A Cellular Automaton to Model Logistic Growth of Tumors

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Introduction

A Cellular Automaton (CA) is a mathematical model that explores how complex behaviors emerge from simple rules. They can be used to visualize tumor growth with each cell of the CA corresponding to a biological cell. **The model proposed in this project is based on deterministic neighborhood rules of at least 1 neighbor being cancerous and stochastic processes of a random number generated being less than the growth, mutation, and apoptosis probability, respectively.**

Methods

A 2D cross-section of the tumor growth is modeled with isotropic assumption. [1].The modeled tissue size is 0.025 mm^2 (each cell is 10 μm. [2]. The initial tumor is 1 % of the total tissue size, and configured as a random-walk ni the center.

Initial Conditions:

Tissue size: 50 x 50 cells

Tumor size: 25 cells

Neighborhood: Von-Neumann neighborhood

Boundary conditions: NA

Growth probability: $GP = r \cdot \rho \cdot \left(1 - \frac{\rho}{k}\right)$ [4]

Simulation Steps: 1000 steps

Simulations: 50

Carrying capacity density, k: 0.5

Growth rate, r: 0.5

Mutation rate, mp = 0

Apoptosis rate, ap = 0

A Von-Neumann neighborhood was chosen because all neighbors are equidistant to the center cell[1]. Boundary conditions were not considered as carrying capacity < tissue size.

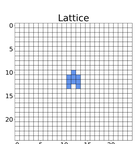


Figure 1. Example initial configuration where blue cells indicate cancer.

Figure 2. Von Neumann neighborhood: Yellow: $C(i,j)$, Blue: Neighbors.

Rules

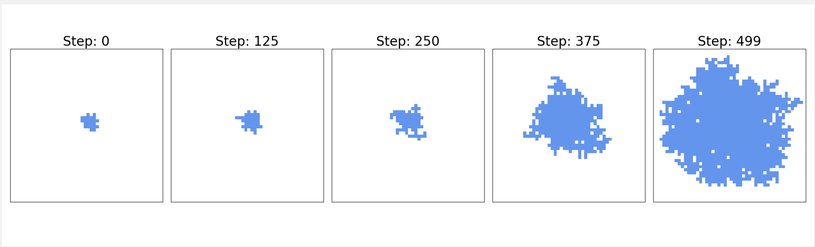
$$C(i,j) = \begin{cases} 1 & \text{if Cancer} \in \text{Neighbors} \\ & \wedge\ \text{RN} < \text{GP}, \\ C(i,j) & \text{otherwise.} \end{cases}$$

$$C(i,j) = \begin{cases} 1 & \text{if RN} < \text{MP}, \\ C(i,j) & \text{otherwise.} \end{cases}$$

$$C(i,j) = \begin{cases} 0 & \text{if RN} < \text{AP}, \\ C(i,j) & \text{otherwise.} \end{cases}$$

Legend: 1 = Cancer, 0 = Normal, RN = Random Number, GP = Growth Probability, MP = Mutation Probability, AP = Apoptosis Probability.

Results



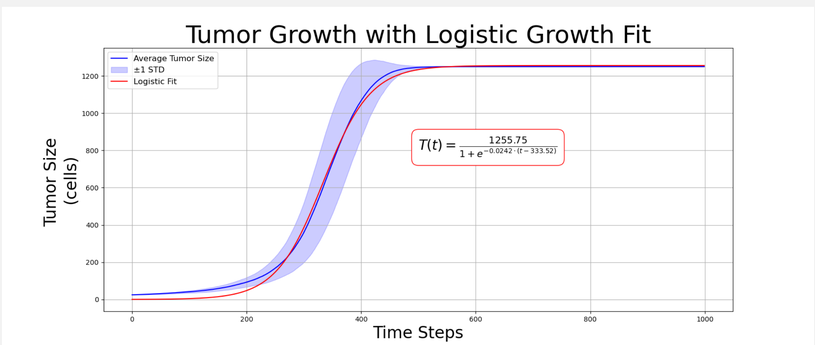


Figure 4. Average tumor growth vs. step across 50 simulations fit to a logistic-growth theoretical model. Mean Absolute Error (MAE) = 16.70 cells, Root Mean Squared Error = 21.90 cells

Discussion

The visual agreement of the theoretical model with the CA across 50 simulations shows that **the discrete CA aligns with the theoretical model.** Quantitatively, this is shown by the MAE of 16.70 cells (1.33% of the resulting tumor size), and the RMSE of 21.90 (1.74% of the resulting tumor size). Although there is agreement between the model and the CA, there is variation between each simulation as shown by the standard deviation plotted.

Further investigations could analyze the effect of the initial configuration in terms of lattice size, initial tumor size, and initial tumor configuration on the tumor growth. **Further investigations can also build upon the MP and AP to model treatment plans that increase the chance of apoptosis, and personalized tumor biology that affects the chance of mutation.**

References

[1] Ruben Interian, Reinaldo Rodríguez-Ramos, Fernando Valdés-Ravelo, Ariel Ramírez-Torres, Celso C. Ribeiro, and Aura Conci. Tumor growth modelling by cellular automata. *Mathematics and Mechanics of Complex Systems*, 5(3-4):239–253, 2017. doi: 10.2140/memocs.2017.5.239. URL `https://dx.doi.org/10.2140/memocs.2017.5.239`.

[2] Carlos A. Valentim, José A. Rabi, and Sergio A. David. Cellular-automaton model for tumor growth dynamics: Virtualization of different scenarios. *Computers in Biology and Medicine*, 153:106481, 2023. ISSN 0010-4825. doi: 10.1016/j.compbiomed.2022.106481. URL `https://doi.org/10.1016/j.compbiomed.2022.106481`.

[3] H. Weedon-Fekjaer, B. H. Lindqvist, L. J. Vatten, O. O. Aalen, and S. Tretli. Breast cancer tumor growth estimated through mammography screening data. *Breast Cancer Research*, 10(3):R41, 2008. doi: 10.1186/bcr2092. URL `https://doi.org/10.1186/bcr2092`. Epub 2008 May 8.

[4] A. Yin, D. J. A. R. Moes, J. G. C. van Hasselt, J. J. Swen, and H. J. Guchelaar. A review of mathematical models for tumor dynamics and treatment resistance evolution of solid tumors. *CPT Pharmacometrics Syst Pharmacol*, 8(10):720–737, 2019. doi: 10.1002/psp4.12450. URL `https://doi.org/10.1002/psp4.12450`. Epub 2019 Aug 9.

This QR code will bring you to my GitHub repository where there is a Quick and Full Simulation. The parameters of both can be adjusted at the top.