Mathematical Modelling and Applications
2023; 8(1): 13-19
http://www.sciencepublishinggroup.com/j/mma
doi: 10.11648/j.mma.20230801.12
ISSN: 2575-1786 (Print); ISSN: 2575-1794 (Online)

Mathematical Modelling and Simulation of the Factors Associated with Targeted Cells, Virus-Producing Cells, and Infected Cells

Kubugha Wilcox Bunonyo[1, *], Liberty Ebiwareme[2]

[1]Department of Mathematics and Statistics, Federal University Otuoke, Yenagoa, Nigeria

[2]Department of Mathematics, Rivers State University, Port Harcourt, Nigeria

Email address:

wilcoxbk@fuotuoke.edu.ng (Kubugha Wilcox Bunonyo)

[*]Corresponding author

To cite this article:

Kubugha Wilcox Bunonyo, Liberty Ebiwareme. Mathematical Modelling and Simulation of the Factors Associated with Targeted Cells, Virus-Producing Cells, and Infected Cells. *Mathematical Modelling and Applications*. Vol. 8, No. 1, 2023, pp. 13-19.
doi: 10.11648/j.mma.20230801.12

Received: June 28, 2023; **Accepted**: July 14, 2023; **Published**: July 24, 2023

Abstract: Mathematical modeling and simulation of the effective parameters in targeted, virus-producing, and infected cells were carried out. The research involved mathematical models that represent the targeted cell population, the virus-producing cell population, and the infected cell population, respectively. The numerical simulation was carried out using Wolfram Mathematica, version 12, where the pertinent parameters in the various models were varied within a specified range to study their effect on the dynamic system. The simulated results revealed that the production of the target infected cells, the elimination rate of infected cells, the elimination rate of virus cells, the elimination rate of tissue cells, the infected cell rate constant, and the constant rate of infection affect the various cell populations. The novelty of this research is the fact that the interaction between macrophage and other cells was modeled and direct numerical simulation was carried out to ascertain the effect of pertinent parameters on the system using Wolfram Mathematica. The results revealed that the production rate of tissue and infected cells affects the targeted tissue cells growth, the elimination rate affects the rate of infected cells, and the infected cell rate constant also affects the dynamic system. In addition, the virus's increase per infected cell affects the system, and finally, the elimination rate of tissue cell affects the system.

Keywords: Modeling, Simulation, Cells, Virus, Infected Cells, Effective Parameters

1. Introduction

The process of creating a mathematical representation of a real-world scenario to predict or gain insight is known as mathematical modeling. There are many different kinds of mathematical models, such as game-theoretic models, statistical models, dynamical systems, and differential equations. The most important type of representation is mathematical models of reality. Basically, anything in the physical or natural world, whether regular or including innovation and human mediation, is dependent upon examination by numerical models in the event that it very well may be portrayed concerning numerical articulations. Thus, industrial processes, traffic patterns, sediment transport in streams, and other scenarios can all be modeled using optimization and control theory; Modeling things like message transmission and linguistic characteristics can be done with information theory; The growth and development of landforms, patterns of atmospheric circulation, stress distribution in engineering structures, and a wide range of other processes in science and engineering can all be modeled using dimensional analysis and computer simulation.

Simulating the flow of real-world processes and systems over time is called simulation. A model is required for simulation. A simulation represents the evolution of a model over time, and the model represents key characteristics or behaviors of a selected system or process. Simulations are often performed with the aid of computers [1].

Viruses are still smaller than bacteria, but they are a type of very small micro-organism. They are very different from

bacteria and come in all shapes and sizes. Viruses act as parasites. Specifically, it requires tissue or living cells to grow. Viruses invade human cells and use part of the cells to multiply. Some viruses even destroy host cells during their life cycle. There are mathematicians and modelers who have studied the spread of disease through studies involving the creation of mathematical models. Their names are:

Boianelli*et al.* [2] reviewed pandemics and influenza A virus (IAV) outbreaks. Streptococcal pneumonia is a bacterium that causes infection. This study shows that despite advances in knowledge, the interaction between IAVs and the host immune response (IR) still remains largely fragmented. The IAV dynamics were quantified and described using a mathematical model. Development of a mathematical modeling framework to account for secondary bacterial infection, immunosenescence, host genetic factors, response to vaccination, and secondary bacterial infection will improve our understanding of IAV infection and optimize its treatment. Important to make Burg *et al*. [3] studied primary HIV infection characterized by an initial exponential increase in peripheral blood viral load followed by a rapid decline to viral setpoint. This investigation showed that some of the viral dynamics could be explained by a model restricted to target cells. Furthermore, target cell-restricted models fail to predict long-term viral dynamics unless a delayed immune response is assumed by Stafford *et al*. [4].

