

Statistical Mechanics of Proteins

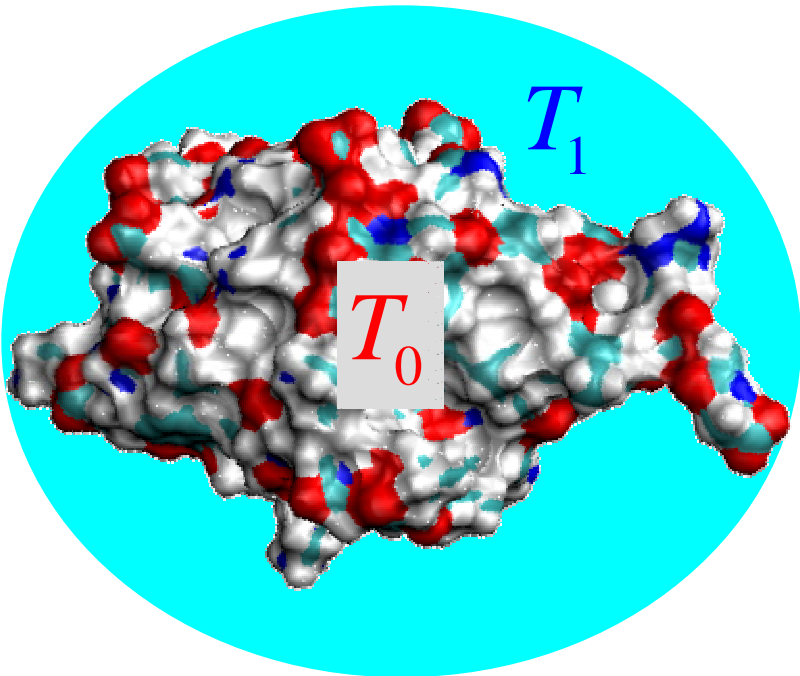
Ioan Kosztin

Department of Physics & Astronomy
University of Missouri - Columbia

- ▶ Equilibrium and non-equilibrium properties of proteins
 - ▶ Free diffusion of proteins
- ▶ Coherent motion in proteins:
temperature echoes
- ▶ **Simulated cooling of proteins**

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

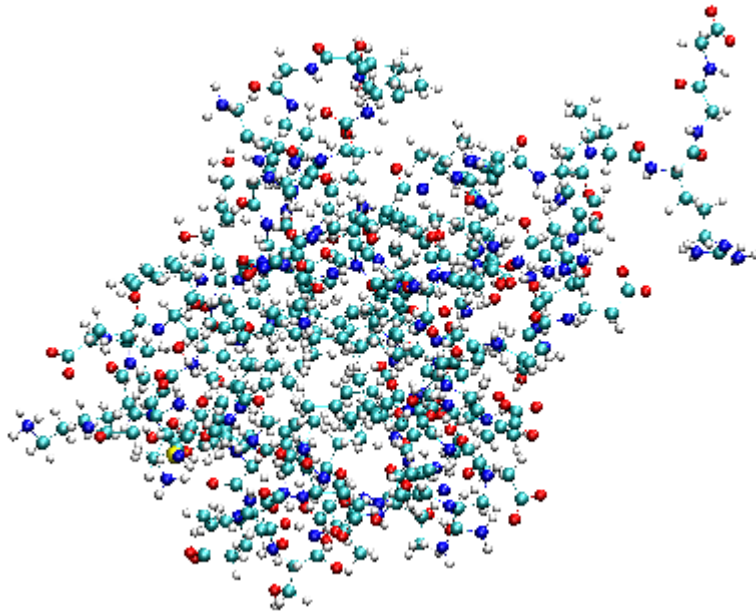
- ▶ macromolecular properties of proteins, which are related to their biological functions, often can be probed by studying the response of the system to an external perturbation, such as *thermal gradient*
- ▶ “small” perturbations are described by linear response theory (LRT), which relates transport (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 $T(\mathbf{r}, t)$ in the protein is governed by the heat diffusion (conduction) equation

