Chapter 19
Integration of a Visualization Solution with a 3-D Simulation Model for Tissue Growth

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ABSTRACT

Visualizing time-varying phenomena is paramount to ensure correct interpretation and analysis, provoke insights, and communicate those insights to others. In particular, visualization allows us the freedom to explore the spatial and temporal domains of such phenomena. The task of visualizing tissue growth is challenging due to the amount of data that needs to be visualized and the large simulation parameter space. Further, many problems and their solution strategies tend to be extremely heterogeneous: in their models, codes, and applications. Such solutions must be designed to manage this heterogeneity in an integrated way, so that the user is presented with a predictable and consistent computing environment. In this book chapter, the author presents an application of visualization to a three-dimensional simulation model for tissue growth. The chapter reports on the different components of the model where cellular automata is used to model populations of cells that execute persistent random walks on the computational grid, collide, and proliferate until they reach confluence. It discusses the main issues regarding the parallelization of the model and its implementation on a parallel machine. The author then elaborates on the integration of visualization with the said simulation model. This includes presenting the system architecture of the developed visualization solution and the employed rendering techniques. Finally, the chapter demonstrates some of the preliminary performance results and discusses the encountered challenges in this undertaking.

INTRODUCTION

Tissue growth is a complex process affected by many factors including cell activities like adhesion or migration, scaffold properties, and external stimuli that modulate cellular functions. For these reasons the development of bioartificial tissue substitutes involves *extensive* and *time-consuming* experimentation. The complexity of biological behavior is the result of dynamic interactions occurring not only among the various components of a cell, but also among the populations of cells that form human tissues. As such, systems-based approaches must be used to study biocomplexity at the cell population and tissue levels. These approaches must consider cells as system components that migrate, proliferate and interact to generate the complex behavior observed in living systems (Marée & Hogeweg, 2001; Lysaght & Hazlehurst, 2004).

Computational models can provide powerful frameworks for studying biocomplexity at the cell population and tissue level (Levin et al., 1997; Law, 2007). The simulation of biological systems, however, differs in significant ways from traditional computer-science problems. Models of biological systems must be based on a thorough understanding of the fundamental mechanisms governing the behavior of the cellular components of such systems. In addition, such models must accurately describe the dynamic interactions among the multitude of cells forming most biological systems of practical interest. Therefore, employing systems-based approaches could lead to models with high complexity whose solution poses significant computational challenges (Lauffenburger & Linderman, 1993; Lee et al., 1995; Soll & Wessels, 1998). The availability of computational models with *predictive* abilities could greatly speed up progress in this area. Such models will assist us in predicting the dynamic response of cell populations to external stimuli, and in assessing the effect of various system parameters on the overall tissue growth rates.

The fundamental advances in 3-D modeling, simulation, and data capture technologies as well as the tremendous increases in computing power have allowed users to take advantage of the many innovations in algorithmic techniques to generate ever more complex models and datasets. As such, visualization has become an important tool, not only in computational science and engineering but also in many other areas, in using and dealing with these massive amounts of data (Johnson & Weinstein, 2006). However, the modeling and simulation process, which represents one of the many sources of this data, is still seen as quite separate from the visualization process. Integrating the two into one computational environment would allow the user to think in terms of the overall task of problem solving in order to analyze the obtained results, gain further insight, and support important decision making. Having a readily available visualization component would allow the user to enhance his understanding in real time (Telea, 2008). In addition, the ability to interactively change the parameters of the simulation model allows for a form of computational steering that is becoming ever more in demand lately (Wright et al., 2010).

We have developed a three-dimensional computational model for tissue growth using cellular automata. This is a stochastic model that accounts for mammalian cell migration, division, and collision. In this chapter, we begin by presenting some background material on the building of three-dimensional bioartificial tissues. We review the computational model and present its corresponding algorithm next. We then discuss some aspects related to its parallelization and present our work up to this point regarding the integration of visualization with the said simulation model for 3-D tissue growth. We conclude this chapter by providing our summary and future directions for research.

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