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Solution of the simplified tumor-immune system using combined LaPlace transform-adomian decomposition method

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KEY WORDS

Combined Laplace transform-Adomian decomposition method; Runge-Kutta fourth-fifth order method; Runge-Kutta second-third order method; Simplified model; Tumor-immune system.

ABSTRACT

In this paper, combined Laplace transform-Adomian decomposition method (CLTADM) is presented to solve simplified Tumor-immune system at two different values of the parameter of interaction between tumor cells and effector cells ω . The system is presented to show the ability of the method for non-linear systems of differential equations. The results obtained are in good agreement with those obtained by the Runge-Kutta fourth-fifth order method (ode45 solver in matlab) and better than those obtained by Runge-Kutta second-third order method (ode23 solver in matlab) in small interval beginning from the point at which the initial values are considered.

1. Introduction

The immune system response consists of two different interacting responses: the cellular response (T lymphocytes) and the humoral response (B lymphocytes). The immune system identifies any stranger cells or tumor cells and destroys them. The immune response (in vivo) starts when tumor cells are recognized as being nonself. Then tumor cells are caught and absorbed by macrophages which can be found in all tissues in the body and circulate round in the blood stream. Macrophages release series of cytokines which activate T helper cells which send signals to natural killers (NKs). Antibodies circulate in the blood and are attached to tumor cells, which implies that they are more

quickly engulfed by macrophages or killed by natural killer cells.

Kuznetsov and Taylor's model describes the interaction between the immune system and tumor cells in vivo (inside animal body) [8]. Magda's model is simplified model of Kuznetsov and Taylor's model where she replaces the Michaelis-Menten form with a Lotka-Volterra form [9]. We will solve Magda's model by CLTADM (approximations to the solutions with four terms) and compare this solution with Runge-Kutta fourth-fifth order method (ode45 solver in matlab) and Runge-Kutta second-third order method (ode23 solver in matlab).

2. Combined Laplace Transform–Adomian Decomposition Method

A system of ordinary differential equations of the first order can be considered as, see [10]

$$\begin{aligned} \dot{y}_1 &= f_1(x, y_1, y_2, \dots, y_n) \\ \dot{y}_2 &= f_2(x, y_1, y_2, \dots, y_n) \\ &\vdots \\ \dot{y}_n &= f_n(x, y_1, y_2, \dots, y_n) \end{aligned} \quad (2.1)$$

where each equation represents the first derivative of each unknown functions as a mapping depending on the independent variable x , and n unknown functions f_1, f_2, \dots, f_n and the initial conditions $y_1(0), y_2(0), \dots, y_n(0)$ are prescribed. We can present the system (2.1), by using the i th equation as:

$$\dot{y}_i = g_i(x, y_1, y_2, \dots, y_n) + F_i(x, y_1, y_2, \dots, y_n), \quad i = 1, 2, \dots, n. \quad (2.2)$$

Here $g_i(x, y_1, y_2, \dots, y_n)$ and $F_i(x, y_1, y_2, \dots, y_n)$ are linear and nonlinear parts of $f_i(x, y_1, y_2, \dots, y_n)$ respectively. Applying the Laplace transform to both sides of (2.2) gives

$$s.L\{y_i\} - y_i(0) = L\{g_i(x, y_1, y_2, \dots, y_n)\} + L\{F_i(x, y_1, y_2, \dots, y_n)\}, \quad i = 1, 2, \dots, n. \quad (2.3)$$

Then

$$L\{y_i\} = \frac{y_i(0)}{s} + \frac{1}{s}L\{g_i(x, y_1, y_2, \dots, y_n)\} + \frac{1}{s}L\{F_i(x, y_1, y_2, \dots, y_n)\}, \quad i = 1, 2, \dots, n. \quad (2.4)$$

The solutions are represented as infinite series in this method, such that

$$y_i = \sum_{k=0}^{\infty} y_{ik}, \quad i = 1, 2, \dots, n, \quad (2.5)$$

where the components y_{ik} are to be recursively computed. However, the nonlinear term $F_i(x, y_1, y_2, \dots, y_n)$ at the right side of equation (2.5) will be represented by an infinite series of the Adomian polynomials A_{ik} in the form

$$F_i(x, y_1, y_2, \dots, y_n) = \sum_{k=0}^{\infty} A_{ik}, \quad i = 1, 2, \dots, n \quad (2.6)$$

where $A_{ik}, k \geq 0$ are defined by

$$A_{ik} = \frac{1}{k!} \frac{d^k}{d\lambda^k} [F_i(x, \sum_{j=0}^k \lambda^j y_{1j}, \sum_{j=0}^k \lambda^j y_{2j}, \dots, \sum_{j=0}^k \lambda^j y_{nj})], \quad \text{at } \lambda = 0, \quad k = 0, 1, 2, \dots; i = 1, 2, \dots, n. \quad (2.7)$$