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

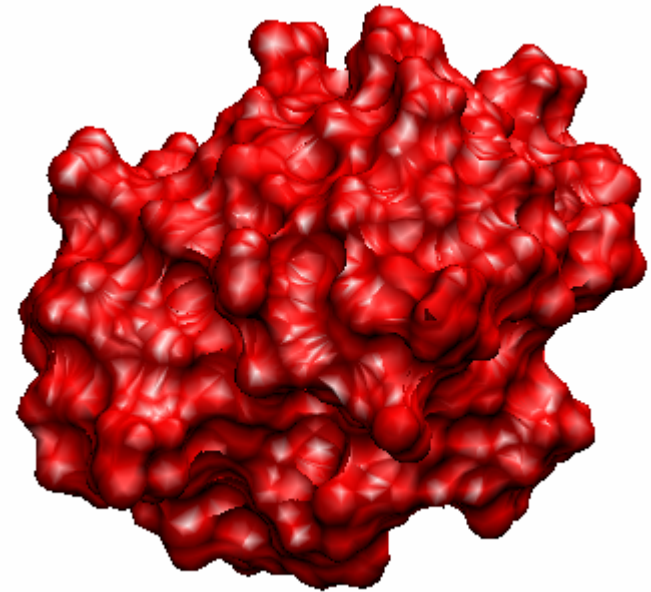
Atomic

vs

Mesososcopic



- each atom is treated individually
- length scale $\sim 0.1 \text{ \AA}$
- time scale $\sim 1 \text{ fs}$



- one partitions the protein in small volume elements and average over the contained atoms
- length scale $\geq 10 \text{ \AA} = 1 \text{ nm}$
- time scale $\geq 1 \text{ ps}$

Heat Conduction Equation

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

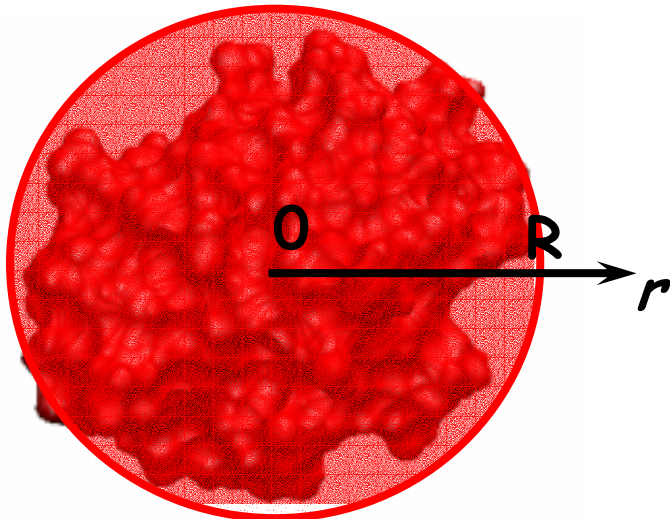
thermal diffusion
coefficient

$$D = K / \rho c$$

mass density

specific heat

thermal conductivity



- approximate the protein with a homogeneous sphere of radius $R \sim 20 \text{ \AA}$
- calculate $T(r, t)$ assuming initial and boundary conditions:

$$T(r, 0) = T_0 \text{ for } r < R$$

$$T(R, t) = T_{bath}$$

Thermal diffusion coefficient $D=?$

D is a phenomenological transport coefficient which needs to be calculated either from a microscopic (atomistic) theory, or derived from (**computer**) **experiment**

