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Stability Analysis and Numerical simulations of a Tumor-immune Interaction Model with Constant Chemotherapy Infusion

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ABSTRACT
Considering the effect of constant chemotherapy infusion, a mathematical model of tumor–immune interaction is formulated and analyzed. Building upon the framework of de Pillis-type models, the present work incorporates immune response, tumor dynamics, and steady drug infusion. We establish the positivity and boundedness of solutions to ensure biological feasibility. Local and global stability analyses of equilibrium points are carried out, with special emphasis on tumor-free and coexistence equilibria. Numerical simulations are presented to validate the analytic findings and illustrate the impact of chemotherapy on tumor suppression. The results indicate that constant chemotherapy infusion can effectively stabilize the tumor-free equilibrium under suitable dosing conditions, highlighting its potential in controlling tumor growth and improving treatment outcomes.

Keywords: Tumor-immune interaction model; Constant chemotherapy infusion; Stability; Numerical simulations

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1. INTRODUCTION

Globally, cancer remains a predominant contributor to disease burden and mortality, posing significant obstacles to the effectiveness and sustainability of healthcare systems and researchers [1,2,3]. Although significant advances have been made in early diagnosis, targeted treatments, and immunotherapies, the challenges of tumor relapse and therapy resistance still hinder long-term clinical outcomes [4,5]. Comprehending the complex interactions among tumor cells, the immune system, and therapeutic procedures is essential. In this context, mathematical modelling serves as a powerful tool to elucidate tumor–immune dynamics, forecast treatment responses, and design optimized therapeutic strategies [6,7,8,9]. To do this researcher made extensive use of mathematical models

In recent decades' numerous researchers have investigated mathematical models of tumor evolution, cellular interactions, and tumor proliferation, leading to the development of a wide range of models [10–16].

The method of chemotherapy administration plays an essential role in determining therapeutic efficacy. Although many models adopt time-dependent dosing schemes, de Pillis et al. demonstrated that incorporating a constant infusion term allows for analytical simplification while retaining clinical relevance. Continuous infusion regimens, including pump-assisted and prolonged intravenous delivery, are widely employed in oncology. However, mathematical models that integrate such infusion strategies with rigorous stability analyses and simulation studies remain relatively scarce.

Classical models of tumor–immune dynamics have provided valuable understanding of how effector immune cells contribute to the regulation of tumor growth [17,18,19]. Early works such as those by Kuznetsov et al. and De Pillis et al. demonstrated how nonlinear differential equations can capture complex immune–tumor dynamics, including tumor escape and immune-induced dormancy. More recent studies have extended these models by incorporating treatment effects, such as chemotherapy, radiotherapy, virotherapy and immunotherapy, to explore the synergistic impact of combined approaches [20,21,22,23].

Chemotherapy continues to represent one of the most common and effective approaches for cancer treatment [24,25]. To capture the balance between therapeutic benefits and adverse effects, various mathematical models of chemotherapy delivery have been proposed, encompassing both periodic pulsed dosing and continuous infusion approaches [26]. Continuous infusion has been demonstrated to maintain steadier plasma drug concentrations, which may enhance therapeutic efficacy while reducing systemic toxicity [27].

In this work, we construct and analyse a tumor–immune interaction model with constant chemotherapy infusion. Three interacting populations are incorporated into the model: effector immune cells, tumor cells, and the concentration of chemotherapy drug. Effector cells become activated in response to tumor antigens and are crucial in tumor elimination, whereas the chemotherapy drug contributes both to tumor cell destruction and to the modulation of immune activity. To validate the biological relevance of the model, we demonstrate the positivity and boundedness of solutions, which validate that all state variables remain non-negative and uniformly bounded for all time. These characteristics confirm the model's well-posedness and applicability for long-term dynamical analysis.

