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Parameter Estimation of a Tumor Growth Model under Data-driven Approach and Its Numerical Solution in Matlab

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Abstract: This paper focuses on the numerical solution of a tumor growth model under a data-driven approach. Based on the inherent laws of the data and reasonable assumptions, an ordinary differential equation model for tumor growth is established. Nonlinear fitting is employed to obtain the optimal parameter estimation of the mathematical model, and the numerical solution is carried out using the Matlab software. By comparing the clinical data with the simulation results, a good agreement is achieved, which verifies the rationality and feasibility of the model.

Keywords: MATLAB; Tumor growth model; Data-driven approach; Ordinary differential equation

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1. Introduction

Malignant tumors, as major diseases that pose a serious threat to human health, have long been a key research focus in the medical field. In today's era, with the continuous progress and rapid development of science and technology, tumor treatment methods are becoming increasingly diverse. Surgical treatment has become more precise and efficient, enabling the maximum resection of tumor tissues while minimizing damage to surrounding normal tissues. Radiotherapy technology has been constantly innovating, evolving from traditional radiotherapy methods to more precise intensity-modulated radiotherapy, proton and heavy ion radiotherapy, etc., which significantly enhances the lethality to tumor cells and reduces the side effects on normal tissues. Chemotherapy has also achieved numerous breakthroughs. New types of chemotherapy drugs keep emerging, not only improving the treatment effect but also alleviating the pain of patients to a certain extent. These advancements have significantly extended the survival period of tumor patients and remarkably improved their quality of life.

However, the survival mechanism of tumors is extremely complex, involving numerous factors from multiple disciplinary fields such as cell biology, molecular biology, and immunology. Tumor cells have abnormal proliferation ability, can escape the immune surveillance of the body, and can also induce angiogenesis through various pathways to provide nutrients and channels for their own growth and metastasis. In addition, the genetic mutations of tumor cells are diverse and complex, and there may be differences between different tumor cells in different patients or even within the same patient. Due to the intertwined influence of these complex factors, there is still no complete model that can accurately explain the occurrence and evolution laws of tumors.

In order to overcome this challenge, researchers from multiple fields are actively exploring and constructing various basic models to simulate the characteristics of tumors. Among them, mathematical models, with their unique advantages, have become an important branch in the study of tumors. Mathematical models can quantitatively describe various phenomena in the tumor growth process by establishing mathematical equations, thus revealing the internal laws of tumor growth. For example, differential equations are used to describe the proliferation and migration processes of tumor cells, and probability models are applied to analyze the risk of tumor occurrence [1–6].

Tumors are formed by tumor cells with genetic mutations. These tumor cells are significantly different from normal cells. The division and proliferation of normal cells are strictly regulated to maintain the normal functions and structures of body tissues and organs. However, the genetic mutations in tumor cells disrupt this regulatory mechanism, enabling their division and proliferation rate to far exceed that of normal cells. This rapid division and proliferation cause the continuous growth of tumor tissues, which exerts pressure on surrounding tissues and organs, affects their normal functions, and thus triggers a series of serious health problems. In this study, based on the clinical cases of a certain X tumor, its growth data were collected and collated. These data record the changes in the size of the tumor at different time points in detail, providing valuable information for studying the growth law of tumors. The aim of this study is to attempt to use these growth data and mathematical methods to construct a mathematical model that can accurately describe the growth law of tumors, providing theoretical support for a deeper understanding of the tumor growth process, prediction of tumor development trends, and formulation of more effective treatment plans.

2. Mathematical model of tumor growth based on data drive

Regression analysis was used to explore the changes in tumor size over time as shown in **Table 1**.

Table 1. Clinical data of X tumor growth over time

Time (day)	The volume of the tumor (mm^2)	Time (day)	The volume of the tumor (mm^2)	Time (day)	The volume of the tumor (mm^2)	Time (day)	The volume of the tumor (mm^2)
0	1.0	26	48.4	51	1120.4	76	2337.2
2	1.3	27	56.1	52	1210.3	77	2345.8
3	1.6	28	64.9	53	1300.1	78	2353.3
4	1.8	29	75.1	54	1388.7	79	2359.6
5	2.1	30	86.8	55	1475.3	80	2365.1
6	2.5	31	100.3	56	1559.1	81	2396.9
7	2.9	32	115.7	57	1638.0	82	2374.1
8	3.3	33	133.4	58	1714.7	83	2377.6
9	3.9	34	153.6	59	1785.7	84	2380.7

Table 1 (Continued)