This result suggests that the immune response may have a significant impact on viral control during primary infection and may support experimental observations that anti-HIV immune responses are already operational during peak viremia. Cancer research by Mukhopadhyay and Bhattacharyya [5] suggested that viruses that specifically infect and destroy tumor cells could be used as therapeutics to inhibit tumors. This study demonstrates that the dynamics of interactions between tumor hosts, invading viruses and immune system responses are highly non-linear and complex, thus the need to incorporate mathematical models to properly understand these dynamics as showed. Additionally, this study incorporates a mathematical model of the dynamics of the oncoviral immune system. A basic deterministic model was analyzed to determine the importance of various host, viral and immune system parameters in controlling system dynamics. In this study, the random noise inherent in physiological processes was also taken into account by extending the deterministic model to a stochastic one. The resulting probabilistic model is analyzed using the mean-square stability approach, and the stochastic stability criterion is derived using the key system parameters. Numerical simulations are performed to confirm the accuracy of the analysis results. Bunonyo et al. [6] studied tumor growth and cell proliferation. This work involved developing a mathematical model to study tumor cell proliferation and using therapeutics to control and reduce cell proliferation. His investigation was divided into two parts:

First, the model describes tumor spread by cell proliferation driven by carcinogens (pathogens), resulting in exponential tumor growth. Second, the model as formulated was solved analytically. The Wolfram Mathematica software was used to generate graphical and tabular results from the simulation. This study found that cell proliferation increased with increasing rates of exposure to carcinogens, indicating rapid tumor spread, and chemoimmunization to control and reduce carcinogens and cell proliferation. We concluded that the use of therapeutic agents can cause tumor spread. Bunonyo and Ebiwareme [7] proposed a model representing tumor growth driven by carcinogens from the first diagnosed level and a fixed dose of chemotherapy; immunotherapy and they proposed several therapeutic models of radiotherapy. The proposed model was solved analytically to obtain tumor cell function with or without therapeutic effect. Numerical simulations have been performed that show that continuous radiation exposure can cause pain and normal cell death, thereby promoting tumor cell proliferation. However, chemotherapeutic and immunotherapeutic drugs have helped shrink tumors and reduce cell proliferation.

Leyden and co. [8] described biological processes such as modeling cell growth and decay, binding of receptors to ligands, regulation of enzymes and genes, or any of the many other areas where mathematical modeling is used. The common denominator was big discoveries and sharp guesses that prompted important researchers to analyze existing ideal models. Numerical measures were used to understand the prevalence patterns of some intractable viral infections that have a significant impact on quality of life, longevity, health care costs, work and daily life. Using these principles, the life cycle of chronic HIV, hepatitis C virus (HCV) and hepatitis B virus (HBV) infections, which currently affect the health of more than one billion patients worldwide, have been specifically studied. Zhao et al. (In China, an area where HBV infection is endemic, universal vaccination of infants against the virus (HBV) was discussed in 2000. Studies show that approximately 10% of the population is chronically infected with HBV. (60% of the population is chronically infected with HBV). This study presents a mathematical model developed to predict the dynamics of HBV transmission and assess the long-term efficacy of vaccination programs. is explained. Based on the features of HBV infection, we used a compartmental model. It is represented by a set of partial differential equations. Parameters were estimated using survey data expressed in the model as nonlinear functions of age and time post-vaccination. Both pre- and post-vaccination studies are compatible with the model. This result suggests that HBV infection in China can be contained in one generation and eventually eradicated. Bunonyo and co. [9] discussed how temperature affects drug distribution in the human stomach and bloodstream. This study shows that drug-taking behavior is related to high and low ambient temperatures in the examined compartments (stomach and circulatory system). Scientific answers to drug fixation in the gastric and circulatory systems were obtained using factor distributions and boundary strategies for processing tributes, and mathematical systems and graphical results were obtained using Wolfram Mathematica. As a

result, we found that drugs introduced into the system diffused faster between compartments when the temperature increased, and slowed down when the temperature decreased.

