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Special Guest Lectures

Using Multi-Scale and Multi-Resolution Model With Graphics Processing Unit (GPU) to Simulate Real-Time Actual Cancer Progression

Le Zhang, Michigan Tech University

Johnston Hall 338
May 24, 2011 - 02:00 pm

Abstract:
Multi-scale agent based model (ABM) has been wildly employed to simulate Glioma tumor cells' interaction and tumor progression. In this type of ABM, computational scientists always use a quantitative molecular pathway of the intracellular level to determine cell's phonotype switch of extracellular level as well as simulate the diffusion of the chemoattractants which are the input factors of the molecular pathway of the tissue level. And then, we can investigate which molecules play important roles to determine cells' phonotype switch and drive the whole Glioma tumor expansion. However, most of the recent ABM models are too theoretic to predict real-time actual cancer progression due to the following reasons. First, it is hard to employ conventional ABM to simulate the large system restricted to the limited compute resource and memory of the computer. Second, we should employ relative fine grids and small time interval for ABM to simulate real-time cancer progression, but it takes long time for the conventional numerical diffusion solver to approximate the exact solution with relative fine grids. For the first problem, we use novel multi-resolution algorithm to relieve the heavy compute requests. The multi-resolution algorithm divides the cancer cells into homogeneous group and heterogeneous group. And then, it concentrates limited compute resource onto the cells in the heterogeneous group. The results demonstrate that multi-resolution ABM can have high predictive power with light compute requests. For the second problem, our study employs cutting-edge graphics processing unit (GPU) technology to speed up the conventional sequential numerical solver for diffusion with relative fine grids. Our research output shows that GPU based parallel compute algorithm can accelerate diffusion processing time around 50 folders than sequential algorithm. Finally, we plan to develop a parallel ordinary differential equation numerical solver to speed up the molecular pathway computation for each cancer cells in the heterogeneous group. In general, GPU based multi-scale and multi-resolution model has great potentiality for us to model real-time actual cancer progression in the 2D and 3D space which could provide more valuable information for the clinical personnel to forecast Glioma tumor expansion. Access Grid viewing is in 338 Johnston Hall. Live presentation is at 234 Nethken Hall, Louisiana Tech University.

Speaker's Bio:
The goal of the proposed research is to develop a multi-scale, multi-resolution parallel agent based model to simulate real-time Glioma tumor progression. Until now, I already have 10 years experience in computational biology of cancer field with a number of publications. Especially, in last three years, I worked for Harvard Medical School as a postdoc to employ agent based modeling technology to develop the multi-scale predictive Glioma model. Recently, I am working in Michigan Tech University as an assistant professor of Math to employ high performance computing to accelerate the previous agent based models. In summary, I have a demonstrated record of successful and productive research projects in an area of high relevance for our computational biology research, and my expertise and experience have prepared me to lead the proposed project.