

A Mathematical Model of Tumor Growth in Human Body with the Rough Set

Arvind Kumar Sinha*, Nishant Namdev

Department of Mathematics, National Institute of Technology, Raipur 492010, India

Received 14 January 2020; Received in revised form 20 August 2020 Accepted 5 October 2020; Available online 16 March 2021

ABSTRACT

Tumors are a significant issue in the world. They are a substantial cause of death and put a heavy load on medical services. Many researchers' have been trying to develop a new medical treatment model for tumors. The growth of tumor cells is uncertain due to their abnormal behavior. The Rough set method is an emerging interventional technique and the most powerful mathematical tool to deal with unpredictable situations. Metastasis dispersal is the procedure by which a few cells from the tumor leave and make another tumor. Subsequently, the danger can scatter through the entire living organism. In this paper, the dynamics of tumor cells are established with the metastasis process in the human body and verified by the Rough set method's technique. This paper develops a connection between applied mathematics, numerical computation, and applications of biological systems.

Keywords: Tumor; Nonlinear; Carrying capacity; Tumor cells; Rough set

1. Introduction

Tumors are a significant issue around the world. They are a significant cause of death and put a heavy load on medical services [1-2]. Many researchers' have been working to develop a novel medical practice model for tumors. The growth of tumor cells is unpredictable due to their irregular behavior [1-2]. Possible signs and reactions of the tumor cell growth include a bump, anomalous dying, unexplained weight decrease, and bowel movements [3]. Tobacco consumption is one of the major causes of around twenty-two percent of tumor deaths [1]. Another ten percent is due to heaviness, poor diet, lack of physical activity, and unreasonable drinking of liquor [1, 4-5]. A different component includes biological pollutants, contaminations, and ionizing radiation [6]. Various hereditary changes are required before tumors develop [7]. Around ten percent of growth results from gained inherited imperfections from a person's parents [8].

Tumors are recognized by particular signs and screening tests [1]. They are then regularly inquired about by therapeutic imaging and avowed by biopsy [9]. Tumor growths may be prevented by not smoking, keeping up a healthy weight, not drinking too much alcohol, eating vegetables, immunization against certain diseases, and keeping up an essential separation from sunlight [10-11]. Early identification through screening is vital for tumors [12-13].

In decades. continuous past advancement related to tumor analysis has been presented [14]. Several mathematical principles are used to identify and treat the tumor. Models are being applied to examine how tumors form [15] and develop [16-19]. They are being used to customize current treatment, anticipate the viability [20-24], or the blend of different treatments [25-27] and provide insight into the development of resistance [28-29]. Many ODE models are suggested to address tumor development [30-31] and are consistently utilized to make expectations about the sufficiency of growth medications [32].

The growth of tumor cells is uncertain due to their abnormal behavior. The Rough set method is an emerging interventional technique and the most powerful mathematical tool to deal with unpredictable situations. Metastasis dispersal is the procedure by which a few cells from the tumor leave and make another tumor. Subsequently, the threat can spread through in the entire organism.

In this paper, a scientific model is given for tumor cells population development with the human body's metastasis process and approved by the Rough set in uncertain circumstances. In this methodology, the mathematical analysis of the nonlinear behavior of the tumor cells population is set up via carrying capacity with the human body's metastasis process and is approved by the Rough set. This paper develops a connection between mathematics, applied numerical computation, and applications of biological systems. These advances offer novel

insights for tumor growth, further supporting research in tumor cell dynamics.

2. Mathematical Model

In this segment, a mathematical model is given. This model is centered on the number of tumor cells and carrying capacity. The following assumptions are for the development of the model.

2.1 Assumption taken

In this model, three assumptions taken as follow:

(A1) A per capita tumor cell development subject to tumor size concerning carrying limit is given by the logistic model [14].

(A2) The carrying capacity growth is proportional to the tumor surface [33].