Assuming that the nonlinear functions are $F_i(x, y_1, y_2, \dots, y_n)$, therefore the Adomian polynomials are given by

$$\begin{aligned} A_{i0} &= F_i(y_{i0}), \\ A_{i1} &= y_{i1} \dot{F}_i(y_{i0}), \\ A_{i2} &= y_{i2} \dot{F}_i(y_{i0}) + \frac{1}{2!} y_{i1}^2 \ddot{F}_i(y_{i0}), \end{aligned} \quad (2.8)$$

$$A_{i3} = y_{i3} \dot{F}_i(y_{i0}) + y_{i1} y_{i2} \ddot{F}_i(y_{i0}) + \frac{1}{3!} y_{i1}^3 \dddot{F}_i(y_{i0}).$$

Substituting (2.5) and (2.6) into (2.4) leads to

$$\begin{aligned} \{\sum_{k=0}^{\infty} y_{ik}\} &= \frac{y_i(0)}{s} + \\ &\frac{1}{s}L\{g_i(x, \sum_{k=0}^{\infty} y_{1k}, \dots, \sum_{k=0}^{\infty} y_{nk})\} + \\ &\frac{1}{s}L\{\sum_{k=0}^{\infty} A_{ik}(x)\}, \quad i = 1, 2, \dots, n, \end{aligned} \quad (2.9)$$

Matching both sides of (2.9) yields the following iterative algorithm

$$\begin{aligned} L\{y_{i0}\} &= \frac{y_i(0)}{s}, \\ L\{y_{ik+1}\} &= \frac{1}{s}L\{g_i(x, y_{1k}, \dots, y_{nk})\} + \\ &\frac{1}{s}L\{A_{ik}(x)\}, \quad i = 1, 2, \dots, n. \end{aligned} \quad (2.10)$$

We get the solutions by applying the inverse Laplace transform on (2.10).

3. Solution of The Simplified Tumor-Immune System Model by CLTADM

The nonlinear system describes the interaction between tumor cells and effector cells in-vivo (inside animal body), see [8, 9] is

$$\frac{dx}{dt} = \sigma - \delta x + \omega xy, \quad (3.1)$$

$$\frac{dy}{dt} = r_2 y(1 - \beta y) - xy,$$

where x denotes the dimensionless density of effector cells, y stands for the dimensionless density of the population of tumor cells, $\sigma = 0.1181$ (The parameter of normal production

of effector cells), $\delta = 0.3743$ (The parameter of death of effector cells), $r_2 = 1.636$ (The parameter of maximal growth rate of tumor cells), $\beta = 0.002$ (β^{-1} is the parameter of maximal carrying capacity of the biological environment for tumor cells) and ω (the parameter of interaction between tumor cells and effector cells.) takes any value. We solve this system with initial values $x(0) = 1$ and $y(0) = 1$. We take two suitable values for ω , first $\omega = -0.04 < 0$ where the tumor cells destroy effector cells through interaction between them, second $\omega = 0.04 > 0$ where the effector cells destroy tumor cells through interaction between them. We compare the solution of the system by three numerical methods: CLTADM, the Runge-Kutta second-third order method(RK23) and the Runge-Kutta fourth-fifth order method(RK45) (as exact solution).

First, using the Laplace transformation to the considered system (3.1), we get

$$L[x] = \frac{1}{s} + \frac{\sigma}{s^2} - \frac{1}{s}L[\delta x] + \frac{1}{s}L[\omega xy], \tag{3.2}$$

$$L[y] = \frac{1}{s} + \frac{1}{s}L[r_2 y] - \frac{1}{s}L[r_2 \beta y^2] - \frac{1}{s}L[xy].$$

Substituting $x = \sum_{k=0}^{\infty} x_k$, $y = \sum_{k=0}^{\infty} y_k$, $F_1 = xy = \sum_{k=0}^{\infty} A_{1k}$, $F_2 = y^2 = \sum_{k=0}^{\infty} A_{2k}$ into (3.2), we get

$$L[\sum_{k=0}^{\infty} x_k] = \frac{1}{s} + \frac{\sigma}{s^2} - \frac{1}{s}L[\delta \sum_{k=0}^{\infty} x_k] + \frac{1}{s}L[\omega \sum_{k=0}^{\infty} A_{1k}], \tag{3.3}$$

$$L[\sum_{k=0}^{\infty} y_k] = \frac{1}{s} + \frac{1}{s}L[r_2 \sum_{k=0}^{\infty} y_k] - \frac{1}{s}L[r_2 \beta \sum_{k=0}^{\infty} A_{2k}] - \frac{1}{s}L[\sum_{k=0}^{\infty} A_{1k}].$$

