

Rare Events

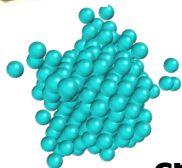
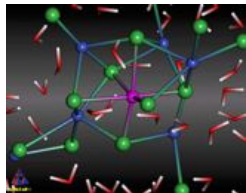
Transition state theory 16.1-16.2

Bennett-Chandler Approach 16.2

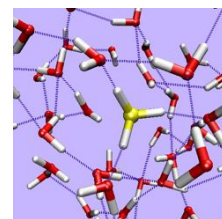
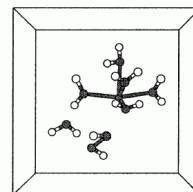
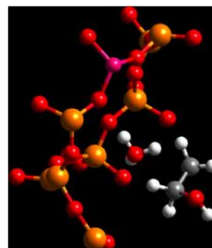
Transition path sampling 16.4

Outline

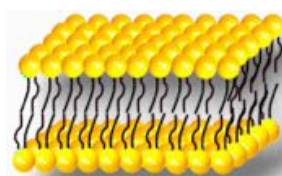
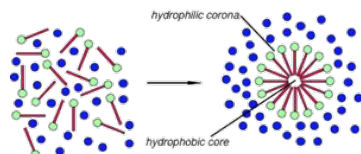
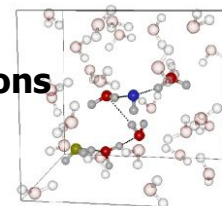
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 - Linear Response theory
 - Transition state theory
 - Free energy methods
 - Bennet Chandler approach
 - Example zeolites
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 - Transition path sampling
 - Rate constants
 - Reaction coordinate analysis
 - Application to biomolecules



crystallisation



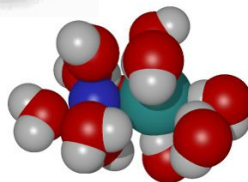
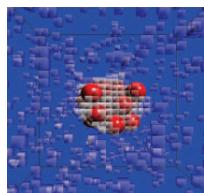
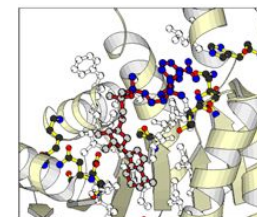
catalysis solution reactions



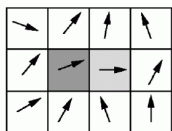
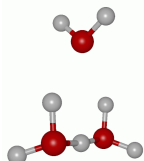
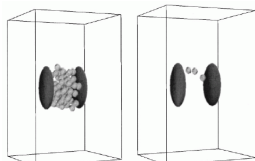
complex fluids

RARE EVENTS

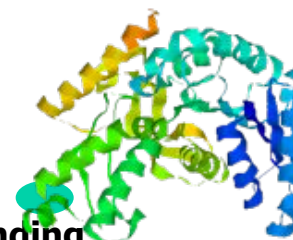
enzyme reactions



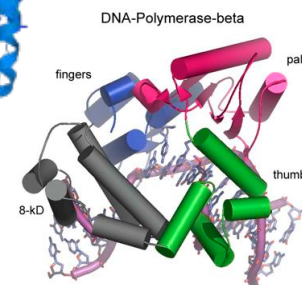
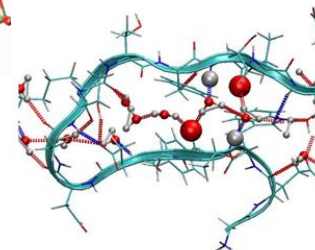
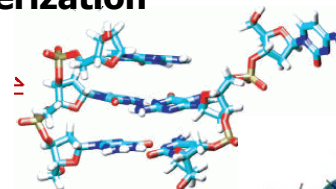
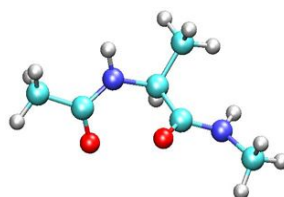
solvent effects



folding & binding



isomerization



Rare events

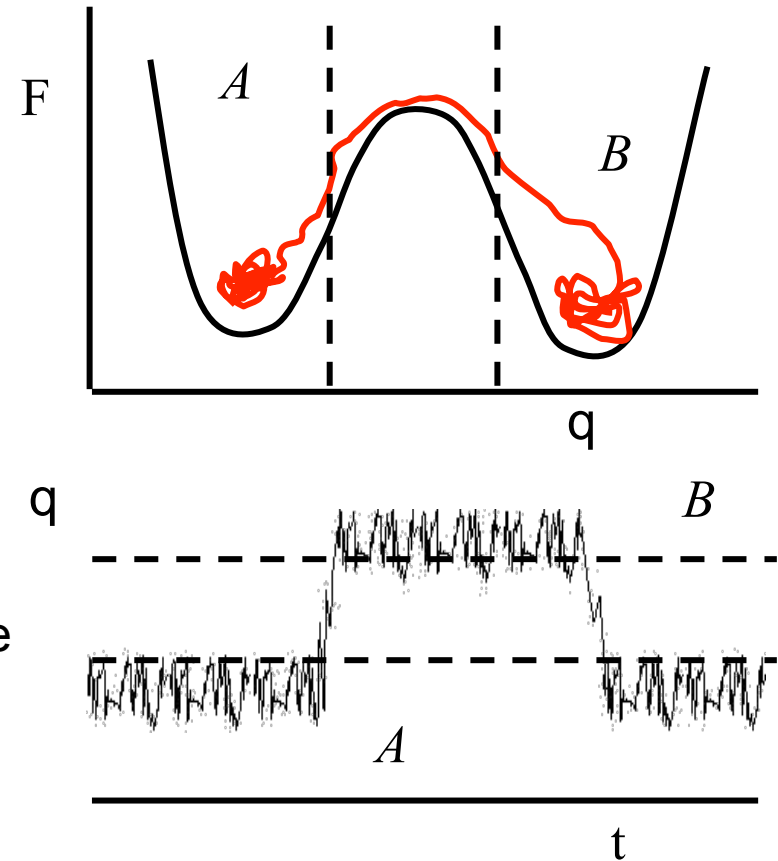
Interesting transitions in complex systems

- solution chemistry
- protein folding
- enzymatic reactions
- complex surface reactions
- diffusion in porous media
- nucleation

