UNIVERSITY OF THE PHILIPPINES

A Comparative Study between Gompertz Equation and Cellular Automata in Modelling Tumor Growth

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ABSTRACT

Cancer cell growth have been studied through different models such as differential equations and automata. The aim of this study is to make a proper transition of the Gompertz equation into a stochastic cellular automata and test both models' capabilities to describe tumor volume growth. Laird (1964) proved on her paper the effectiveness of Gompertz equation in describing tumor cell proliferation. Meanwhile, Qi et.al, (1993) and Boondirek A. et. al. (2006) have proposed cellular automata models to simulate and study tumor growth behavior. The researchers use the methodology of Hu, R., & Ruan, X. (2003) in combining these two models by constructing a cellular automata with gompertz equation. Then, the researchers simulate both of the models in a Java Program and gathered each tumor volume computations. Finally, a comparison between the two sets of results were examined to infer the advantages of each models. The continuous Gompertz equation yielded results of higher precision while the discrete cellular automata yielded real-life probabilistic behavior of tumor growth. The researchers concluded that both models hold different modelling capabilities and, thus, suggest to future researchers to consider appropriate model from the two in dealing with specific tumor growth problems.

Introduction

Up until now, tumor growth rate is still considered to be a puzzling phenomena for many scientists and mathematicians. Modelling such behavior needs to consider a huge amount of variables and complex rules in order to simulate the real abnormal growth of cells. This is because probability and certain conditions are some of the important factors for a realistic tumor growth model.

It was believed that tumor grows at exponential rate but survey of experiments suggested that after an amount of time, the increase of population growth decays in an asymptotic manner. Researchers have used different mathematical models such as the exponential and logistic growth curve to describe tumor cells volume increment. Cube root growth was also empirically established to be a good model. (Mayneord 1932). Paek, Jayeong and Choi, Ils (2017) used a stochastic Gompertz equation to lessen the discrepancies of using the deterministic Gompertz equation with clinical and empirical data.

Cellular Automata is also widely used computational model to simulate the spatial and temporal change of tumor growth. The dynamics of the cellular system to grow under certain conditions can be shown through such model. Jan Poleszczuk and Heiko Enderling (2014) proposed a cellular automaton model with a domain capable of expanding as the the tumor population increases, greatly simulating the complex behavior of tumor cells. Their paper considered the proliferation, migration and death of

the cells under stochastic rules. This model greatly supports how complex cancerous cells growth is, considering probabilistic and behavioral rules.

Since the two models (i.e. Gompertz equation and Cellular automata) are some of the commonly used models for cancerous cells, there must be some bridge or connection that can either strengthen the modelling capability or deepen the knowledge to tumor growth.

The aim of this study is to make a proper transition of the Gompertz equation into a stochastic cellular automata and test both models' capabilities to describe tumor growth.. The researchers start on giving introductory knowledge and definitions about cellular automata and Gompertz equation. Then, the transition process is explained why and how it works. Finally, the researchers simulate the two models to gather data and have them compared to each other to infer the advantages of each models.

The study is delimited to the study of cancer cells, a malignant type of tumor cells. The researchers are focused only making on a one-dimensional cellular automata and are to use Laird's Gompertz function. Tumor growth is the only phenomenon monitored by the researchers; behaviors such movement and death of tumor cells are not considered in this research..

1.1 Cellular Automata

1.1.1 History

During the 1940s, John von Neumann and Stanislaw Ulam proposed the concept of Cellular Automata (CA) to describe the process of self-reproduction on machines. von Neumann was concerned about this possibility as described in his paper, “The General and Logical Theory of Automata”, and only after Ulam suggested the usage of cells made the successful formalization of the theoretical model of self-reproduction.

Another book of von Neumann, Theory of Self-Producing (1966), describes the main idea behind his proposed model. Originally called as Cellular Space, CA is centralised around the usage of cell as the structure unit for lattices up to the third dimension. The machine depends on discrete time intervals where for every specified clock tick, the overall machine state changes. The change or so called “evolution” is under the global rule followed by every cell and group of cells of the specific automata. This change is portrayed as state change of the cells.

As an example, Von Neumann gave a CA that has 29 possible states for each cell. Every cell is related and connected to the top, bottom, left and right cell which is called the von Neumann neighborhood. The CA showed dynamism and complexity like a biological process would such as DNA evolution. Such behavior of the system would later help in analyzing other biological systems such as growth, evolution and self-reproduction.

1.1.2 Overview Definition

According to Hoogduin [10], Cellular Automata is a computing model that computes through a system of discrete elements called cells that have 3 following characteristics :

A. Spatial location. The cells are located in a grid or a space and has unique spatial characteristics as their identities.

B. State Change. The cells undergo changes in state, commonly in binary mode.

The rules of the system tells what a cell's current state should be.

C. Neighborhood. The cells interacts with other cells close to them. The neighborhood holds importance in undergoing state change, considering the rules of the model.

For every discrete time interval, the current configuration of the cell grid evolves to the next one under the evolutionary rules, whether arbitrary or conceptual, of the system. It may evolve or change under 4 patterns - (1) Uniform (2) Repetition (3) Random (4) Complex.

1.1.3 Application and Uses

Cellular automaton has many application for its capability to exhibit dynamic complex behavior even in a simple space under simple rules. For example, fluid flow and dynamics can be simulated through CA, a variation of the automaton called as the

Lattice-Gas automaton. Traffic models in a single lane and forest-fire models are also a variation of CA. [3]

1.2 Gompertz Equation

1.2.1 History

Proposed by Benjamin Gompertz (1825), Gompertz equation or Gompertz curve was derived from Gompertz's Law of Mortality that proposes death probability depends on the age of the person. According to Wesstein [11], it is used in actuarial science for specifying a simplified mortality law (Kenney and Keeping 1962, p. 241). This behavior of such model was used by Charles Winsor (1932) to describe growth processes. [1]

1.2.2 Overview Definition

Gompertz equation is a sigmoid function of time t having an asymptote as t approaches gets larger. It is a type of mathematical model describing a very slow growth at the beginning and the end of the curve where the approach to the ending asymptote is more gradual than the beginning.

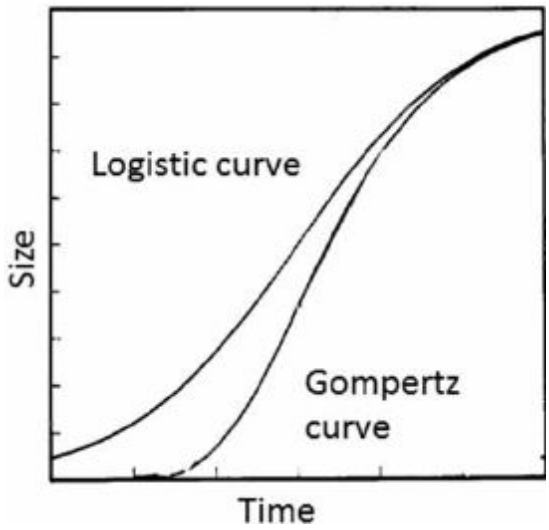

Figure 1: Comparison of logistic curve and Gompertz curve in time-size graph

1.2.3. Application and Uses

Gompertz function has many uses on fields other than engineering. In biology, a modified Gompertz equation was convenient to use as a predictive modelling for *Lactobacillus plantarum* bacterial growth curve (M. H. Zwietering*, I. Jongenburger, F. M. Rombouts and K. VAN 'T Riet, 1990)

In addition, one of Gompertz function uses is to model population growth in a limited space over time taking limited resources into consideration. The medicine field uses the said equation to model what supposed to be the object of the study, tumor growth. (Laird, A.K. 1964)

2. Review of Related Literature

2.1 Transition of DE to Cellular Automaton

Both differential equations and cellular automata are used to characterize the behaviors of different systems, especially in the fields of Science and Math. Despite the latter's promising approach in modelling complex systems, the former is the standard tool for this endeavor. This is because users of cellular automata are limited by the difficult task of coming up with suitable rules needed to model real events [5].

In the paper of Ruanxiaogang, he discussed a method to bridge differential equations and cellular automata. This is done by simplifying differential equations (DE) to an equivalent finite difference equation (FDE) and converting FDEs to cellular automaton. Converting DEs to FDEs is possible because DEs follow the definition of derivatives which is shown in Equation 2.1.1:

$$\frac{dy}{dx} = \lim_{x \to 0} \frac{f(x) - f(a)}{x - a} \tag{2.1.1}$$

Thus, given a typical DE of this form:

$$\frac{dx}{dt} = f(x, y) \tag{2.1.2}$$

It can be converted to an equivalent FDE of this form:

$$x(t+1) = x(t) + f(x(t), y(t)) \tag{2.1.3}$$

This is a simple rearrangement of terms using the definition of derivatives.