“Back of the envelope” estimate:

$$\frac{\partial T(\mathbf{r}, t)}{\partial t} = D \nabla^2 T(\mathbf{r}, t) \Rightarrow \frac{\Delta T}{\tau_0} \sim D \frac{\Delta T}{R^2} \Rightarrow D \sim R^2 / \tau_0$$

$$R \sim 10 \text{ \AA} = 10^{-9} \text{ m}, \quad \tau_0 \sim 10 \text{ ps} = 10^{-11} \text{ s} \quad ???$$

$$\Rightarrow D \sim R^2 / \tau_0 \sim 10^{-7} \text{ m}^2 / \text{s} = 10^{-3} \text{ cm}^2 / \text{s}$$

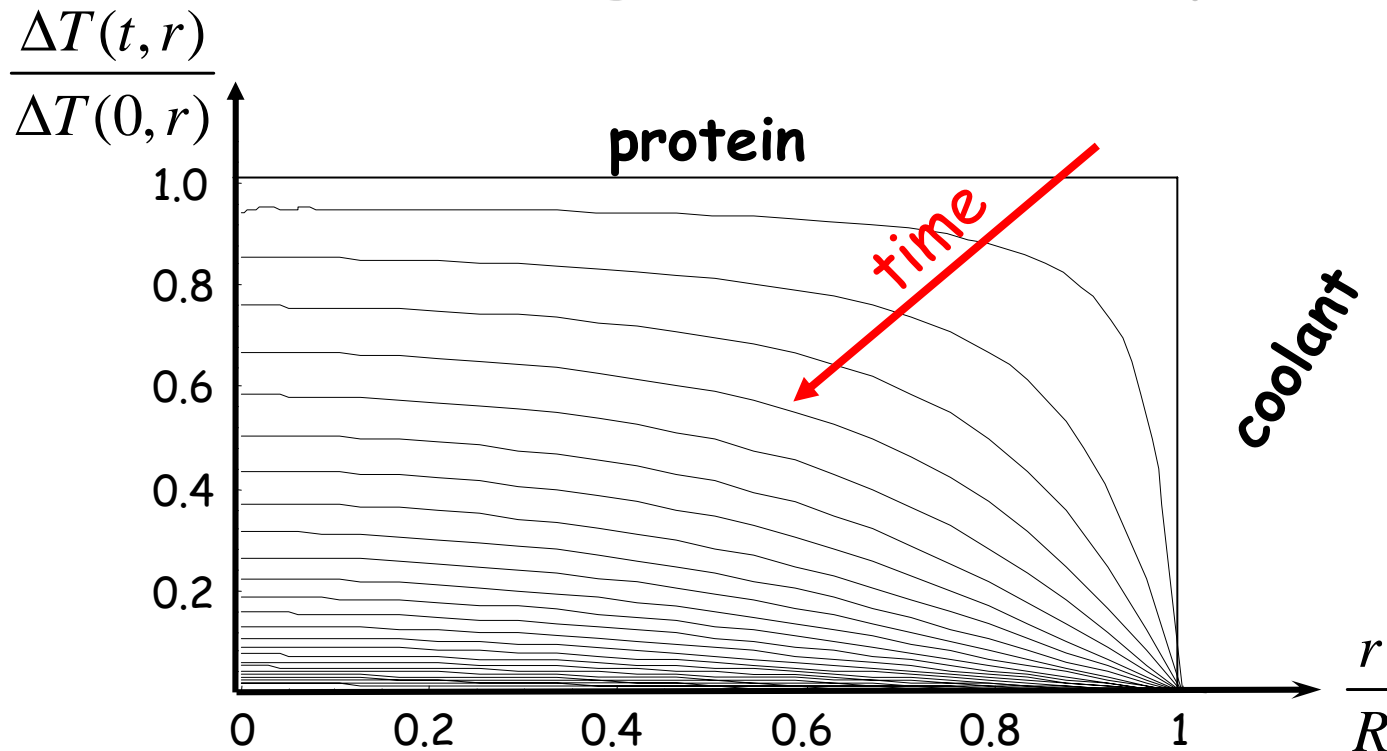
From MD simulation !