These reactions happen on a long time scale compared to the molecular timescale

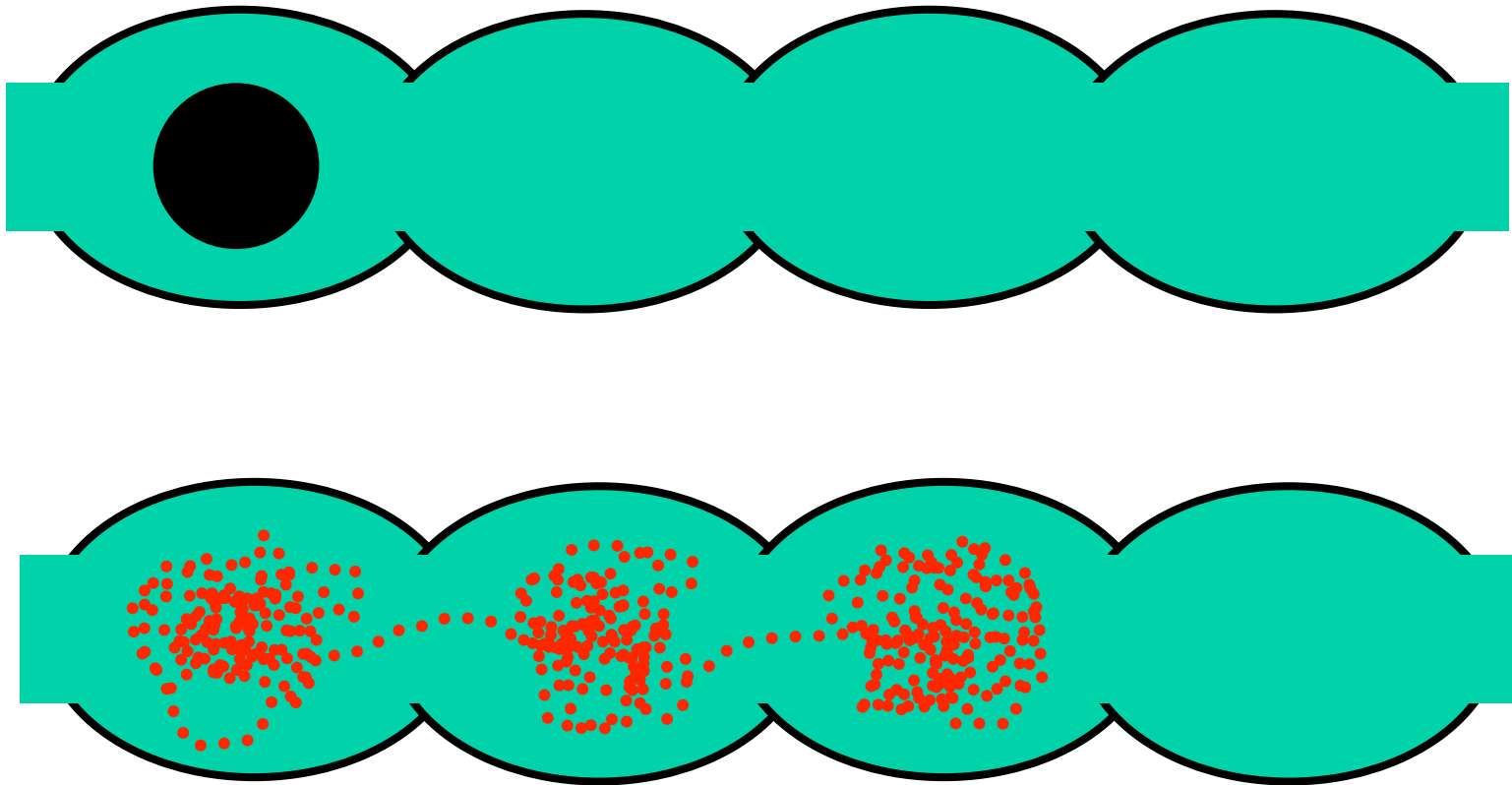


dominated by collective, rare events
Straightforward MD very inefficient



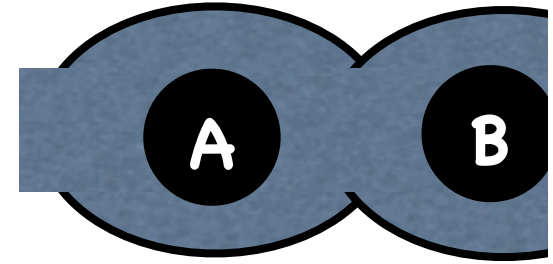
$$\tau_{mol} \ll \tau_{stable}$$

Example: Diffusion in porous material



Phenomenological reaction kinetics

A rare event can be seen as a chemical reaction between **reactant A** and **product B**



The change in population $c(t)$ is ($0 < c < 1$)

$$\frac{dc_A(t)}{dt} = -k_{A \rightarrow B} c_A(t) + k_{B \rightarrow A} c_B(t) \quad \frac{dc_B(t)}{dt} = +k_{A \rightarrow B} c_A(t) - k_{B \rightarrow A} c_B(t)$$

Total number change in population

$$\frac{d[c_A(t) + c_B(t)]}{dt} = 0$$

Equilibrium:

$$\dot{c}_A(t) = \dot{c}_B(t) = 0$$

This gives a relation between equilibrium population and reaction rates

$$\frac{\langle c_A \rangle}{\langle c_B \rangle} = \frac{k_{B \rightarrow A}}{k_{A \rightarrow B}}$$

Relaxation time

Let us make a perturbation of the equilibrium populations.