After converting the DE to an equivalent FDE, it will now be easier to create an equivalent cellular automaton. This is done by replacing the variables x and y to discrete variables of a cellular automaton and limit the scope of these variables to a finite scope, thus, the state variables will now be represented by finite small sets. We can represent the *f*+1 as the state transition function of the cellular automaton we are constructing. This shows that cellular automaton can be converted to an *equivalent* differential equation depending on the rules that will be set to the cellular automaton. [5]

2.2 Modelling Tumor Growth by Gompertz Function

It is commonly believed that tumor grows at an exponential rate terminated by the lack of nutritional support provided by the host. However, it was proven by several experiments that this behavior of tumors is rarely the case [4]. According to the studies Laird has gathered, tumors only grow exponentially at a certain period of time and slows down its growth when it is already large enough [4].

In her paper, Laird used Gompertz function to model the behavior of Tumor Growth. This function was chosen to model the tumor growth because gompertz function models the behavior that exhibits slow growth at the beginning, exponential growth in a certain period of time and slows down again. Laird used the Gompertz equation of this form:

$$\frac{W}{W_o} = e^{\frac{A}{\alpha}(1-e^{-\alpha t})} \tag{2.2.1}$$

In the equation above, W is the tumor size, Wo is the initial tumor size, t is time, and A, *e* and α are constants.

The above equation was simplified in the paper according to the assumptions that were stated. For our paper, we will also use this form of gompertz equation to model tumor growth and be later compared to the model based on a cellular automaton. [4]

2.3 Cellular Automata

Informally, a CA is a lattice of cells with finite, predetermined, discrete states. Each cell in the CA has a neighborhood relation defined over the lattice which indicates which cells are to be considered when state transition rules are applied. Time in CAs are considered discrete. On each time step, every cell is updated synchronously based on the transition rules. The same set of rules is applied at each time step. The transition function is deterministic in nature meaning the transition function should yield the same result for with same inputs. CAs can be extended for it to have stochastic rules yielding stochastic results.

We can outline a formal definition of CAs as follows. First, let the set of all cells be denoted as *C*. Then, let the neighborhood function *N*

$$N : C \times C \rightarrow \{True, False\} \tag{2.3.1}$$

return true if and only if the input pair of cells are neighbors of each other. Next, let *S* be the set of all possible cell states. Then, we let *u* be the state transition function. Typically it is applied synchronously to every element of *C. u* is of the form

$$u : S|N| \rightarrow S \tag{2.3.2}$$

There exists many variations of CAs. They can be of any dimensions but are typically one-dimensional and two-dimensional. They can also be either finite or infinite. Transition rules can be applied synchronously or asynchronously. Transitions can be deterministic or stochastic. Other variations exist but these are the typical ones [18].

2.4 Cellular Automaton on Tumor Growth

There are two main cellular automata methods that can be used to model tumor growth. One model in particular is the Mass-Action Model proposed by D. Ting-Chao Chou in 2011 [14]. Essentially, the mass action-model allows for a randomly chosen cell to multiply to another randomly chosen location on the grid. This model is based off of the chemical and epidemiological laws in which any cell in a homogenous mixture has an equal probability of interacting with another cell on the grid.

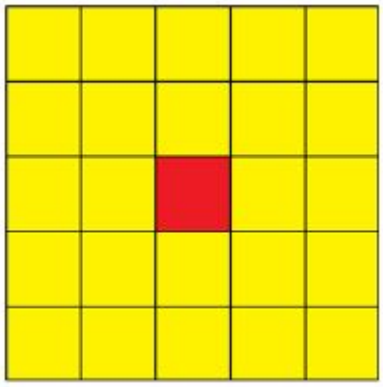

Figure 2: A chosen cell and the cells it can interact with using Mass-Action model

Another commonly used model in cancer modeling is the Spatial Model [17]. The spatial model is similar to the Mass-Action Model except that the cell can only interact with a random location within its neighborhood. The neighborhood for a cell in the Spatial Model used is a Moore neighborhood with range r = 1. The radius that defines the Moore neighborhood of a cell is called the Chebyshev distance which in the Spatial Model is equal to 1.

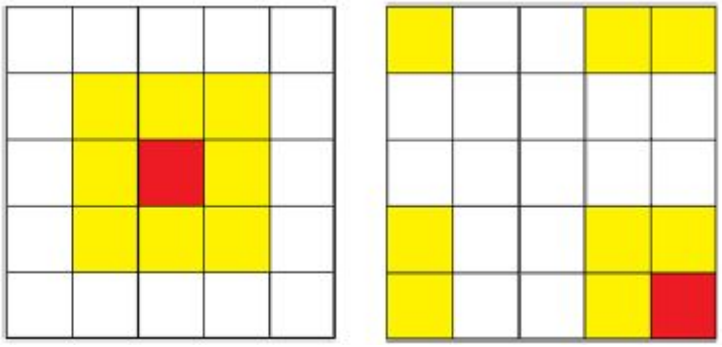

Figure 3: A chosen cell and the cells it can interact with using Spatial model

The area of the Moore neighborhood can be described by the equation $(2r + 1)^2$. These numbers, such as 9, 25, 49, etc., are odd squares. In the given figure with Chebyshev distance r = 1, the total area is 9. In addition, the spatial model wraps over and around itself to create a torus as shown in the figure above.

The Moore neighborhood is defined by the following set:

$$N^{M}_{(x_0,y_0)} = \{(x, y) : |x - x_0| \leq r, |y - y_0| \leq r\} \qquad (2.3.1)$$

Furthermore, the model can be transposed into a von Neumann neighborhood with range r = 1, and r = 2. The range of a von Neumann neighborhood is diagonal and the radius that defines its neighborhood is call the Manhattan distance.

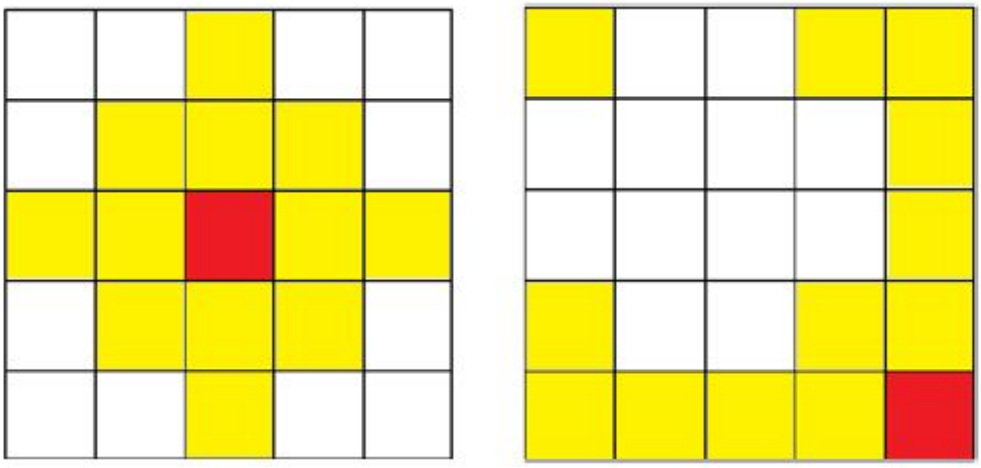

Figure 4: A chosen cell and the cells it can interact with using diagonal von Neumann neighborhood with r = 2

Qi,. et al. [16] and Boondirek, et al. [17] proposed a two-dimensional cellular automaton model of tumor growth with immune response. The growth curve represented from their model shows a growth similar to Gompertz curve which describes the growth of tumor. The cellular automaton model used by Boondirek, et al. can also be extended to three-dimensional model with von Neumann neighborhood.

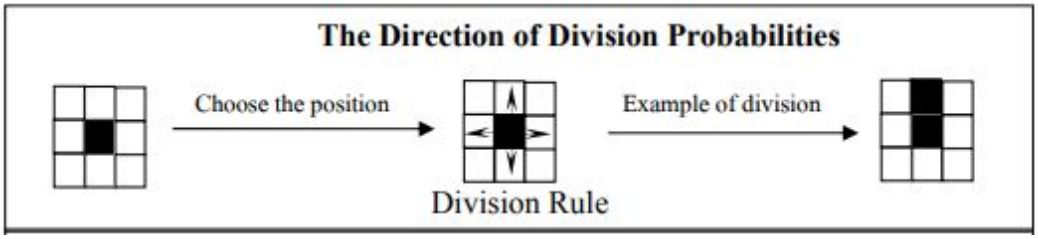

Figure 5: Division Rule of two-dimensional cellular automata.

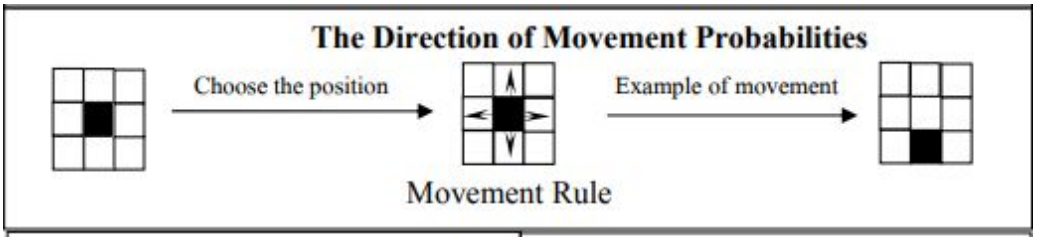

Figure 6: Movement Rule of two-dimensional cellular automata.

