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# STABILITY ANALYSIS FOR GLIAL CELLS INTERACTION BETWEEN IMMUNOTHERAPY AND CANCER CELLS

**Vargees Kaviyan E** Department of Mathematics, Sri Ramakrishna Mission Vidyalaya College of Arts and Science, Coimbatore-641020, India. (E-mail: vargeeskaviyan@gmail.com)
**Jayakumar T** Department of Mathematics, Sri Ramakrishna Mission Vidyalaya College of Arts and Science, Coimbatore-641020, India. (E-mail: jayakumar.thippan68@gmail.com)
**Sujitha S** Department of Science and Humanities, Sree Sakthi Engineering College, Coimbatore-641104, India. (E-mail: sujithaskr5@gmail.com)
**Maheskumar D** Department of Science and Humanities, Sri Krishna College of Technology, Coimbatore-42, India. (E-mail: madhana2010@gmail.com)

**Abstract**
In the past decade, brain tumours have been one of the major problems to cure completely in the medical field, and it has become evident that the treatment of cancer and the control of tumour growth require a greater understanding of the interactions among the key components involved in the cancer network. In this article, we propose a new system of differential equations that explains the interaction of glial (healthy) cells, glioma (cancer) cells, macrophages, CD8+ T cells, and immunotherapy. Positivity and boundedness are investigated. Stability analysis is discussed in two categories: without any treatment and with immunotherapy treatment. Moreover, numerical simulations are also given for our proposed model. The discussion and conclusion are discussed. In the final analysis, we discuss potential future paths and existing research endeavours that are targeted at improving the methods of immunotherapy for the purpose of achieving better results in the treatment of brain cancer. Overall, immunotherapy is a therapeutic method that has a great deal of potential as an independent treatment for brain cancer. It also marks a paradigm shift in the treatment landscape for this debilitating illness.

**Keywords and phrases:**
Brain tumour, Immunotherapy, Glial cells, Glioma cells, Stability Analysis.
**2010 AMS Classification:** 34D20, 37M05, 92C50.

## 1. Introduction

The National Brain Tumour Society estimates that 7,00,000 Americans are currently coping with primary brain tumours, and that 78,980 additional cases will be reported in 2018 [1]. It is not unexpected that scientists and academics from all around the world have been working to simulate the brain tumour. The goal is to better understand the intricate biological process in order to develop new treatment plans or enhance those that are already in place in order to cure brain tumours or at the very least enhance patient quality of life. Numerous types of mathematical models have previously been created, and each one helps us comprehend the tumour and the dynamics that affect the patient's prognosis in a unique way. Malignant gliomas' immune-suppressed state can be reversed by administering mem brane glycoprotein T11 target structure as a therapeutic agent by improving the functional state of immune cells such macrophages and activated CD8+ T cells in animals. According to computer modelling of this therapy, treatment with T11 target structure may enable immune system cells to pass through the blood-brain barrier (BBB) impermeability, resulting in increased phagocytic activity and a decrease in malignant gliomas [2]. Iarosz et al. [3] built a mathematical model of a brain tumour with biological underpinnings in which they used the heavy step function to simulate the interaction between glial cells and neurons. In their simulation, they employed chemotherapy to stop the growth of aggressive glioma cells. Using a cellular automaton model, Tektonidis et al. [4] examined a computational data-driven investigation of the growth and invasive of malignant glioma cells in vitro. They concentrated on identifying the biological components that determine the malignant gliomas' in vitro cultured aggressiveness. In glioblastoma patients, a cellular immunodeficiency condition has been noted. Skin specific energy to a number of antigens and a decline in T cell blastogenic reactivity in vitro are symptoms of defective cell-mediated immunity [5, 6, 7]. Additionally, it is well known that the majority of glioblastoma patients experience humoral immune reactions to their tumours [8, 9].

However, there is less concrete and disputed evidence of strong T cell-mediated anti-tumour responses [10, 11, 12]. Glioblastoma tissue obtained after surgery from tumour-infiltrating lymphocytes has no sensitivity to T cell mitogens in vitro [13]. According to Kikuchi and Neuwelt [14] (1983), the tumour cyst fluid of glioblastoma patients contains immunosuppressive substances that prevent the growth of normal lymphocytes caused by mitogens and antigens, as well as the blood of the patient before but not after tumour excision [5].

