a_3 L ... + n(n-1) a_n L^{n-2} = x_{L_2} \\ \vdots \end{cases} \quad (7)$$

After substituting Eq. (5) into Eq. (3) and applying the boundary conditions to it, we arrive at the following system of equations:

$$\begin{cases} h_0 = f(x(0), x'(0), x''(0), ..., x^{(m)}(0)) \\ h_1 = f(x(L), x'(L), x''(L), ..., x^{(m)}(L)) \\ \vdots \end{cases} \quad (8)$$

Applying the boundary conditions to the derivatives, we have:

$$h'_k : \begin{cases} f(x'(0), x''(0), x'''(0), ..., x^{(m+1)}(0)) \\ f(x'(L), x''(L), x'''(L), ..., x^{(m+1)}(L)) \end{cases} \quad (9)$$

$$h''_k : \begin{cases} f(x''(0), x'''(0), x''''(0), ..., x^{(m+2)}(0)) \\ f(x''(L), x'''(L), x''''(L), ..., x^{(m+2)}(L)) \end{cases} \quad (10)$$

In the end, we obtain a system of equations from which we can calculate the unknown coefficients a_0 , a_1 , a_2 ..., and a_n . This allows us to determine the solution for the differential Eq. (3).

2.3. Padé approximation

Henri Padé is recognized as the originator of the Padé approximation, a classical rational approximation initially proposed by George Frobenius. This method is founded on the principles of rational power approximation and consists of the quotient of two polynomials with distinct degrees. The Padé approximation excels at approximating functions and surpasses the accuracy of the Taylor series. It has found widespread applications in computer science, particularly in the determination of time delays [17-19].

The Padé approximation is expressed as a ratio of two polynomials derived from the Taylor series expansion of a function $x(t)$, and it is defined as [9]:

$$P_m^l = \frac{\sum_{n=0}^{l} a_n t^n}{\sum_{n=0}^{m} b_n t^n}, \quad (11)$$

where $b_0 = 1$, l represents the degree of the numerator polynomial.

m signifies the degree of the denominator polynomial.

The function $x(t)$ can be represented as:

$$x(t) = \sum_{n=0}^{\infty} c_n t^n. \quad (12)$$

Furthermore:

$$x(t) - P_m^l = o(t^{l+m+1}).$$

Thus,

$$\sum_{n=0}^{\infty} c_n t^n = \frac{\sum_{n=0}^{l} a_n t^n}{\sum_{n=0}^{m} b_n t^n}, \quad (13)$$

or

$$c_0 + c_1 t^1 + c_2 t^2 + \cdots = \frac{a_0 + a_1 t^1 + a_2 t^2 + \cdots}{1 + b_1 t^1 + b_2 t^2 + \cdots}.$$

From Eq. (13), obtain the following system equations

$$a_0 = c_0$$
$$a_1 = c_1 + c_0 b_1$$
$$a_2 = c_2 + c_1 b_1 + c_0 b_2$$
$$\vdots$$

where c_n is given.

Consequently, we derive the following system of equations from Eq. (13), where $x(t)$ is a given function. To solve this system for a_n and b_n, we set the degree of the numerator to l and the denominator to m. Additionally, we perform a Taylor series expansion of $x(t)$ up to a specified order.

In summary, the following steps encapsulate the core concept of the SAGPM algorithm [20]. We consider the following system:

$$\left.\begin{aligned} \frac{dx_1}{dt} &= f(x_1(t), x_2(t), a_1(t), \dots, a_n(t)) \\ \frac{dx_2}{dt} &= g(x_1(t), x_2(t), b_1(t), \dots b_n(t)) \end{aligned}\right\} \quad (14)$$

with initial conditions:

$x_1(0) = \alpha$, $x_2(0) = \beta$

Step 1: Begin by applying the Shehu transformation to both sides of Eq. (14) to yield:

$$\left.\begin{aligned} S\left(\frac{dx_1}{dt}\right) &= S(f(x_1(t), x_2(t), a_1(t), \dots a_n(t))), \\ S\left(\frac{dx_2}{dt}\right) &= S(g(x_1(t), x_2(t), b_1(t), \dots b_n(t))), \end{aligned}\right\} \quad (15)$$

Utilizing the differentiation property of the Shehu transformation and incorporating the provided initial conditions, we arrive at:

$$\left.\begin{aligned} X_1(u,v) &= \frac{\alpha u}{v} + \frac{u}{v} S(f(x_1(t), x_2(t), a_1(t), \dots a_n(t))), \\ X_2(u,v) &= \frac{\beta u}{v} + \frac{u}{v} S(g(x_1(t), x_2(t), b_1(t), \dots b_n(t))), \end{aligned}\right\} \quad (16)$$