We further conduct a stability analysis of the tumor-free, immune-free, and coexistence equilibria, identifying the conditions under which each state attains locally stability. This analysis allows us to compute the biological scenarios in which chemotherapy can eradicates the tumor, where the tumor persists due to insufficient immune response, or where tumor–immune coexistence arises under treatment influence. Moreover, numerical simulations are performed to validate the theoretical findings, demonstrate the influence of treatment parameters, and investigate possible outcomes of constant chemotherapy infusion strategies.

2. MODEL FORMULATION

We consider the model developed by de Pillis et al. [5] in which set of nonlinear ordinary differential equation are used to investigate the interaction between tumor cells, immune effector cells, and chemotherapy. It is worth noting that in our model, chemotherapy is used as a constant infusion rate V_0, following the approach of de Pillis et al. [5]. Biologically, this assumption reflects to a continuous drug administration strategy, such as a long term infusion pump, which maintains a steady concentration of chemotherapy in bloodstream. Although time-dependent or periodic chemotherapy dosing $V(t)$ may capture more realistic clinical protocols, the constant infusion assumption provides a tractable framework for mathematical analysis but still gives useful insights into how tumors, the immune system, and drugs interact

The cell populations and drug concentration in this model at time t are denoted by:
• T(t), tumor cell population
• E(t), effector–immune cell population
• M(t), chemotherapy drug concentration
The system of differential equations describing the growth, death, and interactions of these populations with a chemotherapy treatment is given by

$$\frac{dE}{dt} = s + \frac{pET}{h+T} - mET - \mu E - K_E ME$$
$$\frac{dT}{dt} = rT(1 - bT) - a\frac{ET}{T+g} - K_T MT \qquad \ldots (2.1)$$
$$\frac{dM}{dt} = -\gamma M + V_0$$

Table 1:

Parameter	definition	Biological Interpretation	Baseline (Unit)	Unit	source
p	degree of recruitment of maximum immune-effector cells in relation with cancer cells	Represents how strongly immune cells are activated by tumor antigens; higher values mean stronger immune response	0.1245	day^{-1}	[3]
r	rate of tumor growth	Indicates the rate at which tumor cells proliferate; higher values correspond to more aggressive tumors	0.18	day^{-1}	[28]
b	capacity of the tumor cell	Maximum number of tumor cells that can be sustained in the environment	1.02×10^{-9}	$cell^{-1}$	[2]
a	parameter of cancer clean-up	Measure the cytotoxic efficiency of immune cells; larger values mean stronger immune-mediated tumor destruction	3.41×10^{-10}	$cell^{-1}.Day^{-1}$	[2]
g	half-saturation for cancer clean-up	Efficiency with which immune cells clear tumor	10^5	cells	[2]

		cells			
s	growth rate of normal/effector cell	Represents the baseline production of immune cells from bone marrow/thymus independent of tumor presence	1.2×10^{4}	Cells.day^{-1}	[3]
m	degree of inactivation of effector cells by tumor cells	Represent immune suppression by tumors; higher values mean stronger tumor-induced immune suppression	10^{-7}	Cells^{-1}.day^{-1}	[3]
μ	rate of natural demise of effector cells	Reflects the natural turnover or apoptosis of immune cells.	0.03	day^{-1}	[3]
γ	rate of decrease in concentration of chemotherapy drug	Drug clearance rate; higher values indicate faster removal of chemotherapy from the body	0.9	day^{-1}	[5]
h	steepness coefficient of the recruitment curve of effector immune cells	Control how sharply immune cell recruitment increases with tumor size	2.02×10^{10}	cells	[2]
K_E	Chemotherapy-induced death rate of effector cells	Side-effect of chemotherapy on immune system	0.01	day^{-1}	[5]
K_T	Chemotherapy-induced death rate of tumor cells	Cytotoxic effect of chemotherapy on tumor cells	0.3	day^{-1}	[5]

3. POSITIVITY INVARIANCE AND BOUNDEDNESS

In this section we will investigate whether the model (2.1) solutions are biological feasible or not for the considered value of all parameter. To do this we must show that the solutions of the model are positive and bounded using standard compression theory [29]