We investigated whether glioma cells secrete T cell suppressor factors in light of the link between glioblastoma and aberrant T cell function that has been shown in recent years. Some authors [15, 16, 17] have also investigated brain tumours in the context of other therapies. In [3] K. C. Iarosz et al. presented that healthy cells respond among most tumours and Chemotherapy. S. Khajanchi et al. [18] address the proliferation of cancer, macrophages, and CD8+ T cells while not affecting the growth of healthy cells. Building on these foundational studies, another investigation [19] examined both analytical and numerical solutions for modelling the interactions among glial cells, immunotherapy, and cancerous cells. Drawing inspiration from these findings, the present study seeks to develop an innovative computational framework that integrates stability analysis to model brain tumour responses to immunotherapy. This framework aims to advance mathematical modelling by incorporating stability analysis methodologies into the immunotherapy treatment model for brain tumours, as described in [19].

We construct the work as follows: In Section two, A (NLODE) is constructed using (IT). In Section three, positivity and boundedness are discussed. In Section 4, stability analysis is investigated. In Section 5, numerical solutions are discussed, and in Section 6, the discussion and conclusion are provided.

## 2. Mathematical Modelling

In this dynamic model of brain tumours (gliomas), healthy (glial) cells interact with Immunotherapy (IT) treatment. Our model describes the growth, death, and interaction between these cells as given by:

$$\frac{dX_1(t)}{dt} = \Psi_1 X_1(t)\left(1-\frac{X_1(t)}{M_1}\right) - \Delta_1 X_1(t)X_2(t), \tag{1}$$

$$\frac{dX_2(t)}{dt} = \Psi_2 X_2(t)\left(1-\frac{X_2(t)}{M_2}\right) - \Delta_2 X_1(t)X_2(t) - \frac{\left(\overline{\gamma}_1 X_3(t)+\overline{\gamma}_2 X_4(t)\right)X_2(t)}{X_2(t)+\overline{M}_1}, \tag{2}$$

$$\frac{dX_3(t)}{dt} = rX_3(t)\left(1-\frac{X_3(t)}{V_1}\right) - \frac{\overline{\gamma}_3 X_2(t)X_3(t)}{\overline{M}_2+X_2(t)}, \tag{3}$$

$$\frac{dX_4(t)}{dt} = \frac{\nu_1 X_2(t)X_4(t)}{\overline{M}_3+X_2(t)} - \mu_1 X_4(t) - \frac{\overline{\gamma}_4 X_2(t)X_4(t)}{\overline{M}_4+X_2(t)} + s_1 u_1. \tag{4}$$

The system comprises four different components, namely density of Glial cells ($X_1$(Kg/m$^3$)), the density of cancer cells ($X_2$(Kg/m$^3$)), the density of Macrophages ($X_3$(Kg/m$^3$)), the concentrations of CD8+ T cells ($X_4$(Kg/m$^3$)).

In equations (1), (2), and (3), 1st term represents the proliferation of glial cells, glioma cells, macrophages. In equations (1) and (2), 2nd term represents interaction between healthy and cancer cells. In equation (2) final term indicates elimination of $X_2$ owing to interplay with $X_3$ and $X_4$. In equation (3), last term represents deactivation of $X_3$ owing to interaction with $X_2$. In equation (4), 1st term indicates the $X_4$ are recruited by $X_2$, 2nd term indicates death rate of $X_4$, third term indicates the $X_4$ eliminated by $X_2$, and last term $s_1$ is the treatment strength, $u_1$ is a source of $X_4$.