where A_{1k} and A_{2k} are Adomian polynomials defined by

$$A_{1k} = \frac{1}{k!} \frac{d^k}{d\lambda} [F_1(t, \sum_{j=0}^k \lambda^j x_j, \sum_{j=0}^k \lambda^j y_j)]_{\lambda=0}, \tag{3.4}$$

$$k = 0, 1, 2, \dots,$$

$$A_{2k} = \frac{1}{k!} \frac{d^k}{d\lambda} [F_2(t, \sum_{j=0}^k \lambda^j x_j, \sum_{j=0}^k \lambda^j y_j)]_{\lambda=0},$$

$$k = 0, 1, 2, \dots$$

We obtain the following procedure by using CLTADM

$$L[x_0] = \frac{1}{s} + \frac{\sigma}{s^2},$$

$$L[x_{k+1}] = -\frac{\delta}{s}L[x_k] + \frac{\omega}{s}L[A_{1k}], \tag{3.5}$$

$$L[y_0] = \frac{1}{s},$$

$$L[y_{k+1}] = \frac{r_2}{s}L[y_k] - \frac{r_2\beta}{s}L[A_{2k}] - \frac{1}{s}L[A_{1k}],$$

$$k \geq 0.$$

We conclude A_{1k} and A_{2k} where $k=0,1,\dots,4$ as follows

$$A_{10} = x_0 y_0,$$

$$A_{11} = x_0 y_1 + x_1 y_0,$$

$$A_{12} = x_0 y_2 + x_1 y_1 + x_2 y_0, \tag{3.6}$$

$$A_{13} = x_0 y_3 + x_1 y_2 + x_2 y_1 + x_3 y_0,$$

$$A_{14} = x_0 y_4 + x_1 y_3 + x_2 y_2 + x_3 y_1 + x_4 y_0,$$

And

$$A_{20} = y_0^2,$$

$$A_{21} = 2y_0 y_1,$$

$$A_{22} = 2y_0 y_2 + y_1^2, \tag{3.7}$$

$$A_{23} = 2y_0 y_3 + 2y_1 y_2,$$

$$A_{24} = 2y_0 y_4 + 2y_1 y_3 + y_2^2.$$

By the inverse Laplace Transform, using MAPLE, at $\omega = -0.04$, approximations to the solutions with four terms are as follows:

$$x(t) = 1 - 0.2962 t + 0.04870327 t^2 - 0.00885689739 t^3 + 0.00045113927 t^4 - 0.0001549607718 t^5 - 0.0000260090272 t^6 - 0.000001291177405 t^7 - 0.0000002452898539 t^8 - 0.000000004519831192 t^9 - 0.0000000002393195927 t^{10}, \tag{3.8}$$

$$y(t) = 1 + 0.632728 t + 0.3472372180 t^2 + 0.1186571286 t^3 + 0.03853607950 t^4 + 0.0093516923 t^5 - 0.001911623021 t^6 + 0.0000820933656 t^7 - 0.000007161751237 t^8 - 0.000000002784255454 t^9 - 0.0000000005982989818 t^{10}.$$

Also, by using MAPLE at $\omega = 0.04$, approximations to the solutions with four terms are as follows:

$$x(t) = 1 - 0.2162 t + 0.04879239000 t^2 - 0.00316454632 t^3 + 0.00084257250 t^4 +$$

$$\begin{aligned}
& 0.00007851914576 t^5 + \\
& 0.000006833308624 t^6 + \\
& 0.0000003649894864 t^7 + \\
& 0.0000002128031675 t^8 - \\
& 0.0000000006935230475 t^9 + \\
& 0.0000000002393195927 t^{10},
\end{aligned} \tag{3.9}$$

$$\begin{aligned}
y(t) = & 1 + 0.632728 t + \\
& 0.3072372180 t^2 + 0.09336192927 t^3 + \\
& 0.02405300230 t^4 + 0.0041597225 t^5 - \\
& 0.001332765159 t^6 + \\
& 0.00009832898095 t^7 - \\
& 0.000007539936183 t^8 + \\
& 0.0000001275496005 t^9 - \\
& 0.000000005982989818 t^{10}.
\end{aligned}$$

4. Numerical results and discussion

4.1. First case, the tumor cells destroy the effector cells in their interaction at $\omega = -0.04$. By using MATLAB, tables (1,2) show the results of the solution of the simplified model for equation (3.8) and present the absolute errors between the solution obtained by using RK23, the solution obtained by using CLTADM and the solution obtained by using RK45. We get a good approximation by using presented method with only five iterations. Figure (1) shows the solutions obtained by the considered three methods. It is clear that the three curves are almost equal.

