

Designing Treatment Protocols via Tumor Growth Simulations

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EXTENDED ABSTRACT

Cellular adaptation to changing environments is intricately coordinated through many molecular and mechanical responses. As cells evolve, abnormal growth patterns occur (that cannot be controlled by normal mechanisms) leading to cancer. With mathematical modeling we can integrate different characteristics of tumor growth for a non-experimental study of cancer. Through integration of some of the prior clinical, experimental, and mathematical studies, we utilize a cellular automata model to take into account multiple factors affecting tumor growth in healthy tissue. This in silico simulation model of tumor growth is based upon molecular and life cycle features that affect the growth rates of cancer. The life cycle parameters used in this model include replication rate, nutrient and oxygen concentrations, and possible drug effects in a 3-D simulation. The in silico model is used to study the effects of drugs upon the growth and development of the tumor and optimize a drug treatment protocol under various conditions.

Discussion

At this stage in the project, we are able to model tumor growth on a 3-D grid and simulate the different effects that a drug can have on tumor growth by changing the ages and probabilities of death and division. This is crucial to ensure that the simulation parameters can regulate the growth of tumor. By varying not only the growth but also the life of each cell, we can compare and contrast different parameters and study the impacts prototype drugs may have in detail. We have seen (qualitatively) that the four major parameters (age of death, death probability, age of division, division probability) can have a significant regulatory effect upon the growth and development of a tumor when modeling different stages of tumor growth by varying the Gompertzian parameter, α .