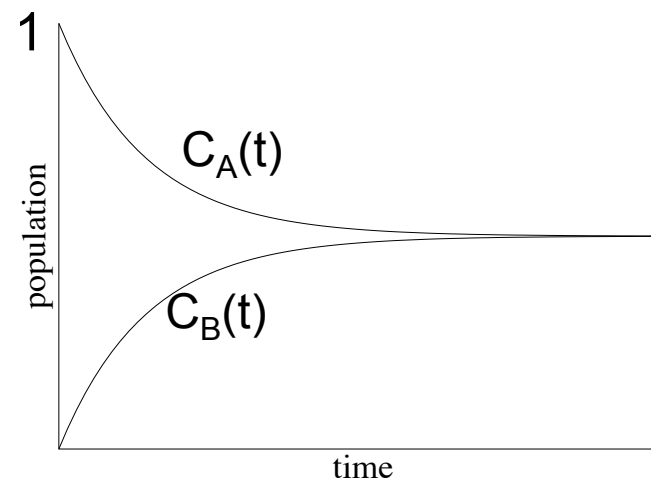
The dynamics of such an equilibrium fluctuation gives the desired information on the response of the system to an external field

For state A $c_A(t) = \langle c_A \rangle + \Delta c_A(t)$ For state B: $c_B(t) = \langle c_B \rangle - \Delta c_A(t)$

We can rewrite the kinetics in terms of the perturbation:

$$\frac{d\Delta c_A(t)}{dt} = -k_{A \rightarrow B} \Delta c_A(t) - k_{B \rightarrow A} \Delta c_A(t)$$

$$\begin{aligned} \Delta c_A(t) &= \Delta c_A(0) \exp[-(k_{A \rightarrow B} + k_{B \rightarrow A})t] \\ &= \Delta c_A(0) \exp[-t/\tau] \end{aligned}$$



With

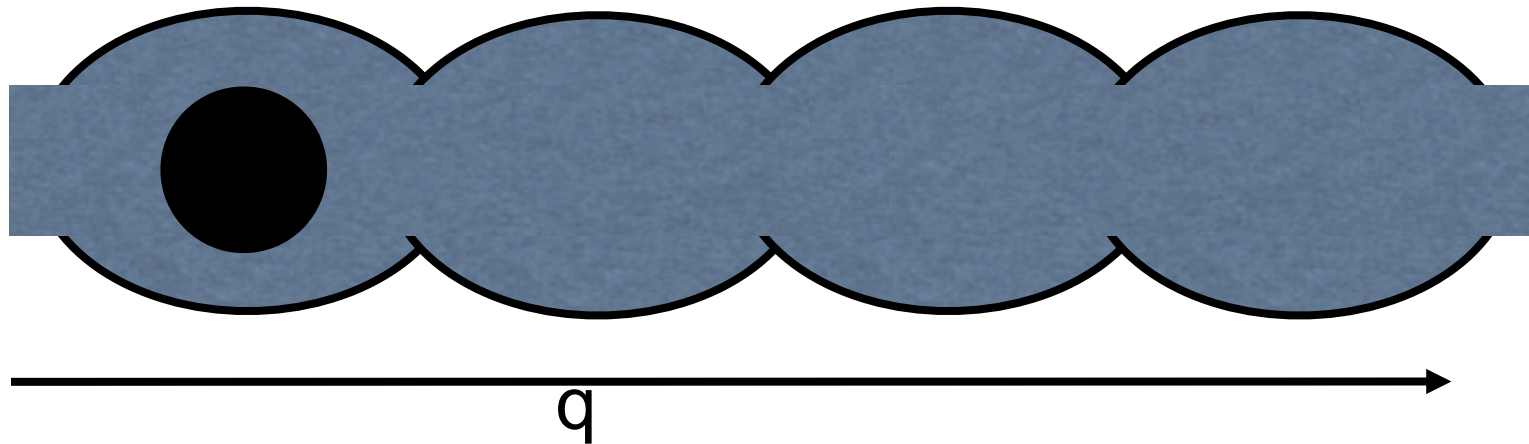
$$\tau = (k_{A \rightarrow B} + k_{B \rightarrow A})^{-1} = k_{A \rightarrow B}^{-1} \left(1 + \langle c_A \rangle / \langle c_B \rangle\right)^{-1} = \frac{\langle c_B \rangle}{k_{A \rightarrow B}}$$

$$c_A(t) + c_B(t) = 1$$

An arrow points from this equation to the term $\langle c_A \rangle / \langle c_B \rangle$ in the equation above.

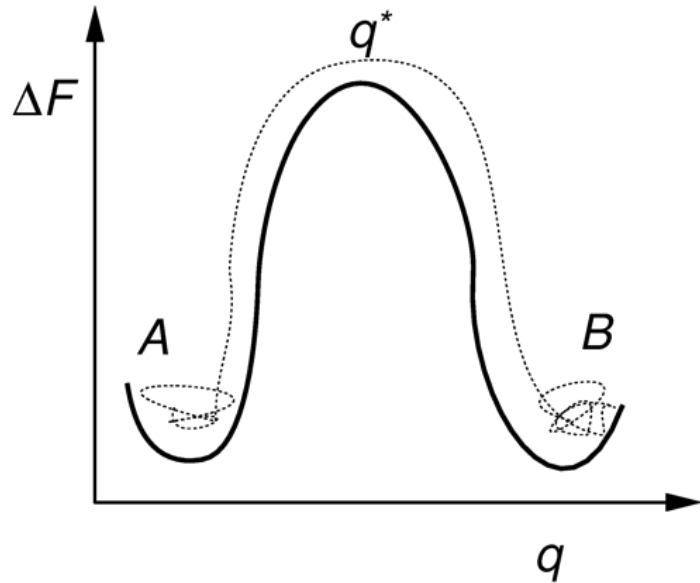
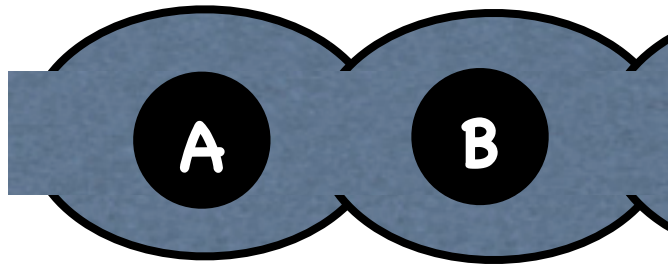
Microscopic theory

Microscopic description of the progress of a reaction



Reaction coordinate: in this case the z-coordinate of the particle

We need to write the kinetics of the reaction in terms of this microscopic reaction coordinate q