The system of (NLODE) from (1) - (4) are normalized, is given by

$$\begin{cases} \dfrac{dx_1(t)}{dt} &= \Psi_1 x_1(t)\big(1-x_1(t)\big) - \delta_1 x_1(t)x_2(t), \\ \dfrac{dx_2(t)}{dt} &= \Psi_2 x_2(t)\big(1-x_2(t)\big) - \delta_2 x_1(t)x_2(t) - \dfrac{\big(\gamma_1 x_3(t)+\gamma_2 x_4(t)\big)x_2(t)}{x_2(t)+m_1}, \\ \dfrac{dx_3(t)}{dt} &= r x_3(t)\big(1-x_3(t)\big) - \dfrac{\overline{\gamma}_3 x_2(t)x_3(t)}{m_2+x_2(t)}, \\ \dfrac{dx_4(t)}{dt} &= \dfrac{\nu_1 x_2(t)x_4(t)}{m_3+x_2(t)} - \mu_1 x_4(t) - \dfrac{\overline{\gamma}_4 x_2(t)x_4(t)}{m_4+x_2(t)} + s_1 u_1. \end{cases} \quad (5)$$

Where,

$x_1(t) = \frac{X_1(t)}{M_1}$, $x_2(t) = \frac{X_2(t)}{M_2}$, $x_3(t) = \frac{X_3(t)}{V_1}$, $x_4(t) = \frac{X_4(t)}{\overline{M_3}}$, $\delta_1 = \Delta_1 M_2$, $\delta_2 = \Delta_2 M_1$, $\gamma_1 = \frac{\overline{\gamma_1} V_1}{M_2}$, $\gamma_2 = \frac{\overline{\gamma_2}\overline{M_3}}{M_2}$, $m_1 = \frac{\overline{M_1}}{M_2}$, $m_2 = \frac{\overline{M_2}}{M_2}$, $m_3 = \frac{\overline{M_3}}{M_2}$, and $m_4 = \frac{\overline{M_4}}{M_2}$.

**Table 1: List of symbols and abbreviations.**

| Parameter | Values | Descriptions |
|---|---|---|
| $\Psi_1$ | $0.0068\ day^{-1}$ | Proliferation rate [20, 21] |
| $\Psi_2$ | $0.012\ day^{-1}$ | Proliferation rate [20, 21] |
| $\Delta_1$ | $3.6 \times 10^{-5} day^{-1}$ | Competition Coefficients [20] |
| $\Delta_2$ | $3.6 \times 10^{-6} day^{-1}$ | Competition Coefficients [20] |

**Table 2: Values of Normalized Parameter**.

| Parameter | Values | Source |
|---|---|---|
| $\gamma_1$ | 0.069943 | [22] |
| $\gamma_2$ | 2.74492 | [22] |
| $m_1$ | 0.90305 | [23] |
| $r$ | 0.3307 | [22] |
| $\overline{\gamma_3}$ | 0.0194 | [22] |
| $m_2$ | 0.030584 | [23] |
| $\nu_1$ | 0.1245 | [24] |
| $m_3$ | 2.8743 | [24] |
| $\mu_1$ | 0.0074 | [22] |
| $\overline{\gamma_4}$ | 0.01694 | [22] |
| $m_4$ | 0.378918 | [23] |
| $\delta_1$ | $1.8 \times 10^{-2} (day^{-1})$ | [3] |
| $\delta_2$ | $1.8 \times 10^{-3} (day^{-1})$ | [3] |

## 3. Positivity and Bounded

The positivity and boundedness of the equations (5) with initial values are investigated in these sections.

**Theorem 3.1.** *The (NLODE) (5) solution remains positive.*

*Proof.* The equations (5) give,

$$\frac{dx_1(t)}{dt} = \Psi_1 x_1(t)\big(1-x_1(t)\big) - \delta_1 x_1(t)x_2(t),$$

$$\frac{dx_1(t)}{x_1(t)} = \Big(\Psi_1(t)\big(1-x_1(t)\big) - \delta_1 x_2(t)\Big)\,dt,$$

we can get,

$$x_1(t) = x_1(0)exp\left(\int_0^t \left[\Psi_1\left(1 - x_1(s)\right) - \delta_1 x_2(s)\right] ds\right).$$