(A3) Metastatic discharge is relative to the 2/3 power of essential tumor estimate, which compares to surficial metastatic outflow [34].

2.2 Dynamics of growth of the number of tumors cells in terms of carrying capacity

To find the number of diseased cells in the tumor in a human body is a hard task because of constant changes in tumor growth over time [14]. The number of cells changes according to time [14],

$$\frac{dB}{dt} = \eta_1 B - \eta_2 B \tag{2.1}$$

where *B* stands for the number of tumor cells at time *t* (in days), η_1 and η_2 respectively, are producing and dying tumor cells, $\frac{dB}{dt}$ is the per capita growth rate of tumor cells population and $\eta_1 - \eta_2 = \gamma$ represents the tumor population growth.

A per capita tumor cell development, subject to tumor size, and concerning carrying limit K, is given by the logistic model [33]. So

$$\frac{dB}{dt} = \gamma B(1 - \frac{B}{K}) \quad . \tag{2.2}$$

Let
$$f(B) = \gamma(1 - \frac{B}{K})$$
 and thus per

capita growth rate of tumor cell decreases as well as increases. In a real-life situation, the growth of cells cannot grow exponentially because, after some time, the cells' growth will reach a constant position. So now from Eq. (2.2),

$$\frac{dB}{dt} = Bf(B). \qquad (2.3)$$

The carrying limit K is considered as a variable representing the tumor cell growth. So

$$\frac{dK}{dt} = \gamma B^{2/3}.$$
 (2.4)

The fraction $\frac{2}{3}$ is taken because the

carrying capacity is proportional to the tumor surface [34]. Here, we can deduce two cases as follows [14]:

- (i) If $\lim_{t\to\infty} B(t) = K$, then shows that the growth of the tumor cell converges to the carrying capacity.
- (ii) The relative growth $\frac{1}{B}\frac{dB}{dt}$ decreases with the increase of tumor cell. For the solution of the carrying capacity, now

solution of the carrying capacity, no from the Eq. (2.5),

$$\frac{dK}{dt} = \gamma \left\{ \frac{KB_0}{B_0 + (K - B_0)e^{-\gamma t}} \right\}^{2/3}$$

Moreover, when the above equation is solved, we obtain

$$\gamma dt = K^{-2/3} [1 + \frac{2}{3} (\frac{K}{B_0} - 1) e^{-\gamma t}] dK$$
 (2.5)

We simplify the Eq. (2.5),

$$\gamma dt = [(1 - \frac{2}{3}e^{-\gamma t})K^{-2/3} + \frac{2}{3B_0}e^{-\gamma t}K^{\frac{1}{3}}]dK.$$

Now, integrating the above equation we obtain

$$\gamma t + c = \left[(1 - \frac{2}{3}e^{-\gamma t}) 3K^{1/3} + \frac{1}{2B_0}e^{-\gamma t}K^{\frac{4}{3}} \right]$$
(2.6)

at $t = 0, K = K_0$. So, from Eq. (2.7), we obtain

$$c = K_0^{1/3} + \frac{1}{2B_0} K_0^{4/3}.$$

By Eq. (2.6), we obtain

$$\gamma t + c = [(aK^{1/3} + bK^{4/3}],$$
 (2.7)

where $a = 3(1 - \frac{2}{3}e^{-\gamma t})$ and $b = \frac{1}{2B_0}e^{-\gamma t}$.

This implies that

$$\gamma t + c = abK^{\frac{4}{3}}$$

That gives

$$K = \left[\frac{\gamma t + c}{ab}\right]^{\frac{3}{4}}.$$
 (2.8)

where $a = 3(1 - \frac{2}{3}e^{-\gamma t})$, $b = \frac{1}{2B_0}e^{-\gamma t}$ and $c = K_0^{1/3} + \frac{1}{2B_0}K_0^{4/3}$.

This shows that K is the maximum number of tumor cells in the human body at any part; it means, it forms a tumor of the maximum size.