Let us introduce the function g_A :

$$g_A(q - q^*) = 1 - \theta(q - q^*) = \theta(q^* - q)$$

With this function we write for the **probability** $c_A(t)$ the system is in state A:

$$\langle c_A(t) \rangle = \langle g_A(t) \rangle$$

Reaction coordinate

Reactant A: $q < q^*$

Product B: $q > q^*$

Transition state: $q = q^*$

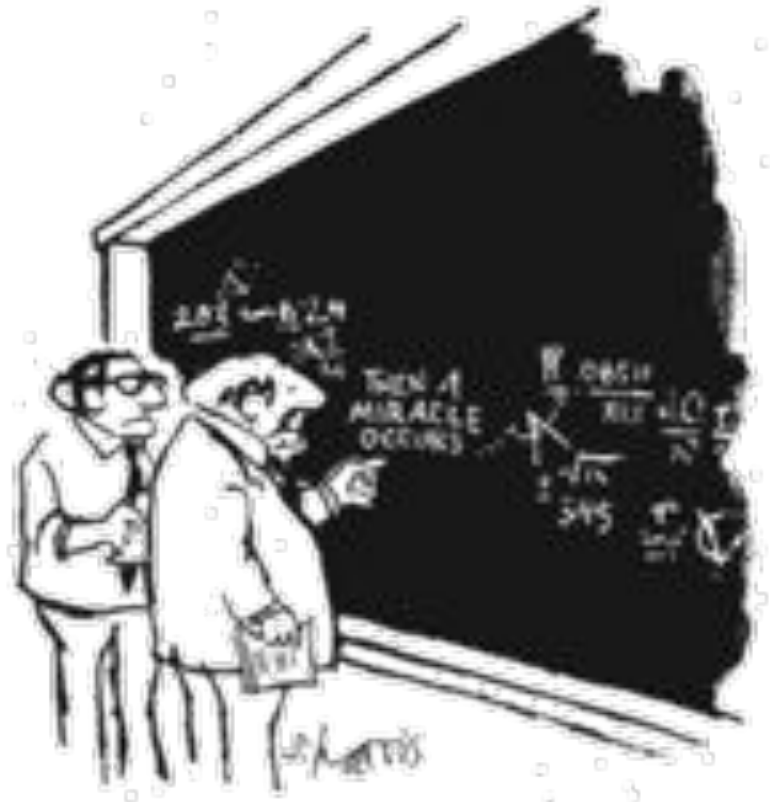
Heaviside θ -function

$$\theta(q - q^*) = \begin{cases} 0 & q - q^* < 0 \\ 1 & q - q^* > 0 \end{cases}$$

Microscopic theory

Is going to give us the
macroscopic relaxation in terms of a
microscopic time correlation function

$$\exp[-t/\tau] = \frac{\langle \Delta g_A(0) \Delta g_A(t) \rangle}{\langle c_A \rangle \langle c_B \rangle}$$



"I THINK YOU SHOULD BE MADE
EXPLICIT HERE IN STEP TWO."

Perturbed Hamiltonian

Let us consider the effect of a static perturbation:

$$H = H_0 - \varepsilon g_A (q - q^*)$$

This external potential increases the concentration of A

For the equilibrium concentration as a function of ε :

$$\Delta c_A = \langle c_A \rangle_\varepsilon - \langle c_A \rangle_0 = \langle g_A \rangle_\varepsilon - \langle g_A \rangle_0$$

We need to compute the ensemble average in the form of :

$$\langle A \rangle_0 = \frac{\int d\Gamma A \exp[-\beta H_0]}{\int d\Gamma \exp[-\beta H_0]}$$

Linear Response theory (static)

The original Hamiltonian (H_0) is perturbed by εD :

$$H = H_0 - \varepsilon D$$

This gives as change in the expectation value of A :

$$\langle \Delta A \rangle = \langle A \rangle - \langle A \rangle_0$$

with

$$\langle A \rangle = \frac{\int d\Gamma A \exp[-\beta(H_0 - \varepsilon D)]}{\int d\Gamma \exp[-\beta(H_0 - \varepsilon D)]} \quad \langle A \rangle_0 = \frac{\int d\Gamma A \exp[-\beta H_0]}{\int d\Gamma \exp[-\beta H_0]}$$

If the perturbation is small we can write

$$\langle A \rangle = \langle A \rangle_0 + \frac{\partial \langle A \rangle_0}{\partial \varepsilon} \varepsilon$$

For such a small perturbation

$$\langle \Delta A \rangle = \frac{\partial \langle A \rangle_0}{\partial \varepsilon} \varepsilon = \left\langle \frac{\partial A}{\partial \varepsilon} \right\rangle_0 \varepsilon$$

with

$$\left\langle \frac{\partial A}{\partial \varepsilon} \right\rangle = \frac{\partial \langle A \rangle}{\partial \varepsilon} = \frac{\int d\Gamma \beta A D \exp[-\beta(H_0 - \varepsilon D)] \int d\Gamma \exp[-\beta(H_0 - \varepsilon D)]}{\left\{ \int d\Gamma \exp[-\beta(H_0 - \varepsilon D)] \right\}^2} - \frac{\int d\Gamma A \exp[-\beta(H_0 - \varepsilon D)] \int d\Gamma \beta D \exp[-\beta(H_0 - \varepsilon D)]}{\left\{ \int d\Gamma \exp[-\beta(H_0 - \varepsilon D)] \right\}^2}$$

Evaluated for $\varepsilon = 0$

$$\left\langle \frac{\partial A}{\partial \varepsilon} \right\rangle_0 = \frac{\int d\Gamma \beta A D \exp[-\beta H_0]}{\left\{ \int d\Gamma \exp[-\beta H_0] \right\}} - \frac{\int d\Gamma A \exp[-\beta H_0]}{\int d\Gamma \exp[-\beta H_0]} \times \frac{\int d\Gamma \beta D \exp[-\beta H_0]}{\int d\Gamma \exp[-\beta H_0]}$$

Giving:

$$\left\langle \frac{\partial A}{\partial \varepsilon} \right\rangle_0 = \beta \left\{ \langle AD \rangle_0 - \langle A \rangle_0 \langle D \rangle_0 \right\}$$

If we apply this result for c_A : $\left\langle \frac{\partial A}{\partial \varepsilon} \right\rangle_0 = \beta \left\{ \langle AD \rangle_0 - \langle A \rangle_0 \langle D \rangle_0 \right\}$

with $H = H_0 - \varepsilon g_A (q - q^*)$

$$\Delta c_A = \langle g_A \rangle_\varepsilon - \langle g_A \rangle_0$$

Since $g_A = 0$ or 1 :
 $g_A(x) g_A(x) = g_A(x)$

$$\frac{\partial \Delta c_A}{\partial \varepsilon} = \beta \left(\langle (g_A)^2 \rangle_0 - \langle g_A \rangle_0^2 \right)$$

$$= \beta \left(\langle g_A \rangle_0 (1 - \langle g_A \rangle_0) \right)$$

$$= \beta \left(\langle c_A \rangle_0 (1 - \langle c_A \rangle_0) \right) = \beta \langle c_A \rangle_0 \langle c_B \rangle_0$$