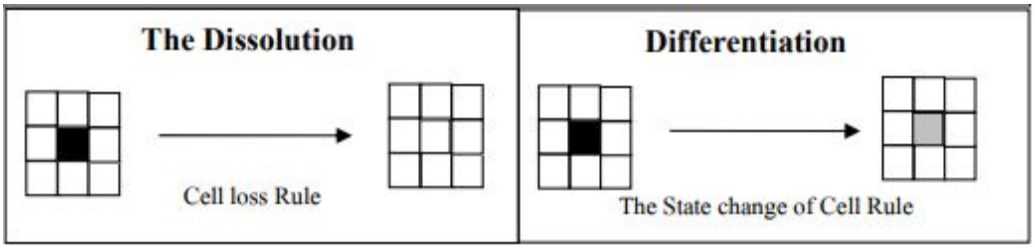

Figure 7: Dissolution and Differentiation Rule of two-dimensional cellular automata.

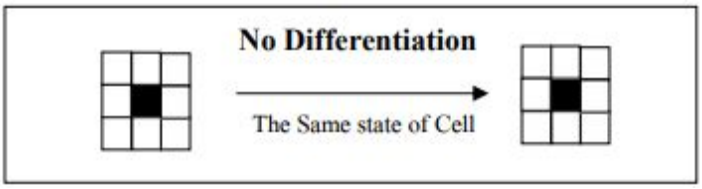

Figure 8: No Differentiation Rule of two-dimensional cellular automata.

As for one-dimensional CA, the neighborhood is commonly the cells adjacent to the chosen cell.

3. Methodology

Many physicists and mathematicians utilized both DE and CA to model continuum-based phenomena. DE was used even centuries before CA was found to numerically describe continuous system with real-life variables. Meanwhile, CA is known for its capability to simulate dynamic and complex system under simple rules. Combining their computing power would tell us if they have a connection and could yield a model better than the two. To combine them, we need to have a transition process from a DE to CA.

3.1 General Concept of the Transition Process

3.1.1 Transition from Continuous Space to Discrete Space

Following Huricha and Ruanxiaogang [5] procedures, the transition depends on the transformation of a continuous system into a discrete one. Since CA undergoes evolution at discrete time intervals with discrete and sometimes finite units, we need to make a continuous DE discrete so that the CA can use it as rules for the CA's system.

First step or first thing to consider is the dependency of the equation to time. Since CA states evolve at every discrete time interval, FDE must change also depending on time . Thus, the equation to consider is of the form

$$\frac{dx}{dt} = f(x, y) \qquad 2.1.2$$

Second step is to transform the DE into a Finite Difference Equation (FDE). FDE is a method of discretization where derivatives are approximated to difference of variables. The principle of the approximation is shown in 3.1.1.1.

$$\frac{df(x)}{dx} = \lim_{\Delta x \to 0} \frac{\Delta f}{\Delta x} \approx \frac{\Delta f}{\Delta x} \qquad 3.1.1.1$$

The equation above states that better and closer approximation depends on how small the value of Δx. Thus, the equation must be like 3.1.1.2.

$$x(t+1) = x(t) + f(x(t), y(t)) \qquad 3.1.1.2$$

Now that it is in discrete space, the equation can be used in the evolutionary rules of a CA. Since this study's CA needs to be stochastic because of the tumor growth's randomness, the equation is needed for the probabilistic rules of the automata. Generally, the CA can be considered as a system of FDE upon application of the equation.

3.1.2 Stochastic CA building

Given the FDE, the task now is to build the CA that follows probabilistic behavior. According to Guinot (2001) [19], a CA's transition probability should incorporate an exponentially decreasing function. To infer the evolutionary rules, the function to be used in the rules must be exhibiting an exponential decrease. From there, the CA states must also be probabilistically dependent on the function.

Based on Guinot's methodology, consider $\mathbf{U}$ as a set of state u_i^n of a CA with M cells at cell i and level n that takes only 2 values i.e. 0 and 1. At level n, $\mathbf{U^n}$ holds the CA at time n :

$$\mathbf{U}^n = (u_1^n, ..., u_M^n)^T, i = 1, ..., M \qquad 3.1.2.1$$

Given set of rules **F** that defines the transition rule from level n to n+1 :

$$\mathbf{F} : \mathbf{U}^n \mapsto \mathbf{U}^{n+1} \qquad 3.1.2.2$$

$$\mathbf{F} = (f_1, ..., f_M)^T, f_i : u_i^n \mapsto u_i^{n+1} \qquad 3.1.2.3$$

there is a quantity:

$$Z^n = \sum_{i=1}^{M} u_i^n \qquad 3.1.2.4$$

where Z^n is the cardinality of CA that have state 1. Guinot's description of the transition rule is given as

$$f_i(u_i^n) = u_i^n \ if \ \chi \leqslant g(u_i^n, k, \Delta t, Z^n, M) \qquad 3.1.2.5$$

Where χ is a random variable generated and uniformly distributed between 0 and 1. g is the function that gives only values between 0 and 1 and k is the function describing the probabilistic behavior of the system. For every cell and every time interval, χ is randomly generated and the transition function decides that a cell will not change its state when a χ is less than or equal to the function g.

Given f_i, we can now define the probability of a cell to persist its value as described by Eq. 3.1.2.6 and Eq. 3.1.2.7

$$Pr(u_i^{n+1} = 1 | u_i^n = 1) \equiv P_{1,1}(r, \Delta t) = g(1, r, \Delta t, Z^n, M) \qquad 3.1.2.6$$

$$Pr(u_i^{n+1} = 0 | u_i^n = 0) \equiv P_{0,0}(r, \Delta t) = g(0, r, \Delta t, Z^n, M) \qquad 3.1.2.7$$

where r is taken as function k. One of the assumed rule in Guinot's methodology is the restriction of cell going from state 1 back to state 0 if the function r is positive and vice versa if the function r is negative . For the sake of limiting the study to the use of Gompertz equation, the succeeding concept is assumed to have r as positive. Thus, the form is expressed as

$$Pr(u_i^{n+1} = 0 | u_i^n = 1) \equiv P_{0,1}(r, \Delta t) = 0 \; if \; r > 0 \qquad 3.1.2.7$$

The probability to persist state 0 of a cell exhibits decreasing exponential growth. To prove the statement, the probability at 2 step time interval must be first known as described at Eq. 3.1.2.8

$$\begin{aligned} Pr(u_i^{n+2} = 0 | u_i^n = 0) \; = \; & Pr(u_i^{n+2} = 0 | u_i^{n+1} = 0) Pr(u_i^{n+1} = 0 | u_i^n = 0) \; + \\ & Pr(u_i^{n+2} = 0 | u_i^{n+1} = 1) Pr(u_i^{n+1} = 1 | u_i^n = 0) \end{aligned} \qquad 3.1.2.8$$

Since as stated at Eq. 3.1.2.7., the equation is reduced to

$$Pr(u_i^{n+2} = 0 | u_i^n = 0) = Pr(u_i^{n+2} = 0 | u_i^{n+1} = 0) Pr(u_i^{n+1} = 0 | u_i^n = 0) \qquad 3.1.2.9$$

which is also equal to

$$Pr(u_i^{n+2} = 0 | u_i^n = 0) = [P_{0,0}(r, \Delta t)]^2 \quad \text{3.1.2.10}$$

Taking into account that the number of level increase is equal to the number of time interval. Then,

$$Pr(u_i^{n+2} = 0 | u_i^n = 0) = P_{0,0}(r, 2\Delta t) = [P_{0,0}(r, \Delta t)]^2 \quad \text{3.1.2.11}$$

It can be generalized that at time interval q,

$$P_{0,0}(r, q\Delta t) = [P_{0,0}(r, \Delta t)]^q \quad \text{3.1.2.12}$$

Thus, Eq. 3.1.2.12 exhibits an exponential decreasing behavior and it also tells that g must also exponentially decrease.

Since as stated by Laird, a power series of e^{-at} in the Gompertz equation expressed in αt would turn the equation into a simple exponential growth/decay function, if αt were small enough.

Given these general functions, rules and proof, a stochastic CA model can now be designed even with the use of a DE. Specifically, the researchers can now build a stochastic CA given the Gompertz equation.