Step 2: Apply the inverse Shehu transformation to both sides of Eq. (16) to obtain:

$$\left.\begin{aligned} x_1(t) &= \alpha + S^{-1}\left(\frac{u}{v} S(f(x_1(t), x_2(t), a_1(t), \dots a_n(t)))\right), \\ x_2(t) &= \beta + S^{-1}\left(\frac{u}{v} S(g(x_1(t), x_2(t), b_1(t), \dots b_n(t)))\right), \end{aligned}\right\} \quad (17)$$

Step 3: Examine the AGM polynomial series characterized by constant coefficients, expressed as follows:

$$x_1(t) = \sum_{i=0}^{n} a_i t^i \quad , \quad x_2(t) = \sum_{i=0}^{n} b_i t^i \quad (18)$$

After substituting Eq. (18) into Eq. (17), Eq. (17) takes the form:

$$\left.\begin{aligned} \sum_{i=0}^{n} a_i t^i &= \alpha + S^{-1}\left(\frac{u}{v} S(f(\sum_{i=0}^{n} a_i t^i, \sum_{i=0}^{n} b_i t^i, a_1(t), \dots, a_n(t)))\right), \\ \sum_{i=0}^{n} b_i t^i &= \beta + \left(\frac{u}{v} S(g(\sum_{i=0}^{n} a_i t^i, \sum_{i=0}^{n} b_i t^i, b_1(t), \dots b_n(t)))\right). \end{aligned}\right\} \quad (19)$$

By applying the initial conditions, we can determine certain coefficients, and through continued derivation of Eq. (19) while incorporating the initial conditions, we can calculate the remaining coefficients.

Step 4: Apply the Padé approximation of order $[l/m]$ to a power series solution obtained via the SAGPM. Select appropriate values for l and m. In this stage, we derive the final solution.

3. The mathematical model

In this section, we hypothesize a dynamic model that describes the interaction between tumor cells and lymphocytes [2]

$$\left.\begin{aligned}\frac{dx_1}{dt} &= \alpha x_1 - x_1 x_2 \\ \frac{dx_2}{dt} &= x_1 x_2 - \frac{1}{\alpha} x_2 - k x_1 + \sigma + v\cos^2(\beta t)\end{aligned}\right\}, \tag{20}$$

with initial conditions

$$x_1(0) = 2.1\ , x_2(0) = 2.7,$$

where

$v = \frac{Fb}{af}, k = \frac{Kb}{d\sqrt{af}}, \alpha = \sqrt{\frac{a}{f}}, \sigma = \frac{ub}{af}, \beta = \frac{w}{\sqrt{af}}$, and the definitions of the other parameters are shown in Table 1.

Table 1: Variables and parameters used in system (20).

	Description
x_1	Number of malignant cells
x_2	Lymphocyte count
a	The growth rate of malignant cells
b	The reaction rate between malignant cells and lymphocytes
u	Lymphocyte proliferation
F	The net worth of doses
f	The rate of decline of lymphocytes
w	Repeating the cyclic behavior of cytokines within the body
d	The frequency of the immune systems recognition of cancer cells
K	The rate of decline of malignant cells

By taking the Shehu transformation on both sides of (20), we obtain

$$\left.\begin{aligned}X_1(u,s) &= \frac{2.1\ u}{s} + \frac{u}{s} S(\alpha x_1 - x_1 x_2) \\ X_2(u,s) &= \frac{2.7\ u}{s} + \frac{u}{s} S(x_1 x_2 - \frac{1}{\alpha} x_2 - k x_1 + \sigma + v\cos^2(\beta t))\end{aligned}\right\} \tag{21}$$

Taking the inverse Shehu transformation on both sides of (21), we obtain

$$\left.\begin{aligned}x_1(t) &= 2.1 + S^{-1}\left(\frac{u}{s} S(\alpha x_1 - x_1 x_2)\right) \\ x_2(t) &= 2.7 + S^{-1}\left(\frac{u}{s} S\left(x_1 x_2 - \frac{1}{\alpha} x_2 - k x_1 + \sigma + v\cos^2(\beta t)\right)\right)\end{aligned}\right\} \tag{22}$$

