Using Web Technologies and Meta-Computing to Visualize a Simplified Simulation Model of Tumor Growth *in vitro*

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Abstract

The aim of this paper is to demonstrate the impact that web technologies and meta computing can have on the simulation of biological processes such as tumor growth. A client-server architecture allowing real-time surface and volume rendering using a standard Web browser is proposed. A simplified three-dimensional cytokinetic simulation model of tumor growth in vitro is developed and results are obtained concerning the development of a small cell lung cancer (SCLC) tumor spheroid in cell culture. A Gaussian distribution of the cell cycle phase duration's is considered. The behavior of the model is compared with both published data and laboratory experience. The application of Web technologies and meta computing leads to a spectacular three-dimensional visualization of both the external and the internal structure of a growing tumor spheroid.

Editorial Synopsis

Dr. Andy Marsh, co-chair of ITIS-ITAB'99, introduced a 'cancer in vitro' experiment to the conference participants. The application allows the use of visualizations on the Web and involves meta-computing techniques. A research team, under the lead of Dr. Georgios Stamatakos, attached to the Department of Electrical and Computer Engineering at NTUA, the National Technical University of Athens, applied a Monte Carlo type of simulation to predict the proliferation of cancer cells. The research team examined how this process leads to the origin and growth of a tumour. Dr. Marsh, who was involved in the experiment, explicitly stressed the major interest of prediction models that are generated with Web and High Performance Computing (HPC) technologies, for the future of medical research.

In medical science, models of tumour growth are developed to achieve a deeper insight into the molecular origin of cancer and to improve therapeutic approaches in oncology. The complex process of uncontrolled cell proliferation has recently been captured in a simplified 3D cytokinetic simulation model of a small cell lung cancer (SCLC) tumour in vitro by the scientific team of NTUA. The experiment is innovative in the sense that a special visualization method is used to allow real time surface and volume rendering on affordable computer hardware for application in daily medical practice. The idea is to set up a client-server architecture for this purpose. Future extension of the system will imply the introduction of various therapeutic schemes as well as a suitable procedure to animate volumes or triangulated surfaces.

For the initial model, the NTUA researchers have selected the specific case of a rapidly growing SCLC tumour in cell culture. After the installation of the cell at the center of the nutrient medium, a number of mesh snapshots, taken at seven different instants ranging from 1 to 240 hours, has been stored for the actual visualization processing. A standard mathematical software package, MATLAB, is used to visualize an equatorial section of the spheroid cell in its various registered moments. The outcome is compared with published simulation data as well as laboratory experience. The 3D processing leads to spectacular 3D views of both the external surface and internal structure of the developing tumour.

The simulation code has been implemented on a Silicon Graphics Challenge XL machine, a shared memory parallel system with 16 x R4400 processors and 320 Mflops. One single run lasts forty minutes but when the number of cells are increasing, a parallelization of the code will be necessary. In fact, the system's input consists of raw data to which voxels are labelled through a code number corresponding to a specific cell state. The output amounts to a set of triangulated surfaces, which are suitable for real time surface and volume rendering. The visualization process involves more than 3D volume structures since the medical expert needs a dynamically evolving 4D imaging modality to properly assess the tumour growth development. Therefore, a novel version of the marching cubes (MC) algorithm is implemented in order to produce an optimized number of small polygons.

The triangulated surfaces are stored in a VRML or Virtual Reality Modelling Language 2.0 format file. VRML 2.0 perfectly enables the generation of 4D animations to display the tumour growth evolution in a graphical as well as interactive way. Hospitals may lack the required computational power to run the simulation. In this case, a client-server approach can easily solve the problem via access to a remote HPC site. The client only has to submit a request for the tumour prediction programme through a Web page, initiating the common gateway interface (CGI) script on the server. As a result, the generated volumes are triangulated, stored in VRML files, sent to the client via e-mail or accessed through a password.

The application of VRML files constitutes only a first stage in the process of implementing advanced virtual reality techniques for the simulation and visualization of tumour growth. The NTUA researchers plan on exploring augmented reality and fully immersive virtual reality to represent the tumour development as a holographic image.