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Research Article

Use of Differential Equations for Modelling Cancer Cell Growth

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ABSTRACT

The research work presents a study on the effectiveness of the use of differential equations in modelling cancer growth. The research determines that there exist numerous differential equations that models growth and progression of differential equations, but they often omit essential progression parameters associated with the disease's prognosis. The research work concludes that if efficient differential equation modelling of cancer growth is to be performed inclusion of essential parameters such as cell interactive effects and therapeutic effects should be included in the model along with its cross validation through real world cancer growth data.

Keywords: parameters, determines, essential, validation

INTRODUCTION

Cancer is a leading cause of death in India and across the world. The disease is the second leading cause of in the world and 4th in India. In India Cardiovascular diseases takes the first podium in terms of cause of death, respiratory diseases steps on second, while tuberculosis steps on third. Cancer appears on fourth platform. In India on a yearly basis cancer contributes to 9.4 percent of deaths. Medical science has attained the cure of cancer. Number of cancer survivors are increasing day by day, but the prognosis of disease is still not very effective. Cancer still needs tremendous research work especially in field of effective early identification. Even if identified early how the cancer progress is still a field of research in modern medical science. The cure for the cancer is known. Surgery, immunotherapy, chemotherapy, and radiation therapy have presented their efficacy in successful treatment of cancer. However, the treatment outcomes are not always positive. It depends upon number of factors such as degree of tumor, time of detection, implementation of treatment schemes, and body's auto immune response. Mathematical models have been developed that predicts the time of treatment and the quantity of drug required to treat the cancer. The cure of cancer is costly. Treatment involves use of costly imaging techniques, medicines, consultation, and radiation therapy. Every step requires use of costly technology. In India the disease is spreading fast. The disease is not only genetically linked but has also become a part of lifestyle disease segment.

To identify cancer growth, its cancer imaging is required. Cancer imaging requires exposing the patient to the radiations. This exposure to radiation results in imaging of the tumor. Repeated exposure to radiation is not possible as it can further result in cell mutation and damage of existing healthy cells. Further, interval between two successive imaging requires a cooling period which can range from fifty to ninety days. Imaging is also a costly process. A full body MRI requires 15 to 20 thousand rupees. Apart of being costly MRI presents result of tumor progress at the time of detection

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and period after subsequent intervention. The disease is a complex mechanism. At times it progresses rapidly even after intervention. Therefore, a overcome such complexities it is essential to model the tumor progression. Differential equations present a promising success in this field. Differential equations help in –

1. Identifying growth dynamics of tumor cells.
2. Spread of cancer cells.
3. To optimally control chemotherapy.
4. To understand work of chemotherapy in reducing tumor cell volume.

STUDY OF MODELLING TECHNIQUES

At present there exists numerous differential equation cancer modelling techniques. Each techniques have its own added advantage and shortcomings. The research work presents study of existing literature that deals with modelling of cancer progression through differential equation and will identify the technique that is frequently utilized in this study area. (Trisilowati, 2012) in her research work incorporated the immune component, dendritic cell therapy, cytotoxic T cell effect, lymphocyte effect, helper T Cell effect, $CD4^+$ and $CD8^+$ effects on ODE for prediction of tumor growth. The research work utilized the Runge-Kutta method for determining the solution of differential equation.

Use of this Method – The work adopts Runge-Kutta Method for solving differential equation. The method is one of the best suited ones when it comes to solving problems that require temporal discretization. In other words, the method is one of the best suited ones for simulation of a complex problem such as cancer cell progression.

(Endeling and Chaplain, 2014) in their research work focused on analysing the tumor growth through ordinary differential equation and how it shrinks under the treatment. The research work utilized the Gompertz differential equation and incorporated the anti tumor treatment and the anti-angiogenic treatment component in it. With the help of a graph the research work indicated a fast exponential decaying tumor size with time with the introduction of tumor treatment.

Gompertz Model	$V = aV \ln \frac{b}{(V + C)}$
V is the volume of the tumor and V is its progression a, b, and c are the constant coefficient defining the growth model.	

Use of this Method – The Gompertz differential equation is well known to model biological processes. The equation is easy to use and results in faster simulations. However, the method is infested with drawbacks such as non-inclusion of important parameter 'time of infection'. Researchers have improved upon the model. But the improved model is case wise and is tailor fitted to individuals' simulation processes. Despite model lacking important parameters it has been used extensively for cancer modelling. Once such case is presented by (Vaghi and Ebos, 2019). They focused on Population modeling of tumor growth curves and the reduced Gompertz model improve prediction of the age of experimental tumors. The reduced Gompertz model was found to exhibit the best results, with drastic improvements when using Bayesian inference as compared to likelihood maximization alone, for both

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accuracy and precision. Specifically, mean accuracy (prediction error) was 12.2% versus 78% and mean precision (width of the 95% prediction interval) was 15.6 days versus 210 days, for the breast cancer cell line. These results demonstrate the superior predictive power of the reduced Gompertz model, especially when combined with Bayesian estimation. Examples of improved Gompertz model are also present. One such case was presented by (Yin, Moes, Hasselt, Swen, Guchelaar, 2019). In their research focused on the review of different ordinary differential equation used for determination of tumor dynamics. The research work stated that Linear growth, exponential growth, logistic growth, Gompertz growth and the combination of exponential and linear growth are basic functions that describes natural tumor growth. The Tumor burden model is helpful in integrating tumor heterogeneity. The research work indicated that immune system model helps in understanding the interaction of tumor dynamics with immune system responses. The research work also indicated the non-linear drug exposure relationship.