Wodarz and Nowak [10] introduced a basic model of viral infection and demonstrated how it has been used to study HIV dynamics and measure key parameters leading to new understandings of disease processes, reviews mathematical models of HIV dynamics, illness and treatment. They considered breed boundary models to explain the general law that the evolution of infection can drive disease spread and eradication of resistance frameworks. This study demonstrates how mathematical models can be used to understand the relationships behind long-term immune regulation of HIV and to design treatment regimens that can lead patients with advanced disease to long-term non-progression. A separate numerical model is created for the elements in between immobilization of proliferating cells, normal cells, resistant cells, chemotherapeutic agents and drugs toxicity of Gafari and Nacerifal [11]. Treatment plans were developed using the Lyapunov stability theorem.

2. Materials and Methods

This research is based on mathematical modeling of the interaction between cells and numerical simulation of the sensitive parameters on the system using Mathematica, version 12. Before formulating the mathematical models to investigate the interactions between the cells, let's consider the following assumptions:

2.1. Assumptions

Following the diagram below, it pictorially showing the interaction between the cells:

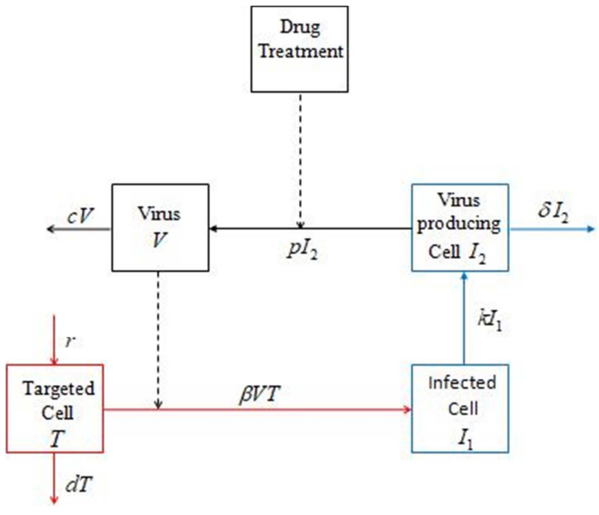

Figure 1. *Diagram showing the relationship between different cells.*

Based on the figure 1 above, we consider the following assumptions:

1. The targeted tissue cells decays naturally over time.
2. The interaction between virus producing cells and infected cells lead to the reduction of infected cells.
3. The interaction between virus cells with T cells lead to per capita growth of infected cells.
4. The rate of production of tissue and infected cells lead to the growth of T cells.
5. The per capita growth of the virus cells is as a result of the production of virus cells from the producing cells.
6. The growth of the infected cells is as result of the per capita growth of virus producing cells.

2.2. Models Formulation

Following the assumptions in section 2.1, we shall formulate the models as:

$$\frac{dT}{dt} = r - dT - \beta TV \tag{1}$$

$$\frac{dI_1}{dt} = \beta TV - kI_1 \tag{2}$$

$$\frac{dI_2}{dt} = kI_1 - \delta I_2 \tag{3}$$

$$\frac{dV}{dt} = pI_2 - cV \tag{4}$$

Equations (1)-(4) are subject to the following initial conditions:

$$\left.\begin{aligned} T(0) &= T_0 \\ I_1(0) &= I_{10} \\ I_2(0) &= T_{20} \\ V(0) &= V_0 \end{aligned}\right\} \tag{5}$$

2.3. Definition of the Parameters

T : Targeted Tissue cell
I_1 : Infected cell
I_2 : Virus producing cell
V : Viruses at time
$r(t)$: Producing Rate of Tissue and Infected cells
δ : Elimination Rate of Infected cells
d : Elimination Rate of Tissue cell
c : Elimination Rate of Virus cells
β : Infected Rate constant
p : Rate of virus increase per infected cells