Giving:

$$\Delta c_A = \beta \langle c_A \rangle_0 \langle c_B \rangle_0 \varepsilon$$

Linear Response theory (dynamic)

Let us now switch off the perturbation at $t=0$

$$H = H_0 - \varepsilon D$$

$$H = H_0 \quad \text{at } t > 0:$$

Let us see how the system relaxes to equilibrium (dynamical perturbation)

$$\langle \Delta A(t) \rangle = \langle A(t) \rangle - \langle A \rangle_0 = \langle A(t) \rangle$$

We take $\langle A \rangle_0 = 0$

Similar as for the static case for small values of ε , we have

$$\left\langle \frac{\partial A(t)}{\partial \varepsilon} \right\rangle_0 = \frac{\int d\Gamma \beta A(t) D \exp[-\beta H_0]}{\left\{ \int d\Gamma \exp[-\beta H_0] \right\}} = \beta \langle D(0) A(t) \rangle$$

Giving:
$$\langle \Delta A(t) \rangle = \beta \varepsilon \langle D(0) A(t) \rangle$$

$$\langle \Delta A(t) \rangle = \beta \varepsilon \langle D(0) A(t) \rangle$$

If we apply this result to $D = \Delta g_A$ and $A = \Delta g_A$

We obtain: $\langle \Delta c_A(t) \rangle = \beta \varepsilon \langle \Delta g_A(0) \Delta g_A(t) \rangle$

From static perturbation:

$$\beta \varepsilon = \frac{\Delta c_A(0)}{\langle c_A \rangle \langle c_B \rangle}$$

$$\langle \Delta c_A(t) \rangle = \Delta c_A(0) \frac{\langle \Delta g_A(0) \Delta g_A(t) \rangle}{\langle c_A \rangle \langle c_B \rangle}$$

Compare linear response expression with the macroscopic expression

$$\Delta c_A(t) = \Delta c_A(0) \exp[-t/\tau]$$

Microscopic rate expression

$$\exp[-t/\tau] = \frac{\langle \Delta g_A(0) \Delta g_A(t) \rangle}{\langle c_A \rangle \langle c_B \rangle}$$

Δ has disappeared because of the derivative

Derivative

$$-\frac{1}{\tau} \exp[-t/\tau] = \frac{\langle g_A(0) \dot{g}_A(t) \rangle}{\langle c_A \rangle \langle c_B \rangle} = -\frac{\langle \dot{g}_A(0) g_A(t) \rangle}{\langle c_A \rangle \langle c_B \rangle}$$

Stationary (t is arbitrary, only depends on τ)

$$\frac{d}{dt} \langle A(t) B(t + \tau) \rangle = 0$$

$$\langle A(t) \dot{B}(t + \tau) \rangle + \langle \dot{A}(t) B(t + \tau) \rangle = 0$$

$$\langle A(0) \dot{B}(\tau) \rangle = -\langle \dot{A}(0) B(\tau) \rangle$$

We have
$$\frac{1}{\tau} \exp[-t/\tau] = \frac{\langle \dot{g}_A(0) g_A(t) \rangle}{\langle c_A \rangle \langle c_B \rangle}$$

Using
$$\tau = k_{A \rightarrow B}^{-1} \left(1 + \langle c_A \rangle / \langle c_B \rangle \right)^{-1} = \frac{\langle c_B \rangle}{k_{A \rightarrow B}}$$

For sufficiently short t, we obtain

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{g}_A(0) g_A(t) \rangle}{\langle c_A \rangle}$$

Using the definition of g_A we can write

$$\dot{g}_A(q - q^*) = \dot{q} \frac{\partial g_A(q - q^*)}{\partial q} = -\dot{q} \frac{\partial g_B(q - q^*)}{\partial q}$$

$$k_{A \rightarrow B}(t) = \frac{\left\langle \dot{q}(0) \frac{\partial g_B(q(0) - q^*)}{\partial q} g_B(t) \right\rangle}{\langle c_A \rangle}$$

We now have an expression that relates the macroscopic reaction rate to microscopic properties

$$k_{A \rightarrow B}(t) = \frac{\left\langle \dot{q}(0) \frac{\partial g_B(q(0) - q^*)}{\partial q} g_B(t) \right\rangle}{\langle c_A \rangle}$$

$$g_B(t) = \theta(q(t) - q^*)$$

$$\frac{\partial g_B(q(0) - q^*)}{\partial q} = \frac{\partial \Theta(q(0) - q^*)}{\partial q} \\ = \delta(q(0) - q^*)$$

$$\dot{q}(0)$$

$$\langle c_A \rangle = \langle \Theta(q^* - q) \rangle$$

Let us look at the different terms in this equation

Only when the system is in the product state we get a contribution to the ensemble average

Only when the system starts at the transition state, we get a contribution to the ensemble average

Velocity at t=0

Concentration of A

$$k_{A \rightarrow B}(t) = \frac{\left\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \right\rangle}{\langle \theta(q^* - q) \rangle}$$

Transition state theory

$$k_{A \rightarrow B}(t) = \frac{\left\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \right\rangle}{\left\langle \theta(q^* - q) \right\rangle}$$