We show that if $E(0), T(0), M(0) \geq 0$

Then $E(t), T(t), M(t) \geq 0$ for all $t \geq 0$

M-equation is linear

$$\frac{dM}{dt} = -\gamma M + V_0$$

If $M(t) = 0$ then $\frac{dM}{dt} = V_0 > 0$

So trajectory cannot cross from nonnegative to negative hence $M(t) \geq 0$ for all $t \geq 0$

For T- equation we write

$$\frac{dT}{dt} = T[r(1 - bT) - \frac{aE}{T+g} - K_T M]$$

At any time when $T = 0$ and $E, M \geq 0$, We have $\frac{dT}{dt} = 0$

Thus T cannot become negative hence $T(t) \geq 0$

For E- equation

$$\frac{dE}{dt} = s + E[\frac{pT}{h+T} - mT - \mu - K_T M]$$

If $E = 0$ then $\frac{dE}{dt} = s > 0$, E cannot cross to negative value hence $E(t) \geq 0$

So $(E, T, M) \epsilon R_+^3 : E \geq 0, T \geq 0, M \geq 0$ is forward invariant solutions starting non-negative remain non-negative.

Now to check boundedness of the model (2.1)

From M- equation

$$\frac{dM}{dt} = -\gamma M + V_0$$

$$\Rightarrow \frac{dM}{dt} + \gamma M = V_0$$

The above linear ODE gives the solution

$$\Rightarrow M = M_0 e^{-\gamma t} + \frac{V_0}{\gamma}(1 - e^{-\gamma t})$$

$$\Rightarrow \lim_{t \to \infty} \sup [M(t)] \leq \frac{V_0}{\gamma}$$

From T- equation

$$\frac{dT}{dt} - rT(1 - bT) - u\frac{ET}{T+g} - K_T MT \leq rT(1 - bT)$$

As immune and chemo terms are nonnegative

$$\Rightarrow \frac{dT}{dt} \leq rT(1 - bT)$$

Integrating above we get solution

$$\Rightarrow T(t) \leq \frac{1}{b + T(0)e^{-rt}}$$

$$\Rightarrow \lim_{t \to \infty} \sup [T(t)] \leq \frac{1}{b}$$

Similarly, for the E-equation can be written as

$$\frac{dE}{dt} = s + \frac{pET}{h+T} - mET - \mu E - K_E ME \leq s - \mu E$$

$$\frac{dE}{dt} \leq s - \mu E$$

Integrating the above linear-ODE we get solution

$$\Rightarrow E(t) = (1 - e^{-\mu t}) + E_0 e^{-\mu t}$$

$$\lim_{t \to \infty} \sup [E(t)] \leq \frac{s}{\mu}$$

Consequently, the corresponding domain region for the system (2.1) is

$$\Delta = \left\{(E,T,M) \epsilon R_+^3 \mid E(t) \leq \frac{s}{\mu}, T(t) \leq \frac{1}{b}, M(t) \leq \frac{V_0}{\gamma}\right\}$$

The domain region Δ is positively invariant, which verifies that the model system (2.1) is biological feasible

4. EQUILIBRIUM POINTS

Equilibrium points of the system (2.1) obtained when $\frac{dE}{dt} = 0, \frac{dT}{dt} = 0, \frac{dM}{dt} = 0$ it will discuss in following lemma

Lemma 1

(i) If $E = 0, T = 0,$ then system (2.1) has an equilibrium point $P_0(0,0,\frac{V_0}{\gamma})$

(ii) If $E = 0,$ then system (2.1) has an immune- free equilibrium point $P_1(0,\frac{r-K_T\frac{V_0}{\gamma}}{rb},\frac{V_0}{\gamma})$

(iii) If $T = 0,$ then the system (2.1) has an tumour free equilibrium point $P_2(\frac{s\gamma}{\mu\gamma+K_E V_0},0,\frac{V_0}{\gamma})$

Proof.