3. Simulated Results

The numerical simulation was done using Mathematica, version 12, where the effective parameters were varied in the system to investigate the roles they play in the system. The initial conditions were considered at $T_0 = 0.4, I_{10} = 0.2, I_0 = 0.5$ and $V_0 = 0.3$ and the investigation run from zero to 10 months. The results are

presented as follows:

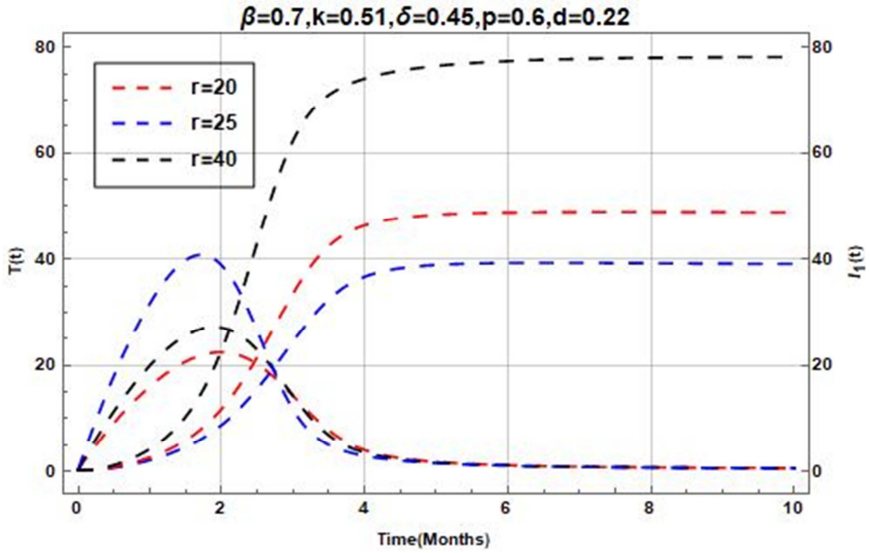

Figure 2. *Effect of Production Rate on Targeted and Infected Cells.*

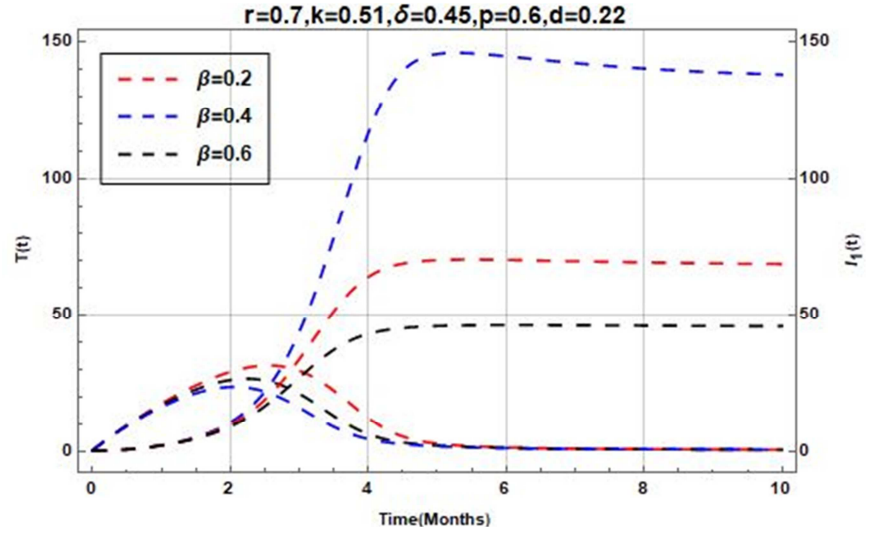

Figure 3. *Effect of the Constant Rate of Infection on Targeted and Infected Cells.*