In similar way, we obtain from 2nd to 4th equations of (5), we get

$$x_2(t) = x_2(0)exp\left(\int_0^t \left[\Psi_2\left(1 - x_2(s)\right) - \delta_2 x_1(s) - \frac{\left(\gamma_1 x_3(s) + \gamma_2 x_4(s)\right)}{x_2(s) + m_1}\right] ds\right),$$

$$x_3(t) = x_3(0)exp\left(\int_0^t \left[r\left(1 - x_3(s)\right) - \frac{\gamma_3 x_2(s)}{x_2(s) + m_2}\right] ds\right),$$

$$x_4(t) = x_4(0)exp\left(\int_0^t \left[\frac{\nu_1 x_2(s)}{x_2(s) + m_3} - \mu_1 - \frac{\gamma_4 x_2(s)}{x_2(s) + m_4}\right] ds\right).$$

$$R_+^4 = \{x_1(t), x_2(t), x_3(t), x_4(t): x_1(t), x_2(t), x_3(t), x_4(t) > 0\}.$$

Next, we are going to demonstrate that the system (5) is bounded by using the system's positivity.

**Theorem 3.2.** *The (NLODE) (5) is bounded.*

*Proof.* First, we take 1st equations of (5):

$$\frac{dx_1(t)}{dt} \leq \Psi_1 x_1(t)\left(1 - x_1(t)\right),$$

$$-\frac{1}{x_1^2}\frac{dx_1}{dt} - \frac{\Psi_1}{x_1} \leq -\Psi_1.$$

After solving we can get the solutions,

$$\bar{x_1} = \lim_{t \to +\infty} \sup x_1(t) \leq 1.$$

Similarly, we can take 2nd, 3rd of equations of (5),

$$\frac{dx_2(t)}{dt} \leq \left(1 - x_2(t)\right)\Psi_2 x_2(t),$$

$$\frac{dx_3(t)}{dt} \leq r x_3(t)\left(1 - x_3(t)\right).$$

The equations follow that,

$$\bar{x_1} = \lim_{t \to +\infty} \sup x_1(t) \leq 1, \qquad \bar{x_2} = \lim_{t \to +\infty} \sup x_2(t) \leq 1,$$

$$\bar{x_3} = \lim_{t \to +\infty} \sup x_3(t) \leq 1.$$

Since $0 < \mu_1$, from the fourth equation of (4) is that

$$\frac{dx_4(t)}{dt} \leq \nu_1 x_2(t) x_4(t) - \mu_1 x_4(t).$$

$$\bar{x_4} = \lim_{t \to +\infty} \sup x_4(t) \leq 0, \quad if \;\; \nu_1 x_4(t) < \mu_1.$$

$$R_+^4 = \{x_1(t),\, x_2(t),\, x_3(t),\, x_4(t):$$
$$0 \leq x_1(t) \leq 1,\;\; 0 \leq x_2(t) \leq 1,\;\; 0 \leq x_3(t) \leq 1,\;\; 0 \leq x_4(t)\}.$$

## 4. Stability Analysis

Our focus is on their stability of the system of the equation.

### 4.1 Equilibria and their local stability analysis

The eigenvalues $\lambda_i$(i = 1, 2, 3, 4) of the variational matrix decide the local stability of the system (8) around each of the singular points:

$$J_{E_n} = \begin{bmatrix} M_{11} & M_{12} & 0 & 0 \\ M_{13} & M_{14} & M_{15} & M_{16} \\ 0 & M_{17} & M_{18} & 0 \\ 0 & M_{19} & 0 & M_{20} \end{bmatrix}, \qquad (6)$$

where,

$$M_{11} = \Psi_1 - 2\Psi_1\overline{x_1} - \delta_1\overline{x_2}, M_{12} = -\gamma_1\overline{x_1}, M_{13} = -\delta_2\overline{x_2},$$
$$M_{14} = \Psi_2 - 2\Psi_2\overline{x_2} - \delta_2\overline{x_1} - \frac{m_1(\gamma_1\overline{x_3} + \gamma_2\overline{x_4})}{(m_1 + \overline{x_2})^2},$$
$$M_{15} = -\left(\frac{\gamma_1\overline{x_2}}{\overline{x_2} + m_1}\right), M_{16} = -\left(\frac{\gamma_1\overline{x_2}}{\overline{x_2} + m_1}\right), M_{17} = -\frac{\overline{\gamma}_3 m_2\overline{x_3}}{(\overline{x_2} + m_2)^2},$$
$$M_{18} = r - 2r\overline{x_3} - \frac{\overline{\gamma}_3\overline{x_2}}{(\overline{x_2} + m_2)}, M_{19} = \frac{\nu_1 m_3\overline{x_4}}{(m_3 + \overline{x_2})^2} - \frac{\overline{\gamma}_4 m_4\overline{x_2}}{(\overline{x_4} + m_4)^2},$$
$$M_{20} = \frac{\nu_1\overline{x_2}}{m_3 + \overline{x_2}} - \mu_1 - \frac{\overline{\gamma}_4\overline{x_2}}{\overline{x_2} + m_4}.$$