(i) If $E = 0, T = 0$, then equation (2.1) and $\frac{dM}{dt} = 0$

$\Rightarrow -\gamma M + V_0, \Rightarrow M = \frac{V_0}{\gamma},$ we get $P_0(0,0,\frac{V_0}{\gamma})$

(ii) If $\frac{dM}{dt} = 0, \Rightarrow M = \frac{V_0}{\gamma},$ by putting $E - 0$ and $\frac{dT}{dt} = 0$ in T- equation of (2.1) we get

$$rT(1-bT) - K_T MT = 0$$

$$\Rightarrow T[r(1-bT) - K_T\frac{V_0}{\gamma}] = 0$$

$$such\ that\ T = 0\ or\ r(1-bT) - K_T\frac{V_0}{\gamma} = 0$$

$\rightarrow T - \frac{r-K_T\frac{V_0}{\gamma}}{br}$ and we get, $P_1(0,\frac{r-K_T\frac{V_0}{\gamma}}{rb},\frac{V_0}{\gamma})$

and for $T = 0$, we will get same equilibrium point as in (i)

(iii) If $\frac{dM}{dt} = 0, \Rightarrow M = \frac{V_0}{\gamma}$ by putting $T = 0$ and $\frac{dE}{dt} = 0$ in E- equation of (2.1) and then substituting $M = \frac{V_0}{\gamma}$, we have

$$\Rightarrow s - \mu E - K_E\frac{V_0}{\gamma}E = 0$$

$$\Rightarrow E = \frac{S}{\mu + K_E\frac{V_0}{\gamma}}, \Rightarrow E = \frac{s\gamma}{\mu\gamma + K_E V_0}$$

Therefore we obtain $P_2(\frac{s\gamma}{\mu\gamma+K_E V_0},0,\frac{V_0}{\gamma})$

4.1. Coexistence equilibrium point

In this section we will find coexistence equilibrium point $P_3 = (E^*,T^*,M^*)$

Now if $\frac{dM}{dt} = 0, \Rightarrow M^* = \frac{V_0}{\gamma}$

This means both immune cells (E^*) and tumor cells (T^*) are positive

So we look equilibria with:

$M^* = \frac{V_0}{\gamma}, \quad E^* > 0, \quad T^* > 0$

From the tumor equation $\left(\frac{dT}{dt} = 0\right)$:

$$0 = rT^*(1-bT^*) - \alpha\frac{E^*T^*}{T^*+g} - K_T M^* T^*$$

Since $T^* \geq 0$, divide through by T^*

$$0 = r(1 - bT^*) - a\frac{E^*}{T^*+g} - K_T\frac{V_0}{\gamma}$$

Now solve for E^* we get

$$E^* = \frac{T^*+g}{a}\left(r(1 - bT^*) - K_T\frac{V_0}{\gamma}\right) \qquad \ldots(3)$$

Now put this expression for E^* in to the immune equation $\left(\frac{dE}{dt} = 0\right)$:

$$0 = s + \frac{pE^*T^*}{h+T^*} - mE^*T^* - \mu E^* - K_E M^* E^*$$

$$\Rightarrow 0 = s + \frac{p\left(\frac{T^*+g}{a}\left(r(1 - bT^*) - K_T\frac{V_0}{\gamma}\right)\right)T^*}{h+T^*} - m\left(\frac{T^*+g}{a}\left(r(1 - bT^*) - K_T\frac{V_0}{\gamma}\right)\right)T^*$$
$$- \mu\frac{T^*+g}{a}\left(r(1 - bT^*) - K_T\frac{V_0}{\gamma}\right) - K_E\frac{V_0}{\gamma}\frac{T^*+g}{a}\left(r(1 - bT^*) - K_T\frac{V_0}{\gamma}\right) \qquad \ldots(4)$$