3.2 Conversion of Gompertz Equation to Finite Difference Equation

In this paper, the Gompertz equation used in the paper of Laird will be converted to an equivalent cellular automaton using the method done in the paper of Ruanxiaogang. To do so, we must derive the equivalent Finite Difference Equation (FDE) of the differential equation that can be generated by getting the derivative of the Gompertz equation (2.2.1) with respect to time [5].

$$\frac{W}{W_o} = e^{\frac{A}{\alpha}(1-e^{-\alpha t})} \qquad 2.2.1$$

As stated in the previous chapter, W stands for the tumor size, Wo stands for the initial tumor size, t is time, and A, *e* and α are constants. Following the work of Ruanxiaogang, we get the differential equation describing the rate of tumor growth by first rearranging 2.2.1 to have an equation where only W is on the left side.

$$W = W_o e^{\frac{A}{\alpha}(1-e^{-\alpha t})} \qquad 3.2.1$$

The equation above can be simplified by applying natural logarithmic function on both sides.

$$ln(W) = ln(W_o e^{\frac{A}{\alpha}(1-e^{-\alpha t})}) \qquad 3.2.2$$

It should be noted that all the variables and constants present in the 3.2.1 are positive numbers, thus, applying the logarithmic function in both sides will not give undefined values. Simplifying 3.2.2 will yield to 3.2.3, as shown below.

$$\begin{aligned} ln(W) &= ln(W_o) + ln(e^{\frac{A}{\alpha}(1-e^{-\alpha t})}) \\ &= ln(W_o) + \frac{A}{\alpha}(1 - e^{-\alpha t}) \\ ln(W) &= ln(W_o) + \frac{A}{\alpha} - \frac{A}{\alpha}e^{-\alpha t} \end{aligned} \qquad 3.2.3$$

Simplifying 3.2.1 by using natural logarithmic function will make it easier to apply implicit differentiation.

$$\frac{1}{W}(\frac{dW}{dt}) = Ae^{-\alpha t} \qquad 3.2.4$$

Multiplying both sides of 3.2.4 by W will give 3.2.5. This was done to isolate $\frac{dW}{dt}$ to the other side of the equation.

$$\frac{dW}{dt} = WAe^{-\alpha t} \tag{3.2.5}$$

The final step in deriving the Gompertz equation is by substituting 3.2.1 to 3.2.5. This will give the differential equation 3.2.6.

$$\frac{dW}{dt} = AW_o e^{\frac{A}{\alpha}(1-e^{-\alpha t})} e^{-\alpha t} \tag{3.2.6}$$

The FDE of 3.2.6 can be approximated, using the definition of derivative (2.1.1). Assuming T_o, also known as the discrete time interval, is small enough,then the derivative of W with respect to t can be approximated as shown below.

$$\frac{dW}{dt} \approx \frac{W(t+T_o) - W(t)}{T_o} \tag{3.2.7}$$

In the equation 3.2.7, t is discrete time, and T_o is discrete time interval. This means that t is equal to kT_o where k is a positive integer. Treating the approximation as an equality and substituting t= kT_o, we can change 3.2.7 to 3.2.8.

$$\frac{dW}{dt} = \frac{W(kT_o + T_o) - W(kT_o)}{T_o} \qquad 3.2.8$$

The equation above can be manipulated by multiplying T_o in both sides of 3.2.8. Thus, making it closer to the FDE form described by Ruanxiaogang.

$$T_o \frac{dW}{dt} = W(kT_o + T_o) - W(kT_o) \qquad 3.2.9$$

In line with the goal to convert 3.2.1 to an equivalent FDE, we can still rearrange the equation above to fully follow the FDE form. Thus by rearranging 3.2.9, the FDE form of W can be derived as shown in 3.2.10.

$$W(kT_o + T_o) = T_o \frac{dW}{dt} + W(kT_o) \qquad 3.2.10$$

However, the form above is still not simplified. The equation 3.2.6 can still be substituted to $\frac{dW}{dt}$. Thus the final form of the FDE that we will use to create the cellular automaton is shown by 3.2.11.

$$W((k+1)T_o) = AT_oW_oe^{\frac{A}{\alpha}(1-e^{-\alpha t})}e^{-\alpha t} + W(kT_o) \qquad 3.2.11$$

3.3 Transition of Gompertz FDE to Cellular Automaton

In the previous section, we have seen how the Gompertz differential equation was converted to an equivalent finite difference equation. In this section, we will see how the Gompertz FDE derived from 3.2 can be translated to a cellular automaton.

It should be noted that the function 3.2.11 models the future state of the tumor size using the present state of the tumor size. This observation is important because it shows that this function works similar to the transition function of a cellular automaton, since cellular automaton computes its next state depending on its current state. With this we can define an ideal increment in the tumor size using a Gompertz cellular automaton [5].

$$\Delta W_{CA} = \Delta W \tag{3.3.2}$$

Assuming that the change in the tumor size is with respect to time and the change in time is equal to T_o, then we can say that 3.3.2 is can be represented as the equation below.

$$\Delta W_{CA} = W(t + T_o) - W(t) \tag{3.3.3}$$

Thus, using the equation 3.2.11, we can define ΔW_{CA} as 3.3.4.

$$\Delta W_{CA} = AT_o W_o e^{\frac{A}{\alpha}(1-e^{-\alpha t})} e^{-\alpha t} \qquad 3.3.4$$

For one-dimensional cellular automaton, the maximum possible growth of the tumor at discrete time t at each discrete interval is represented by ΔW_{max}. In this equation (3.3.5) V_c is the volume of the Gompertz CA cell, and r_c is the radius of the Gompertz CA cell.

$$\Delta W_{max}(t) = 2 \times V_c = \frac{8\Pi}{3} {r_c}^3 \qquad 3.3.5$$

The equation 3.3.5 shows that the maximum tumor growth is equal to the maximum volume of the cells that will turn into a tumorous cell. In the case of one-dimensional cellular automaton, the maximum number of cells that can possibly be tumorous at every discrete time is two. This is because it can only affect its neighboring cells [5].

Each cell in the CA can either be a tumor cell or not a tumor cell. For simplicity, we let a cell representing a tumor cell to be one and zero otherwise. Since the CA for

the Gompertz Equation has an element of randomness, we use $p^i(t)$ to describe the stochastic property of cell i. $p^i(t)$ is defined as follows:

$$p^i(t) = \begin{cases} 0 & s_{i-1}(t) = 0 \text{ and } s_{i+1}(t) = 0 \\ 1 & s_{i-1}(t) = 1 \text{ and } s_{i+1}(t) = 1 \\ \frac{\Delta W_{CA}(t)}{\Delta W_{max}(t)} & otherwise \end{cases} \quad 3.3.6$$

where $s_i(t)$ is the state of cell i at a given discrete time t. We assume that the state of any cell in the CA to be irreversible meaning it can not go from one to zero but it can go zero to one. Using the above equations we can now construct a CA from the Gompertz model. We construct the CA as follows: first, we let the states be one and zero as explained above. Next, using a one-dimensional CA we identify each cell using i where $i \in \{-I_{max},...,-2,-1,0,1,-2,...,I_{max}\}$ where I_{max} is used to define the range of the one-dimensional CA. Then, we use a left and right cell neighborhood. We identify the left cell and right cell of cell i to be $i - 1$ and $i + 1$ respectively. As for the rules, we use

$$s_i(t + T_o) = \begin{cases} s_i(t) & p^{(i)}(t) \leq P_T \\ s_i(t) + 1 & otherwise \end{cases} \quad 3.3.7$$

where P_T is the probable threshold ranging from 0 to 1 and T_0 is the amount of time between each state transition. P_T is generated using a uniform probability density function. There will be cases where $p^{(i)}(t)$ is greater than 1 meaning the chosen cell will surely be converted to a tumor cell. To account for this excess in $p^{(i)}(t)$, the same

process will be applied to the adjacent cells of the chosen cell. To apply this CA model, we need to simply code using these conditions and follow these rules. The CA constructed using this method should yield similar results to the DE.

4. Results and Discussion

In this section, we will be discussing the difference between the tumor growth modelled by the Gompertz equation and the tumor growth simulated by the cellular automaton that we have created in the previous section. For the first two section, we will discuss in detail the results of the gompertz equation and cellular automata. Then, we discuss their difference and the stochastic behavior of the automaton. Throughout the simulation, radius will only affect the overall volume constantly and will not affect the behavioral change of volume per se. Although the cellular automata is finite, we used a significantly large amount of automata space for the tumor growth to simulate, ensuring that the volume will not exceed the cell space. A java program was used to simulate the differential equation and cellular automata and the data directly given by the program was used as the results. Only one cell was considered as the stem cell of the tumor, located in the middle of the cell space.

4.1 Modelling Walker W26B1 using Gompertz Equation

We recall from equation 2.2.1 that the Gompertz equation has two constants namely the A and the α. The constant α represents the retarding effect in growths of tumor. The retarding effect is the tendency of tumors to slow down its growth [21]. In equation 2.2.1,

it can be observed that the larger the α is the faster it is for the 2.2.1's value to stop growing exponentially. It can also be seen that when the retarding effect is zero ($\alpha = 0$), the growth modelled by the Gompertz equation will just always be exponential. The constant A represents the initial growth of the tumor. The sign of A determines whether the tumor is growing or regressing. These two constants has different values depending on the type of tumor growth it is modelling.