By AGM , we substitute (18) into (22) to obtain

$$\left.\begin{aligned}\sum_{i=0}^{n} a_i t^i &= 2.1 + S^{-1}\left(\frac{u}{s} S(\alpha \sum_{i=0}^{n} a_i t^i - \sum_{i=0}^{n} a_i t^i * \sum_{i=0}^{n} b_i t^i)\right) \\ \sum_{i=0}^{n} b_i t^i &= 2.7 + S^{-1}\left(\frac{u}{s} S\left(\sum_{i=0}^{n} a_i t^i x_2 - \frac{1}{\alpha}\sum_{i=0}^{n} b_i t^i - k\sum_{i=0}^{n} a_i t^i + \sigma + v\cos^2(\beta t)\right)\right)\end{aligned}\right\} \tag{23}$$

When n = 3, after simplification and offset values of

$\alpha = 2, k = 0.2, \sigma = 0.05, v = 0.25\ and\ \beta = 0.30$, Eq. (23) becomes:

$$f(x_1(t)) = -2\mu_1 + \mu_1\mu_2 = 0 \quad (24)$$
$$g(x_2(t)) = 0.5\mu_2 - \mu_1\mu_2 + 0.2\mu_1 - 0.05 - 0.25\cos^2(0.3t) = 0, \quad (25)$$

where

$$\mu_1 = a_0 + a_1 t + a_2 t^2 + a_3 t^3,\ \mu_2 = b_0 + b_1 t + b_2 t^2 + b_3 t^3.$$

The constant coefficients of Eqs. (24) and (25), which are $\{a_0, \ldots, a_3 \text{ and } b_0, \ldots, b_3\}$ can be computed by applying initial conditions in the form of:

$$x_1(t=0) = 2.1 \rightarrow a_0 = 2.1, \quad x_2(t=0) = 2.7 \rightarrow b_0 = 2.7.$$

On both Eqs. (24) and (25) and their derivatives, the initial conditions are applied as follows:

$$f(x_1(t=0)): a_0 b_0 - 2a_1 + a_1 = 0,$$
$$g(x_2(t=0)): -0.3 + b_1 + 0.5b_0 - a_0 b_0 + 0.2a_0 = 0$$
$$f'(x_1(t=0)): a_0 b_1 + a_1 b_0 - 2(a_1 + a_2) = 0,$$
$$g'(x_1(t=0)): 2b_2 + 0.5b_1 - a_1 b_0 - a_0 b_1 + 0.2a_1 = 0,$$
$$f''(x_1(t=0)): 2(a_0 b_2 + a_1 b_1 + a_2 b_0) - 4a_2 + 6a_3 = 0,$$
$$g''(x_1(t=0)): 0.045 + 6b_3 + b_2 - 2(a_2 b_0 + a_1 b_1 + a_0 b_2) + 0.4a_2 = 0,$$

Maple software facilitates the determination of unknown constant coefficients a_i and b_i by solving the aforementioned equations.

Then the solutions are

$$x_1(t) = 2.1 - 1.47t - 3.8955t^2 + 1.9012t^3$$
$$x_2(t) = 2.7 + 4.2t + 1.5225t^2 - 4.49975t^3$$

Now, takeing the Padé approximation, with l = 0, m= 3 for $x_1(t)$ and l = 1, m= 2 for $x_2(t)$, we obtain the solutions of the system

$$x_{1[0,3]} = \frac{2.1}{0.9999999998 + 0.6999999999t + 2.345t^2 + 2.034666666t^3}$$

$$x_{2[1,2]} = \frac{2.7 + 0.4992532845t}{1.0 - 1.370646932t + 1.568228560t^2}$$

4. Results and discussion

This section delves into the numerical computations for the mathematical model, obtained through the application of SAGPM. **Table 2** shows the comparison between the new method SAGPM and AGM and the Adomian decomposition method (ADM) by measurements of errors and CPU time at $\alpha = 2,\ k = 0.2, \sigma = 0.05\ and\ \beta = 0.30$, and different values of v. We note from the error tables that the new method is more accurate and efficient compared to AGM and ADM in terms of fewer errors and a lower CPU time. **Table 3** shows the compatibility of the solutions obtained using the new SAGPM method with the results of the AGM for different values of β. It also shows the effect of parameter β which correlates with repeat dosing on tumor and lymphoid cells over time. **Fig. 1** demonstrates a comparative analysis between the solutions provided by the new method SAGPM and AGM for the given system (20), at $\alpha = 2, \sigma = 0.05,\ k = 0.2, \beta = 0.30\ and\ v = 0.25$. **Fig. 2** demonstrates approximate analytical solutions for cancer cells and lymphocytes before and after the administration of doses of cytokines**.** In this figure, we notice that the tumor size decreases when additional doses of cytokines are given.