The existence of equilibrium points and their stability analysis are discussed further below in three types:

- Without therapy.
- With immunotherapy.

**4.1.1. Without therapy**

The system [5] has a "extinct" equilibrium point $E_0$ (0,0,0,0) for any set of parameters, in which all four cell populations are dead.

$$J_{E_0} = \begin{bmatrix} \Omega_1 & 0 & 0 & 0 \\ 0 & \Omega_2 & 0 & 0 \\ 0 & 0 & r & 0 \\ 0 & 0 & 0 & -\mu_1 \end{bmatrix}. \quad (7)$$

The corresponding eigenvalues for this equilibrium point $E_0$ are

$$\lambda_1 = \Omega_1 > 0, \lambda_2 = \Omega_2 > 0, \lambda_3 = r_2 > 0, \lambda_4 = -\mu_1 < 0.$$

This Eigenvalue clearly shows that the system is unstable and also figures representation are also given in Section 5.1.

**4.1.2 With Immunotherapy**

The system [5] has an "extinct" equilibrium point $E_1(\overline{x_1}, 0, \overline{x_3}, \overline{x_4})$ for any set of parameters,

$$J_{E_1} = \begin{bmatrix} M_{11} & -\beta\,\overline{x_1} & 0 & 0 \\ 0 & M_{12} & 0 & 0 \\ 0 & -\frac{\overline{\gamma}_3\overline{x_3}}{m_2} & r - 2r\overline{x_3} - \frac{\overline{\gamma}_3}{m_2} & 0 \\ 0 & \frac{\nu_1\overline{x_4}}{m_3} - \frac{\overline{\gamma}_4\overline{x_4}}{m_4} & 0 & -\mu_1 \end{bmatrix}, \quad (8)$$

where,

$$M_{11} = \Omega_1 - 2\Omega_1\overline{x_1},$$
$$M_{12} = \Omega_2 - \delta_2\overline{x_1} - \frac{\gamma_1\overline{x_3} + \gamma_2\overline{x_4}}{m_1}.$$

The corresponding eigenvalues for this equilibrium point $E_1$ are

$$\lambda_1 = -\Omega_1 < 0, \lambda_2 = M_{12} < 0, \lambda_3 = -r < 0, \lambda_4 = -\mu_1 < 0.$$

This Eigenvalue clearly shows that the system is locally asymptotically stable and also figures representation are also given in Section 5.2.

**4.2 Global Stability Analysis**

Global stability analysis investigates the behaviour of system solutions across the entire state space, rather than focusing solely on the vicinity of an equilibrium point. The objective is to determine whether solutions originating from any initial conditions will converge to a specific equilibrium or, at the very least, remain bounded throughout. This broader perspective of global stability provides a more thorough insight into the overall dynamics of the system across all possible states. One of the most widely used approaches for such an analysis is the application of Lyapunov functions.

In this section, we rigorously explore the global stability of the tumour-free equilibrium point by employing LaSalle's Invariance Principle [25], combined with a carefully chosen Lyapunov function. Our goal is to formally establish the global stability of the tumour-free equilibrium $E(\overline{x_1}, 0, \overline{x_3}, \overline{x_4})$. To this end, we construct and define the Lyapunov function with precision, recognizing it as a crucial tool

in our stability analysis. This function will form the mathematical foundation needed to validate the robustness of the tumour-free equilibrium point in the absence of tumour cells.