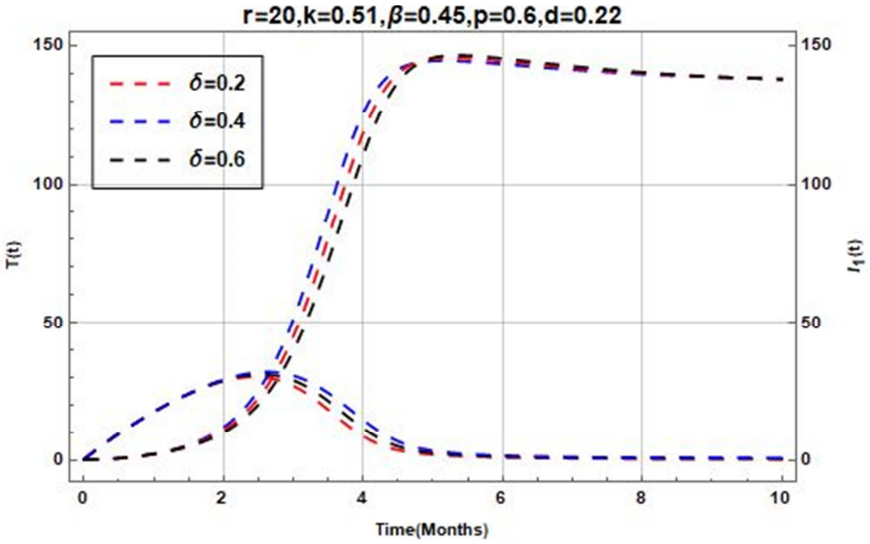

Figure 4. *Effect of Elimination Rate of Infected Cells on Targeted and Infected Cells. and Infected Cells.*

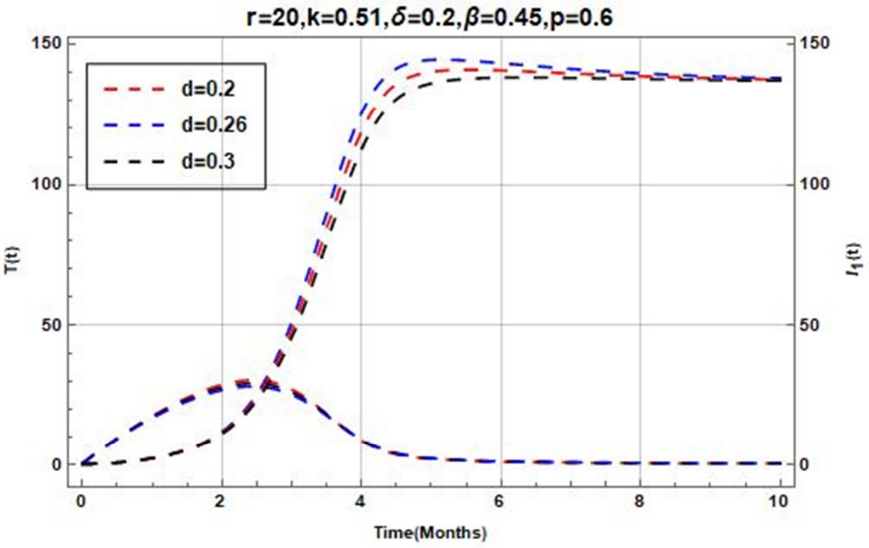

Figure 5. *Effect of Elimination Rate of Tissue Cell on Targeted and Infected Cells.*