Table 2: Compare of the errors and CPU time for ADM, AGM and SAGPM, with a step size of $h = 0.05$, over the time interval at $t \in (0,1)$.

	Functions	*Errors*	*ADM*	*AGM*	*SAGPM*
$v = 0$	$x_1(t)$	L_2	0.06751368080	0.06751368076	0.04412635052
		L_∞	0.2321812500	0.232181250	0.1210824527
		CPU(s)	0.063	0.047	0.015
	$x_2(t)$	L_2	0.1547555780	0.1547555778	0.02522920002
		L_∞	0.532208333	0.532208333	0.086802633
		CPU(s)	0.063	0.047	0.015
$v = 0.25$	$x_1(t)$	L_2	0.0683087826	0.06910388441	0.04628084687
		L_∞	0.2349156251	0.237650000	0.1259219291
		CPU(s)	0.047	0.031	0.015
	$x_2(t)$	L_2	0.1590188379	0.1635547040	0.07009076560
		L_∞	0.546869792	0.562468750	0.238824051
		CPU(s)	0.047	0.031	0.015

where; the measurement errors are defined as the follows:

$$\|E\|_{L_2} = \sqrt{h\sum_{i=0}^{n}|x_{i+1} - x_i|^2}, \|E\|_{L_\infty} = max_{i=0..n}(|x_{i+1} - x_i|).$$

Table 3: Comparison between approximate solutions obtained by AGM and SAGPM when $v = 0.25$ and for different values of β.

Methods	Time	*Functions*	$\beta = 0.30$	$\beta = 0.32$	$\beta = 0.34$
AGM	$t = 0.15$	$x_1(t)$	1.798267800	1.798267800	1.798267800
		$x_2(t)$	3.349069594	3.349066106	3.349062394
	$t = 0.35$	$x_1(t)$	1.189815200	1.189815200	1.189815200
		$x_2(t)$	4.163579469	4.163535165	4.163488002
SAGPM	$t = 0.15$	$x_1(t)$	1.803148555	1.803148555	1.803148555
		$x_2(t)$	3.344495339	3.344490272	3.344484879
	$t = 0.35$	$x_1(t)$	1.296697446	1.296697446	1.296697446
		$x_2(t)$	4.035391652	4.035304344	4.035211398

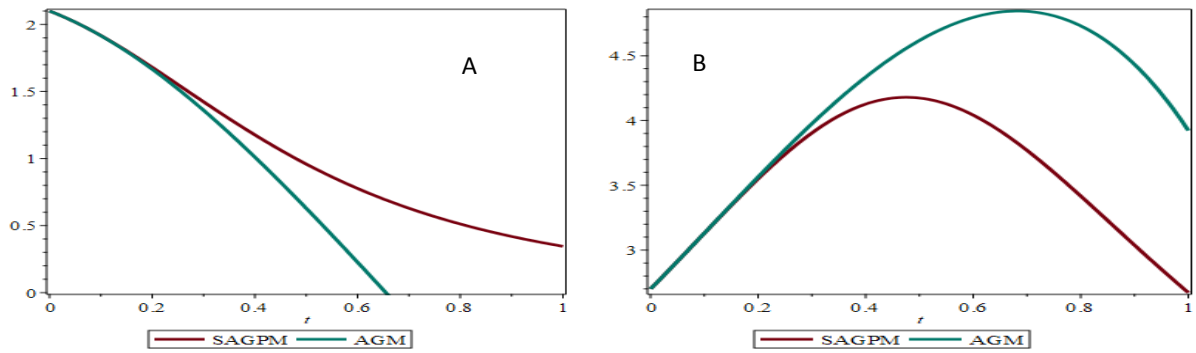


Fig.1: Comparison the approximate solutions obtained by AGM and SAGPM for $x_1(t)$ in (A) and $x_2(t)$ in (B) for system (20).

