Modeling Cell Cycle Dynamics in Cell Cultures: Implications for Cancer Therapy in Well Mixed and Spatial Structured Models

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The cell cycle is a series of precisely regulated events crucial for cell growth and division. This complexity poses challenges in mathematical modeling and simulation of cell cultures. Particularly, employing an exponentially distributed cell cycle length may lead to erroneous interpretations, as highlighted by Yates et al. [4], "the most probable time for a cell to divide is the current time". Further, Vittadello et al. [3] have shown that synchronization among individual cells can spontaneously emerge in a cell culture due to the cell cycle, even in the absence of direct intercellular coupling.

In this presentation, we introduce a novel stochastic simulation algorithm designed to model cell populations with realistic cell cycle lengths in well-mixed environments. We particularly explore its applications in cancer therapy scenarios. Based on our lattice based stochastic cell population simulation method [1], we then expand this method to simulate spatially heterogeneous populations. This extension reveals challenges linked to the finite carrying capacity of environments. To address these, we propose four model assumptions that facilitate overcoming these challenges. Finally, we characterize the parameter space, identifying regions where synchronization is evident in spatial models. We conclude by demonstrating the robustness of synchronization effects across different model assumptions. The presentation is partly based on the phd thesis of the author [2].

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