Table 1. The effector cells $x(t)$ at $\omega = -0.04$, the absolute error between the RK23 and CLTADM along with the result obtained by the RK45

t	x(t) with CLTADM	RK23 - RK45	x(t) - RK45
0	1	0	0
0.005	0.998520216474919	3.80806497446429e-13	1.11022302462516e-16
0.010	0.997042861474598	3.68760577629246e-12	7.77156117237610e-16
0.015	0.995567928366442	6.42363939817869e-12	3.33066907387547e-16
0.020	0.994095410524506	9.64806012859754e-12	1.11022302462516e-15
0.025	0.992625301329435	1.23115961869757e-11	7.43849426498855e-15
0.030	0.991157594168409	1.54534163243625e-11	2.14273043752655e-14
0.035	0.989692282435078	1.80437886854179e-11	5.65103519534205e-14
0.040	0.988229359529509	2.11026751628651e-11	1.24567023362943e-13
0.045	0.986768818858117	2.36196617819928e-11	2.53796983429311e-13
0.050	0.985310653833614	2.65952815325932e-11	4.76174655261730e-13
0.055	0.983854857874942	2.90384383205833e-11	8.44657677134819e-13
0.060	0.982401424407214	3.19302362328244e-11	1.42175160533498e-12
0.065	0.980950346861655	3.42992301227696e-11	2.29838370557900e-12
0.070	0.979501618675536	3.71068731297441e-11	3.58268970046538e-12
0.075	0.978055233292116	3.94012600324345e-11	5.41899858319539e-12
0.080	0.976611184160580	4.21244150672351e-11	7.97784061035145e-12
0.085	0.975169464735972	4.43436398711583e-11	1.14750431379207e-11
0.090	0.973730068479137	4.69817518222726e-11	1.61632929263078e-11
0.095	0.972292988856658	4.91254814605213e-11	2.23518981101734e-11
0.100	0.970858219340789	4.91208185238179e-11	3.03979064142368e-11

Figure 1. The effector cells at $\omega = -0.04$ where the effector cells with RK45 blue [—], the effector cells with RK23 blue [---] and the effector cells with CLTADM $x(t)$ blue [...] (lower line). The tumor cells at $\omega = -0.04$ where the tumor cells with RK45 red

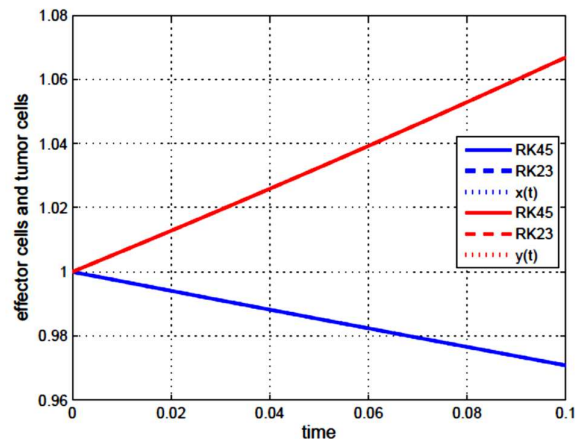


Table 2. The tumor cells $y(t)$ at $\omega = -0.04$, the absolute error between the RK2-3 and CLTADM along with the result obtained by the RK4-5

t	y(t) with CLTADM	RK23 - RK45	y(t) - RK45
0	1	0	0
0.005	1.00317233578671	7.37654382021447e-12	2.22044604925031e-16
0.010	1.00636212276522	9.15525433242692e-11	1.15463194561016e-14
0.015	1.00956945079983	1.27126531523913e-10	4.52970994047064e-14
0.020	1.01279441033980	2.13118633851650e-10	2.75557354711964e-13
0.025	1.01603709242290	2.49917198047456e-10	1.03139718987677e-12
0.030	1.01929758867875	3.37764705093946e-10	3.10396153224701e-12
0.035	1.02257599133230	3.75818487441393e-10	7.82240938690393e-12
0.040	1.02587239320719	4.65561589280128e-10	1.74629199989340e-11
0.045	1.02918688772911	5.04901453979301e-10	3.54163365301474e-11
0.050	1.03251956892917	5.96581006817587e-10	6.66993127396154e-11
0.055	1.03587053144720	6.37239150336200e-10	1.18216769706692e-10
0.060	1.03923987053508	7.30896898559763e-10	1.99374738940605e-10
0.065	1.04262768206000	7.72905295320925e-10	3.22437188060576e-10
0.070	1.04603406250774	8.68583427404701e-10	5.03241892602091e-10
0.075	1.04945910898588	9.11975606143756e-10	7.61652074743324e-10
0.080	1.05290291922707	1.00971764283031e-09	1.12237796834336e-09
0.085	1.05636559159219	1.05452735432721e-09	1.61552193844727e-09
0.090	1.05984722507351	1.15437726044831e-09	2.27750440728869e-09
0.095	1.06334791929792	1.20063892161681e-09	3.15170733955483e-09
0.100	1.06686777452999	1.21318954882099e-09	4.28949409325696e-09