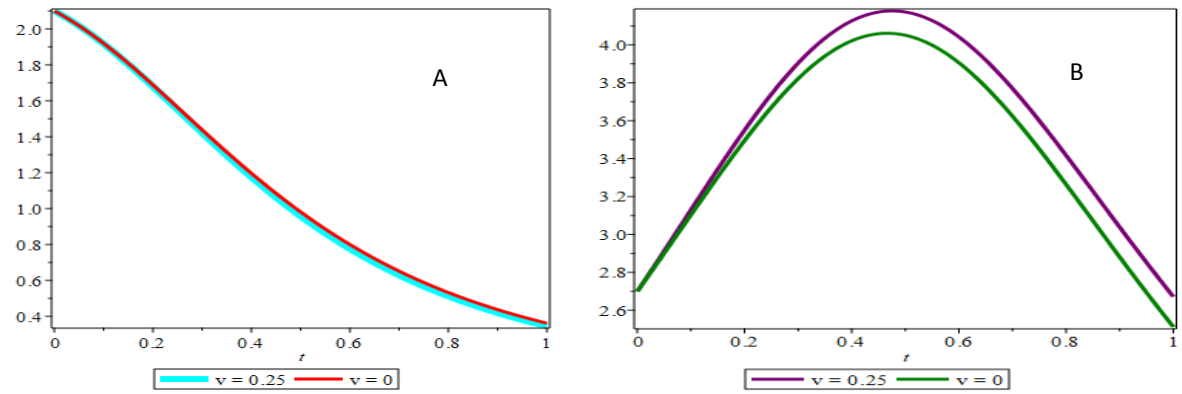


Fig. 2: Approximate analytical solutions of (A) $x_1(t)$ and (B) $x_2(t)$ at $\alpha = 2, \sigma = 0.05,\ \beta = 0.30\ and\ k = 0.2.$

5. The convergence analysis

This section elucidates the convergence of the approximate analytical solutions provided by SAGPM for the given system (20). The system of equations is presented in the following form:

$$x_1 = A(x_1, x_2), \qquad (26)$$
$$x_2 = B(x_1, x_2),$$

In this context, A and B represent nonlinear operators. The solution derived through the current method corresponds to the following sequence:

$$S_n = \sum_{j=0}^{n} x_{1j} = \sum_{j=0}^{n} a_j \frac{t^j}{(j)!}$$
$$K_n = \sum_{j=0}^{n} x_{2j} = \sum_{j=0}^{n} b_j \frac{t^j}{(j)!}$$

Theorem (5.1): (Convergence of System)[21]

Consider H as a Hilbert space, where A and B are operators mapping from H to H. Let x_1 and x_2 denote the exact solutions of Eq. (26). The approximate solutions

$$\sum_{j=0}^{\infty} x_{1j} = \sum_{j=0}^{\infty} a_j \frac{t^j}{(j)!}$$

and

$$\sum_{j=0}^{\infty} x_{2j} = \sum_{j=0}^{\infty} b_j \frac{t^j}{(j)!}$$

are convergence to exact solutions x_1 and x_2 respectively, and

$$\left\| x_{1_{j+1}} \right\| \leq \rho \left\| x_{1_j} \right\|, \forall i \in N \cup \{0\}\ and\ \exists\ 0 \leq \sigma < 1, \left\| x_{2_{j+1}} \right\| \leq \sigma \left\| x_{2_j} \right\|, \forall j \in N \cup \{0\},$$

hold, when $0 \leq \rho < 1,$

Definition (5.2): For every $j \in N \cup \{0\}$,we define

$$\rho_j = \begin{cases} \frac{\|x_{1_{j+1}}\|_2}{\|x_{1_j}\|_2}, & \left\|x_{1_j}\right\|_2 \neq 0 \\ 0, & otherwise \end{cases} \quad \text{and} \quad \sigma_j = \begin{cases} \frac{\|x_{2_{j+1}}\|_2}{\|x_{2_j}\|_2}, & \left\|x_{2_j}\right\|_2 \neq 0 \\ 0, & otherwise \end{cases},$$

where

$$\|x\|_2 = \sqrt{h \sum_{i=0}^{n} |x_i|^2}.$$

Corollary(5.3): From theorem (5.1), $\sum_{j=0}^{\infty} x_{1j} = \sum_{j=0}^{\infty} a_j \frac{t^j}{(j)!}$ and $\sum_{j=0}^{\infty} x_{2j} = \sum_{j=0}^{\infty} b_j \frac{t^j}{(j)!}$ converge to exact solutions x_1 *and* x_2 when $0 \leq \rho_j < 1$ *and* $0 \leq \sigma_j < 1, j = 0,1,2, \ldots$

To illustrate the convergence of analytical approximations, we applied Definition (5.2) as follows:

where $v = 0.25, at\ t \in (0,1)$,

for $x_1(t)$, we obtain

$$\rho_1 = 0.9678426340 < 1,$$
$$\rho_2 = 0.4864082922 < 1,$$
$$\rho_3 = 0.001359839944 < 1,$$

and for $x_2(t)$, we obtain

$$\sigma_1 = 0.3396280847 < 1,$$
$$\sigma_2 = 0.3049554300 < 1,$$
$$\sigma_3 = 0.2955500820 < 1.$$

These results confirm that the convergence of approximate solutions resulting from the use of the new method is valid and show that its algorithm helped to achieve the acceleration of convergence by increasing iterations.