In the paper of Laird, she summarized the constants commonly used in some types of tumor and compared how close the Gompertz equation modelled the growth of these tumors. For this study, we will be modelling the tumor Walker W26B1, and follow the constants used by Laird in her study. Thus, the value of A that will be used is 0.220 and the value of α that will be used is 0.0218. It should also be noted that the cell volume is solved by fixing the cell radius as 1 unit.

$$\frac{W}{W_o} = e^{\frac{0.220}{0.0218}(1-e^{-(0.0218)t})} \qquad 4.1.1$$

The function above is the function that will be used to compute the predicted Walker W26B1 growth. Since we know that W_o is the initial tumor size, we can further reduce 4.1.2 to 4.1.2.

$$W = e^{\frac{0.220}{0.0218}(1-e^{-(0.0218)t})} \qquad 4.1.2$$

The transition from 4.1.1 to 4.1.2 is just done by setting the initial tumor size to 1. This just means that the initial volume of the cell is 1 unit, or can also be interpreted as only one cell is a tumor cell at the beginning.

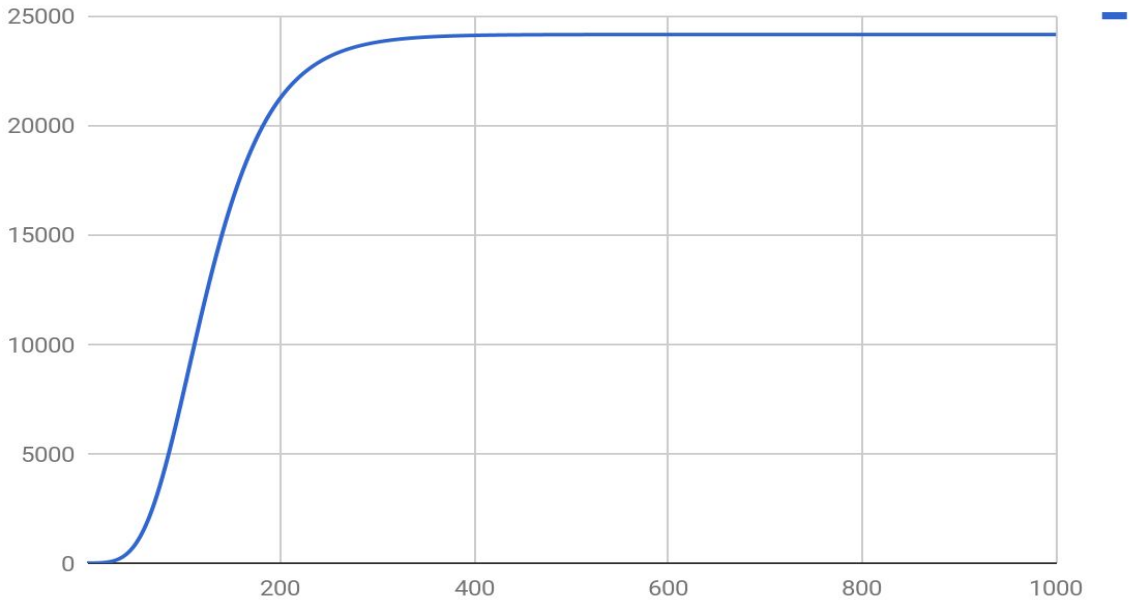

Figure 4.1.3: Tumor Growth as Modelled by 4.1.2

Figure 4.1.3 shows the theoretical tumor growth at each time step from the 1st hour to the 1000th hour when equation 4.1.2 was used (The actual values that are used to plot the graph is linked to the graph above. To access the spreadsheet, one can do so by clicking the figure above and opening the source.) The x-axis shows the

independent variable which is time and the y-axis shows the tumor size. It can be noticed that when the variable *t* (x-axis) was still small, the retarding effect of α was still negligible. This was shown by the part where the tumor size is still growing exponentially.

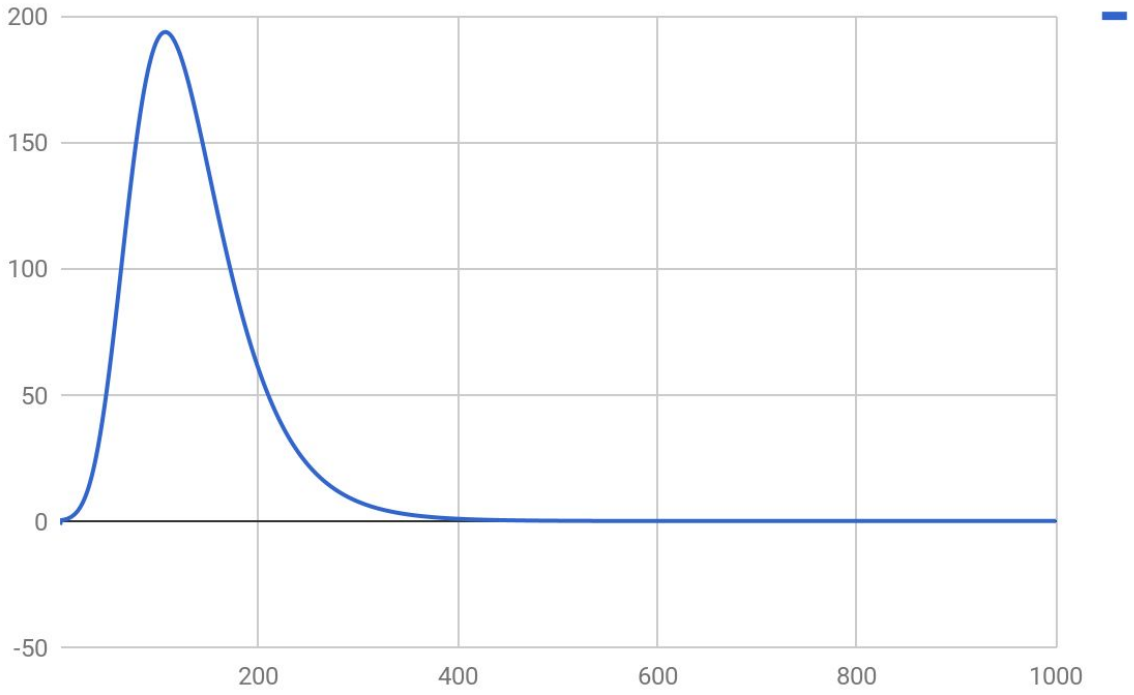

Figure 4.1.4: ΔW per time step

Figure 4.1.4 shows the change in tumor size per time step with respect to the previous hour. This means that every point in this graph shows the *W(n)-W(n-1)*. Using this graph, it can be seen the time step when the rate of change in tumor size started decreasing. Looking at the values per point, it was during the 104th hour when the rate of change decreased.

This shows that the Gompertz equation models the tumor size as exponential in growth for the first few time steps until the retardation constant finally takes effect, when the value of *t* is not that small.

4.2 Modelling Walker W26B1 using Cellular Automaton

The Cellular Automaton was implemented in Java following the methodology as described. The CA will be constructed based on a user input for the size and the user has control of which cell index will be planted with a tumor cell initially. The program prompts the user for the constants *A* and α as described in chapter 4.1. As for stochasticity, the package Random in Java was used to generate the random double numbers. The program was run up to 1000 time steps for five trials to show the stochastic properties of the CA and the output of the program was printed to a file and graphed as follows.