Let us consider the limit: $t \rightarrow 0^+$

$$\lim_{t \rightarrow 0^+} = \theta(q(t) - q^*) = \theta(\dot{q}(t))$$

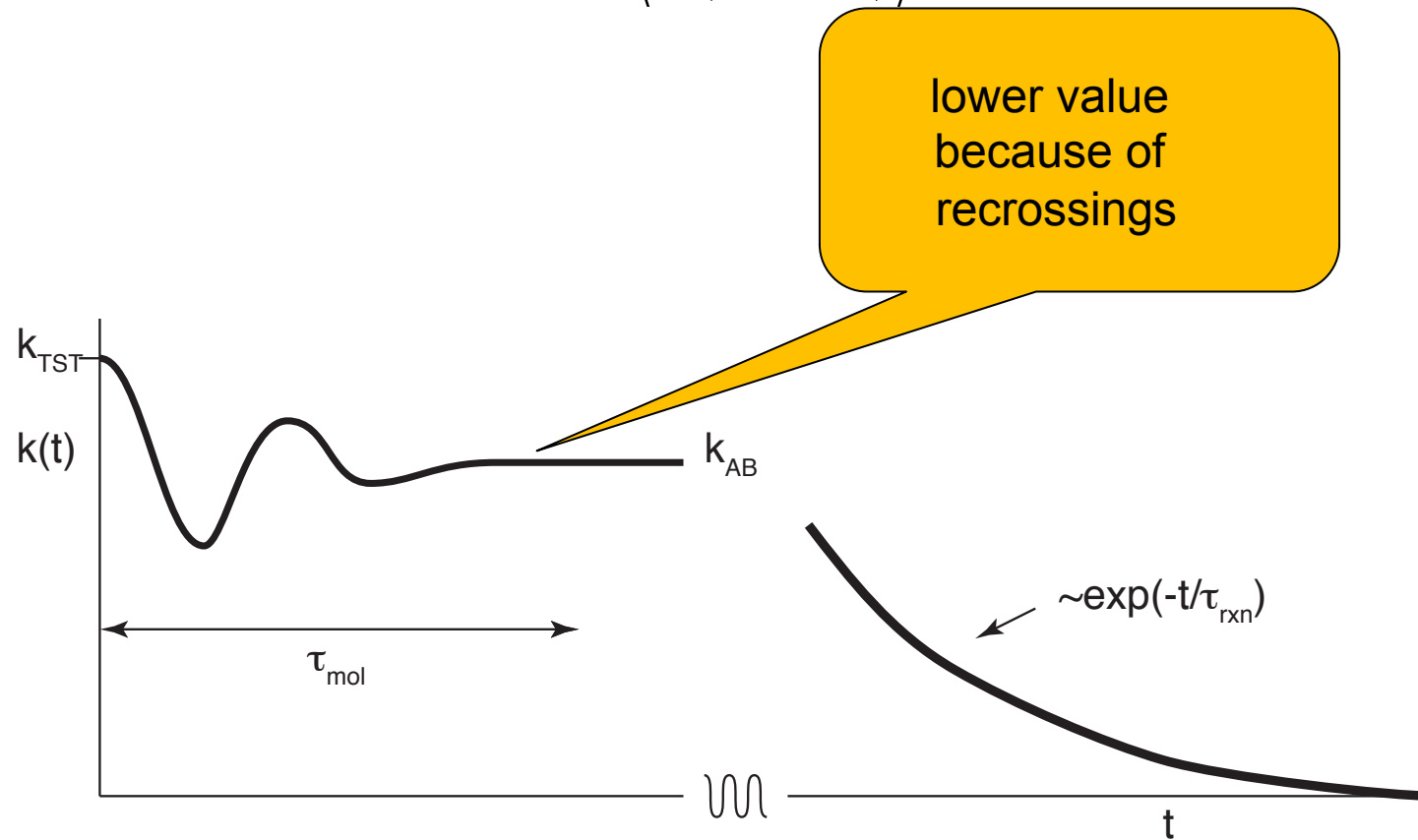
This gives:

$$k_{A \rightarrow B}^{TST} = \frac{\left\langle \dot{q}(0) \delta(q(0) - q^*) \theta(\dot{q}) \right\rangle}{\left\langle \theta(q^* - q) \right\rangle}$$

Eyring's transition state theory

Decay of rate expression

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$



Transition state theory

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$

We can rewrite this expression as a product

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \rangle}{\langle \delta(q(0) - q^*) \rangle} \times \frac{\langle \delta(q(0) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$

Conditional “probability” to find a particle on the top of the barrier with a positive velocity

Ratio of probabilities to find particle on top of the barrier and in the state A

$$k_{A \rightarrow B}(t) = \left\langle \dot{q}(0) \theta(q(t) - q^*) \right\rangle_{q=q^*} \times \frac{\langle \delta(q(0) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$

Free energy barrier

$$\frac{\langle \delta(q(0) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$

Ratio of the probabilities to find a particle on top of the barrier and in the state A

Probability to be on top of the barrier:

$$\langle \delta(q^* - q) \rangle = C \int dq \delta(q - q^*) \exp(-\beta F(q)) = C \exp(-\beta F(q^*))$$

Probability to be in state A:

$$\langle \Theta(q^* - q) \rangle = C \int dq \Theta(q - q^*) \exp(-\beta F(q)) = C \int_{q < q^*} dq \exp(-\beta F(q))$$

This gives:

$$\frac{\langle \delta(q(0) - q^*) \rangle}{\langle \theta(q^* - q) \rangle} = \frac{\exp(-\beta F(q^*))}{\int_{q < q^*} dq \exp(-\beta F(q))}$$

We need to determine the free energy as a function of the order parameter

$\left\langle \dot{q}(0) \theta(q(t) - q^*) \right\rangle_{q=q^*}$ Conditional “probability” to find a particle on the top of the barrier with a positive velocity

$\dot{q}(0)$ Assume that on top of the barrier the particle is in equilibrium: use Maxwell-Boltzmann distribution to generate this velocity

$\dot{q}(0) \theta(q(t) - q^*)$ Only particles with a positive velocity end up in the product state. We assume that once in the product state they stay there.

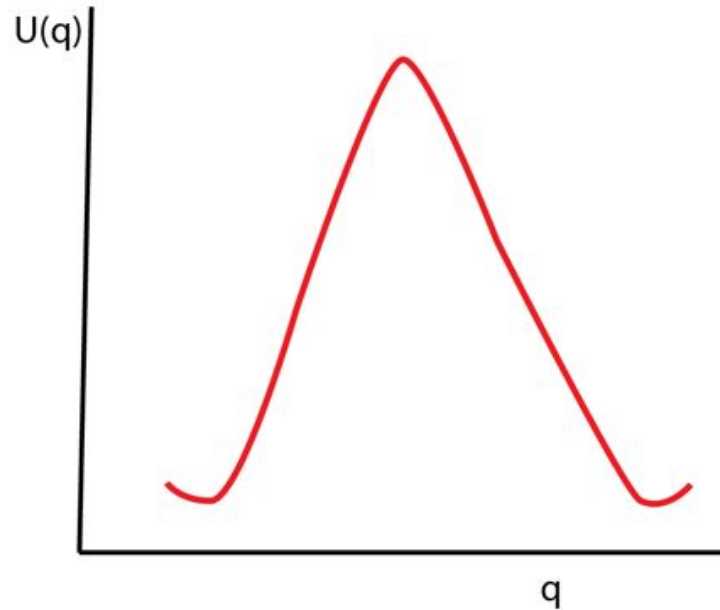
$$\lim_{t \rightarrow 0^+} \dot{q}(0) \theta(q(t) - q^*) = \dot{q}(0) \theta(\dot{q}(0)) = 0.5 |\dot{q}(0)|$$