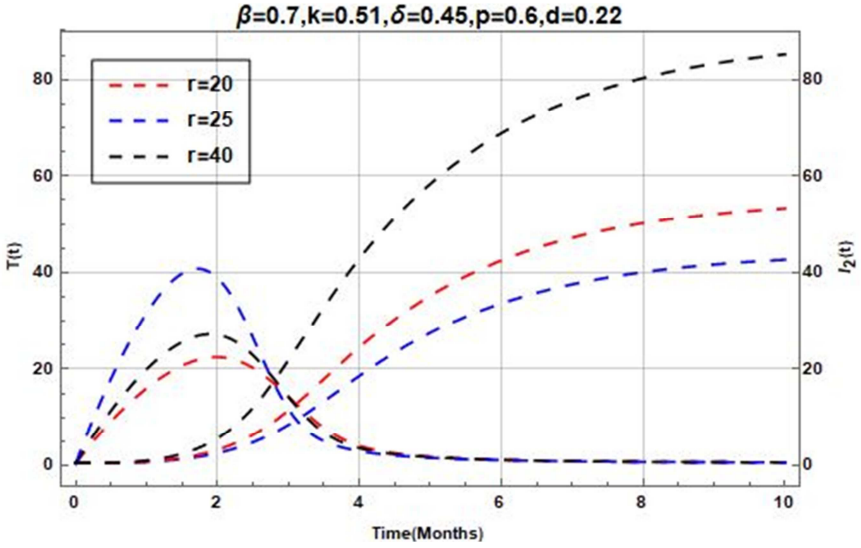

Figure 6. *Effect of the Production Rate on Targeted and Virus Cells.*

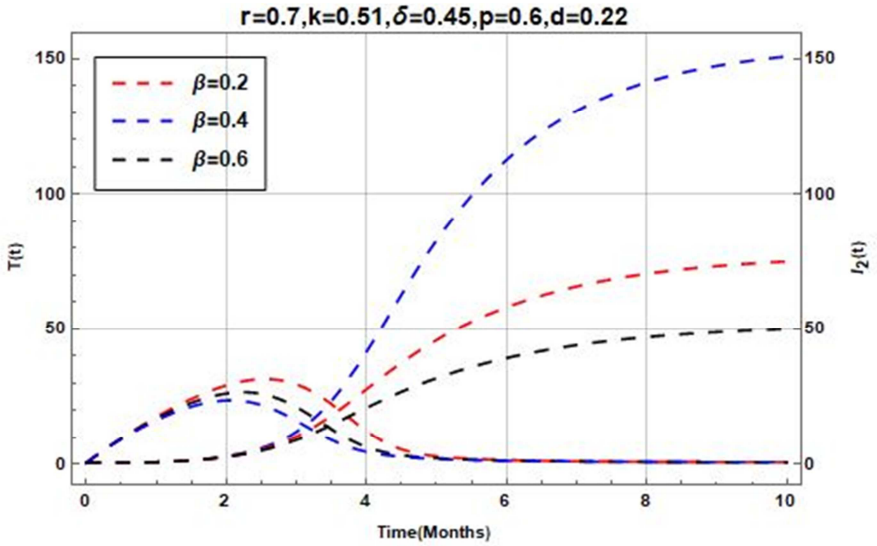

Figure 7. *Effect of the Rate of Infection on Targeted and Virus Cells.*

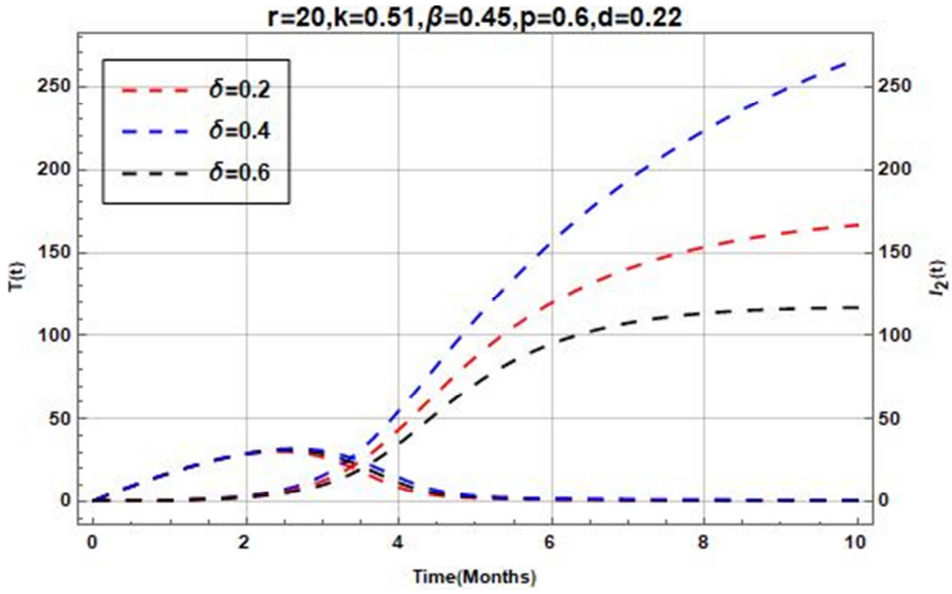

Figure 8. *Effect of the Tissue Production Rate on Targeted and Virus Cells.*

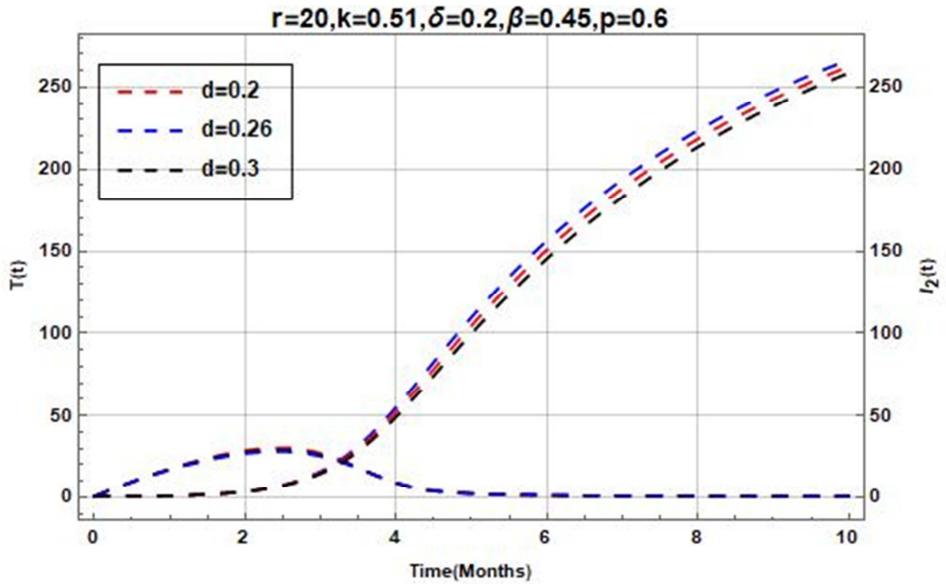

Figure 9. *Effect of Elimination Rate on Targeted and Virus Cells Producing Cells.*

4. Discussions

Figure 2 shows the effect of product rate on tissue and infection cells. The figure showed that the tissue cell growth started at 0.4 and increased to 22.4691 at a production rate of 20 units before decreasing from 14.2709 to 0.623841. In addition, for a change in growth rate from 20 to 22, and then to 40 units, we noticed a relative growth of the tissue cells. Furthermore, we noticed a growth in infectious cell rate with an increase in production rate from 20 to 25 units. Figure 3 depicts the effect of the constant rate of infection on the tissue cells and infected cells. It is seen that the number of tissue cells increases from a reference point of 0.4 and begins to increase to 17.6016 and gets to a peak of 29.4716 before decreasing to 0.628693 as the constant infection rate increases from 0.2 to 0.6 units. In a similar vein, the number of infected cells increases with a constant rate of infection. Figure 4 illustrates the effect of the elimination rate of infected cells on tissue cells and infected cells. The figure showed that for the elimination rate of infected cells to be 0.2, 0.4, and 0.6, the tissue cells increase from 0.4 to 28.7079 before decreasing to 0.386974, and in a similar vein, the infection cells decrease from 2.35959 to 2.2239, and the infection cells increase to 138.059 and 137.928.