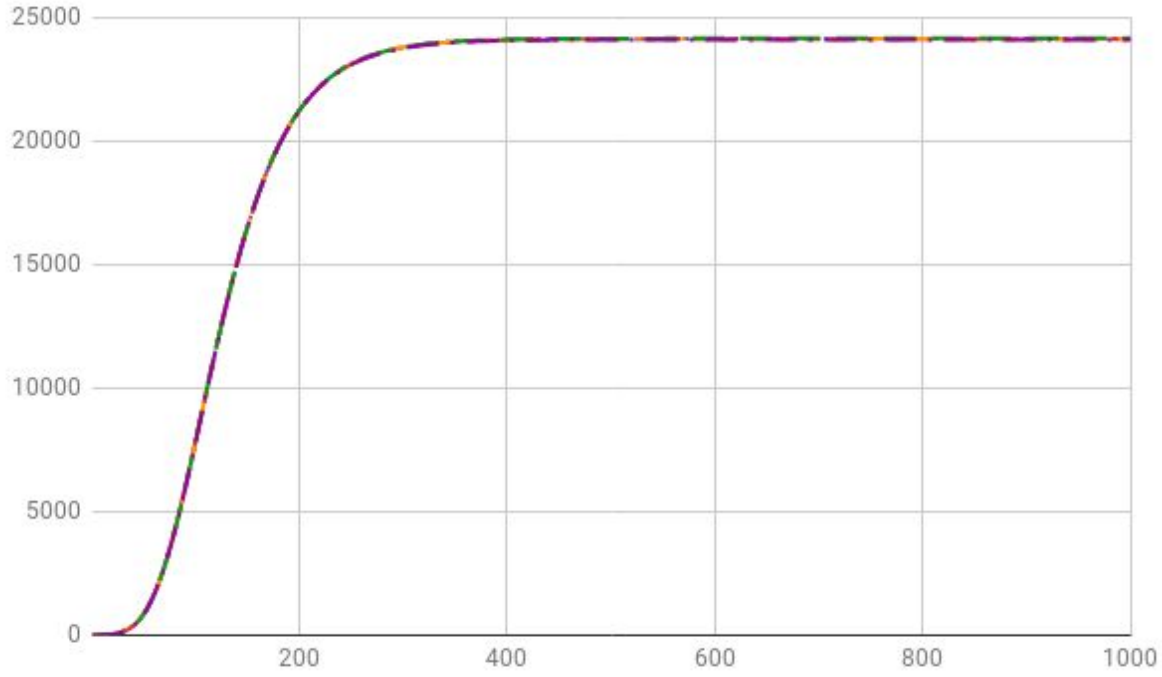

Figure 4.2.1: Tumor Growth as Modelled by Cellular Automaton 3.3.7

Note that Figure 4.2.1 was based on discrete time steps and the graph is only made for visual purposes despite it depicting continuous time variable. The x-axis shows the independent variable which is time and the y-axis shows the tumor size of each of the trial. There are five trials in the graph each represented by a different color and line dashing.

4.3 Comparing Gompertz Equation Results and Cellular Automaton Results

From the previous parts, we have already seen the values generated by the Cellular Automaton 3.3.7 and the values computed using the Gompertz equation 2.2.1 in

describing the Walker 26B1 tumor. Ideally, these values per time step should be close, if not the same since CA 3.3.7 is just derived from Gompertz equation 2.2.1.

Figure 4.3.1: Difference of Cellular Automaton Values and Gompertz Equation Values

However, as shown in the graph above, the difference in their values aren't close to the ideal setting.

In the 1st hour up until the 104th hour, the growth of their difference is exponential. This is because the retarding effect of the constant α is still negligible during the small values of *t*. As the simulation progresses, it can be observed that the difference is gradually getting lower and demonstrates an oscillating behavior. The behavior of the graph can be attributed to the probabilistic behavior of the cellular automaton. Unlike the Gompertz equation that always just gives a value that grows

smoothly with respect to time, cellular automaton may not grow in a given time step. It should also be noted that the growth of Gompertz equation can be half a cell volume while the growth of cellular automaton are multiples of cell volume. Thus, as shown in Figure 4.3.1, there is a part where the graph oscillates (104th hour to the 502nd hr).

From the 502nd hour to the 1000th hour, it can be noticed that the graph "stabilized" compared to the previous period. This is because the retardation effect has already taken its effect and the models has already reached the "maximum growth".

Test no.	Mean Absolute Difference
Test 1	18.51426937
Test 2	20.13813407
Test 3	20.79268662
Test 4	30.45496448
Test 5	24.20424447

Figure 4.3.2: Mean Absolute Error of each Test compared to Gompertz Equation

The Mean Absolute Error with respect to the Gompertz equation is computed for each stochastic test. The results of the computation is shown in Figure 4.3.2. We can see that for each test, it yields different results because of the stochastic behavior of the CA in comparison with the Gompertz equation which is deterministic. The results are

relatively low since we can see that there are only a few volume difference between the two tests relative to the size of the whole CA.

The two models have their own disadvantages and advantages. For the Gompertz model, the time is continuous so it is more accurate as compared to the discrete time steps of the CA. This is because it does not grow by multiples of cell volume but rather by fractions of the cell volume. The DE is also accurate in a sense that since it is deterministic, it will always give similar values and results given that the constants used are the same. However, this does not mean that the Gompertz model is better than the CA. Since CA is stochastic, it is fit for modeling real life tumor growth system because tumor growth is stochastic in nature since tumor growth is subject to irregular growth. In some cases, the observed tumor size is far from what the DEs can predict since it is deterministic [22]. The CA can also be considered dynamic because of its stochasticity and dependence on the cells and its interaction with its neighbors as well as other computing limitations. A reason as to why conversion of DE to cellular automaton is important.

Conclusion

In this research paper, a stochastic cellular automata was designed based on Gompertz equation for modeling tumor growth. Comparing these two models, the researchers conclude that Gompertz equation yielded consistent and higher precision of volume computation. Meanwhile, cellular automata yielded dynamic and higher performance of the probabilistic behavior of tumor growth. Considering their modelling power for the given phenomenon, the researchers do not state which model is better. However, this study proves that both models are able to simulate tumor volume growth but holds different advantages. Depending on the conditions and behavior needed, one of the two models are fit to be used than the other. Understanding how to fully utilize these two models may help in simulating more accurate real life systems and phenomena.

This research also concludes that a differential equation such as Gompertz equation can be designed into a cellular automaton to model real biological systems. The transition bridged a way for a continuous system be described into a finite system. Through the integration of concepts and models, our understanding to real life systems can be further improve.

We hope that this paper helped the readers understand the computing and modelling capabilities of cellular automata and differential equations. Hopefully, this

paper give the future researchers the idea of innovating and utilizing different models of scientific systems.

Appendix

Time	Value	Time	Value	Time	Value
1	1.243114	31	142.2486	61	1672.664
2	1.538097	32	158.9024	62	1771.779
3	1.89436	33	177.0826	63	1874.44
4	2.322684	34	196.8824	64	1980.641
5	2.835363	35	218.3963	65	2090.374
6	3.446351	36	241.7199	66	2203.623
7	4.171408	37	266.9496	67	2320.366
8	5.02826	38	294.1822	68	2440.575
9	6.03675	39	323.5145	69	2564.217
10	7.218995	40	355.0431	70	2691.254
11	8.599542	41	388.8637	71	2821.64
12	10.20552	42	425.0712	72	2955.327
13	12.06678	43	463.7588	73	3092.26
14	14.21604	44	505.018	74	3232.378
15	16.68902	45	548.938	75	3375.619
16	19.52456	46	595.6057	76	3521.912
17	22.76469	47	645.1048	77	3671.185
18	26.45481	48	697.5157	78	3823.361
19	30.64365	49	752.9154	79	3978.359
20	35.38341	50	811.3769	80	4136.095
21	40.72979	51	872.9688	81	4296.481
22	46.74194	52	937.7555	82	4459.426
23	53.48252	53	1005.796	83	4624.837
24	61.01764	54	1077.146	84	4792.618
25	69.41679	55	1151.853	85	4962.671
26	78.75278	56	1229.962	86	5134.895
27	89.1016	57	1311.511	87	5309.189
28	100.5423	58	1396.532	88	5485.449
29	113.1569	59	1485.052	89	5663.57
30	127.0299	60	1577.091	90	5843.448

Table 1: Gompertz Equation Values (t=1 to t=90)

Time	Value	Time	Value	Time	Value
91	6024.975	121	11731.08	151	16588.47
92	6208.044	122	11915.09	152	16723.25
93	6392.548	123	12097.93	153	16856.2
94	6578.38	124	12279.53	154	16987.29
95	6765.432	125	12459.86	155	17116.55
96	6953.598	126	12638.86	156	17243.97
97	7142.77	127	12816.5	157	17369.57
98	7332.843	128	12992.71	158	17493.33
99	7523.711	129	13167.47	159	17615.29
100	7715.272	130	13340.74	160	17735.44
101	7907.422	131	13512.48	161	17853.78
102	8100.059	132	13682.66	162	17970.35
103	8293.083	133	13851.23	163	18085.13
104	8486.397	134	14018.19	164	18198.15
105	8679.902	135	14183.49	165	18309.41
106	8873.505	136	14347.11	166	18418.94
107	9067.111	137	14509.03	167	18526.74
108	9260.631	138	14669.23	168	18632.82
109	9453.975	139	14827.69	169	18737.2
110	9647.055	140	14984.38	170	18839.9
111	9839.789	141	15139.3	171	18940.93
112	10032.09	142	15292.43	172	19040.3
113	10223.89	143	15443.76	173	19138.04
114	10415.09	144	15593.27	174	19234.15
115	10605.64	145	15740.96	175	19328.66
116	10795.44	146	15886.82	176	19421.58
117	10984.45	147	16030.84	177	19512.93
118	11172.58	148	16173.01	178	19602.72
119	11359.77	149	16313.35	179	19690.98
120	11545.96	150	16451.83	180	19777.72

Table 2: Gompertz Equation Values (t=91 to t=180)