4.2. Second case, the effector cells destroy the tumor cells in their interaction at $\omega = 0.04$. Again, by using MATLAB, tables (3,4) show the results of the solution of the simplified model for equation (3.9) and present the absolute errors between the solution obtained by using RK23, the solution obtained by

using CLTADM and the solution obtained by using RK45. We obtain a good approximation by using presented method with only five iterations. Figure (2) shows the solutions obtained by the considered three methods. It is clear that the three curves are almost equal.

Table 3. The effector cells $x(t)$ at $\omega = 0.04$, the absolute error between the RK23 and CLTADM along with the result obtained by the RK45

t	x(t) with CLTADM	RK23 - RK45	x(t) - RK45
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0	1	0	0
0.005	0.998920219414709	3.71258579434652e-13	0
0.010	0.997842876082887	3.87656573508366e-12	0
0.015	0.996767967650121	6.32649488352399e-12	0
0.020	0.995695491774693	9.85356241045565e-12	5.55111512312578e-16
0.025	0.994625446127612	1.23203669488703e-11	1.99840144432528e-15
0.030	0.993557828392646	1.58697499585969e-11	6.43929354282591e-15
0.035	0.992492636266348	1.83539849984982e-11	1.67643676718399e-14
0.040	0.991429867458090	2.19262386025321e-11	3.78586051397178e-14
0.045	0.990369519690086	2.44281261885249e-11	7.72715225139109e-14
0.050	0.989311590697433	2.80235834537734e-11	1.46327394645596e-13
0.055	0.988256078228128	3.05436786973701e-11	2.60458321577062e-13
0.060	0.987202980043111	3.41628947353456e-11	4.41091607683575e-13
0.065	0.986152293916285	3.67017527480584e-11	7.15205672463526e-13
0.070	0.985104017634552	4.03453936925757e-11	1.11932685342708e-12
0.075	0.984058148997843	4.29032365190096e-11	1.69786407155925e-12
0.080	0.983014685819145	4.65716354369761e-11	2.50743870111592e-12
0.085	0.981973625924535	4.91490181886434e-11	3.61599639120413e-12
0.090	0.980934967153212	5.28427301915713e-11	5.10713693557818e-12
0.095	0.979898707357522	5.54402079799843e-11	7.07989222803462e-12
0.100	0.978864844402993	5.58925128402166e-11	9.65238999839357e-12

Table 4. The tumor cells $y(t)$ at $\omega = 0.04$, the absolute error between the RK23 order and CLTADM along with the result obtained by the RK45 order method

t	y(t) with CLTADM	RK23 - RK45	y(t) - RK45
0	1	0	0
0.005	1.00317133261574	4.96869212440743e-12	4.44089209850063e-16
0.010	1.00635809732467	6.03284089351064e-11	5.10702591327572e-15
0.015	1.00956036469139	8.54623039003855e-11	1.57651669496772e-14
0.020	1.01277820564434	1.41850975410307e-10	1.14575016141316e-13
0.025	1.01601169147740	1.67753588797837e-10	4.40536496171262e-13
0.030	1.01926089385133	2.25187868352350e-10	1.34914301952449e-12
0.035	1.02252588479534	2.51874299195265e-10	3.41970896045041e-12
0.040	1.02580673670847	3.10371284228950e-10	7.66009478070373e-12
0.045	1.02910352236115	3.37856631560385e-10	1.55568891102575e-11
0.050	1.03241631489659	3.97433641552425e-10	2.93201019019307e-11
0.055	1.03574518783222	4.25732782360910e-10	5.19737586301972e-11
0.060	1.03909021506112	4.86407136790490e-10	8.76470007682428e-11
0.065	1.04245147085345	5.15535614198370e-10	1.41701539391192e-10
0.070	1.04582902985778	5.77325076633883e-10	2.21068718886386e-10
0.075	1.04922296710250	6.07298655808108e-10	3.34414718139442e-10
0.080	1.05263335799721	6.70220989817949e-10	4.92521579076310e-10
0.085	1.05606027833401	7.01055435925468e-10	7.08491709744408e-10
0.090	1.05950380428885	7.65128627122635e-10	9.98172877686443e-10
0.095	1.06296401242288	7.96840149419609e-10	1.38040046060439e-09
0.100	1.06644097968372	8.04944111365558e-10	1.87746151958379e-09