Time (day)	The volume of the tumor (mm^2)	Time (day)	The volume of the tumor (mm^2)	Time (day)	The volume of the tumor (mm^2)	Time (day)	The volume of the tumor (mm^2)
10	4.5	35	176.6	60	1851.8	85	2383.2
11	5.2	36	202.7	61	1912.6	86	2385.7
12	6.0	37	232.3	62	1968.3	87	2387.7
13	7.0	38	265.9	63	2018.9	88	2389.3
14	8.1	39	303.5	64	2064.5	89	2390.8
15	9.5	40	345.5	65	2105.5	90	2391.1
16	10.9	41	392.3	66	2142.2	91	2393.2
17	12.7	42	444.0	67	2174.7	92	2394.2
18	14.8	43	500.9	68	2203.5	93	2394.9
19	17.2	44	562.9	69	2229.2	94	2395.7
20	19.9	45	630.1	70	2251.3	95	2396.3
21	23.1	46	702.2	71	2270.8	96	2396.9
22	26.8	47	779.0	72	2288.0	97	2397.2
23	31.1	48	859.9	73	2303.0	98	2397.6
24	36.1	49	944.3	74	2316.1	99	2397.9
25	41.8	50	1031.4	75	2327.4	100	2398.4

First, draw the scatter diagram of the data, as shown in **Figure 1**. The scatter diagram of the specific data is drawn in Matlab code:

```
data=xlsread(‘data1.xlsx’);Time=data(:,1)’;
Num=data(:,2)’;plot(Time,Num,’bo’)； grid on
xlabel(‘Time(day)’)； ylabel(‘the volume of the tumor(mm^3)’)
```

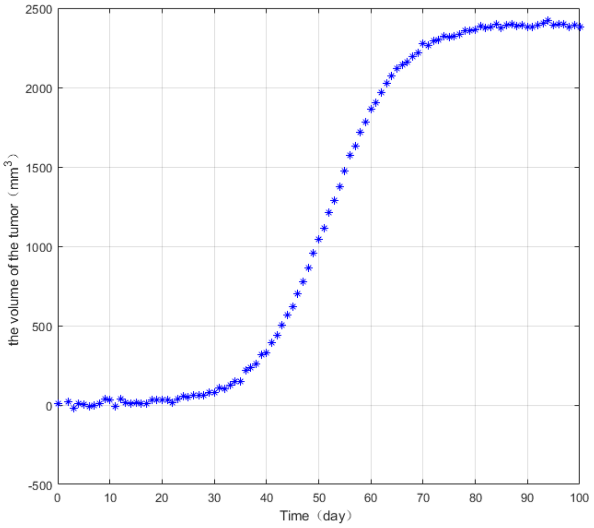

Figure 1. Scatter plot of clinical data

The trend of tumor size change over time can be visually seen from **Figure 1**, but the law of tumor change cannot be accurately obtained. The scatter points in the figure show a general upward trend, indicating that the tumor is growing over time, but this trend only provides a vague overall impression. Due to the dispersion of the scatter point distribution, the spacing between the points is not uniform, and there is no obvious linear or simple curve relationship, it is impossible to determine the specific growth rate change of the tumor at each stage and whether there is a turning point in the growth pattern based on these scattered points.

The mechanism analysis and data regression analysis were combined to build a mathematical model of tumor change over time. Mechanism analysis can start from the biological principles of tumor growth, such as considering the effects of internal factors, such as the division mechanism of tumor cells and the supply and consumption of nutrients on tumor growth. Data regression analysis can use mathematical methods to dig deep into a large number of existing clinical data and find the mathematical relationship behind the data [7]. The two complement each other, and it is expected to build a mathematical model that accurately reflects the law of tumor growth.

It can be seen from **Figure 1** that in the process of rapid tumor growth, when the tumor volume reaches a certain level, the growth rate slows down and becomes stable due to the limited supply of nutrients. This change rule is consistent with the characteristics of Logistic model, which can be described by the ordinary differential equation model as follows:

$$\begin{cases} \dfrac{dX(t)}{dt} = aX(t) - bX^2(t), \\ X(t_0) = X_{0,} \end{cases} \tag{1}$$

Where X=$X(t)$ represents the volume of the tumor (mm^3), t is time(day), a is the growth rate of the tumor per unit time, $b = \dfrac{a}{K}$, K is the maximum tumor volume, X_0 is the volume of the tumor at the initial moment t=t_0. Transform the equation into $\dfrac{dX}{dt} = aX(1 - \dfrac{X}{K})$, and the analytical solution of the model can be obtained by using the method of separating variables

$$X(t) = \frac{K}{1 + Ce^{-a(t - t_0)}}, \tag{2}$$

Where $C = \dfrac{K - N_0}{N_0}$.

