Organization of NAMD Tutorial Files



2.1.1. RMSD for individual residues

<u>**Objective</u></u>: Find the average RMSD over time of each residue in the protein using VMD. Display the protein with the residues colored according to this value.</u>**



2.1.2 Maxwell-Boltzmann Distribution

<u>**Objective</u>:** Confirm that the kinetic energy distribution of the atoms in a system corresponds to the Maxwell distribution for a given temperature.</u>





<u>Objective</u>: Plot the various energies (kinetic and the different internal energies) as a function of temperature.



2.1.4 Temperature Fluctuations

Temperature time series: $T(t) = \frac{2}{3k_B} \langle K(t) \rangle = \frac{1}{3Nk_B} \sum_{i=1}^{N} m_i v_i^2(t)$ $= \sum_{i=1}^{N} X_i(t) , \quad X_i(t) = \frac{m_i v_i^2(t)}{3Nk_B} = \frac{2\varepsilon_i}{3Nk_B}$

According to the central limit theorem:

$$\langle T \rangle = N \langle X \rangle = \frac{2}{3k_B} \left\langle \frac{m_i v_i^2}{2} \right\rangle = \frac{2}{3k_B} \frac{3}{2} k_B T_0 = T_0 \quad \text{thermodynamic} \\ \sigma_0^2 = \left\langle X^2 \right\rangle - \left\langle X \right\rangle^2 = \frac{2T_0^2}{3N^2} \implies \sigma^2 = \sigma_0^2 / N = \frac{2T_0^2}{3N} \\ \boxed{\left(4\pi T_1^2 \right)^{-1/2} \left[3(T - T_0)^2 \right]}$$

 $\left| p(x) = \left(\frac{m T_0}{3N} \right) \right| \exp \left| -\frac{\sqrt{3} + \frac{1}{2}}{4T_0^2} \right|$

Analysis of MD Data

- 1. Structural properties
- 2. Equilibrium properties

3. Non-equilibrium properties

Can be studied via both **equilibrium** and/or **non-equilibrium** MD simulations

Time Correlation Functions

$$C_{AB}(t-t') = \underbrace{\langle A(t) B(t') \rangle = \langle A(t-t') B(0) \rangle}_{\text{since } \rho_{eq} \text{ is } t \text{ independent } !}$$

$$A \neq B$$
 cross-
 $A = B$ auto-
 f correlation function

Correlation time:
$$\tau_c = \int_0^\infty dt C_{AA}(t) / C_{AA}(0)$$

Estimates how long the "memory" of the system lasts In many cases (but not always): $C(t) = C(0) \exp(-t/\tau_c)$

Free Diffusion (Brownian Motion) of Proteins

- In living organisms proteins exist and function in a <u>viscous environment</u>, subject to <u>stochastic</u> (random) <u>thermal forces</u>
- the motion of a globular protein in a viscous aqueous solution is diffusive



 e.g., ubiquitin can be modeled as a spherical particle of radius R~1.6nm and mass M=6.4kDa=1.1x10⁻²³ kg

Diffusion can be Studied by MD Simulations!

ubiquitin in water



total # of atoms: 7051 = 1231 (protein) + 5820 (water)

simulation conditions: NpT ensemble (T=310K, p=1atm),
periodic BC, full electrostatics, time-step 2fs (SHAKE)

simulation output: Cartesian coordinates and velocities of all atoms saved at every other time-step (10,000 frames = 40 ps) in separate DCD files

Goal: calculate D and τ

by fitting the theoretically calculated center of mass (COM) velocity autocorrelation function to the one obtained from the simulation

• theory:
$$C_{vv}(t) = \langle v(t) v(0) \rangle = \langle v_0^2 \rangle e^{-t/\tau}$$

 $\langle v_0^2 \rangle = \frac{k_B T}{M} = \frac{D}{\tau}$ (equipartition theorem)

▶ simulation: consider only the x-component $(v_x \rightarrow v)$ replace ensemble average by time average

$$C_{vv}(t) \approx C_i = \frac{1}{N-i} \sum_{n=1}^{N-i} v_{n+i} v_n$$

 $t \equiv t_i = i\Delta t$, $v_n = v(t_n)$, N = # of frames in vel.DCD

Velocity Autocorrelation Function



Probability distribution of $V_{x,y,z}$



with
$$v \equiv v_{x,y,z}$$