2.3 Tumor cells growth with metastasis process

Metastasis dispersal is the strategy by which a couple of cells from the tumor will leave and make another tumor. In this way, the threat can disperse through the entire organism [34]. This metastasis procedure is in charge of ninety percent of the patients' demise. Here from Eq. (2.7), if

$$\lim_{t \to \infty} B(t) = K. \tag{2.9}$$

The growth of tumor cells reaches the carrying capacity. So, it can be said that after reaching the state of carrying capacity, a couple of cells from the tumor will leave and make another tumor [34]. In the case of the absence of the dead cells, the tumor cells grow at a rate proportional to the current population of the tumor cells

$$\frac{dB}{dt} = \mu B. \tag{2.10}$$

The above Eq. (2.10) shows the growth of the tumor cell in any other part of the human body since the metastatic discharge is relative to the 2/3 power of essential tumor estimate, which compares to surficial metastatic outflow [34]. Both primary tumor and metastases make new metastases at the rate given by,

$$\gamma(B) = aB^{2/3}.$$
 (2.11)

Now, we can also write

$$\gamma(B) = a \left[\frac{KB_0}{B_0 + (K - B_0)e^{-\gamma t}} \right]^{2/3}.$$
 (2.12)

The above equation shows the tumor cells' growth rate in other parts of the human body with the metastasis process. The tumor cells in this part will get the same carrying capacity again like (2.12) and still with the metastasis process; it will reach like (2.8) and so on.

In the above expression, since K is the carrying capacity of tumor cells, that means K is the maximum number of tumor cells in the human body, which shows that it forms the tumor of the maximum size.

3. Result of the Model

Eq. (2.8) shows the expression of the carrying capacity. The number of cells increases with time (days), and after some time growth of the number of tumor cells reaches the constant state (Fig. 1). By changing the integral width, the number of tumor cells increases with time (days), and after some time the constant behavior is shown in Figs. (1)-(3).

If tumor cells' growth reaches the carrying capacity, then a few cells from the tumor leave and make another tumor. In the case of the absence of the dead cells, the tumor cells grow at a rate proportional to the current population of the tumor cells.



Fig. 1. Tumor cell population growth as a function of time shows that the number of tumor cells increased with time (days), and after some time, the growth of the tumor cells shows constant behavior.



Fig. 2. Tumor cell population growth as a function of time shows that the number of tumor cells increased with time (days), and after some time, the growth of the tumor cells shows constant behavior.



Fig. 3. Tumor cell population growth as a function of time shows that the number of tumor cells increased with time (days), and after some time, the growth of the tumor cells shows constant behavior.

4. The Rough Set

The area of the Rough set applications utilized today is considerably more extensive than before, basically in the zones of the drug, investigation of database traits, and process control. The Rough set has a few covers with different strategies for information examination. e.g., cluster investigation, fuzzy sets, statistics, proof hypothesis. [35-37].

4.1 Validation with the rough set

The data [38] used for describing the model is further relevant because we only require the estimated quantity of tumor cells with time (days) for the validation of the model, and in seeking for the expected quantity of tumor cells, we noticed this preliminary data in the precise form. The data is robust and very proper for work, so we have used it for the model. This work can be utilized in the same type of trial data.

The data [38] of the number of tumor cells and its approximation are taken from the real world, and by using Rough Set Exploration System (RSES 2.2.2) [39], it is observed that the amount of tumor cells grows with time (days), and later sometimes the growth of the tumors cells explicates the consistent form (Fig. 4). 4.2 The mechanism used for the rough set A data frame comprising information $S = (\rho, \sigma)$, where ρ is the nonempty finite collection of objects and ϑ is the nonempty finite collection of attributes, $\vartheta \subseteq \rho$ and $\lambda \subseteq \sigma$. The two sets $\lambda_*(\vartheta)$ and $\lambda^*(\vartheta)$ represent the lower and upper approximation of ϑ , respectively, and are defined as follows:

$$\lambda_*(\mathcal{G}) = \bigcup_{x \in \rho} \{\lambda(x) : \lambda(x) \subseteq \mathcal{G}\}$$
$$\lambda^*(\mathcal{G}) = \bigcup_{x \in \rho} \{\lambda(x) : \lambda(x) \cap \mathcal{G} \neq \phi\}.$$