Modelling of cancer cell requires involvement of multiple parameters. Such as effect of T- cells, immune systems, and interaction between healthy and cancer cells. This multi- parameter model when includes the use of chemotherapy in it results in efficient modelling of cancer progression one such case was demonstrated by (Abernathy, Abernathy, and Stevens, 2020). In their research work focused on developing a mathematical model for determination of tumor growth. They focused on how tumor growth and shrinks before and after the introduction of virotherapy. The research work with the help of Hopf bifurcation differential equation presents the interaction between the tumor cells, uninfected tumor cells, virions, and effector T- Cells. Such differential equations could be modelled as –

For modelling of effects of therapeutics on cancer the following differential equation would be used.

$$N'(t) = aN(t)(1 - bN(t)) - \alpha_1 N(t)T(t) - \mathrm{k}_N u(t)N(t)$$

$$L'(t) = rN(t)T(t) - \boldsymbol{\mu} L(t) - \mathrm{Q}_1 L(t)T(t) - \mathrm{k}_L u(t)L(t)$$

$$T'(t) = cT(t)(1 - dT(t)) - \alpha_2 N(t)T(t) - \mathrm{Q}_2 L(t)T(t) - \mathrm{k}_T u(t)T(t)$$

$$u'(t) = v - \boldsymbol{\omega} u(t)$$

The model variables are T(t) for tumor cell population at time t, N(t) for NK cell population, L(t) for cytotoxic T cell (CTLs) population, and u(t) for quantity of drug at the tumor site.

Example of inclusion of therapeutics in differential model was also presented by (Sharpe and Dobrovolny, 2021). In their research work used the ordinary differential equation to predict the effectiveness of the chemotherapy. The research work in their ODE incorporated the stochastic process. The research work utilized ten different ODE to simulate the tumor growth and effect of chemotherapy in reducing the tumor growth to a level of being classified as cured. The stochastic process incorporation changed the level of chemotherapy and time needed to cure the tumor.

Cancer modelling through differential equation is only possible when the growth and progression data points are available with the researcher. To determine the same Xenografting techniques are available.

Benefit of Xenografting – Human trials is not possible when it comes to repeated recording of cancer cell progression. Therefore, human xenograft trials on nude mice open dimensions of cancer cell progression measurement. Efficient use of xenograft models was exhibited by (Varna, Bertheau, and Legres, 2014). In their research work focused on generation of tumor growth data for research

purpose. The researchers focused on generating the tumor growth data through xenografting of human tumor in nude mouse. The researchers stated that in nude mouse site specific engraftment is possible. Nude mice possess immunocompromised systems which act as an excellent environment for studying human tumor growth.

CONCLUSION

The research work focused on determining the use of differential equation in modelling cancer progression. From the study the research work concludes that –

1. Gompertz model of modelling cancer growth is a convenient means to understand the cancer progression. However, the model lacks essential inclusion of critical parameters such as time of infection and effect of chemotherapy on the cancer cell progression.
2. Effective modelling of cancer cell progression is possible only when the combined effect of immune system, chemotherapy, and cancer – healthy cell interaction is considered. Therefore, it is concluded that either the Gompertz model should be rectified to include the above stated parameters or existing differential equations such as Hopf bifurcation model be used those accounts for such parametric effects.
3. Efficacy of differential equations can only be determined when tested upon the real- world examples. Therefore, it is concluded that the progression obtained through the developed model should always be tested against the real progression of infection. For the sample nude mice xenograft studies were found to be a helpful data assimilation source.

REFERENCES

[1] Varna M. (2014). Tumor Microenvironment in Human Tumor Xenografted Mouse Models, Journal of Analytical Oncology

[2] Sharpe, S., & Dobrovolny, H. M. (2021). Predicting the effectiveness of chemotherapy using stochastic ODE models of tumor growth. In Communications in Nonlinear Science and Numerical Simulation (Vol. 101, p. 105883). Elsevier BV. https://doi.org/10.1016/j.cnsns.2021.105883

[3] Trisilowati (2012). Varna M. (2014). Tumor Microenvironment in Human Tumor Xenografted Mouse Models, Journal of Analytical Oncology, Queensland University Technology

[4] Enderling H. (2014). Mathematical Modeling of Tumor Growth and Treatment, Current Pharmaceutical Design

[5] Vaghi (2019). Mathematical Modeling, Analysis, and Simulation of Tumor Dynamics with Drug Interventions. In Computational and Mathematical Methods in Medicine (Vol. 2019, pp. 1–13). Hindawi Limited. https://doi.org/10.1155/2019/4079298

[6] Abernathy, Z., Abernathy, K., & Stevens, J. (2020). A mathematical model for tumor growth and treatment using virotherapy. In AIMS Mathematics (Vol. 5, Issue 5, pp. 4136–4150). American Institute of Mathematical Sciences (AIMS). https://doi.org/10.3934/math.2020265