6. Stability analysis

In this section, we delve into the stability analysis of the system (20). The system's dynamic characteristics are assessed by examining the eigenvalues of the associated Jacobian matrix at each equilibrium point, presented as follows:

$$J = \begin{pmatrix} \alpha - x_2 & -x_1 \\ x_2 - k & x_1 - \frac{1}{\alpha} \end{pmatrix}.$$

The system (20) has two fixed points, which are given in Table 4.

Table 4: Classification of the equilibrium points for the system (20), at

$$\alpha = 2, k = 0.2, \sigma = 0.25\ , and\ v = 0.$$

Equilibrium points	*Eigenvalues*	*Stability*
$(0,0.5)$	$1.5, -0.50$	*Unstable*
$(0.41,2)$	$-0.042 + 0.864i$, $-0.042 - 0.864i$	*Stable*

In Fig.3, there are two states of the tumor: the first state where the tumor remains dormant, meaning it doesn't progress over time, and the second state where the tumor is active. We will investigate the impact of cytokine dosages on these two states. In Fig.4, we observe a noticeable transformation in the cellular interactions over time, influenced by the dosage of cytokines. The closed loops gradually diminish, and the central region expands as the cytokine dosage increases. This change can be attributed to the effect of cytokines on the dynamics of the immune response. The observed changes imply that cytokines play a pivotal role in modulating the relationship between lymphocytes and cancer cells. Furthermore, the dose-dependent effect highlights the significance of cytokine concentration. As the cytokine dosage escalates, the transformation becomes more pronounced. In Fig.5, we notice that cytokines have a limited role in improving lymphocyte response and eliminating cancer cells. This suggests that cytokines alone are not sufficient for cancer treatment. In conclusion, cytokine therapy can be beneficial in the case of a dormant tumor, but it is not enough on its own in the case of an active tumor.

