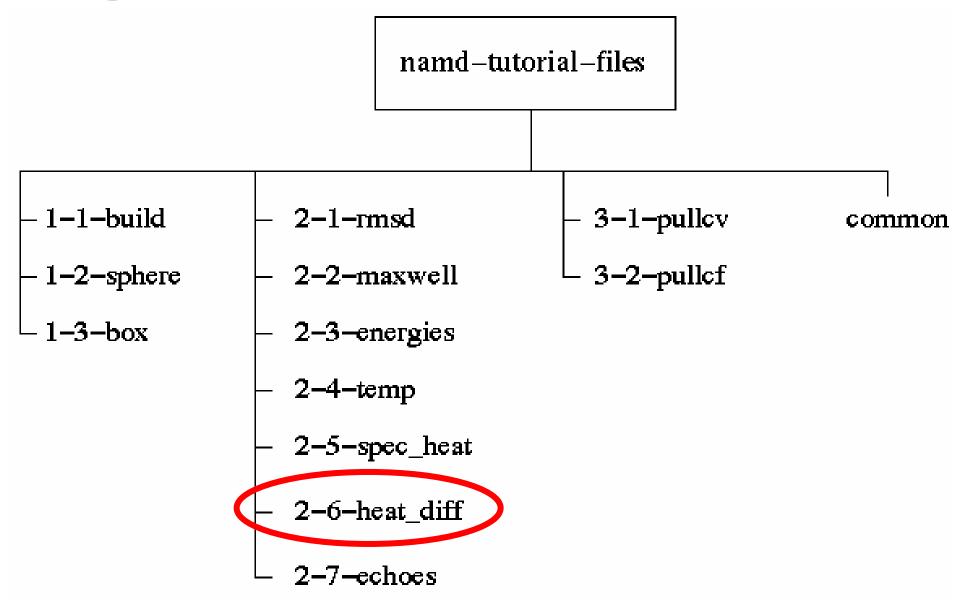
# NAMD Tutorial (Part 2)

#### 2 Analysis

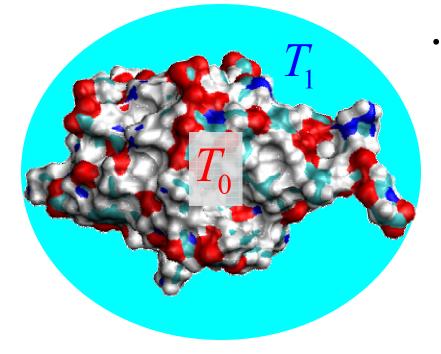
- > 2.1 Equilibrium
  - > 2.1.1 RMSD for individual residues
  - > 2.1.2 Maxwell-Boltzmann Distribution
  - > 2.1.3 Energies
  - 2.1.4 Temperature distribution
  - > 2.1.5 Specific Heat
- 2.2 Non-equilibrium properties of protein
  2.2.1 Heat Diffusion
  - > 2.2.2 Temperature echoes

### **Organization of NAMD Tutorial Files**



### Simulated Cooling of Ubiquitin

- Proteins function in a narrow (physiological) temperature range. What happens to them when the temperature of their surrounding changes significantly (temperature gradient) ?
- Can the heating/cooling process of a protein be simulated by molecular dynamics ? If yes, then how?



What can we learn from the simulated cooling/heating of a protein ?

# Nonequilibrium (Transport) Properties

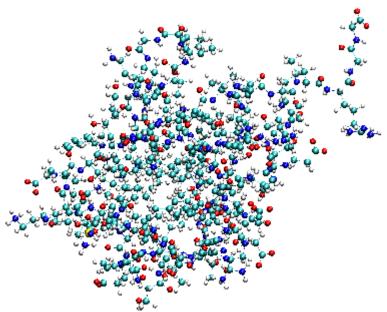
- macromolecular properties of proteins, which are related to their biological functions, often can be probed by studying the response of the system to an external perturbation, such as *thermal gradient*
- "small" perturbations are described by linear response theory (LRT), which relates transport (nonequilibrium) to thermodynamic (equilibrium) properties
- on a "mesoscopic" scale a globular protein can be regarded as a continuous medium  $\Rightarrow$  within LRT, the local temperature distribution T(r,t) in the protein is governed by the heat diffusion (conduction) equation