The above equation in the T^* variable obtains T^* solution so that the coexistence equilibrium point of the model is $P_3\left(E^*, T^*, \frac{V_0}{\gamma}\right)$ where E^* and T^* like the above equation (3) & (4)

5. STABILITY ANALYSIS OF EQUILIBRIUM POINTS

To determine the local stability of the equilibrium points, we need to compute the linearization of the system (2.1), which is obtained from the Jacobian matrix of the system (2.1). See [1] for more information about such calculations. For the system (2.1), the Jacobian is the following:

$$J(E,T,M) = \begin{bmatrix} \frac{pT}{h+T} - mT - \mu - K_E M & \frac{pEh}{(h+T)^2} - \mu E & -K_E E \\ \frac{-aT}{T+g} & r(1 - 2bT) - a\frac{Eg}{(T+g)^2} - K_T M & -K_T T \\ 0 & 0 & -\gamma \end{bmatrix}$$

If we substitute the equilibrium value in the Jacobean matrix J, then the matrix J will represent the linearization of the system of differential equations about the equilibrium points. By the Hartman-Grobman theorem [30], the local dynamics of the nonlinear system will be approximated by the behavior of the linearized system near that equilibrium points, as long as the equilibrium point is hyperbolic (i.e., when none of the Eigenvalues of the Jacobean matrix have zero real parts). Therefore, the stability of each equilibrium point can be determined by analyzing the eigenvalues of the Jacobean evaluated at the equilibrium.

5.1. Equilibrium at $P_0(0,0,\frac{V_0}{\gamma})$

Evaluating J at $P_0(0,0,\frac{V_0}{\gamma})$

$$J(P_0) = \begin{bmatrix} -\mu - K_E\frac{V_0}{\gamma} & 0 & 0 \\ 0 & r - K_T\frac{V_0}{\gamma} & 0 \\ 0 & 0 & -\gamma \end{bmatrix}$$

The eigenvalues of this matrix are $\lambda_1 = -\mu - K_E\frac{V_0}{\gamma} < 0, \lambda_2 = r - K_T\frac{V_0}{\gamma}, \lambda_3 = -\gamma < 0$

Since $\lambda_1 < 0$ & $\lambda_2 < 0$ for positive parameters, the only possible unstable direction is λ_2. Therefore $P_0(0,0,\frac{V_0}{\gamma})$ locally asymptotically stable iff $r - K_T\frac{V_0}{\gamma} < 0 \Leftrightarrow r < K_T\frac{V_0}{\gamma}$ otherwise it is saddle point.

5.2 Equilibrium at $P_1(0,\frac{r-K_T\frac{V_0}{\gamma}}{rb},\frac{V_0}{\gamma})$

$$J(P_1) = \begin{bmatrix} p\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right) & & \\ \left(h+\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)\right) - m\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right) - \mu - K_E\frac{V_0}{\gamma} & 0 & 0 \\ \frac{-a\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)}{\left(\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)+g\right)} & r\left(1-2b\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)\right) - K_T\frac{V_0}{\gamma} & -K_T\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right) \\ 0 & 0 & -\gamma \end{bmatrix}$$

The eigenvalues of this matrix are

$$\lambda_1 = \frac{p\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)}{\left(h+\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)\right)} - m\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right) - \mu - K_E\frac{V_0}{\gamma}, \lambda_2 = r\left(1-2b\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)\right) - K_T\frac{V_0}{\gamma}, \quad \lambda_3 = -\gamma < 0$$

So P_1 locally asymptotically stable iff both $\lambda_1 < 0$ & $\lambda_2 < 0$, i.e. $\frac{p\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)}{\left(h+\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)\right)} < m\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right) + \mu + K_E\frac{V_0}{\gamma}$ &

$$r < \frac{K_T\frac{V_0}{\gamma}}{\left(1-2b\left(\frac{r-K_T\frac{V_0}{\gamma}}{rb}\right)\right)}$$

