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Cellular-automaton simulation of tumor growth dynamics: from computational implementation to case analysis

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Mathematical oncology explores the development and application of models to cancer-related phenomena [5]. As an important advantage, mathematical models can test and reproduce several scenarios, which could be either unfeasible or impossible through in vitro experiments. Among different approaches, cell-based or discrete models are organized frameworks that keep track of fully independent individual parameters depending on time and/or space, as an attempt to mathematically model the heterogeneity and complex phenomena found in cancer. Computationally, they can rely on different approaches including (but not restricted to) Monte-Carlo simulations, energy minimization techniques, volume conservation laws and motion rules [3]. Virtualization (i.e. numerical simulation) involving cell-based models is often referred to as in-silico modeling because of their similarity and logical extension of in vitro experimentation [2]. Concerning cellular-automata (CA) models, relatively simple implementations can go a long way in providing emergent complex behavior [1, 4].

The model herein proposed is a stochastic framework in which a single cell originates a tumor exhibiting different characteristics depending on model configurations and its parameters. Every cell will obligatorily present one of the following exclusive behaviors: apoptosis, proliferation, migration, or quiescence. These behaviors have a predefined probability (which may itself vary with time) and they are checked in the aforesaid order. Healthy cells are considered absent spaces.

The model also comprises a heterogeneous population of tumor cells, in which each cell can either be a regular tumor cell (RTC) or a stem tumor cell (STC). While RTC cells (nonclonogenic cells) compose the bulk of a tumor and are limited, STCs lack internal regulatory mechanisms regarding cell death, thus being immortal. They can be categorized as clonogenic (can only give birth to regular, i.e. mortal cells) or true stem cells (may also generate an identical true stem cell). Differences regarding aforementioned cells are depicted in Figure 1, in which STCs are represented in yellow whereas RTCs are depicted in shades of red.

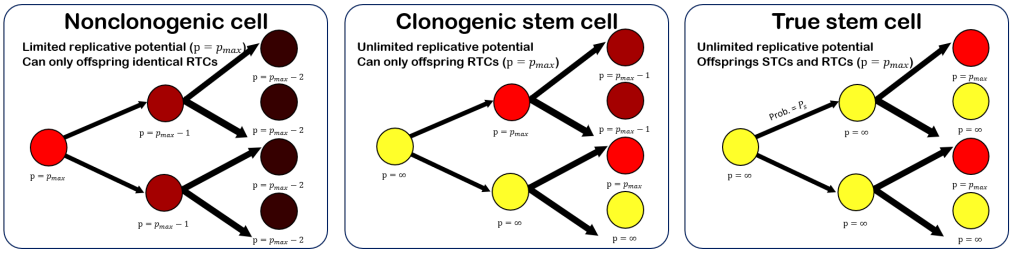

Figure 1: Populations considered in the model: Nonclonogenic, clonogenic and true stem cells.

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In this work, we implemented some high-performance techniques suggested by [4], as for instance coded-lattice and dynamically growing domains. The model was coded in Python due its versatility and accessible learning curve. By varying the progenitor cell type and each movement probability, the stochastic cellular automaton is able to simulate different scenarios such as tumor absence, benignity (stability), invasion (instability), and migrating tumors (clustering).

Figure 2 depicts preliminary results related to the dynamics of two different tumors. The first, originated from a nonclonogenic cell, relates to some types of benign tumors, which can live in patients for up to decades and never reach a dangerous size or malignancy. The other originates from a true STC cell and is larger and unstable, such as an invasive tumor. Indeed, the proposed approach arises as an interesting in silico modeling tool whose capabilities will be fully explored in future studies.

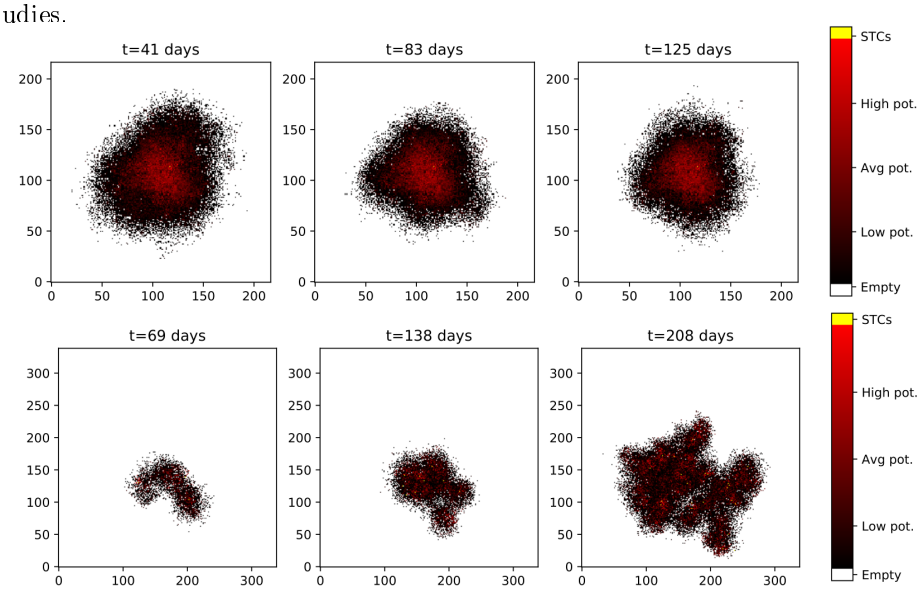

Figure 2: Virtualization of a benign tumor (above) and an invasive tumor (bellow)

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