The set

$$\lambda N_{\lambda}(\vartheta) = \lambda^{*}(\vartheta) - \lambda_{*}(\vartheta),$$

is defined as the boundary region of \mathscr{G} [35-37]. If $\lambda N_{\lambda}(\mathscr{G}) = \phi$ then v is crisp or exact with respect to λ ; and if $\lambda N_{\lambda}(\mathscr{G}) \neq \phi$, v is rough or inexact with respect to λ [35-37].

The Rough set depends on the hypothesis that every event is linked to some of the data; during data processing, discretization is a vital tool for dealing with imprecision when applying the Rough set [35-37].

5. Discussion and Conclusion

Tumors are the principal cause of death and put significant weight on the medical practice because of the disease's enduring aspects. The area of the Rough set applications utilized today is considerably more extensive than before, basically in the zones of the drug, investigation of database traits, and process control.

In circumstances of the modern knowledge and former model presented for the tumor cells, the model has included the growth of the tumor cells in terms of carrying capacity and metastasis process.



Fig. 4. Tumor cell population growth as a function of time shows that the number of tumor cells increased with time (days), and the growth of the tumor cells show constant behavior by the Rough set exploration system (RSES 2.2.2).

tumor cell growth with the metastasis process, which was approved using the Rough set. We observed the association in the tumor cells and time such that the tumor cells grow, and after some period of time, approach steady-state in a continuous curve graph (Fig. 1). By changing the equidistance width, the tumor cells increase with time (days), and, after some period of time, they shows the same constant behavior in the zigzag curve form in Figs. (1-3). In all cases, the same result is obtained.

In Rough set, by using the Rough Set Exploration System (RSES 2.2.2), we found the association between the tumor cells and time such that the tumor cells grow with time and approach the steady-state (Fig. 4).

The simulation process using MATLAB and the Rough Set Exploration System (RSES 2.2.2) exhibits the same results, i.e., the tumor cells grow with time and approach the steady-state.

Hence, we have established a mathematical model for tumor cells growth with the metastasis process in the human body, validated by the Rough set.

Therefore, these advances offer novel insights for tumor growth, further supporting research in tumor cell dynamics.

Acknowledgements

The authors are extremely thankful, to the Department of Mathematics, NIT Raipur (C. G.), India for providing facilities, space and an opportunity for the work.

References

[1] World Health Organization. Cancer. [cited 2018 Sep 12] <u>https://www.who.int/news-room/fact-sheets/detail/cancer</u>.

- [2] National Tumors Institute. [cited 2015 Feb 9] What is cancer? <u>https://www.cancer.gov/about-</u> cancer/understanding/what-is-cancer.
- [3] National Cancer Institute. Symptoms of cancer. [cited 2019 May 16]. <u>https://www.cancer.gov/about-</u> <u>cancer/diagnosis-staging/symptoms</u>.
- [4] National Tumors Institute. Obesity and cance. [cited 2017 Jan 17] <u>https://www.cancer.gov/about-</u> <u>cancer/causesprevention/risk/obesity/obe</u> <u>sity-fact-sheet</u>.
- [5] Jayasekara H, MacInnis RJ, Room R, English DR. Long-term alcohol consumption and breast, upper aerodigestive tract and colorectal tumors risk: a systematic review and metaanalysis. Alcohol and Alcoholism 2016;51:315-30. Doi:10.1093/alcalc/agv110.
- [6] P. Kunnumakkara Anand AB. Sundaram Kunnumakara AB. C. Harikumar KB, Tharakan ST, Lai OS, Sung B, Aggarwal BB. Tumors is a preventable disease that requires major lifestyle changes. Pharmaceutical Research 2008;25:2097-116. Doi:10.1007/s11095-008-9661-9.
- [7] World Health Organization. Cancer. [cited 2018 Feb 20] <u>https://www.who.int/news-room/factsin-pictures/detail/cancer</u>.
- [8] American Tumors Society. Family cancer syndromes. [cited 2020 Aug 05] <u>https://www.cancer.org/cancer/cancerer-causes/genetics/family-cancersyndromes.html</u>.
- [9] American Tumors Society. Understanding genetic for testing [cited] 2017 Apr 10] cancer. https://www.cancer.org/cancer/cancercauses/genetics/understanding-genetictesting-for-cancer.html.

