

CSE 60531  
Computational Biophysics  
Spring 2008

Due Tuesday March 11, 2008.

1. (10 points) Recall that for the canonical ensemble, the probability density is proportional to  $\exp(-H(x, p)/k_B T)$ .
  - (a) Show that if a value of  $\Gamma = [x^T, p^T]$  is chosen randomly from the canonical distribution, then  $x$ ,  $p_{1x}$ ,  $p_{1y}, \dots, p_{N,z}$  are independent assuming the Hamiltonian  $H(x, p) = \frac{1}{2}p^T M^{-1}p + U(x)$ . (The individual components of  $x$  are not independent of each other).
  - (b) Recall that a random variable  $\xi$  from a Gaussian distribution has a probability density

$$\rho(\xi) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{(\xi - \mu)^2}{2\sigma^2}\right),$$

where  $\mu$  is the mean and  $\sigma$  is the standard deviation. Precisely what is the probability density of  $p_{iy}$ ?

- (c) If  $Z$  is a random variable from a standard Gaussian distribution (with mean 0 and standard deviation 1), how can you use  $Z$  to choose  $p_{iy}$ ? the velocity  $v_{iy}$ ?
2. (5 points) Show that replica exchange as presented in the lecture satisfies microscopic reversibility.
3. (5 points) Which amino acids have net positive charge? net negative charge? contain sulfur? have a side chain with two covalent bonds to the backbone?
4. You will repeat the following simulation procedure starting from alanC7equatorial, alanC7axial, and alanC5axial.
  - (a) (5 points each) Minimize each one of the structures using 100 steps of minimization. Save the positions in a file minim.coor. Redirect the output of NAMD to a file minim.log. Plot the potential energy

vs time. Turn in your NAMD configuration file and plot. Use the following force field parameters:

```
paraTypeCharmm on
parameters par_all27_prot_lipid.inp
exclude scaled1_4
fulldirect on
switchdist 10
cutoff 12
```

- (b) (5 points each) Equilibrate the system to 310 K, with positions and velocities in files `equil.coor` and `equil.vel`. Prepare a NAMD configuration that does at least 20 ps of Langevin dynamics with a time step of 1 fs and a damping coefficient of  $5 \text{ ps}^{-1}$ . Output energies and timing every 0.1 ps starting at zero. Redirect the output of NAMD to a file `equil.log`. Plot the temperature vs time. Turn in your NAMD configuration and plot.
- (c) (10 points each) Run 100 ns of simulation of alanine dipeptide using NAMD2. Output energies and timing every 10 ps, and output a DCD file every 1 ps. Use a time step of 2 fs and SHAKE (rigidbonds all). Turn in your NAMD configuration file. In a Vista machine this took about 2 1/2 hours.
- (d) (5 points each) Run a VMD script that will create files for the  $\phi$  and  $\psi$  dihedral angles. Turn in your VMD TCL script.
- (e) (10 points each) Run a MATLAB or Octave script that will create a Ramachadran plot of the free energy ( $-k_B T \log P$ ) in  $\text{kcal mol}^{-1}$ . Use `imagesc` to create the plot. Also, use `colorbar` to place a colorbar in the plot. Turn in your script and the Ramachadran plot of your simulations.