Time	Value	Time	Value	Time	Value
181	19862.96	211	21813.46	241	22902.18
182	19946.71	212	21861.23	242	22928.25
183	20029	213	21908.08	243	22953.78
184	20109.85	214	21954.02	244	22978.8
185	20189.27	215	21999.06	245	23003.3
186	20267.28	216	22043.21	246	23027.29
187	20343.9	217	22086.51	247	23050.8
188	20419.14	218	22128.94	248	23073.82
189	20493.04	219	22170.55	249	23096.36
190	20565.6	220	22211.33	250	23118.44
191	20636.84	221	22251.3	251	23140.07
192	20706.78	222	22290.49	252	23161.24
193	20775.45	223	22328.89	253	23181.98
194	20842.86	224	22366.53	254	23202.3
195	20909.02	225	22403.42	255	23222.19
196	20973.96	226	22439.57	256	23241.66
197	21037.7	227	22475	257	23260.74
198	21100.25	228	22509.72	258	23279.41
199	21161.63	229	22543.75	259	23297.7
200	21221.86	230	22577.09	260	23315.61
201	21280.95	231	22609.76	261	23333.15
202	21338.93	232	22641.76	262	23350.32
203	21395.82	233	22673.13	263	23367.13
204	21451.62	234	22703.86	264	23383.59
205	21506.36	235	22733.96	265	23399.71
206	21560.06	236	22763.46	266	23415.49
207	21612.73	237	22792.36	267	23430.94
208	21664.39	238	22820.67	268	23446.07
209	21715.05	239	22848.4	269	23460.88
210	21764.73	240	22875.57	270	23475.38

Table 3: Gompertz Equation Values (t=181 to t=270)

Time	Value	Time	Value	Time	Value
271	23489.58	301	23800.93	331	23964.45
272	23503.48	302	23808.25	332	23968.29
273	23517.08	303	23815.42	333	23972.04
274	23530.41	304	23822.43	334	23975.71
275	23543.45	305	23829.3	335	23979.3
276	23556.21	306	23836.02	336	23982.81
277	23568.71	307	23842.59	337	23986.25
278	23580.95	308	23849.03	338	23989.62
279	23592.93	309	23855.32	339	23992.91
280	23604.65	310	23861.49	340	23996.14
281	23616.13	311	23867.52	341	23999.29
282	23627.36	312	23873.42	342	24002.38
283	23638.36	313	23879.2	343	24005.4
284	23649.13	314	23884.86	344	24008.35
285	23659.67	315	23890.39	345	24011.24
286	23669.99	316	23895.81	346	24014.07
287	23680.08	317	23901.11	347	24016.84
288	23689.97	318	23906.29	348	24019.55
289	23699.64	319	23911.37	349	24022.21
290	23709.11	320	23916.34	350	24024.8
291	23718.38	321	23921.2	351	24027.34
292	23727.46	322	23925.96	352	24029.83
293	23736.34	323	23930.61	353	24032.26
294	23745.03	324	23935.17	354	24034.64
295	23753.54	325	23939.63	355	24036.96
296	23761.87	326	23943.99	356	24039.24
297	23770.02	327	23948.26	357	24041.47
298	23778	328	23952.44	358	24043.65
299	23785.81	329	23956.53	359	24045.79
300	23793.45	330	23960.54	360	24047.88

Table 4: Gompertz Equation Values (t=271 to t=360)

Time	Value	Time	Value	Time	Value
361	24049.92	391	24094.48	421	24117.68
362	24051.92	392	24095.52	422	24118.22
363	24053.88	393	24096.54	423	24118.76
364	24055.79	394	24097.54	424	24119.27
365	24057.67	395	24098.51	425	24119.78
366	24059.5	396	24099.47	426	24120.28
367	24061.29	397	24100.4	427	24120.77
368	24063.05	398	24101.32	428	24121.24
369	24064.77	399	24102.21	429	24121.71
370	24066.45	400	24103.09	430	24122.16
371	24068.09	401	24103.95	431	24122.61
372	24069.7	402	24104.78	432	24123.04
373	24071.28	403	24105.6	433	24123.47
374	24072.82	404	24106.41	434	24123.89
375	24074.33	405	24107.19	435	24124.3
376	24075.8	406	24107.96	436	24124.7
377	24077.24	407	24108.71	437	24125.09
378	24078.66	408	24109.45	438	24125.47
379	24080.04	409	24110.17	439	24125.84
380	24081.39	410	24110.87	440	24126.21
381	24082.72	411	24111.56	441	24126.57
382	24084.01	412	24112.23	442	24126.92
383	24085.28	413	24112.89	443	24127.26
384	24086.52	414	24113.54	444	24127.6
385	24087.73	415	24114.17	445	24127.93
386	24088.92	416	24114.79	446	24128.25
387	24090.08	417	24115.39	447	24128.56
388	24091.22	418	24115.98	448	24128.87
389	24092.33	419	24116.56	449	24129.17
390	24093.42	420	24117.13	450	24129.47

Table 5: Gompertz Equation Values (t=361 to t=450)

Time	Value	Time	Value	Time	Value
451	24129.76	481	24136.04	511	24139.3
452	24130.04	482	24136.18	512	24139.38
453	24130.31	483	24136.33	513	24139.45
454	24130.58	484	24136.47	514	24139.53
455	24130.85	485	24136.6	515	24139.6
456	24131.11	486	24136.74	516	24139.67
457	24131.36	487	24136.87	517	24139.74
458	24131.61	488	24137	518	24139.8
459	24131.85	489	24137.12	519	24139.87
460	24132.09	490	24137.25	520	24139.93
461	24132.32	491	24137.37	521	24139.99
462	24132.54	492	24137.49	522	24140.06
463	24132.77	493	24137.6	523	24140.12
464	24132.98	494	24137.71	524	24140.17
465	24133.2	495	24137.83	525	24140.23
466	24133.4	496	24137.93	526	24140.29
467	24133.61	497	24138.04	527	24140.34
468	24133.81	498	24138.14	528	24140.4
469	24134	499	24138.24	529	24140.45
470	24134.19	500	24138.34	530	24140.5
471	24134.38	501	24138.44	531	24140.55
472	24134.56	502	24138.53	532	24140.6
473	24134.74	503	24138.63	533	24140.65
474	24134.91	504	24138.72	534	24140.7
475	24135.08	505	24138.81	535	24140.74
476	24135.25	506	24138.89	536	24140.79
477	24135.42	507	24138.98	537	24140.83
478	24135.58	508	24139.06	538	24140.88
479	24135.73	509	24139.14	539	24140.92
480	24135.89	510	24139.22	540	24140.96

Table 6: Gompertz Equation Values (t=451 to t=540)

Time	Value	Time	Value	Time	Value
541	24141	571	24141.88	601	24142.34
542	24141.04	572	24141.9	602	24142.35
543	24141.08	573	24141.92	603	24142.36
544	24141.12	574	24141.94	604	24142.37
545	24141.15	575	24141.96	605	24142.38
546	24141.19	576	24141.98	606	24142.39
547	24141.23	577	24142	607	24142.4
548	24141.26	578	24142.02	608	24142.41
549	24141.29	579	24142.04	609	24142.42
550	24141.33	580	24142.05	610	24142.43
551	24141.36	581	24142.07	611	24142.44
552	24141.39	582	24142.09	612	24142.45
553	24141.42	583	24142.1	613	24142.46
554	24141.45	584	24142.12	614	24142.46
555	24141.48	585	24142.13	615	24142.47
556	24141.51	586	24142.15	616	24142.48
557	24141.54	587	24142.16	617	24142.49
558	24141.57	588	24142.18	618	24142.5
559	24141.6	589	24142.19	619	24142.5
560	24141.62	590	24142.21	620	24142.51
561	24141.65	591	24142.22	621	24142.52
562	24141.68	592	24142.23	622	24142.52
563	24141.7	593	24142.25	623	24142.53
564	24141.73	594	24142.26	624	24142.54
565	24141.75	595	24142.27	625	24142.54
566	24141.77	596	24142.28	626	24142.55
567	24141.8	597	24142.3	627	24142.56
568	24141.82	598	24142.31	628	24142.56
569	24141.84	599	24142.32	629	24142.57
570	24141.86	600	24142.33	630	24142.58

Table 7: Gompertz Equation Value (t=541 to t=630)

Time	Value	Time	Value	Time	Value
631	24142.58	661	24142.71	691	24142.77
632	24142.59	662	24142.71	692	24142.77
633	24142.59	663	24142.71	693	24142.77
634	24142.6	664	24142.71	694	24142.77
635	24142.6	665	24142.72	695	24142.78
636	24142.61	666	24142.72	696	24142.78
637	24142.61	667	24142.72	697	24142.78
638	24142.62	668	24142.72	698	24142.78
639	24142.62	669	24142.73	699	24142.78
640	24142.63	670	24142.73	700	24142.78
641	24142.63	671	24142.73	701	24142.78
642	24142.64	672	24142.73	702	24142.78
643	24142.64	673	24142.74	703	24142.79
644	24142.64	674	24142.74	704	24142.79
645	24142.65	675	24142.74	705	24142.79
646	24142.65	676	24142.74	706	24142.79
647	24142.66	677	24142.74	707	24142.79
648	24142.66	678	24142.75	708	24142.79
649	24142.66	679	24142.75	709	24142.79
650	24142.67	680	24142.75	710	24142.79
651	24142.67	681	24142.75	711	24142.79
652	24142.68	682	24142.75	712	24142.8
653	24142.68	683	24142.76	713	24142.8
654	24142.68	684	24142.76	714	24142.8
655	24142.69	685	24142.76	715	24142.8
656	24142.69	686	24142.76	716	24142.8
657	24142.69	687	24142.76	717	24142.8
658	24142.7	688	24142.76	718	24142.8
659	24142.7	689	24142.77	719	24142.8
660	24142.7	690	24142.77	720	24142.8