- Kushi LH, Doyle C, McCullough M, [10] Rock CL, Wahnefried WD, Bandera EV, Gapstur S, Patel AV, Andrews K, Gansler T. American tumors society guidelines on nutrition and physical activity for tumors prevention: reducing the risk of tumors with healthy food physical choices and activity. Clin 2016;62:30-**CATumors** J 67. Doi:10.3322/caac.20140.
- [11] Parkin DM, Boyd L, Walker LC. 16.The fraction of tumors attributable to lifestyle and environmental factors in the UK in 2010. British Journal of Tumors 2011;105:S77-81. Doi:10.1038/bjc.2011.489.
- [12] World Health Organization. WHO report on cancer: setting priorities, investing wisely and providing care for all. [cited 2020 Feb 3] <u>https://www.who.int/publications/i/item/</u> <u>who-report-on-cancer-setting-priorities-</u> <u>investing-wisely-and-providing-care-for-all</u>
- [13] Gotzsche PC, Jorgensen KJ. Screening for breast tumors with mammography. The Cochrane Database of Systematic Reviews 2013;6. Doi:10.1002/14651858.
- [14] Enderling H, Chaplain AJM. Mathematical modeling of tumors growth and treatment, Current Pharmaceutical Design 2014;20.
- [15] Elias J, Dimitrio L, Clairambault J, Natalini R. The p53 protein and its molecular network: Modelling a missing link between dna damage and cell fate. BiochimBiophys Acta Proteins Proteomics. 2014;1844:232–47. Doi: 10.1016/j.bbapap.2013.09.019.
- [16] Laird AK. Dynamics of tumors growth. British Journal of Cancer 1965;19:278– 91. Doi: 10.1038/bjc.1965.32.
- [17] Laird AK. Dynamics of tumors growth. British Journal of Cancer 1964; 13:490–502. Doi: 10.1038/bjc.1964.55

- [18] Summers W. Dynamics of tumors growth — a mathematical model. Growth 1966;30:333.
- [19] Dethlefsen LA, Prewitt JMS, Mendelsohn ML. Analysis of tumors growth curves. Journal of the National Cancer Institute 1968;40:389–405.
- [20] Brodin NP, Vogelius IR, Eriksson TB, AfRosenschold PM, Maraldo MV, Aznar MC, Specht L, Bentzen SM. Optimizing the radiation therapy dose prescription for pediatric medulloblastoma: Minimizing the life years lost attributable to failure to control the disease and late complication risk. ActaOncologica 2014;53:462–70. Doi: 10.3109/0284186X.2013.858824.
- Batmani Y, Khaloozadeh H. Optimal drug regimens in cancer chemotherapy: A multi-objective approach. Computer in Biology and Medicine 2013;43:2089– 95. Doi: 10.1016/j.compbiomed.2013.09.026.
- [22] Huang X, Ning J, Wahed AS. Optimization of individualized dynamic treatment regimes for recurrent diseases. Statistics in Medicine 2014;33:2363–78. Doi:10.1002/sim.6104.
- [23] Moodie EEM, Richardson TS, Stephens DA. Demystifying optimal dynamic treatment regimes. Biometrics 2014;63:447–55. Doi: 10.1111/j.1541-0420.2006.00686.x.
- [24] Wang Z, Deisboeck TS. Mathematical modeling in cancer drug discovery. Drug Discovery Today 2014;19:45–50. Doi: 10.1016/j.drudis.2013.06.015.
- [25] Panetta JC. A mathematical model of drug resistance: Heterogeneous tumors. Mathematical Biosciences 1998; 147:41–61. Doi: 10.1016/S0025-5564(97)00080-1.
- [26] Sakode CM, Padhi R, Kapoor S, Rallabandi VPS, Roy PK. Multimodal

