Acceleration of large-scale multi-physics simulation for biomedical EMC with many-core architecture based computing

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Recently, computer simulation scale for biomedical EMC becomes extremely huge, because numerical models, which represent shape, structure, configuration, etc., of biological bodies, increase these preciseness. Parallelizing simulation code is one of the effective solutions to deal with such a high definition and massive scale problem. Finite difference methods, frequently used for solving biomedical EMC problem, are classified as the stencil scheme which has the nature of memory-bound feature. Hence, it is desirable to employ many-core architecture with the high-speed memory bandwidth (approximately 200-300GB/s) such as the graphics processing unit (GPU) or the many integrated core (MIC) hardware accelerators. The purpose of this study is to accelerate the multi-physics simulation system for numerical dosimetries by the many-core architecture based computing technique.

In this study, it is described that the multi-physics simulation codes for the dosimetries of millimeter wave (MMW) exposure is accelerated by the GPU cluster by way of example. This simulation system is developed to evaluate power absorptions and time-dependent temperature distributions within ocular tissues exposed to MMWs. The system is consists of the 3D electromagnetic field (EMF) reconstruction code, the EMF analysis code to obtain power absorption caused by MMW irradiation, and bio-heat transfer analysis code considering fluid dynamics to obtain time-dependent temperature distribution.

The finite-difference time-domain (FDTD) method is used as the electromagnetic field solver, and massive parallel code for FDTD method is implemented by the compute unified device architecture (CUDA) to apply multi GPUs consisting of several thousands processing cores. We have achieved 10x speed up for 500 x 500 x 500 cells simulation with Nvidia Tesla M2090 GPU, as compared with 20 threads Open MP parallelization with AMD Opteron 6174. We also apply the MIC hardware accelerator to parallelize FDTD scheme. The comparison applying the GPU and the MIC will discuss in this presentation.

The simplified marker and cell (SMAC) method is employed to solve the nonlinear bio-heat transfer equation systems considering the aqueous humor dynamics. To improve calculation speed, we modified original SMAC method to full implicit scheme. In the modified SMAC (MSMAC) scheme, the predicted velocity and the temperature of next time step is calculated by Crank-Nicolson method. The parallelized algebraic multi grid (AMG) method is applied to large-scale simultaneous equations appeared in the implicit schemes. GPU acceleration by the CUDA is applied to MSMAC scheme partly including the AMG algorithm. We have achieved a 50x speed-up for 170 x 170 x 170 cells with Nvidia Tesla M2090 GPU, as compared with the MSMAC method using 1 CPU (AMD Opteron 6174), and calculation time is reduced to approximately 3 hours to reconstruct actual 6 min phenomenon.

We have accelerated the multi-physics simulation code by the many-core architecture based computing system. However, it is found there is the bottleneck in the I/O performance to access massive amount of data from simulation code. In this presentation, we will discuss about the improvement of I/O processes.