Through a meticulous investigation of the Lyapunov function, we will demonstrate that the system's trajectories eventually converge toward this tumour-free equilibrium, confirming the global stability of the point $E(\overline{x_1}, 0, \overline{x_3}, \overline{x_4})$, and thereby ensuring the system's long-term behaviour in the absence of malignant growth.

$$N = \left[x_1 - \overline{x_1} - \overline{x_1}\ln\left(\frac{x_1}{\overline{x_1}}\right)\right] + \left[x_3 - \overline{x_3} - \overline{x_3}\ln\left(\frac{x_3}{\overline{x_3}}\right)\right] + \frac{1}{2}[x_4 - \overline{x_4}]^2 \quad (9)$$

From the construction of the Lyapunov function, it becomes evident that the function $N$ remains non-negative under the initial conditions within the first quadrant, and it attains the value zero exclusively at the tumour-free equilibrium point. This crucial property confirms that $N$ is a valid candidate for assessing the stability of the equilibrium. To further strengthen this conclusion, we proceed to analyse the time derivative of $N$, denoted as $\frac{dN}{dt}$, within the framework of the proposed model, particularly in reference to equation (5).

The behaviour of $\frac{dN}{dt}$ will provide critical insights into the system's temporal dynamics, and its role in our stability analysis is pivotal. By thoroughly examining $\frac{dN}{dt}$, we aim to demonstrate that it is non-positive, which in turn reinforces the global stability of the tumour-free equilibrium point. This non-positivity will indicate that the system's trajectories tend to evolve toward this stable state, thereby confirming the robustness of the tumour-free equilibrium.

$$N' = (x_1 - \overline{x_1})\frac{x_1'}{x_1} + (x_3 - \overline{x_3})\frac{x_3'}{x_3} + (x_4 - \overline{x_4})x_4'$$

$$N' = (x_1 - \overline{x_1})\big(\Psi_1(1 - x_1)\big) + (x_3 - \overline{x_3})r(1 - x_3) + (x_4 - \overline{x_4})(s_1u_1 - \mu_1x_4) \quad (10)$$

After simplify (10), we obtain

$$= (x_1 - \overline{x_1})\big(-\Psi_1(x_1 - \overline{x_1})\big) + (x_3 - \overline{x_3})\big(-r(x_3 - \overline{x_3})\big) - \mu_1(x_4 - \overline{x_4})^2$$

$$N' = -\Psi_1(x_1 - \overline{x_1})^2 - r(x_3 - \overline{x_3})^2 - \mu_1(x_4 - \overline{x_4})^2$$

Under the condition $\Psi_1 \geq 0, r \geq 0, \mu_1 \geq 0$, the following holds

$$N' \leq 0.$$

We calculated $N'(t)$ to verify our above results numerically by considering initial values, all parameters given in Tables 1 and 2. We can summarize the analytical conditions for global asymptotic stability in the following theorem.

**Theorem 1:** If $\Psi_1 \geq 0, r \geq 0, \mu_1 \geq 0$ then the proposed model (5) is globally stable around the tumour free equilibrium point $E_1$.

## 5. Numerical Simulation

The system (5) will be discussed in this part, and it will be solved using 4th order Runge-Kutta method. The numerical simulation is also completed by means of select out the parameter values represented in Tables 1 and 2 with initial conditions $x_1(0) = \frac{9}{10}, x_2(0) = \frac{1}{10}, x_3(0) = \frac{55}{100}, x_4(0) = \frac{2}{10}$. We have chosen two categories to analyse numerically for our model:

- Without treatment
- With Immunotherapy

### 5.1. Without treatment

First, we now consider without treatment. Figure 1 and 2 show the result of the system without treatment. At this stage, the stability analysis showed that Glial cells have decreased in Figure 1 because of Gliomas gradually maximum size in Figure 2. This has happened at this stage because no treatment has been provided. So, next we recruit immunotherapy treatment for killing tumour cells.

