

Chemistry 478 — Molecular Modeling

Laboratory #6 — Properties of Pure Liquids via Molecular Dynamics Simulation

In this lab you will prepare a cubic periodic box containing a pure organic liquid, and then generate a molecular dynamics trajectory for the liquid. Post-processing analysis of the trajectory can give estimates of the density, heat of vaporization, radial distribution, diffusion constant, *etc.*

Protocol

(1) Below is a table containing the molecular weight, density, melting point and boiling point for several simple liquids. Your goal in this lab is to pick one of these substances, perform a molecular dynamics simulation on a sample of your chosen molecule, and then compute values for the density, heat of vaporization, diffusion constant and radial distribution functions. You can also monitor the approach to conformational equilibrium.

Molecule	MW	Density	MP	BP
Acetic Acid	60.05	1.049	46	118
Acetone	58.08	0.791	-94	56
Acetonitrile	41.05	0.786	-48	82
Ammonia	17.03	0.682	-78	-33
Aniline	93.13	1.022	-6	184
Benzene	78.11	0.874	6	80
Chlorobenzene	112.56	1.107	-45	132
Cyclohexane	84.16	0.779	7	81
Cyclopentene	68.12	0.774	-135	44
Dimethyl Formamide	73.10	0.944	-98	153
Dimethyl Sulfoxide	78.13	1.101	18	189
Ethanol	46.07	0.794	-114	78
Ethane Thiol	62.13	0.839	-145	35
Ethyl Acetate	88.11	0.902	-84	77
Ethyl Iodide	155.97	1.950	-108	71
Ethylene Glycol	62.07	1.113	-13	197
Formamide	45.04	1.134	3	210
Methanol	32.04	0.791	-98	65
Methyl Disulfide	94.20	1.046	-85	109
Methyl t-Butyl Ether	88.15	0.740	-109	52
Nitromethane	61.04	1.127	-29	101
Pentane	72.15	0.626	-130	36
Phenol	94.11	1.017	41	182
Tetrahydrofuran	72.11	0.889	-108	66
Trifluoroethanol	100.01	1.373	-44	79
Trimethyl Amine	59.11	0.636	-117	4
Water	18.02	1.000	0	100

(2) First, obtain a TINKER **.xyz** file containing a single molecule of your chosen substance. Files for isolated molecules, setup to use the OPLS-AA force are provided on the course website for this lab. You will need to use the **oplsaa.prm** file provided along with this lab. This slightly modified version of the parameter file contains extra parameters for some of the molecules in the list. Also copy the **tinker.key** file from the course site, which initially contains just a single line pointing to the OPLS-AA parameters.

(3) Examine the **.xyz** file and compare the atom types in the column just to the right of the x,y,z-coordinates to the OPLS-AA parameter file obtained in the previous step to verify that the correct atom types are used for your molecule.

(4) Minimize your molecule using the TINKER **minimize** program to clean up any distortions in the original geometry. Then copy your molecule to a second file, edit this second file to translate the molecule to some new set of coordinates using any text editor, and finally use the TINKER **xyzedit** program to merge your two molecules into a single file containing a dimer. Use **minimize** to find the optimal energy for the dimer. What is the energy of interaction, *i.e.*, the energy of the dimer minus twice the energy of the monomer? Are you sure that you have found the best dimer structure?

(5) Run the TINKER **xyzedit** program on the minimized monomer, using the option to create a cubic periodic box filled with multiple copies of your molecule. You should try to make a box about 25 Angstroms on a side, and you will need to calculate the number of molecules to place in the box based on molecular weight, density, *etc.* Note that 1 Angstrom is equal to 10^{-10} meters, and Avogadro's number is $6.02214129 \times 10^{23}$.

(6) Make sure the box size in Angstroms is set via the appropriate keyword (**X-AXIS**) in your keyfile, then minimize the solvent box to again remove any bad or high energy contacts. You can also set the cutoff distance for the van der Waals interactions (keyword: **VDW-CUTOFF**). This value must be somewhat less than half the box dimension – a value of 9 Angstroms is typical for OPLS simulations. For electrostatic interactions turn on Ewald summation using the **EWALD** keyword, and set the real-space Ewald cutoff to 7 Angstroms using the **EWALD-CUTOFF 7.0** keyword. Also use of pair neighbor lists for both VDW and electrostatic interactions by adding the **NEIGHBOR-LIST** keyword.

(7) Next run **minimize** to remove bad contacts from your liquid box. You should use a moderate convergence criterion for the minimization of about 1.0 kcal/mol/Ang.

(8) Start an MD simulation using the TINKER **dynamic** program in the isothermal-isobaric ensemble (constant temperature and pressure, also referred to as NPT). We will use an integration method specially formulated for the NPT ensemble; to do this set the keyword **INTEGRATOR NOSE-HOOVER**. Use room temperature (298K = 25°C) for the target temperature, as long as your substance is a liquid at that temperature. Otherwise use a target temperature midway between the melting and boiling points. The target pressure should be 1 Atm. Also add the **ARCHIVE** keyword prior to your MD run, which will cause the full trajectory to be written to a single archive (**.arc**) file.

(9) Collect your MD trajectory, saving coordinate snapshots every 0.1 ps, and using a 2 fs time step for integration. You will generally need to discard the first portion of the trajectory (perhaps 200 ps) as an "equilibration period". Following equilibration, you can use the remaining "production period" in your analysis to determine the density, heat of vaporization, and radial distributions for the OPLS-AA model of your liquid. Ideally, your production period should be at least a nanosecond or longer.

(10) Average properties from your MD run can be determined by running the TINKER **mdavg** script (in the /bin directory of the TINKER distribution) on the log file from the dynamics calculation. This will provide the average temperature, pressure, density, potential energy, *etc.* The instantaneous values of these same quantities can be found by inspecting and using **grep** on the log file. In particular, you should compare your computed density with the experimental value.

(11) You should figure out how to compute the heat of vaporization from your MD results. See the Leach book, or other recommended course books for further information.

(12) Radial distribution functions can be computed from your saved MD coordinates using the TINKER **radial** program. Try, for example, computing the distribution function between pairs of like polar atoms, if your liquid contains a polar functional group. The theory and form of radial distributions is described in section 6.2.5 of Leach.

(13) Use the TINKER **diffuse** program to compute the diffusion constant for individual molecules within your sample of liquid.

(14) Finally, if your liquid can exhibit alternative conformations, such as the "chair" and "boat" conformations of cyclohexane, determine the relative percentage of each conformation as a function of the simulation time. Does it look like your system has reached its conformational equilibrium state?

Questions

(1) Why is it necessary to minimize your liquid box before starting the MD run? What would likely happen if you skipped this step?

(2) Diffusion constants are typically computed via the Einstein relationship. What is this relationship, and how is it used to derive the diffusion constant?

(3) What methods can be used to determine whether an MD simulation is "equilibrated"? Not all properties equilibrate and/or convergence at the same rate. Which kinds of properties tend to converge more slowly?

(4) It is also possible to use an MD simulation to compute an estimate of the heat capacity of your liquid. Find the statistical mechanical fluctuation formula for heat capacity and apply it to your simulation data (see Leach or a similar book). The value you derive will probably be uncertain at best. Why?