$$\frac{\partial T(\mathbf{r},t)}{\partial t} = D \nabla^2 T(\mathbf{r},t)$$

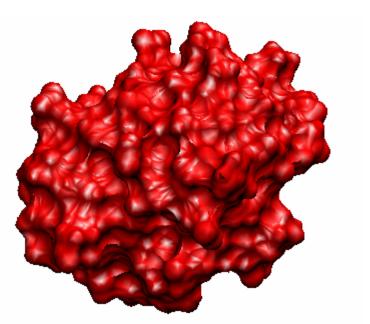


VS

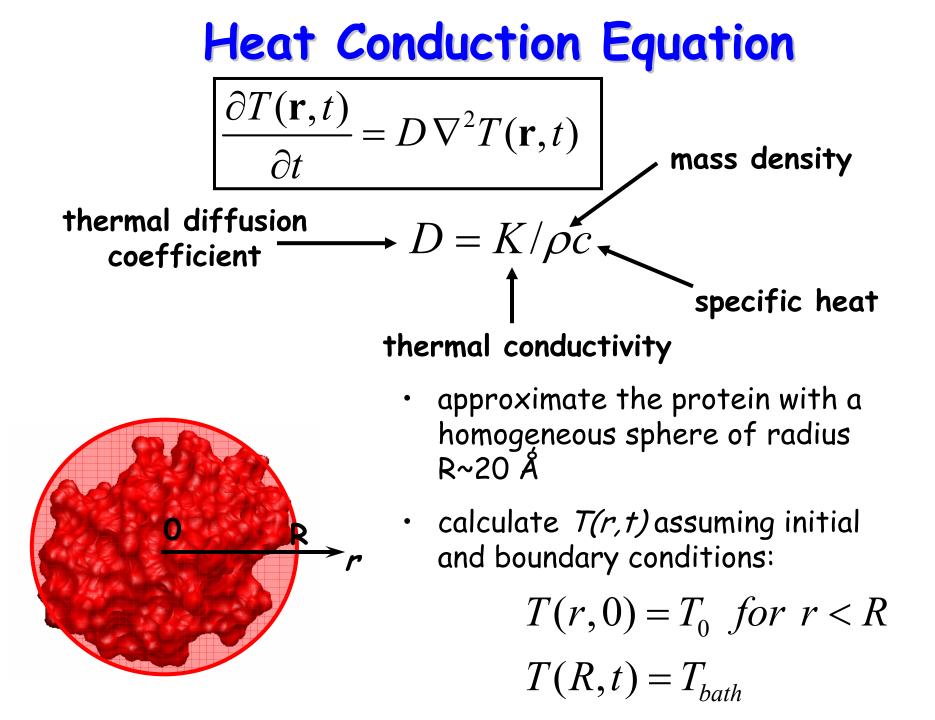
# Mesoscopic

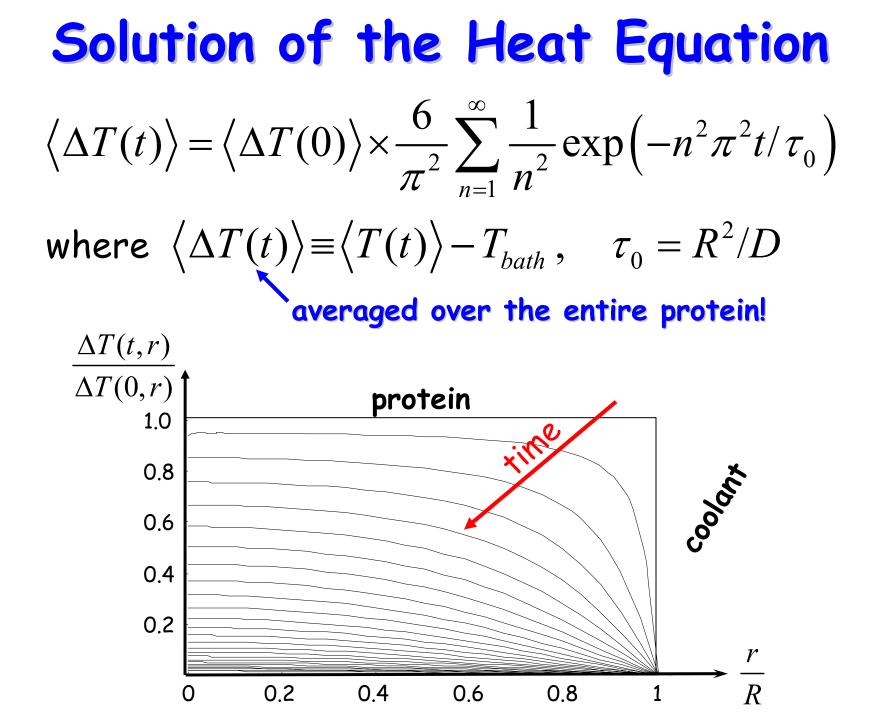


- each atom is treated individually
- length scale ~ 0.1 Å
- time scale ~ 1 fs



- one partitions the protein in small volume elements and average over the contained atoms
- length scale ≥ 10 Å = 1nm
- time scale ≥ 1 ps