Solution of the Heat Equation

$$\langle \Delta T(t) \rangle = \langle \Delta T(0) \rangle \times \frac{6}{\pi^2} \sum_{n=1}^{\infty} \frac{1}{n^2} \exp\left(-n^2 \pi^2 t / \tau_0\right)$$

where $\langle \Delta T(t) \rangle \equiv \langle T(t) \rangle - T_{bath}$, $\tau_0 = R^2 / D$

averaged over the entire protein!



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)

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

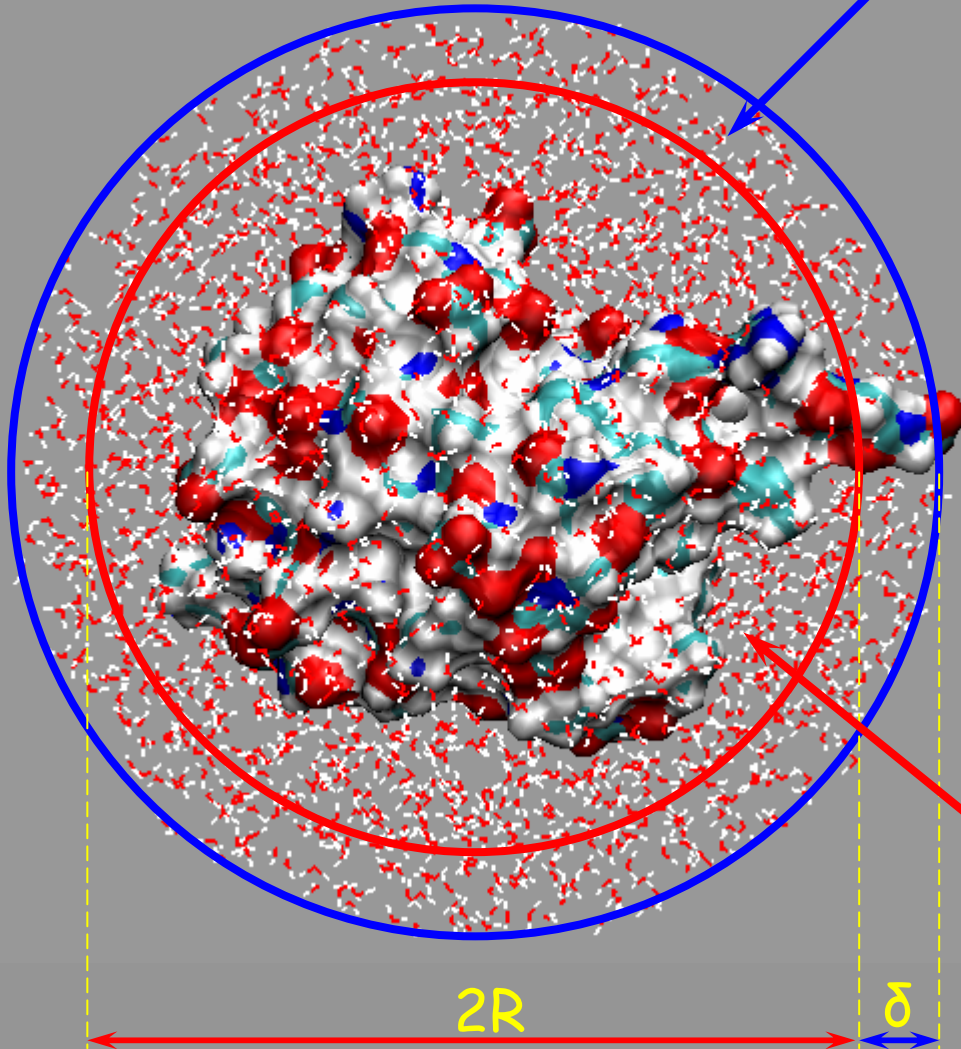
3. Random reassignment of atomic velocities according to Maxwell's distribution for desired temperature (velocity autocorrelation completely lost)

NAMD User Guide: Temperature Control

6.3 Temperature Control and Equilibration . . .	50
6.3.1 Langevin dynamics parameters	
6.3.2 Temperature coupling parameters . . .	
6.3.3 Temperature rescaling parameters . . .	
6.3.4 Temperature reassignment parameters .	