Table 8: Gompertz Equation Values (t=631 to t=720)

Time	Value	Time	Value	Time	Value
721	24142.8	751	24142.82	781	24142.83
722	24142.8	752	24142.82	782	24142.83
723	24142.8	753	24142.82	783	24142.83
724	24142.81	754	24142.82	784	24142.83
725	24142.81	755	24142.82	785	24142.83
726	24142.81	756	24142.82	786	24142.83
727	24142.81	757	24142.82	787	24142.83
728	24142.81	758	24142.82	788	24142.83
729	24142.81	759	24142.82	789	24142.83
730	24142.81	760	24142.82	790	24142.83
731	24142.81	761	24142.82	791	24142.83
732	24142.81	762	24142.82	792	24142.83
733	24142.81	763	24142.83	793	24142.83
734	24142.81	764	24142.83	794	24142.83
735	24142.81	765	24142.83	795	24142.83
736	24142.81	766	24142.83	796	24142.83
737	24142.81	767	24142.83	797	24142.83
738	24142.81	768	24142.83	798	24142.83
739	24142.82	769	24142.83	799	24142.83
740	24142.82	770	24142.83	800	24142.83
741	24142.82	771	24142.83	801	24142.83
742	24142.82	772	24142.83	802	24142.83
743	24142.82	773	24142.83	803	24142.83
744	24142.82	774	24142.83	804	24142.83
745	24142.82	775	24142.83	805	24142.83
746	24142.82	776	24142.83	806	24142.83
747	24142.82	777	24142.83	807	24142.83
748	24142.82	778	24142.83	808	24142.83
749	24142.82	779	24142.83	809	24142.83
750	24142.82	780	24142.83	810	24142.83

Table 9: Gompertz Equation Values (t=721 to t=810)

Time	Value	Time	Value	Time	Value
811	24142.83	841	24142.84	871	24142.84
812	24142.83	842	24142.84	872	24142.84
813	24142.83	843	24142.84	873	24142.84
814	24142.83	844	24142.84	874	24142.84
815	24142.83	845	24142.84	875	24142.84
816	24142.84	846	24142.84	876	24142.84
817	24142.84	847	24142.84	877	24142.84
818	24142.84	848	24142.84	878	24142.84
819	24142.84	849	24142.84	879	24142.84
820	24142.84	850	24142.84	880	24142.84
821	24142.84	851	24142.84	881	24142.84
822	24142.84	852	24142.84	882	24142.84
823	24142.84	853	24142.84	883	24142.84
824	24142.84	854	24142.84	884	24142.84
825	24142.84	855	24142.84	885	24142.84
826	24142.84	856	24142.84	886	24142.84
827	24142.84	857	24142.84	887	24142.84
828	24142.84	858	24142.84	888	24142.84
829	24142.84	859	24142.84	889	24142.84
830	24142.84	860	24142.84	890	24142.84
831	24142.84	861	24142.84	891	24142.84
832	24142.84	862	24142.84	892	24142.84
833	24142.84	863	24142.84	893	24142.84
834	24142.84	864	24142.84	894	24142.84
835	24142.84	865	24142.84	895	24142.84
836	24142.84	866	24142.84	896	24142.84
837	24142.84	867	24142.84	897	24142.84
838	24142.84	868	24142.84	898	24142.84
839	24142.84	869	24142.84	899	24142.84
840	24142.84	870	24142.84	900	24142.84

Table 10: Gompertz Equation Values (t=811 to t=900)

Time	Value	Time	Value	Time	Value
901	24142.84	931	24142.84	961	24142.84
902	24142.84	932	24142.84	962	24142.84
903	24142.84	933	24142.84	963	24142.84
904	24142.84	934	24142.84	964	24142.84
905	24142.84	935	24142.84	965	24142.84
906	24142.84	936	24142.84	966	24142.84
907	24142.84	937	24142.84	967	24142.84
908	24142.84	938	24142.84	968	24142.84
909	24142.84	939	24142.84	969	24142.84
910	24142.84	940	24142.84	970	24142.84
911	24142.84	941	24142.84	971	24142.84
912	24142.84	942	24142.84	972	24142.84
913	24142.84	943	24142.84	973	24142.84
914	24142.84	944	24142.84	974	24142.84
915	24142.84	945	24142.84	975	24142.84
916	24142.84	946	24142.84	976	24142.84
917	24142.84	947	24142.84	977	24142.84
918	24142.84	948	24142.84	978	24142.84
919	24142.84	949	24142.84	979	24142.84
920	24142.84	950	24142.84	980	24142.84
921	24142.84	951	24142.84	981	24142.84
922	24142.84	952	24142.84	982	24142.84
923	24142.84	953	24142.84	983	24142.84
924	24142.84	954	24142.84	984	24142.84
925	24142.84	955	24142.84	985	24142.84
926	24142.84	956	24142.84	986	24142.84
927	24142.84	957	24142.84	987	24142.84
928	24142.84	958	24142.84	988	24142.84
929	24142.84	959	24142.84	989	24142.84
930	24142.84	960	24142.84	990	24142.84

Table 11: Gompertz Equation Values (t=901 to t=990)

Time	Value	Time	Value	Time	Value
991	24142.84	995	24142.84	999	24142.84
992	24142.84	996	24142.84	1000	24142.84
993	24142.84	997	24142.84		
994	24142.84	998	24142.84		

Table 11: Gompertz Equation Values (t=901 to t=1000)

Cellular Automaton Code (Java):

```
import java.util.*;
import java.lang.Math.*;
public class CA{
    public static void main(String[] args){
    Random r = new Random();
    Scanner s = new Scanner(System.in);
    System.out.print("Enter number of cells: ");
    int number_of_cells = s.nextInt();
    int count = 0;
    double p_t = 0;
    int[] ca = new int[number_of_cells];
    for(int i = 0;i < number_of_cells;i++){
        ca[i] = 0;
    }
    System.out.println("CA setup complete!");
    System.out.print("Enter which cells are initially tumor cells
    [0, "+ (number_of_cells - 1) +"] (comma separated): ");
    s.nextLine();
    String input_string = s.nextLine();
    String[] inputs = input_string.split(",");
    System.out.print("Time t at : ");
    String input_time = s.nextLine();

    for(int i = 0;i < inputs.length;i++){
        ca[Integer.parseInt(inputs[i])] = 1;
    }
    int time = Integer.parseInt(input_time);
    System.out.print("A = ");
    input_string = s.nextLine();
    double A = Double.parseDouble(input_string);
    System.out.print("alpha = ");
    input_string = s.nextLine();
    double alpha = Double.parseDouble(input_string);
    System.out.print("radius = ");
    input_string = s.nextLine();
    double radius = Double.parseDouble(input_string);
    double cellVolume = Math.pow(radius,3);
    System.out.println(time);
    for(int j = 1; j <= time; j++){
        int[] ca_next = new int[number_of_cells];
        for(int i = 0;i < number_of_cells;i++){
        ca_next[i] = ca[i];
        }
        System.out.println();
        for(int i = 0;i < number_of_cells;i++){
        if(ca[i] == 1){
```

```
            ca_next[i] = 1;
        }
        else if(ca[Math.floorMod(i + 1,number_of_cells)] ==
        ca[Math.floorMod(i-1, number_of_cells)]){
            ca_next[i] = ca[Math.floorMod(i + 1,number_of_cells)];
        }
        else{
            double w_ca_t = A*(cellVolume)*(Math.exp((A/alpha)*
            (1-Math.exp(-alpha*j)))*Math.exp((-alpha*j)));
            p_t = w_ca_t / (cellVolume*2);
            while (p_t >= 1.0){
            ca_next[i] = 1;
            ca[i] = 1;
            p_t = p_t - 1.0;
            if( i == number_of_cells-1 || i == 0){
                break;
            }
            else{
                if(ca[i+1] == 1){
                i = i-1;
                }
                else if (ca[i-1] == 1){
                i = i+1;
                }
            }
            }
            if(r.nextDouble()<p_t){
            ca_next[i] = 1;
            }
        }
        }
        ca = ca_next;
        ca_next = null;
    }

    for(int i = 0 ; i < number_of_cells ; i++){
        if(ca[i] == 1){
        count = count + 1;
        }
    }
    System.out.println();
    System.out.println("Cellular Automata result : " + cellVolume*count);
    System.out.println("Gompertz Equation result : " + cellVolume*
    Math.exp((A/alpha)*(1-Math.exp(-alpha*time))));
    }
}
```

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