

Chem 860. Homework 3

Protein simulations. I. Structural properties (Due: Feb.18)

February 11, 2009

1 Homework

1.1 Pencil exercises

- Covariance matrix and thermodynamics

Propose a way to estimate the entropy of a macromolecular system based on the covariance matrix from molecular dynamics simulation. *Hint: one may obtain a set of effective frequencies from the quasi-harmonic analysis. The system can be approximated as a set of harmonic oscillators with those effective frequencies. Search for references by I. Andricioaei and M. Karplus.* Give the explicit expression that relates the entropy to the covariance matrix; discuss its value and limitation. **Bonus:** is the method useful for estimating nuclear quantum mechanical contributions to entropy?

1.2 Computational exercises

In the Assignment/hw3 directory, there is a CHARMM input script for performing a short MD simulation for a simple β hairpin with an implicit solvent model (EEF1, which will be discussed briefly in the near future) - so that we don't have to worry about boundary condition, long-range electrostatics etc. Modify the input file such that you carry out 10 ps of equilibration and 50 ps of production run. The calculation should take only several minutes of CPU time. Once again, you can use VMD to visualize the MD simulation. Note the fluctuations in temperature and the typical frequency of updating the non-bond list.

- Statistical error analysis

Store the potential energy (of the production run) into a file by specifying the KUNIT value and an appropriate NPRINT value (10) in the "dynamics" section. Estimate the average and statistical error in the total potential energy using the block average technique. How different is the result compared to the value without any block averaging? You need to write a simple piece of code that reads in the data from data/hair2.ene and performs block

averaging. A useful example for block average can be found at:
http://www.ccp5.ac.uk/SSCCP5/WORKSHOP/Day_2/Basics/block.f

- Structural properties

Plot the following quantities associated with the simulation:

1. RMSD for the backbone atoms relative to the starting structure as a function of time.
2. RMSD for the backbone atoms in the averaged MD structure relative to the the starting structure. Make a figure to illustrate this by overlaying the two structures in VMD.
3. RMSF for C α atoms. **Bonus:** one can map the RMSF onto the structure in VMD (i.e., different color for different magnitude of fluctuation).
4. Covariance matrix for C α atoms, discuss the qualitative pattern you saw. In general, it takes a long time to get converged covariance matrix (because non-local values are influenced by slow fluctuations).
5. End-end distance ($\mathbf{r}_1^{C\alpha} - \mathbf{r}_N^{C\alpha}$); main-chain hydrogen bonds (i.e., between NH and CO).
6. Radius of gyration ($R_g = \sqrt{\frac{1}{N} \sum_{i=1}^N \langle (\mathbf{r}_i - \mathbf{r}_G)^2 \rangle}$, where \mathbf{r}_G is the center of mass). We usually use C α atoms only.