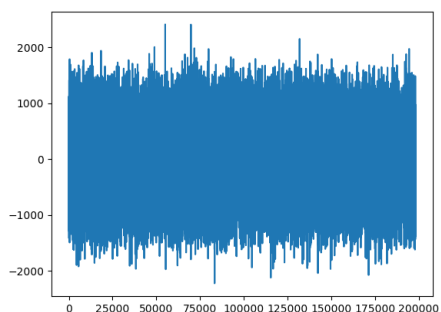


HEXANE WATER RESULTS LOG SUMMER 2018

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1. 8/6/2018

- (1) Downloaded pressure_scalar-press-NPT-1bead-water-lammps to dash_work/interface on laptop. Used pressure_analysis_UPDATE.py leaving out first 2000 records and used 198 blocks 5 ps to get average pressure of 1.41, SE 0.94, SD 511.08:



- (2) Because we accidentally used restart/traj every 1,000 for fulldata-NPT-298 and then restart/traj 10,000 for fulldata-NPT-298-restart1, we will re-do this calculation again using the updated interface file collecting restart/traj every 1,000.
- (3) Submitted simulation no. 1.
- (4) To check pressures in a non-vacuum interfacial system, in DASH we are going to run simulation no. 2, which does NPT equilibration for 200,000 steps and then does an NVT simulation of the interface. Filename press-nonexpanded.
- (5) Submitted simulation no. 2.
- (6) We want to compare the above simulation to LAMMPS, so we will first run the equilibration step in LAMMPS as simulation no. 3. Note, however, that the mixing rules currently used in the LAMMPS file are arithmetic. Also NOTE: to use depablo-tc, must type module load openmpi into terminal first, even if it is already in submit script. After this, we need to run the NVT portion of the simulation for 6M steps.
- (7) Running simulation no. 3.
- (8) Now, let's turn to how pressure is typically computed in DASH. In general, an ideal gas mechanical equation of state is given by

$$P = \frac{Nk_B T}{V} = \rho k_B T \quad (1.1)$$

This assumes that molecules in the gas are point-like and do not interact with each other. However, if interactions between the particles and a finite particle volume is allowed. The virial expansion is a perturbation theory around the ideal gas used when the interactions in the real gas are dominated by two-body interactions. One uses a virial expansion in powers of the density, keeping the temperature dependence of the coefficients. We can then apply manipulations of the time derivative of the classical virial to arrive at

$$P = \rho k_B T - \left[\frac{1}{3V} \left\langle \sum_{i < j}^N r_{ij} F_{ij} \right\rangle \right] \quad (1.2)$$

where the second term is called the virial correction.

- (9) In DASH, it appears as though `DataComputerPressure.cu` is responsible for scalar pressure values. On line 92, we have

$$pressureScalar = (tempScalar_loc * ndf_loc * boltz + sumVirial) / (dim * volume) * state - > units \quad (1.3)$$

`tempScalar_loc` appears to be the temperature of the system, `boltz` is the boltzmann coefficient, `sumVirial` is that second virial correction, `dim` is the dimension of the system. `ndf` I calculated to be 3 per atom, including M sites for the water model (printed values using interface file). So, it does make sense to divide by `dim`, i.e. divide by 3, because that gets us to N. However, we are also including M-sites in the pressure value. So, we are at the very least overcounting the ideal gas term for the pressure. The amount of overcorrection for 3650 water molecules is given by:

$$P_c = \frac{N k_B T}{V} = \frac{3650 \times 1.38 \times 10^{-23} \times 298}{50 \times 10^{-10} \times 50 \times 10^{-10} \times 150 \times 10^{-10}} \quad (1.4)$$

Actually, would it even be incorrect to have four sites per atom? Maybe that's actually the correct ideal model here?

2. 8/7/2018

- (1) First, we will begin by compiling the most recent version of DASH, which should contain Mike's edits to the TIP4P/F fix for accurate pressure computation (avoiding M-site in ideal gas term). Compiling version in folder DASH-8-7-2018.
- (2) DASH pressure computations:

NVT with vacuum: `run_UPDATE_8-7-2018.sh` and `interface_UPDATE_8-7-2018.py`, z length 149.2717, x length 58.45467, y length 58.67825, 3650 TIP4P/F water molecules, 500 hexane molecules, waldman-hagler mixing between the water and hexane molecules, NVT with Andersen thermostat with parameters `nu = 0.01` (a parameter describing the collision frequency of the system with the heat bath) and applying every 10 steps, 298 K, 1M steps equilibration and 1M steps production, `PI false`, `restart/traj` every 10,000, -20/+20 for z change as accounted above, filename `newpress-expanded`, tensor information commented out in input script. This is simulation no. 4.

We will do the same as above, except we will not expand the box by 20 Å in each z direction, and we will apply NPT equilibration for 1M steps and then 1M steps of NVT. This is simulation no. 6.

(3) LAMMPS pressure computations:

NVT with vacuum: interface.sbatch and in.taffi_tip4pF_waldman, x length 149.2717, y length 58.67825, z length 58.45467, 3650 TIP4P/F water molecules, 500 hexane molecules, waldman-hagler mixing, NVT with NoseHoover, 298 K, 1M steps equilibration and 1M steps production, PI false, restart/traj every 10,000, filename newpress-expanded-lammps. We will start with 500,000 steps and restart from there, which is simulation no. 5.

Same as above, except we will not expand the box by 20 Å in each z direction, and we will apply NPT equilibration for 1M steps and then 1M steps of NVT. The first 500,000 steps will be simulation no. 7.

Simulation no. 8 is filename newpress-expanded-lammps-restart1, restarting from newpress-expanded-lammps.restart for 1.5M steps

Simulation no. 9 is filename newpress-nonexpanded-lammps-restart1, restarting from newpress-nonexpanded-lammps.restart for 500K steps

Simulation no. 10 is filename newpress-nonexpanded-lammps-restart2, restarting from newpress-nonexpanded-lammps-restart1.restart, and going for 1M NVT steps.

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