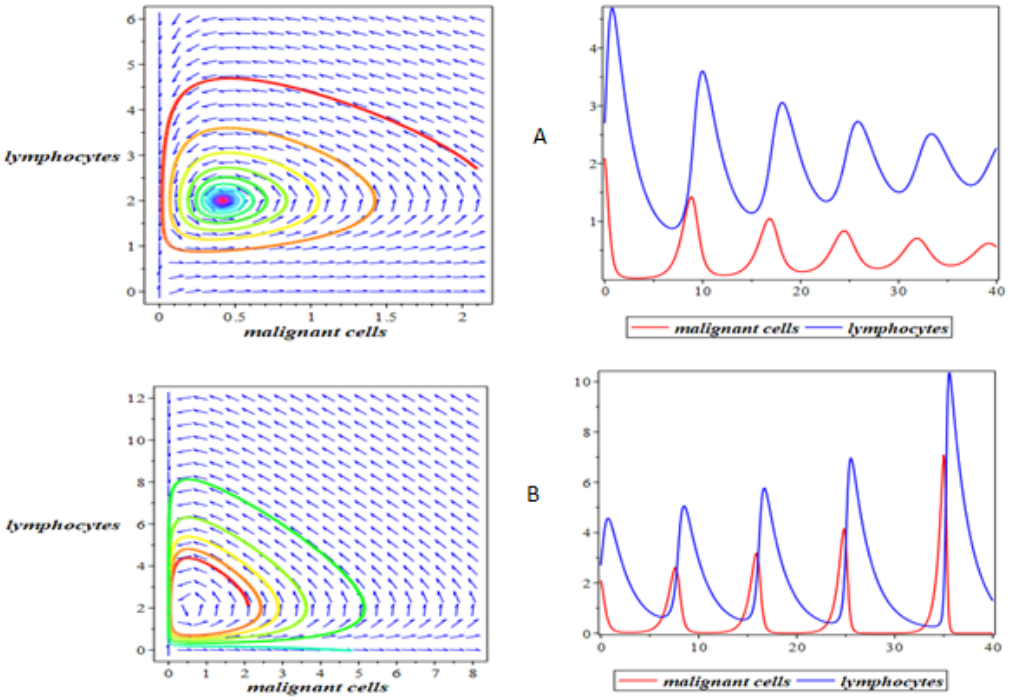
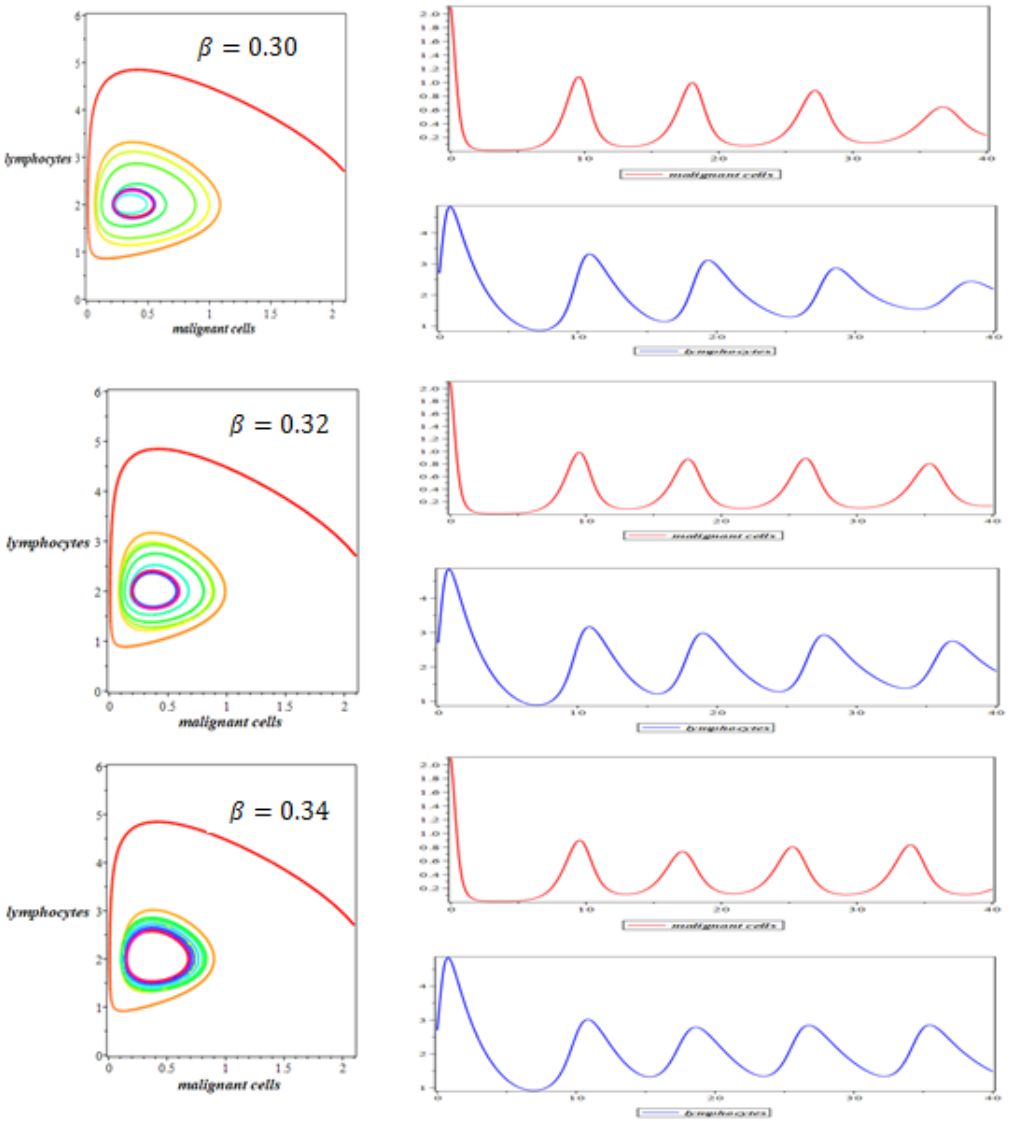


Fig.3: Phase plane of a system (20), at $\alpha = 2, k = 0.2,\ v = 0,$ and $\sigma = 0.25$ in A, $\sigma = 0.05$ in B.



Figu.4: Phase plane of a system (20), at $\alpha = 2, k = 0.2, \sigma = 0.25,\ v = 0.25,$ and for different values of β.