5.3. Equilibrium at $P_2\left(\frac{s\gamma}{\mu\gamma+K_EV_0},0,\frac{V_0}{\gamma}\right)$

$$(P_2) = \begin{bmatrix} \mu - K_E\frac{V_0}{\gamma} & \frac{p\left(\frac{s\gamma}{\mu\gamma+K_EV_0}\right)}{h} - \mu\left(\frac{s\gamma}{\mu\gamma+K_EV_0}\right) & -K_E\left(\frac{s\gamma}{\mu\gamma+K_EV_0}\right) \\ 0 & r - a\frac{\left(\frac{s\gamma}{\mu\gamma+K_EV_0}\right)}{g} - K_T\frac{V_0}{\gamma} & 0 \\ 0 & 0 & -\gamma \end{bmatrix}$$

The eigenvalues of this matrix are $\lambda_1 = \mu - K_E\frac{V_0}{\gamma}$, $\lambda_2 = r - a\frac{\left(\frac{s\gamma}{\mu\gamma+K_EV_0}\right)}{g} - K_T\frac{V_0}{\gamma}, \lambda_3 = -\gamma < 0$

So P_2 locally asymptotically stable iff both $\lambda_1 < 0$ & $\lambda_2 < 0$, i.e. $\frac{V_0}{\gamma} > \frac{\mu}{K_E}$, $r < a\frac{\left(\frac{sT}{\mu T + K_E V_0}\right)}{g} + K_T\frac{V_0}{\gamma}$

5.4. Coexistence equilibrium point $P_3\left(E^*, T^*, \frac{V_0}{\gamma}\right)$

$$J\left(E^*, T^*, \frac{V_0}{\gamma}\right) = \begin{bmatrix} \frac{pT^*}{h+T^*} - mT^* - \mu - K_E\frac{V_0}{\gamma} & \frac{pE^*h}{(h+T^*)^2} - \mu E^* & -K_E E^* \\ \frac{-aT^*}{T^*+g} & r(1-2bT^*) - a\frac{E^*g}{(T^*+g)^2} - K_T\frac{V_0}{\gamma} & -K_T T^* \\ 0 & 0 & -\gamma \end{bmatrix}$$

At P_3 substitute in to the Jacobean and denote the upper 2×2 block entries by

$$a_{11} = \frac{pT^*}{h+T^*} - mT^* - \mu - K_E\frac{V_0}{\gamma}$$

$$a_{12} = \frac{pE^*h}{(h+T^*)^2} - \mu E^*$$

$$a_{21} = \frac{-aT^*}{T^*+g}$$

$$a_{22} = r(1-2bT^*) - a\frac{E^*g}{(T^*+g)^2} - K_T\frac{V_0}{\gamma}$$

One eigenvalue is $\lambda_3 = -\gamma < 0$

The remaining two eigenvalues are the roots of

$$\lambda^2 - (a_{11} + a_{22})\lambda + (a_{11}a_{22} - a_{12}a_{21}) = 0$$

Here we examine the stability analysis of coexistence equilibrium point $P_3\left(E^*, T^*, \frac{V_0}{\gamma}\right)$ when it exists. In this case, analytic techniques fail to yield information about the eigenvalues λ_1 & λ_2, due to the complexity of the system. Conditions such as the Routh-Hurwitz test [31] the coexistence equilibrium P_3 is locally asymptotically stable iff $(a_{11} + a_{22}) < 0$ *and* $(a_{11}a_{22} - a_{12}a_{21}) > 0$

6. NUMERICAL SIMULATIONS

To investigate the dynamics of tumour growth, immune response, and chemotherapy drug administration, we performed numerical simulations of the proposed mathematical model. The system consists of three coupled ordinary differential equations representing:

1. **Tumour cells (T)**
2. **Effector immune cells (E)**
3. **Chemotherapy drug concentration (M)**

6.1. Simulation method

- The model equations were solved using the **fourth-order Runge-Kutta (RK4) method** with a time step of Δt = 0.1 days.
- Initial conditions were set as $T(0) = 10^6, E(0) = 10^5$ and $M(0) = 0$
- Simulations were performed over **200 days** to capture both short- and long-term dynamics.