The effect of the elimination rate of tissue cells on tissue cells and infected cells is shown in Figure 5. The result depicts that the tissue cells start to grow from 0.4 to 28.7079 before decreasing to 0.386974 at a rate of 0.2, but then decrease to 17.2391 as they continue to decrease to 0.395078. Furthermore, the infection cells also increased from 0.2 to

138.059 for the tissue elimination of 0.2, then 0.26 and 0.3, respectively. Figure 6 illustrates the effect of tissue and virus-cell production on the tissue and infection cells, respectively. The figure reveals that the tissue cells start at 0.4 and grow to 22.4691 before decreasing to 0.623841 for the production rate of 20 units, and they increase from 0.4 to 27 before decreasing to 0.6226414 and 0.621008. The result also reveals that the virus grows from 0.5 to 42.6355 for a production rate of 20 units, 53.2911, and 85.2107 for a production rate of 25 and 40, respectively. Figure 7 depicts the effect of a constant rate of infection on the tissue cells and virus cells. The result showed that the tissue cells increased for the infection rate of 0.2, then reduced over time to 0.628693, then to 0.625507 and 0.624241 for the rates of 0.4 and 0.6, respectively. We noticed that the virus cell grows from 0.5 to 150.748, 74.9283, and 49.7964 at different rates of 0.4 and 0.6, respectively.