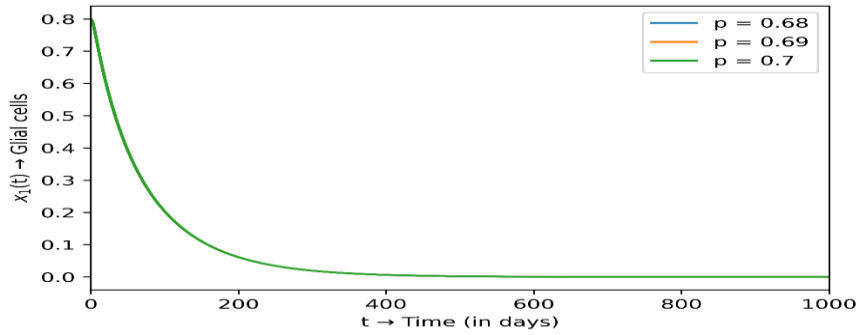


**Figure 1:** Numerical solution of the Glial cells without any therapy

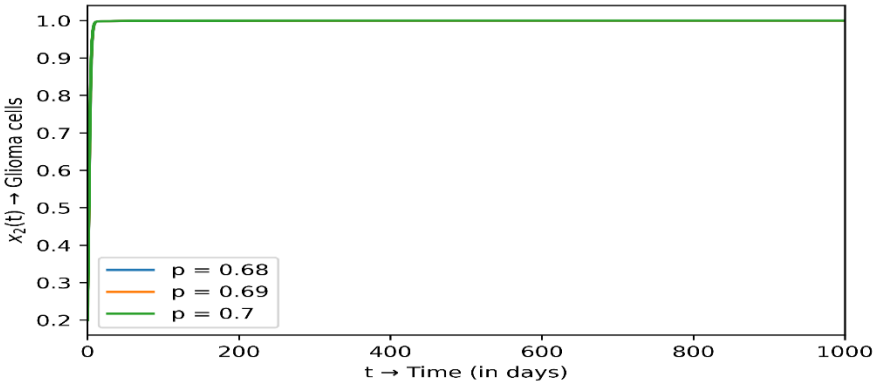


**Figure 2:** Numerical solution of the Glioma cells without any therapy.

### 5.2. With Immunotherapy

At this time, by providing Immunotherapy treatment. We illustrate the findings for the scenario where the treatment regimens were used in Figure 3, 4, and 5. This result can be seen in Figure 3, where glial cells are shown multiplying rapidly while decreasing tumour cells Figure 4 and Figure 5 shows that the concentration of CD8+T cells are also increasing gradually.