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

$$m\ddot{\mathbf{r}} = \mathbf{F}_{FF} + \mathbf{F}_H + \mathbf{F}_f + \mathbf{F}_L$$

\mathbf{F}_{FF} \rightarrow force field

\mathbf{F}_H \rightarrow harmonic restrain

\mathbf{F}_f \rightarrow friction

\mathbf{F}_L \rightarrow Langevin force

atoms in the inner region follow Newtonian dynamics

$$m\ddot{\mathbf{r}} = \mathbf{F}_{FF}$$

2-6-heat_diff: Simulated Cooling of UBQ

Start from a pre-equilibrated system of UBQ in a water sphere of radius 26Å
mol load psf ubq_ws.psf namdbin ubq_ws_eq.restart.coor

Create the a coolant layer of atoms of width 4Å

Select all atoms in the system:

set selALL [atomselect top all]

Find the center of the system:

set center [measure center \$selALL weight mass]

Find X, Y and Z coonidnates of the system's center:

foreach {xmass ymass zmass} \$center { break }

2-6-heat_diff: Simulated Cooling of UBQ

Select atoms in the outer layer:

```
set shellSel [atomselect top "not ( sqr(x-$xmass) + sqr(y-$ymass) +  
sqr(z-$zmass) <= sqr(22) ) "]
```

Set beta parameters of the atoms in this selection to 1.00:

```
$shellSel set beta 1.00
```

Select the entire system again:

```
set selALL [atomselect top all]
```

Create the pdb file that marks the atoms in the outer layer by 1.00 in the beta column:

```
$selALL writepdb ubq_shell.pdb
```

NAMD configuration file: **ubq_cooling.conf**

Spherical boundary conditions

Note: Do not set other boundary conditions and PME if spherical

boundaries are used

if {1} {

sphericalBC on

sphericalBCcenter 30.30817, 28.80499, 15.35399

sphericalBCr1 26.0

sphericalBCK1 10

sphericalBCexp1 2

}

this is to constrain atoms

if {1} {

constraints On

consref ubq_shell.pdb

consexp 2

conskfile ubq_shell.pdb

conskcol B

}

NAMD configuration file: `ubq_cooling.conf`

this is to cool a water layer

```
if {1} {  
tCouple          on  
tCoupleTemp      200  
tCoupleFile      ubq_shell.pdb  
tCoupleCol       B  
}
```

RUN THE SIMULATION FOR 10 ps

(5000 steps; timestep = 2 ps)

The (kinetic) temperature $T(t)$ is extracted from the simulation log (output) file; it can be plotted directly with

