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A Parallel Cellular Automaton Model of Tumor Growth for Multicore and GPU Programming

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Abstract : Tumor growth from a transformed cancer-cell up to a clinically apparent mass spans through a range of spatial and temporal magnitudes. Through computer simulations, Cellular Automata (CA) can accurately describe the complexity of the development of tumors. Tumor development prognosis can now be made -without making patients undergo through annoying medical examinations or painful invasive procedures- if we develop appropriate CA-based software tools. In silico testing mainly refers to Computational Biology research studies of application to clinical actions in Medicine. To establish sound computer-based models of cellular behavior, certainly reduces costs and saves precious time with respect to carrying out experiments in vitro at labs or in vivo with living cells and organisms. These aim to produce scientifically relevant results compared to traditional in vitro testing, which is slow, expensive, and does not generally have acceptable reproducibility under the same conditions. For speeding up computer simulations of cellular models, specific literature shows recent proposals based on the CA approach that include advanced techniques, such the clever use of supporting efficient data structures when modeling with deterministic stochastic cellular automata. Multiparadigm and multiscale simulation of tumor dynamics is just beginning to be developed by the concerned research community. The use of stochastic cellular automata (SCA), whose parallel programming implementations are open to yield a high computational performance, are of much interest to be explored up to their computational limits. There have been some approaches based on optimizations to advance in multiparadigm models of tumor growth, which mainly pursuit to improve performance of these models through efficient memory accesses guarantee, or considering the dynamic evolution of the memory space (grids, trees,...) that holds crucial data in simulations. In our opinion, the different optimizations mentioned above are not decisive enough to achieve the high performance computing power that cell-behavior simulation programs actually need. The possibility of using multicore and GPU parallelism as a promising multiplatform and framework to develop new programming techniques to speed-up the computation time of simulations is just starting to be explored in the few last years. This paper presents a model that incorporates parallel processing, identifying the synchronization necessary for speeding up tumor growth simulations implemented in Java and C++ programming environments. The speed up improvement that specific parallel syntactic constructs, such as executors (thread pools) in Java, are studied. The new tumor growth parallel model is proved using implementations with Java and C++ languages on two different platforms: chipset Intel core i-X and a HPC cluster of processors at our university. The parallelization of Polesczuk and Enderling model (normally used by researchers in mathematical oncology) proposed here is analyzed with respect to performance gain. We intend to apply the model and overall parallelization technique presented here to solid tumors of specific affiliation such as prostate, breast, or colon. Our final objective is to set up a multiparadigm model capable of modelling angiogenesis, or the growth inhibition induced by chemotaxis, as well as the effect of therapies based on the presence of cytotoxic/cytostatic drugs.

Keywords : cellular automaton, tumor growth model, simulation, multicore and manycore programming, parallel programming, high performance computing, speed up
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