6.2. Chemotherapy Scenarios

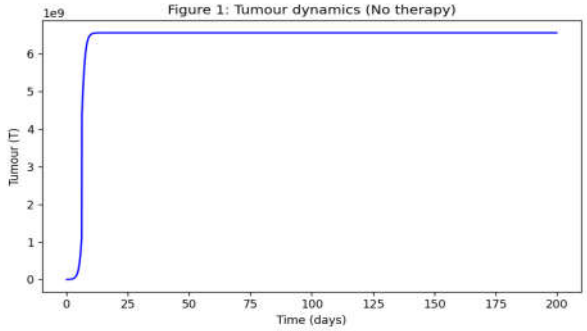
Three therapy protocols were considered:

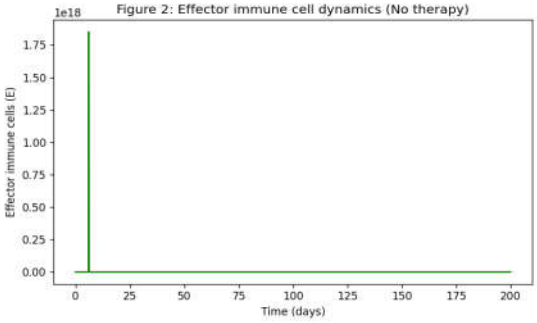
- **No chemotherapy:** $V_0 = 0$, representing natural tumor-immune dynamics.
- **Constant infusion:** $V_0 = 500$, simulating a continuous drug infusion.
- **Pulsed therapy:** $V_0 = 10^4$ administered periodically every 20 days.

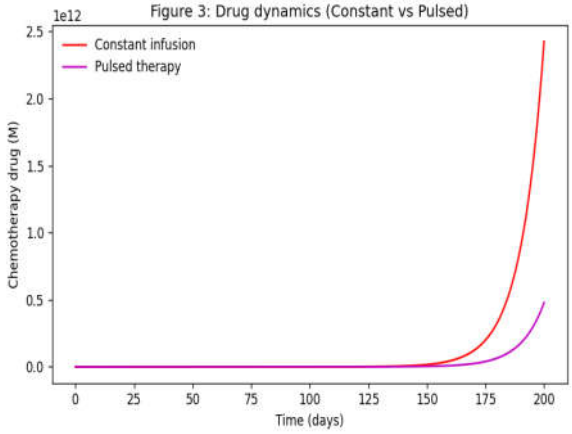
6.3. Parameter Values

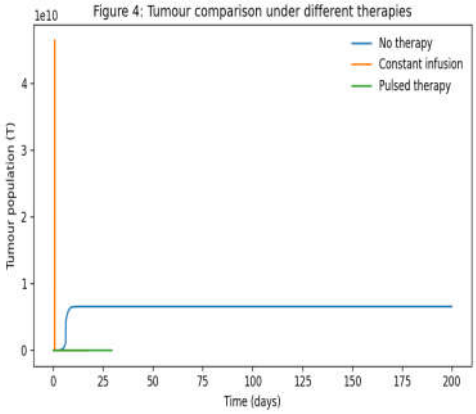
The parameters were chosen based on previous studies (see Table 1)

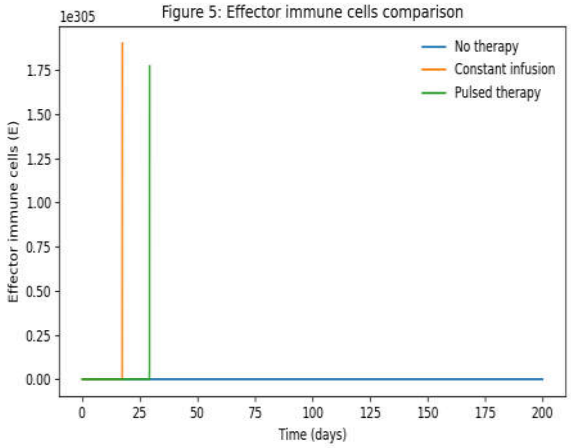
6.4. Graph plots.