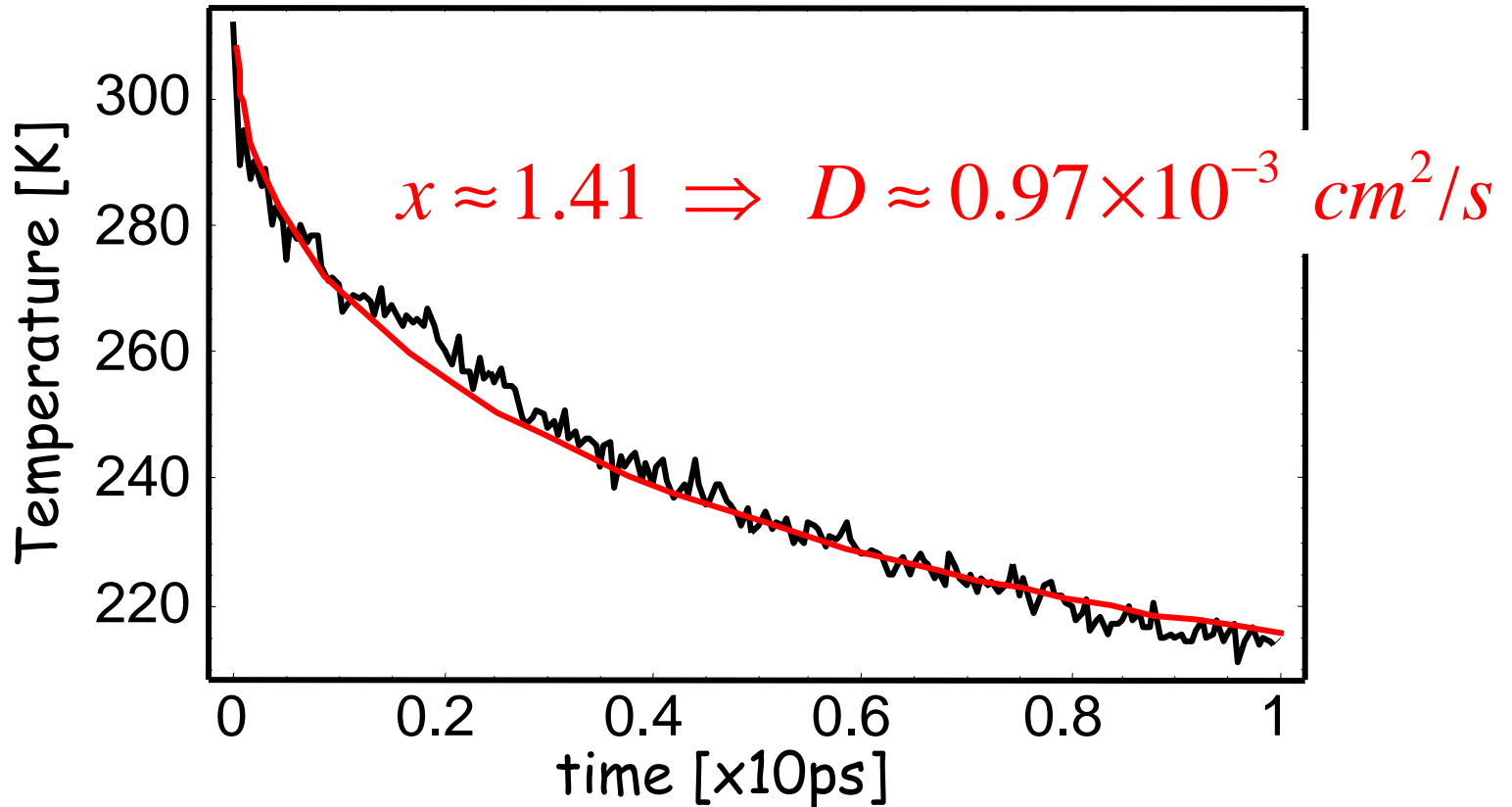
`namdplot TEMP ubq_cooling.log`

Is this procedure of getting $T(t)$ correct ?

Determine D by Fitting the Data

$$\frac{\langle \Delta T(t) \rangle}{\langle \Delta T(0) \rangle} = \frac{6}{\pi^2} \sum_{n=1}^{\infty} \frac{1}{n^2} \exp(-n^2 x t / t_0)$$

$$t_0 = 10 \text{ ps}, \quad x = \text{fitting parameter}, \quad D = \left(\frac{R}{\pi} \right)^2 \frac{x}{t_0}$$



Thermal Conductivity of UBQ

$$K = D \rho c$$

$$C_V = \langle \delta E^2 \rangle / k_B T^2 = \left(\langle E^2 \rangle - \langle E \rangle^2 \right) / k_B T^2$$

$$D \approx 0.97 \times 10^{-3} \text{ cm}^2/\text{s}$$

$$\rho \approx 1 \times 10^3 \text{ kg/m}^3$$