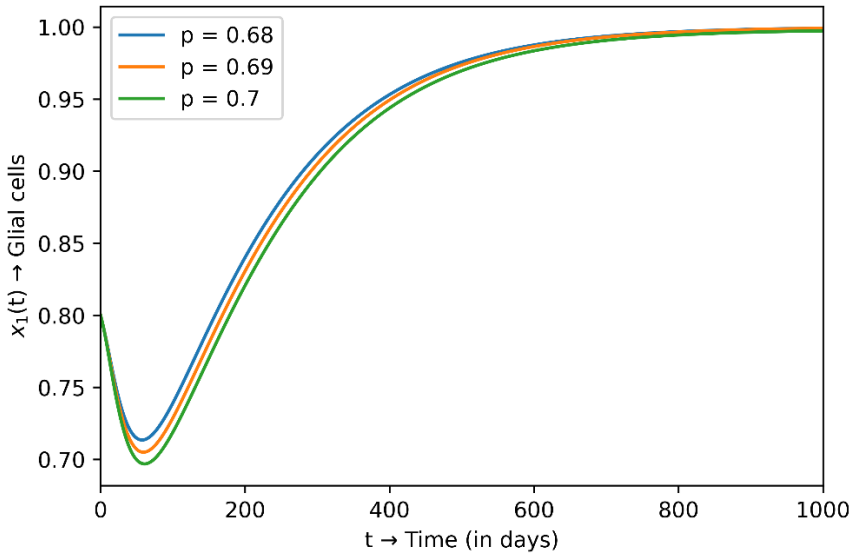


**Figure 3:** Numerical solution of the Glial cells with Immunotherapy.

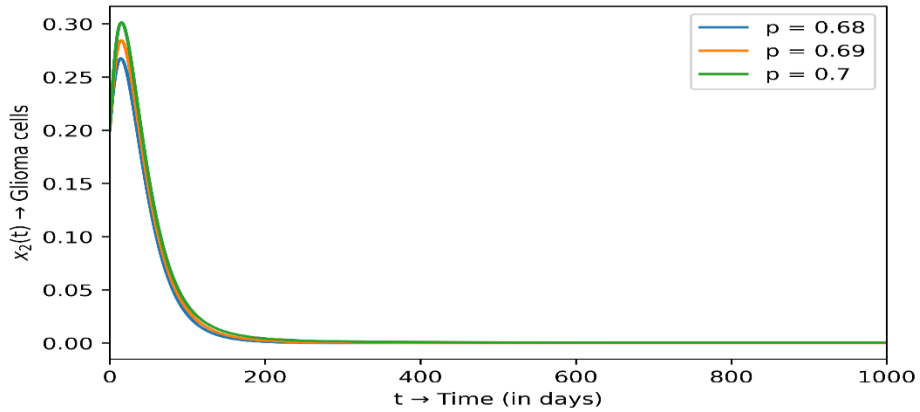


**Figure 4:** Numerical solution of the Glioma cells with Immunotherapy

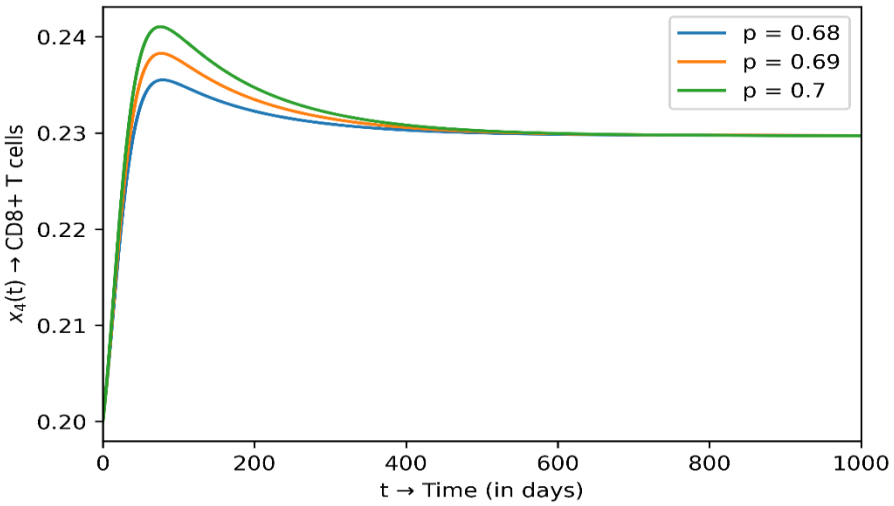


**Figure 5:** Numerical solution of the CD8+ T cells with Immunotherapy.

## 6. Discussion and Conclusion

In this paper, we proposed a mathematical model to observe the dynamics of the cancer cells' interplay with Immunotherapy. We take into the $X_2(t)$ Cancer cells, $X_1(t)$ Glial cells, $X_3(t)$ Macrophages, $X_4(t)$ CD8+ T cells. The positivity and boundedness are discussed. The steadiness of the linear version has been discussed. We construct a characteristics equation and after solve this we could get Eigen values. Next, our system is locally asymptotically stable on account of all our Eigen values are less than zero. We appear out for a numerical simulation for the system of equations. Numerical Simulations are constructed into two different categories. First, we now consider without treatment. Figures 1 and 2 show the result of the system without treatment. Figure 1 shows decrement of Glial cells because increment in Glioma cell counting in Figure 2. Next, we consider the system (5) with Immunotherapy, Figures 3 and 5 show that proliferation of Glial and CD8+T cells while decreasing the concentration of Cancer cells in Figure 4.

We believe that the mathematical modelling is interplaying between most cancers' cells and Immunotherapy, constitutes a step in the direction of enhancing techniques for the curing of malignant tumours. In future research, we would like to examine the mathematical model (5) with fractional derivatives for glial cell interaction between immunotherapy treatment and cancer cells.

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