# How to simulate cooling ?

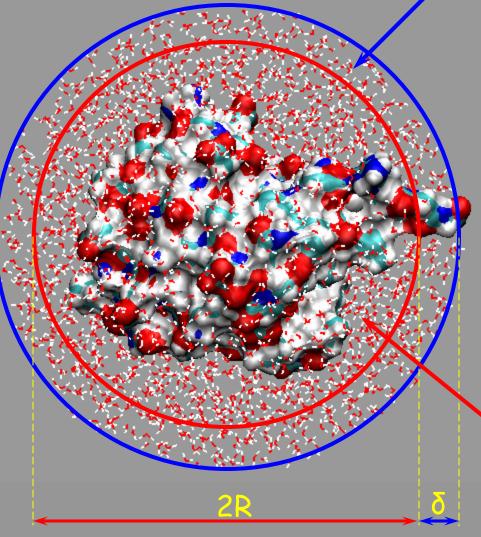
- In laboratory, the protein is immersed in a coolant and the temperature decreases from the surface to the center
- Cooling methods in MD simulations:
  - 1. Stochastic boundary method
  - 2. Velocity rescaling (rapid cooling, biased velocity autocorrelation)

$$\langle T(t) \rangle_{sim} = \frac{\sum_{i=1}^{N_d} m_i v_i^2}{N_d k_B} \implies v_i' = v_i \sqrt{\frac{T_{new}}{T_{old}}}$$

3. Random reassignment of atomic velocities according to Maxwell's distribution for desired temperature (velocity autocorrelation completely lost)

### **Stochastic Boundary Method**

Heat transfer through mechanical coupling between atoms in the two regions



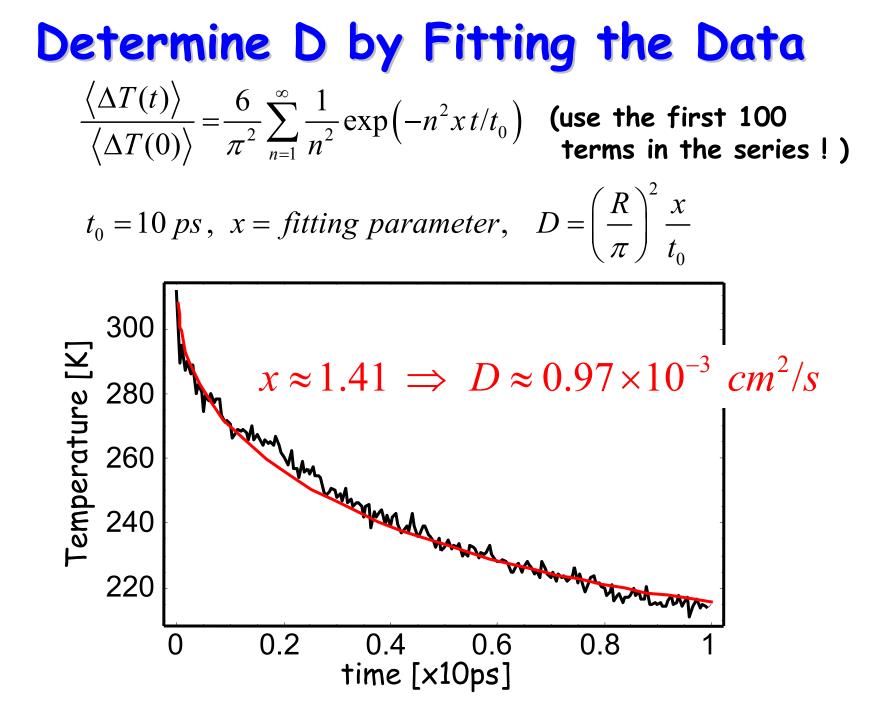
#### coolant layer of atoms

motion of atoms is subject to stochastic Langevin dynamics  $m \ddot{r} = F_{FF} + F_H + F_f + F_L$ 

 $F_{FF} \rightarrow$  force field  $F_{H} \rightarrow$  harmonic restrain  $F_{f} \rightarrow$  friction  $F_{L} \rightarrow$  Langevin force

atoms in the inner region follow Newtonian dynamics

$$m \, \ddot{r} = F_{FF}$$



#### Thermal Conductivity of UBQ

 $K = D\rho c$ 

$$C_{V} = \langle \delta E^{2} \rangle / k_{B} T^{2} = \left( \langle E^{2} \rangle - \langle E \rangle^{2} \right) / k_{B} T^{2}$$

 $D \approx 0.97 \times 10^{-3} \ cm^2/s$  $\rho \approx 1 \times 10^3 \ kg/m^3$ 

# NAMD Tutorial (Part 2)

#### 2 Analysis

- > 2.1 Equilibrium
  - > 2.1.1 RMSD for individual residues
  - 2.1.2 Maxwell-Boltzmann Distribution
  - > 2.1.3 Energies
  - > 2.1.4 Temperature distribution
  - > 2.1.5 Specific Heat
- 2.2 Non-equilibrium properties of protein
  - > 2.2.1 Heat Diffusion

#### 2.2.2 Temperature echoes