## CSCI596 (Scientific Computing and Visualization) Assignment 4 Hybrid MPI+OpenMP Parallel Molecular Dynamics

Due: October 12 (Fri), 2018 — note that HPC will be down starting Oct. 15 (Mon)

- 1. Write a hybrid MPI+OpenMP parallel molecular dynamics (MD) program (name it hmd.c), starting from the MPI parallel MD program, pmd.c, following the lecture note on "hybrid MPI+OpenMP parallel MD". Submit the source code of hmd.c, with your modifications from pmd.c clearly marked.
- 2. (Verification) Run your hmd.c on two 4-core nodes (in total of 8 cores) with 2 MPI processes, each with 4 OpenMP threads, using the following input parameters: InitUcell = {24,24,12}, Density = 0.8, InitTemp = 1.0, DeltaT = 0.005, StepLimit = 100, StepAvg = 10. Use the following number of MPI processes and that of OpenMP threads, vproc = {1,1,2}, nproc = 2, vthrd = {2,2,1}, nthrd = 4, in the header file. Note the global number of atoms is: 4 atoms/unit cell × (24×24×12 unit cells) × 2 MPI processes = 55,296. Submit the standard output from the run. Make sure that the total energy is the same as that calculated by pmd.c using the same input parameters (shown below) at least for ~5-6 digits.

3. (Scalability) Run hmd.c on an 8-core node with one MPI process and the number of threads varying from 1, 2, 4, to 8, with input parameters: InitUcell = {24,24,24}, Density = 0.8, InitTemp = 1.0, DeltaT = 0.005, StepLimit = 100, StepAvg = 101. Plot the strong-scaling parallel efficiency as a function of the number of threads and submit the plot.

## (Potential Final Project)

Optimize the performance of the hybrid MPI+OpenMP MD code. For example, we could enclose the entire MD loop in a parallel clause in the main function to avoid the excessive fork-join overhead. We could also use a lock variable for synchronization.