3. MATLAB numerical simulation and result visualization

To fit the model parameters more easily, take $t_0 = 0$, further deform the model:

$$X(t) = \frac{K}{1 + e^{\ln C - at}} = \frac{K}{1 + e^{-(-\ln C + at)}} = \frac{\beta_1}{1 + e^{-(\beta_2 + \beta_3 t)}}, \tag{3}$$

Where $\beta_1 = K, \beta_2 = -\ln C = -\ln \frac{K - X_0}{X_0} = \ln \frac{X_0}{K - X_0}, \beta_3 = a$. Part of the Matlab code of the numerical solution is as follows [7]:

```
beta1=2400;logist=@(p)log(p./(1-p));
fitlm(x,logist(y/beta1))；
beta0 = [2400, -7.7831, 0.14999];
fun = @(phi,t) phi(1) ./ ( 1 + exp(-(phi(2) + phi(3) * t)));
[beta, errs] = nlinfit(x, y, fun, beta0)；
pred = fun(beta, x);
plot(x,y,’bo’)；  grid on
xlabel(‘Time(day)’)；  ylabel(‘the volume of the tumor(mm^3)’)；  hold on
plot(x, pred, ‘r*’)；  legend(‘Original Data’, ‘Prediction Results’)
```

Estimation of these three parameters β_1,β_2,β_2, requires the use of nonlinear fitting methods, which are more sensitive to the selection of initial values. The appropriate initial value can make the fit converge to the optimal estimate quickly, otherwise, it may not reach the optimal after many iterations. Final run result β_1=2400, β_2=-7.7, β_3=0.11 Thus, the tumor model was obtained:

$$X(t) = \frac{2400}{1 + e^{-(-7.7+0.11t)}}. \tag{4}$$

The fitting results of the mathematical model obtained through numerical simulation are shown in **Figure 2**.

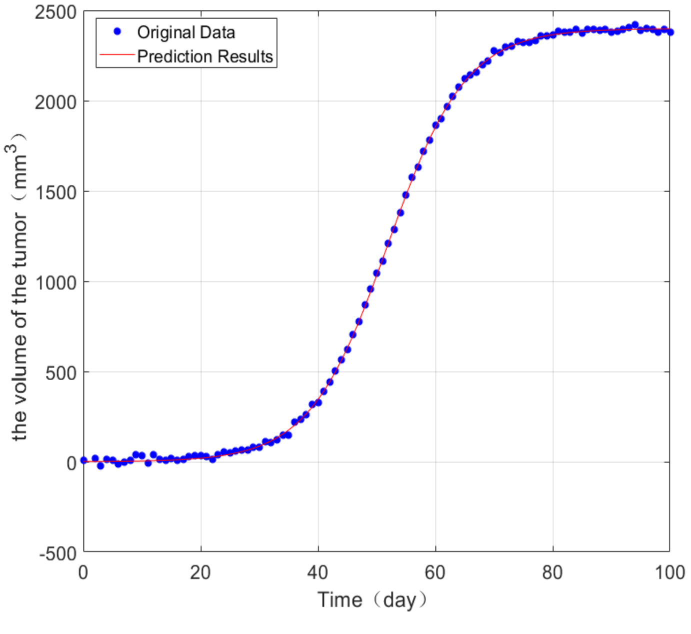

Figure 2. Fitting results

It can be clearly seen from **Figure 2** that the clinical data is in good agreement with the results simulated according to the mathematical model. Each clinical data point is tightly wrapped around the simulation curve, and the two trends are almost exactly the same, which intuitively demonstrates the reliability of the model. Through the nonlinear fitting method of Matlab software, the researchers were able to fit the optimal estimates of these three key parameters. In the fitting process, the powerful computing power of Matlab plays a key role. After several iterations of calculation, the most suitable parameter combination is finally determined. After these optimal estimates are obtained, a mathematical model suitable for tumor growth data can be obtained. With this model, doctors can scientifically predict and accurately make decisions on tumor growth in combination with the actual situation of patients, providing a strong basis for the formulation of follow-up treatment plans.

4. Conclusion

The data-driven tumor growth model constructed in this study, combined with Matlab numerical solution, showed significant advantages. Researchers dig deep into tumor clinical data and build models based on reasonable assumptions. Matlab numerical solution with powerful computing power and visualization function, efficiently solve and optimize the model parameters. The combination of the two can accurately fit tumor growth data, covering all stages of tumor growth.

With the help of this model and solution, researchers can deeply explore the law of tumor growth from a mathematical point of view and understand the influence mechanism of various factors on tumor growth. This provides support for medical experts to develop personalized treatment plans, which helps to predict tumor development in advance and improve the cure rate of patients.

In the field of cancer research, this achievement has both theoretical and practical value. Theoretically, it enriches the theoretical system of mathematical modeling. In practice, it provides strong technical support for tumor diagnosis, treatment evaluation and prognosis prediction, promotes tumor research and development, and brings new hope for overcoming tumor problems.

Disclosure statement

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