Figure 8 illustrates the effect of the elimination rate on virus cells on tissue cells. The figure shows that for the elimination rate of virus cells to be 0.2, 0.4, and 0.6, the tissue cells increase from 0.4 to 28.7079 before decreasing to 0.386974, and in a similar vein, the virus cells increase from 2.35959 to 138.059, and the virus cells increase to 138.059, 138.004, and 137.928. The effect of the elimination rate of tissue cells on targeted and virus cells is shown in Figure 9. The result illustrates that the targeted cells start to grow from 0.4 to 28.7079 before decreasing to 0.386974 at a rate of 0.2, but decrease from 0.4 as they continue to decrease to 0.395078. The virus cell grows from 0.5 to 266.551, then to 262.551 and 258.689, respectively.

5. Conclusion

We have been able to formulate mathematical models that represent effective parameters in targeted, virus-producing, and infected cells, perform numerical simulations of the formulated models using Mathematica, and present and discuss the results. Based on the results obtained, we can conclude as follows:

1. The production rate of tissue and infected cells affects the targeted tissue cell's growth.
2. The elimination rate affects the rate of infected cells.
3. The infected cell rate constant affects the system.
4. The virus's increase per infected cell affects the system.
5. The elimination rate of tissue cells affects the system.

References

[1] Saltelli, A., Bammer, G., Bruno, I., Charters, E., Di Fiore, M., Didier, E.,... & Kay, J. (2020). Samuele Lo Piano, Deborah Mayo, Roger PielkeJr, TommasoPortaluri, Theodore M. *Porter, ArnaldPuy, Ismael Rafols, Jerome R. Ravetz, Erik Reinert, Daniel Sarewitz, Philip B. Stark, Andrew Stirling, Jeroen van der Sluijs, and Paolo Vineis*, 482-484.

[2] Boianelli, A., Nguyen, V. K., Ebensen, T., Schulze, K., Wilk, E., Sharma, N. & Hernandez-Vargas, E. A. (2015). Modeling influenza virus infection: a roadmap forinfluenza research. *Viruses*, *7* (10), 5274-5304.

[3] Burg, D., Rong, L., Neumann, A. U., & Dahari, H. (2009). Mathematical modeling ofviral kinetics under immune control during primary HIV-1 infection. *Journal of Theoretical Biology*, *259* (4), 751-759.

[4] Stafford, M. A., Corey, L., Cao, Y., Daar, E. S., Ho, D. D., &Perelson, A. S. (2000). Modeling plasma virus concentration during primary HIV infection. *Journal of theoretical biology*, *203* (3), 285-301.

[5] Mukhopadhyay, B., & Bhattacharyya, R. (2009). A nonlinear mathematical model ofvirus-tumor-immune system interaction: deterministic and stochastic analysis. *Stochastic Analysis and Applications*, *27* (2), 409-429.

[6] Bunonyo, K. W., Odinga, T., & Ikimi, C. G. (2022). Modeling Tumor Cell Proliferationand Therapeutic Treatment Simulation. *Central Asian Journal of Medical and Natural Science*, *3* (6), 576-586.

[7] Bunonyo, K. W., & Ebiwareme, L. (2022). Tumor growth mathematical modeling andapplication of chemo-immunotherapy and radiotherapy treatments. *International Journalof Statistics and Applied Mathematics*, 7 (2): 125-139; https://doi.org/10.22271/maths.2022.v7.i2b.806,

[8] Layden, T. J., Layden, J. E., Ribeiro, R. M., & Perelson, A. S. (2003). Mathematicalmodeling of viral kinetics: a tool to understand and optimize therapy. *Clinics in liver disease*, *7* (1), 163-178.

[9] Bunonyo, K. W., Ebiwareme, L., & Awomi, P. Z. (2023). Temperature effect on drugdiffusion in the stomach and bloodstream compartments. *World Journal of Biology Pharmacy and Health Sciences*, *13* (02), 178-188.

[10] Wodarz, D., & Nowak, M. A. (2002). Mathematical models of HIV pathogenesis andtreatment. *BioEssays*, *24* (12), 1178-1187.

[11] Ghafari, A., and N. Naserifar. "Mathematical modeling and lyapunov-based drugadministration in cancer chemotherapy." (2009): 151-158.