$$k_{A \rightarrow B}^{TST} = \lim_{t \rightarrow 0^+} \left\langle \dot{q}(0) \theta(q(t) - q^*) \right\rangle_{q=q^*} \times \frac{\left\langle \delta(q(0) - q^*) \right\rangle}{\left\langle \theta(q^* - q) \right\rangle}$$

$$k_{A \rightarrow B}^{TST} = 0.5 |\dot{q}(0)| \frac{\exp(-\beta F(q^*))}{\int_{q < q^*} dq \exp(-\beta F(q))}$$

Eyring's TST

1-D ideal gas particle on a hill



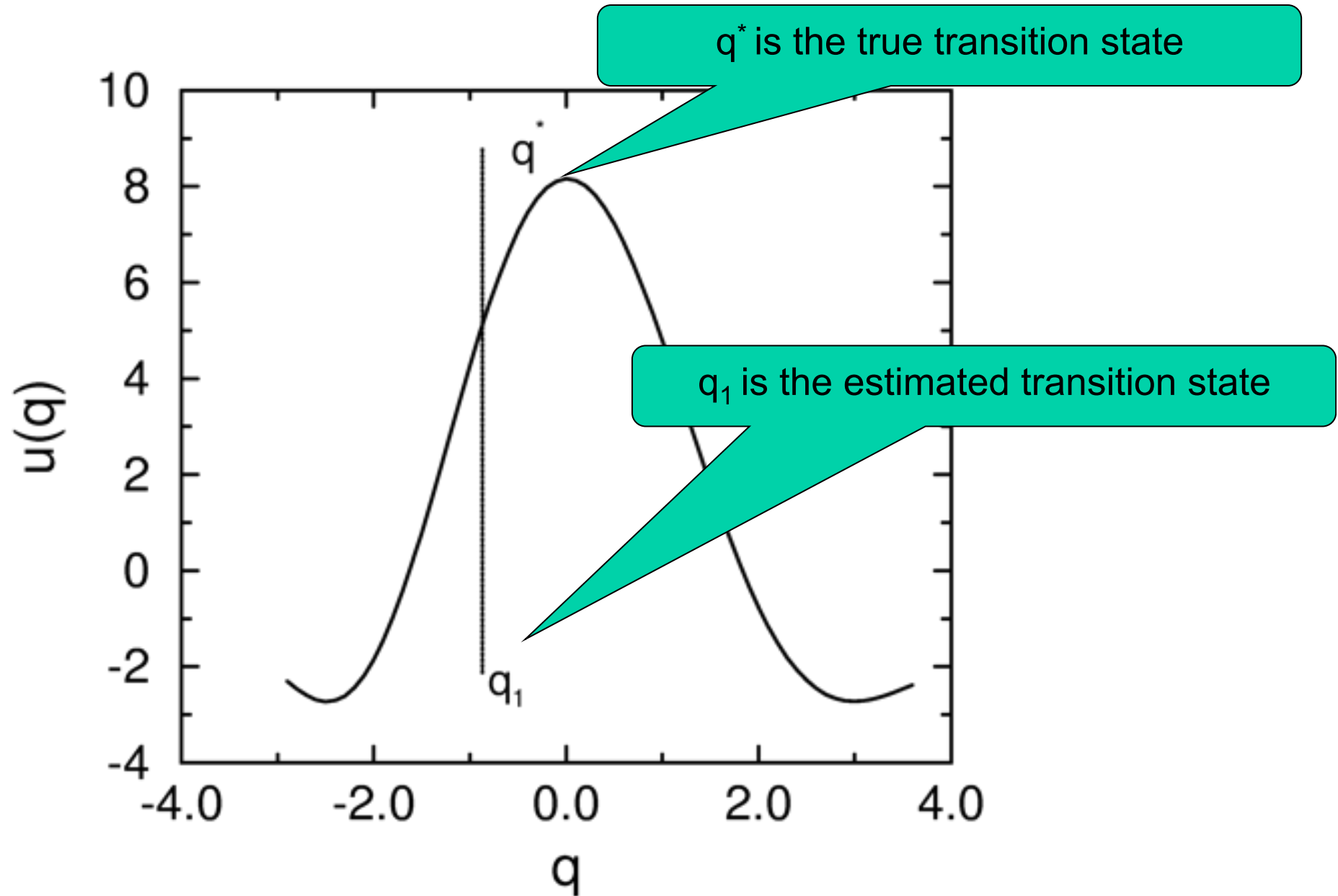
$$k_{A \rightarrow B}^{TST} = 0.5 \left| \dot{q}(0) \right| \frac{\exp(-\beta F(q^*))}{\int_{q < q^*} dq \exp(-\beta F(q))}$$