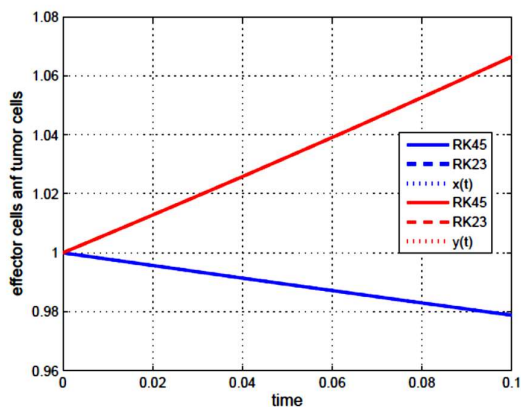


Figure 2. The effector cells at $\omega = 0.04$ where the effector cells with RK45 blue [—], the effector cells with RK23 blue [---] and the effector cells with CLTADM $x(t)$ blue [...] (lower line). The tumor cells at $\omega = -0.04$ where the tumor cells with RK45 red [—], the tumor cells with RK23 red [---] and the tumor cells with CLTADM $x(t)$ red [...] (upper line).

5. Residual Functions and Residual Errors

We consider $\bar{x}(t)$ and $\bar{y}(t)$ are the solutions of system (3.1) by using CLTADM.

Then, $R_1(t)$ and $R_2(t)$ are residual functions which are defined as

$$R_1(t) = \frac{d\bar{x}(t)}{dt} - \sigma + \delta\bar{x}(t) - \omega\bar{x}(t)\bar{y}(t), \quad (5.1)$$

And

$$R_2(t) = \frac{d\bar{y}(t)}{dt} - r_2\bar{y}(t)(1 - \beta\bar{y}(t)) + \bar{x}(t)\bar{y}(t). \quad (5.2)$$

5.1. First case, $\omega = -0.04 < 0$. The residual functions $R_1(t)$ and $R_2(t)$ can be defined as

$$\begin{aligned} R_1(t) = & -3 * 10^{-1} t^2 - 1.9 * 10^{-11} t^3 \\ & - 9.86 * 10^{-11} t^4 \\ & - 0.1832024205 * 10^{-3} t^5 \\ & - 0.1716974171 * 10^{-3} t^6 \\ & + 0.2733195040 * 10^{-4} t^7 \\ & - 0.8872598275 * 10^{-5} t^8 \\ & + 6.999511452 * 10^{-7} t^9 \\ & - 1.855444348 * 10^{-7} t^{10} \\ & + 2.980718910 * 10^{-9} t^{11} \\ & + 4.541564544 * 10^{-10} t^{12} \\ & - 4.007391104 * 10^{-1} t^{13} \\ & + 1.981666379 * 10^{-11} t^{14} \\ & - 1.395145446 * 10^{-13} t^{15} \\ & + 8.009409262 * 10^{-14} t^{16} \\ & + 8.452562677 * 10^{-16} t^{17} \\ & + 1.277639381 * 10^{-16} t^{18} \\ & + 1.108337235 * 10^{-18} t^{19} \\ & + 5.727386745 * 10^{-20} t^{20}, \end{aligned}$$

And

$$\begin{aligned} R_2(t) = & -1 * 10^{-10} t^2 - 1.6 * 10^{-9} t^3 \\ & - 6.8 * 10^{-10} t^4 \\ & - 0.2550738184 * 10^{-1} t^5 \\ & + 0.388150943 * 10^{-4} t^6 \\ & + 0.5966351814 * 10^{-3} t^7 \\ & - 0.1987413684 * 10^{-3} t^8 \\ & + 0.1857644873 * 10^{-4} t^9 \\ & - 0.4775086195 * 10^{-5} t^{10} \\ & - 2.735835871 * 10^{-8} t^{11} \\ & + 2.651288763 * 10^{-8} t^{12} \\ & - 2.472436921 * 10^{-9} t^{13} \\ & + 6.053795521 * 10^{-10} t^{14} \\ & - 7.666606117 * 10^{-12} t^{15} \\ & + 2.243524843 * 10^{-12} t^{16} \\ & + 1.804771929 * 10^{-14} t^{17} \\ & + 3.474525610 * 10^{-15} t^{18} \\ & + 2.781744196 * 10^{-17} t^{19} \\ & + 1.548971745 * 10^{-18} t^{20}. \end{aligned}$$

We can put values of t take numbers $0, 0.005, 0.01, \dots, 0.1$ to calculate the residual errors of $\bar{x}(t)$ and $\bar{y}(t)$. Tables (5) and (6) show the absolute residual errors of $\bar{x}(t)$ and $\bar{y}(t)$ for system (3.1).