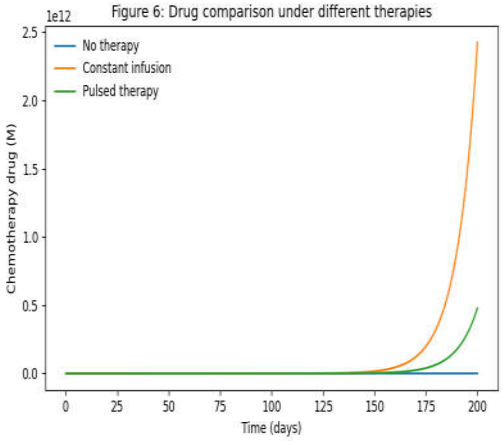












7. RESULT AND DISCUSSION

- **Figure 1** depits tumour growth without therapy. The tumour population rapidly increases and eventually stabilizes near its carrying capacity, while immune cells remain insufficient to control growth.
- **Figure 2** shows the effector immune cell dynamics in the absence of therapy. The immune population initially responds but eventually declines due to diminution by the large tumour burden.
- **Figure 3** shows the drug dynamics under constant infusion and pulsed therapy. Constant infusion yields a stable and sustain drug level, whereas pulsed therapy produces periodic peaks followed by decay between doses.
- **Figure 4** presents a comparative analysis of tumour dynamics under three scenarios. Both constant infusion and pulsed therapy significantly suppress tumour growth compared to the uncontrolled case, with constant infusion providing the strongest suppression
- **Figure 5** comparison of effector immune cell across therapies. Continuous drug infusion reduces immune cells due to cytotoxic effects, but pulsed therapy preserves higher immune activity compared to continuous infusion.
- **Figure 6** Drug concentration comparison across therapeutic strategies. No therapy results in zero concentration, while constant infusion produces a monotonic increase towards equilibrium. Pulsed therapy generates oscillatory peaks aligned with the dosing intervals.

8. CONCLUSION

This study presents formulation and analysis of a nonlinear mathematical model capturing the complex interactions among tumour cells, effector immune cells, and chemotherapy drug concentration. The framework accounts for both immune-mediated tumour suppression and chemotherapy-induced cytotoxic effects under different treatment strategies. Stability analysis of the equilibrium points revealed that tumour-free and tumour-persistent states are highly sensitive to parameter variations, particularly the interplay between tumour proliferation, immune activity, and drug efficacy. The result indicate that chemotherapy and immune response can jointly steer the system towards tumour eradication whenever the effective reproduction number of tumour cells is reduced below unity.

Numerical simulations performed using the fourth-order Runge–Kutta method, we examined the temporal dynamics of tumour growth, immune response, and drug kinetics under three scenarios: no therapy, constant infusion, and periodic pulsed administration. The finding demonstrates that, in the absence of therapy, the tumour population expends rapidly approaches its carrying capacity, while immune cells alone remains inadequate to suppress progression. The inclusion of chemotherapy significantly modifies the system dynamics. Continuous infusion provides sustained tumour inhibition, but at the cost of reducing immune cell viability due to continuous drug exposure. In contrast, pulsed therapy produces oscillatory tumour control while maintaining a comparatively strong immune response, thereby suggesting a potential balance between therapeutic efficacy and immune system preservation.

Overall, the study highlights important trade-offs between tumor elimination and immune preservation across different chemotherapy regimens. These results emphasize the importance of designing optimized dosing strategies that minimize systemic toxicity while maximizing therapeutic efficacy. Future extension of this framework could incorporate tumor heterogeneity, adaptive immune mechanisms, and combined immunotherapy, thereby increasing its applicability to personalized cancer treatment.

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