

Chem 860. Homework 6 Due: Mar. 25 2009

Basic Monte Carlo and Replica Exchange

March 13, 2009

1 Pencil exercises

1. Heat capacity can be calculated from fluctuations in the **total energy** in the canonical ensemble:

$$C_V = \frac{\langle E^2 \rangle - \langle E \rangle^2}{k_B T^2}$$

(a) In a MC NVT simulation, one does not calculate fluctuations in the total energy but in the **potential energy**. Is it then still possible to calculate the heat capacity? Explain. (b) Alternatively, C_V can be calculated from differentiating the total energy of a system with respect to temperature. Discuss the advantages or disadvantages of this approach.

2. Consider an one-dimensional system, whose distribution has the simple form: $\exp(-\beta U(x)) = \Theta(x)\Theta(1-x)$, in which the $\Theta(x)$ is a Heaviside function (i.e., zero when $x < 0$ and 1 when $x > 0$) [Can you guess what the system looks like?:-)] We can consider two MC moves for a canonical sampling of the system:

(a) Generate a random displacement in x between $[-\delta, \delta]$. (b) Generate a random number ϕ between $[1, 1+\delta]$. With a probability of 0.5, invert the value of ϕ thus obtained. The new value of x is obtained by multiplying x with ϕ .

Derive the acceptance/rejection rules for the schemes. Are they the same?

3. Consider developing a GCMC scheme for a mixture of two components - at temperature T and chemical potential for the components μ_1 and μ_2 .

(i). To add/remove particles, the following scheme is used,

- select at random to add or remove a particle
- select at random a component
- add or remove a particle of this component.

Derive the acceptance rules for these trial moves

(ii). Imagine an alternative scheme:

- select at random to add or remove a particle
- select at random a particle, independent of its identity, add or remove.

Does this scheme satisfy detailed balance if the acceptance rules derived in (i) is used? If not, can this be corrected? *Hint: a useful reference is Mol. Phys. 85, 435, 1995*

2 Computational exercises

Sample scripts are in hw5.

2.1 Basic Metropolis Monte Carlo

You will find a CHARMM script that does Monte Carlo simulations for a small protein, BPTI, plus four buried water molecules. Look through the input and mc.doc to understand different types of moves available in CHARMM for protein simulations. A very good reference that talks about the optimization of MC in CHARMM is J. Comp. Chem. 27, 203 (2006)

(1). Run a short MC simulation to optimize the move set (e.g., step size etc.). (2). With this move set, first carry out MC simulations to equilibrate the system - i.e., monitor the structure of the protein and make sure that the RMSD reaches a plateau. (3). Next run MC production runs (you have to write your own script for this!). Estimate the average potential energy and specific heat of the system. (4) **Bonus:** Can you develop a way to compare the efficiency of MC simulations to Molecular Dynamics? What quantities would you look at. Run a short MD to illustrate your point.

2.2 Replica Exchange Molecular Dynamics (thanks to Mr. Xiao Zhu)

This is a simple exercise for REMD with a small peptide in the vacuum with only 4 replicas (not what you would do in real research). The input perl script allows you to modify the frequency of exchange (ν_{Ex}) and the distribution of temperatures. Select a number of values for ν_{Ex} based on the reference of Roitberg et al. (JCP, 128, 024103), and select several temperature ladders (e.g., compare uniform distribution with exponential distribution). Analyze your results in terms of distribution of energies from different replica. Can you reproduce the similar quantities plotted in Fig. 1 & 2 in the paper?

Hint: use ./temp_remd.pl -h for useful info. Also there is a readme file in the directory. For those of you who will use the script on your own machines, make sure the path to CHARMM is set up properly in the perl script.