therapy for complete regression of malignant melanoma using constrained nonlinear optimal dynamic inversion. Biomedical Signal Processing and Control 2014;13:198–211. Doi: 10.1016/j.bspc.2014.04.010.

- [27] De Pillis LG, Gu W, Radunskaya AE. Mixed immunotherapy and chemotherapy of tumors: modeling, applications and biological interpretations. Journal of Theoretical Biology 2006;238:841–62. Doi: 10.1016/j.jtbi.2005.06.037.
- [28] Rihan FA, Lakshmanan S, Maurer H. Optimal control of tumour-immune model with time-delay and immunochemotherapy. Applied Mathematics and Computation 2019;353:147-165. Doi:https://doi.org/10.1016/j.amc.2019.0 2.002.
- [29] Huang Y, Zhang Z, Hu B. Bifurcation for a free-boundary tumor model with angiogenesis. Nonlinear Analysis: Real World Applications 2017;35:483-502. Doi:https://doi.org/10.1016/j.nonrwa.20 16.12.003.
- [30] Deng Y, Liu M. Analysis of a stochastic tumor-immune model with regime switching and impulsive perturbations. Applied Mathematical Modelling 2020;78:482-504. Doi: https://doi.org/10.1016/j.apm.2019.10.01 0
- [31] Jin Y, Yuanshun T, Robert AC. Modelling effects of a chemotherapeutic dose response on a stochastic tumourimmune model. Chaos, Solitons & Fractals 2019;123:1-13. Doi: https://doi.org/10.1016/j.chaos.2019.03. 029.
- [32] Zheng J, Cui S. Analysis of a tumormodel free boundary problem with a nonlinear boundary condition. Journal of Mathematical Analysis and Applications 2019.
 Doi:https://doi.org/10.1016/j.jmaa.2019.

<u>05.056</u>.

- [33] Hahnfeldt P, Panigrahy D, Folkman J, Hlatky L. Tumors development under angiogenic signaling: a dynamical theory of tumors growth, treatment response, and postvascular dormancy. Cancer Research 1999;59:4770-5.
- [34] Iwata K, Kawasaki K, Shigesada N. A dynamical model for the growth and size distribution of multiple metastatic tumors. Journal of Theoretical Biology 2000;203:177–86.
- [35] Polkowski L. Advance in Soft Computing: Rough Sets Mathematical Foundations. Physical-Verlag A Springer-Verlag Company 2002. Doi: 10.1007/978-3-7908-1776-8

- [36] Peters G, Lingras P, Slezak D. Rough Sets Selected Methods and Applications in Management and Engineering. Springer 2012. Doi:10.1007/978-1-4471-2760-4
- [37] Lin TY, Cercone N. Rough Sets and Data Mining Analysis of Imprecise Data. Kluwer Academic Publishers 1997. Doi: 10.1007/978-1-4613-1461-5
- [38] Krug H, Taubert G. Zur praxis der anpassung der logistischen function an das wachstum experimenteller tumoren, Arch. Geschwulstforsch 1985;55:235– 244.
- [39] Skowron A. RSES 2.2 User's Guide. Warsaw University 2005. http://logic.mimuw.edu.pl/»rses.