Table 5. The effector cells $\bar{x}(t)$ and the absolute residual error $|R_1(t)|$ at $\omega = -0.04$

t	$\bar{x}(t)$	$ R_1(t) $
0	1	0
0.005	0.998520216474919	1.32762482936056e-15
0.010	0.997042861474598	2.15116530341577e-14
0.015	0.995567928366442	1.47889548376577e-13
0.020	0.994095410524506	6.09369398179928e-13
0.025	0.992625301329435	1.84992437325431e-12
0.030	0.991157594168409	4.60398715910475e-12
0.035	0.989692282435078	9.97373408243885e-12
0.040	0.988229359529509	1.95082487948044e-11
0.045	0.986768818858117	3.52845555125354e-11
0.050	0.985310653833614	5.99905119490705e-11
0.055	0.983854857874942	9.70095522121443e-11
0.060	0.982401424407214	1.50507270074336e-10
0.065	0.980950346861655	2.25519833161007e-10
0.070	0.979501618675536	3.28044218734774e-10
0.075	0.978055233292116	4.65130261890345e-10
0.080	0.976611184160580	6.44974507107808e-10
0.085	0.975169464735972	8.77015854246335e-10
0.090	0.973730068479137	1.17203299019365e-09
0.095	0.972292988856658	1.54224359751973e-09
0.100	0.970858219340789	2.00140533161579e-09

Table 6. The tumor cells $\bar{y}(t)$ and the absolute residual error $|R_2(t)|$ at $\omega = -0.04$

t	$\bar{y}(t)$	$ R_2(t) $
0	1	0
0.005	1.00317233578671	8.24103402296251e-14
0.010	1.00636212276522	2.56230022240949e-12
0.015	1.00956945079983	1.93970589494933e-11
0.020	1.01279441033980	8.16732879072494e-11
0.025	1.01603709242290	2.49170203747834e-10
0.030	1.01929758867875	6.19921914928230e-10
0.035	1.02257599133230	1.33977834755096e-09
0.040	1.02587239320719	2.61196459953344e-09
0.045	1.02918688772911	4.70663850519875e-09
0.050	1.03251956892917	7.97044619543511e-09
0.055	1.03587053144720	1.28360754416133e-08
0.060	1.03923987053508	1.98318065744816e-08
0.065	1.04262768206000	2.95910607722770e-08
0.070	1.04603406250774	4.28619455152975e-08
0.075	1.04945910898588	6.05167970071762e-08
0.080	1.05290291922707	8.35617193660840e-08
0.085	1.05636559159219	1.13146120392058e-07
0.090	1.05984722507351	1.50572243719619e-07
0.095	1.06334791929792	1.97304697167786e-07
0.100	1.06686777452999	2.54979977102551e-07

5.2. Second case, $\omega = 0.04 > 0$. The residual functions $R_1(t)$ and $R_2(t)$ can be defined as

and

$$\begin{aligned}
 R_1(t) = & 4.4 * 10^{-11}t^2 + 2 * 10^{-1} t^3 \\
 & - 5.60 * 10^{-11}t^4 \\
 & - 0.5577791271 * 10^{-4}t^5 \\
 & + 0.4665493954 * 10^{-4}t^6 \\
 & - 0.2299278246 * 10^{-4}t^7 \\
 & + 0.3147442824 * 10^{-5}t^8 \\
 & - 6.798879130 * 10^{-7}t^9 \\
 & + 4.990283643 * 10^{-8}t^{10} \\
 & - 2.663559442 * 10^{-9}t^{11} \\
 & + 7.157610583 * 10^{-1} t^{12} \\
 & - 2.442820160 * 10^{-11}t^{13} \\
 & + 1.165619359 * 10^{-1} t^{14} \\
 & - 8.197733661 * 10^{-13}t^{15} \\
 & + 7.944007539 * 10^{-14}t^{16} \\
 & - 2.148816072 * 10^{-15}t^{17} \\
 & + 1.266444891 * 10^{-16}t^{18} \\
 & - 1.386978391 * 10^{-1} t^{19} \\
 & + 5.727386745 * 10^{-20}t^{20},
 \end{aligned}$$

$$\begin{aligned}
 R_2(t) = & 1.9 * 10^{-9}t^2 - 1.04 * 10^{-9} t^3 \\
 & + 1.66 * 10^{-9} t^4 \\
 & - 0.1133318574 * 10^{-1}t^5 \\
 & + 0.1915531276 * 10^{-2}t^6 \\
 & + 0.4177937432 * 10^{-3}t^7 \\
 & - 0.6125490202 * 10^{-4}t^8 \\
 & + 0.1678983376 * 10^{-4}t^9 \\
 & - 0.1343303369 * 10^{-5}t^{10} \\
 & + 4.141181886 * 10^{-8}t^{11} \\
 & + 5.578256188 * 10^{-9}t^{12} \\
 & - 4.357074870 * 10^{-10}t^{13} \\
 & - 1.914784796 * 10^{-10}t^{14} \\
 & + 1.436734740 * 10^{-11}t^{15} \\
 & - 1.665731579 * 10^{-12}t^{16} \\
 & + 4.357708965 * 10^{-14}t^{17} \\
 & - 2.817671637 * 10^{-15}t^{18} \\
 & + 2.968055040 * 10^{-17}t^{19} \\
 & - 1.314721627 * 10^{-1} t^{20}.
 \end{aligned}$$