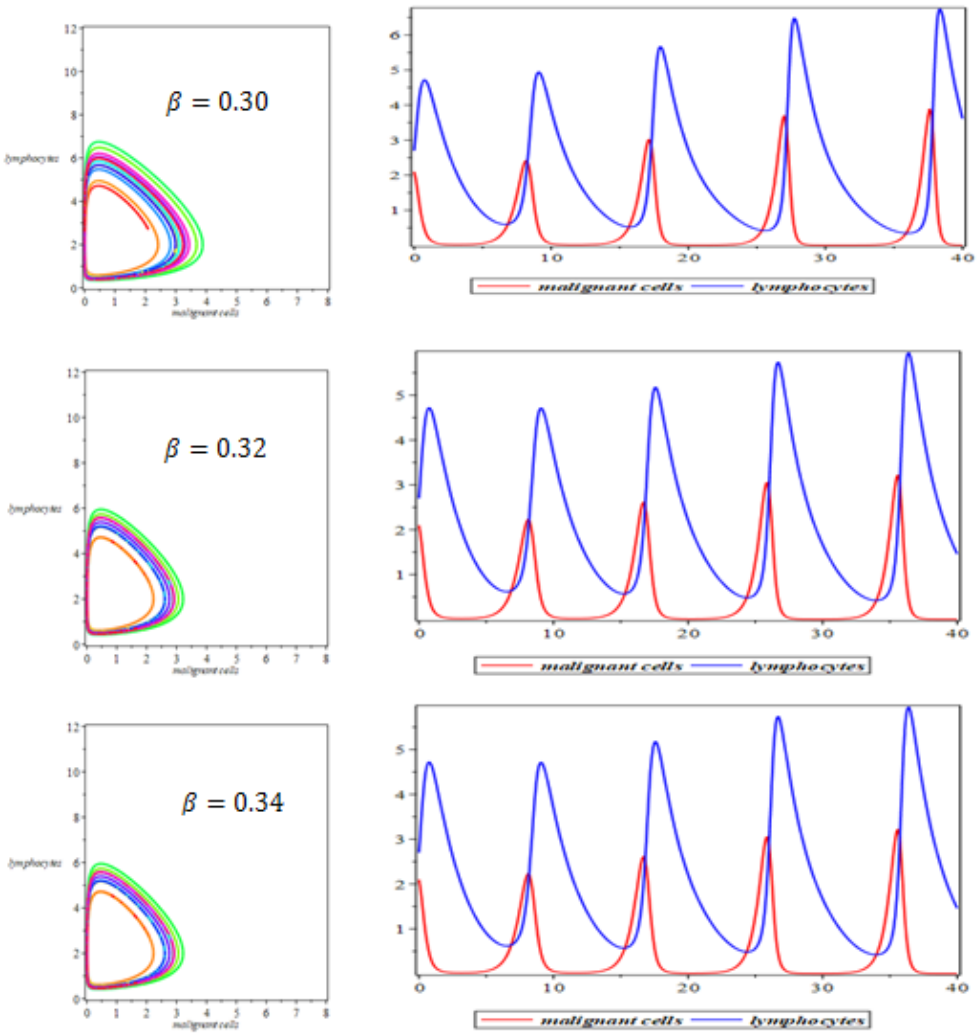


Fig.5: Phase plane of a system (20), at $\alpha = 2, k = 0.2, \sigma = 0.05, \nu = 0.25$, and for different values of β.

7. Conclusion

In this research, the effect of treatment on the reactive behavior of tumors was studied by using a new method based on combining Shehu transformation and Akbari-Ganji's method with the Padé approximation. Mathematical results and graphs were used to conclude the effects of treatment on tumors. The current study concluded that using the proposed method for tumor analysis provides highly accurate and reliable results. Error tables prove that the new method is more accurate and efficient compared to AGM and ADM in terms of fewer errors and less CPU time. It can also be said that the new method is a development of AGM. Convergence analysis was performed, and the accuracy of the resulting approximate solutions was confirmed using the new algorithm. The results showed that the new algorithm facilitated accelerated convergence by increasing the number of iterations. Through the analysis of system stability, significant results were obtained affirming the effectiveness of cytokine treatment in reducing tumor volume when the tumor is dormant. Moreover, increasing the treatment dose resulted in an improvement in its efficacy. However, in the case of an active tumor, relying solely on cytokine doses for treatment is not sufficient. It necessitates additional medical interventions to enhance the condition. These findings highlight the importance of using cytokines as an effective tumor reduction therapy. They also stress the importance of carefully regulating the dose of treatment to balance efficacy and minimize potential side effects. In the future, cytokines are expected to develop into customized therapies for common malignancies, and to form part of integrated cancer treatment alongside other therapies such as chemotherapy, radiotherapy and surgery. It is important to continue research and clinical trials to improve our understanding of the role of cytokines in cancer treatment and to develop new and effective therapies for patients.

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