We can put values of t take numbers **0, 0.005, 0.01, ..., 0.1** to calculate the residual errors of $\bar{x}(t)$ and $\bar{y}(t)$. Tables (7) and (8) show the absolute residual errors of $\bar{x}(t)$ and $\bar{y}(t)$ for system (3.1).

Table 7. The effector cells $\bar{x}(t)$ and the absolute residual error $|R_1(t)|$ at $\omega = 0.04$

t	$\bar{x}(t)$	$ R_2(t) $
0	1	0
0.005	0.998920219414709	9.26636211128575e-16
0.010	0.997842876082887	1.12992594521971e-15
0.015	0.996767967650121	3.19249290354558e-14
0.020	0.995695491774693	1.57925715076045e-13
0.025	0.994625446127612	5.05946296844120e-13
0.030	0.993557828392646	1.28228398839632e-12
0.035	0.992492636266348	2.79136697777873e-12
0.040	0.991429867458090	5.45392167725150e-12
0.045	0.990369519690086	9.82466863916604e-12
0.050	0.989311590697433	1.66095557789198e-11
0.055	0.988256078228128	2.66825376001705e-11
0.060	0.987202980043111	4.11019090717182e-11
0.065	0.986152293916285	6.11262027601558e-11
0.070	0.985104017634552	8.82296577775484e-11
0.075	0.984058148997843	1.24117269059022e-10
0.080	0.983014685819145	1.70739425441226e-10
0.085	0.981973625924535	2.30306144969183e-10
0.090	0.980934967153212	3.05300915816033e-10
0.095	0.979898707357522	3.98494151157639e-10
0.100	0.978864844402993	5.12956266301956e-10

Table 8. The tumor cells $\bar{y}(t)$ and the absolute residual error $|R_2(t)|$ at $\omega = 0.04$

t	$\bar{y}(t)$	$ R_2(t) $
0	1	0
0.005	1.00317133261574	1.19847948549288e-14

0.010	1.00635809732467	9.42422270895282e-13
0.015	1.00956036469139	8.16017355773890e-12
0.020	1.01277820564434	3.53911215498876e-11
0.025	1.01601169147740	1.09033543823954e-10
0.030	1.01926089385133	2.72307629292292e-10
0.035	1.02252588479534	5.89406764515410e-10
0.040	1.02580673670847	1.14962645979546e-09
0.045	1.02910352236115	2.07147075566863e-09
0.050	1.03241631489659	3.50673595130857e-09
0.055	1.03574518783222	5.64457149723556e-09
0.060	1.03909021506112	8.71551789559722e-09
0.065	1.04245147085345	1.29955214521464e-08
0.070	1.04582902985778	1.88099257248892e-08
0.075	1.04922296710250	2.65374395152150e-08
0.080	1.05263335799721	3.66140812481414e-08
0.085	1.05606027833401	4.95370995891275e-08
0.090	1.05950380428885	6.58688701457048e-08
0.095	1.06296401242288	8.62407681029719e-08
0.100	1.06644097968372	1.11357016642777e-07

6. Conclusion

Combined Laplace transform-Adomian decomposition method has been applied to non-linear system of ordinary differential equations; the simplified tumor-immune system. In small interval from the point at which the initial values are considered, the

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absolute error between CLTADM and RK45 (ode45 solver in matlab) is tiny (very small). We find that the absolute error between CLTADM and RK45 (ode45 solver in matlab) is smaller than the absolute error between RK23 (ode23 solver in matlab) and RK45 (ode45 solver in matlab). Therefore, the Combined Laplace transform-Adomian decomposition method is better than RK23 (ode23 solver in matlab) in small interval from the point at which the initial values are considered, i.e. $[0, 0.1]$. Then, the absolute residual errors of solutions by using CLTADM are very small where the solutions by using CLTADM nearly equal the exact solutions in small interval from the point at which the initial values are considered. Also, there are many chemical reactions which start and end in a small time. Therefore, we can use Combined Laplace transform-Adomian decomposition method to solve the mathematical models of chemical reactions.

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