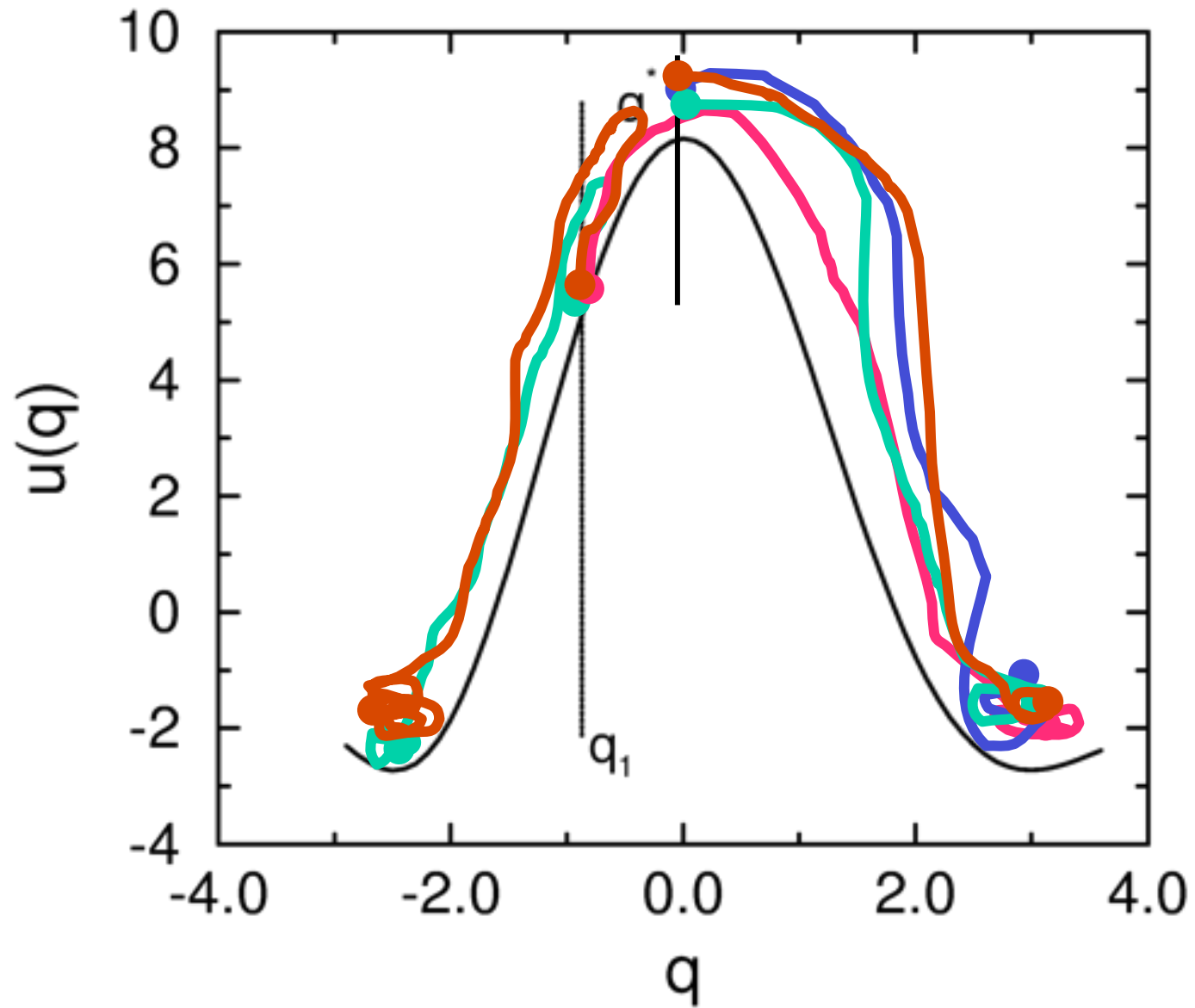
Maxwell-Boltzmann: $\left| \dot{q}(0) \right| = \sqrt{\frac{2k_B T}{\pi m}}$

This gives for the hopping rate

$$k_{A \rightarrow B}^{TST} = \sqrt{\frac{k_B T}{2\pi m}} \frac{\exp(-\beta U(q^*))}{\int_{q < q^*} dq \exp(-\beta U(q))}$$

Ideal gas particle on a not-so-ideal hill



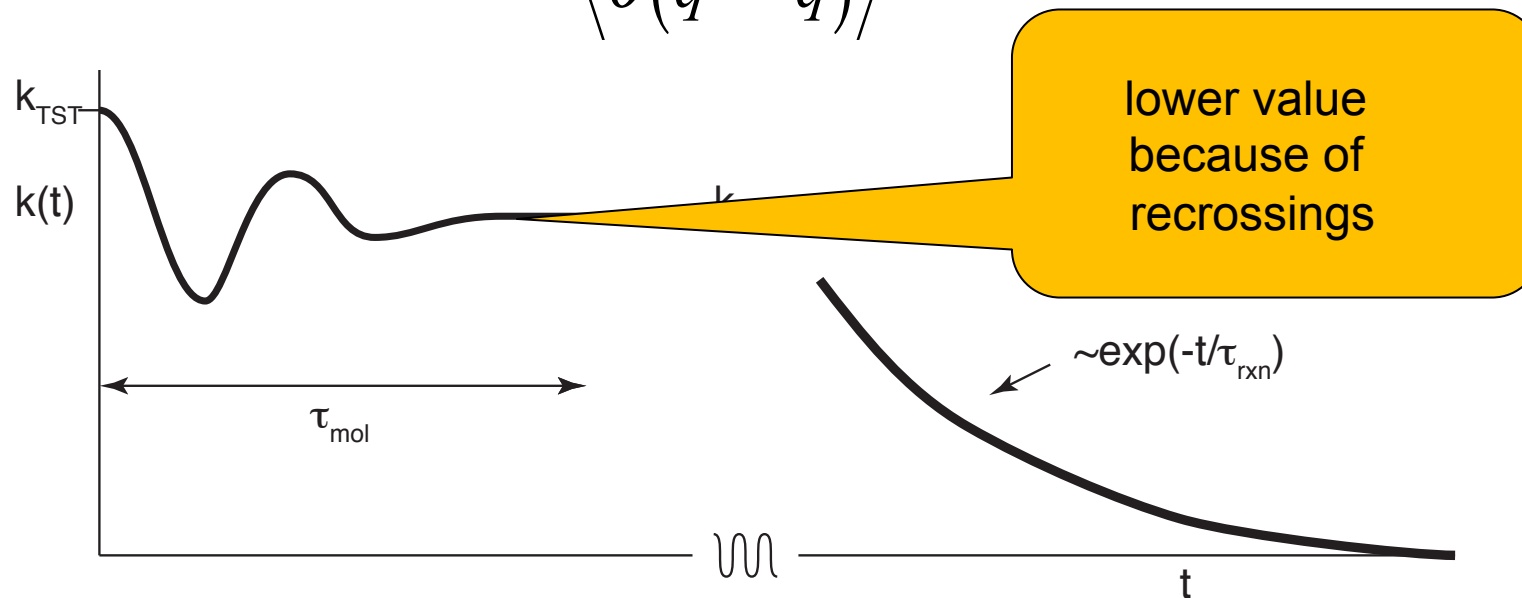


For this case transition state theory will **overestimate** the hopping rate

Transition state theory

- One has to know the free energy accurately (MC/MD)
- Gives only an upper bound to the reaction rate
- Assumptions underlying transition theory should hold: *no recrossings*

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$



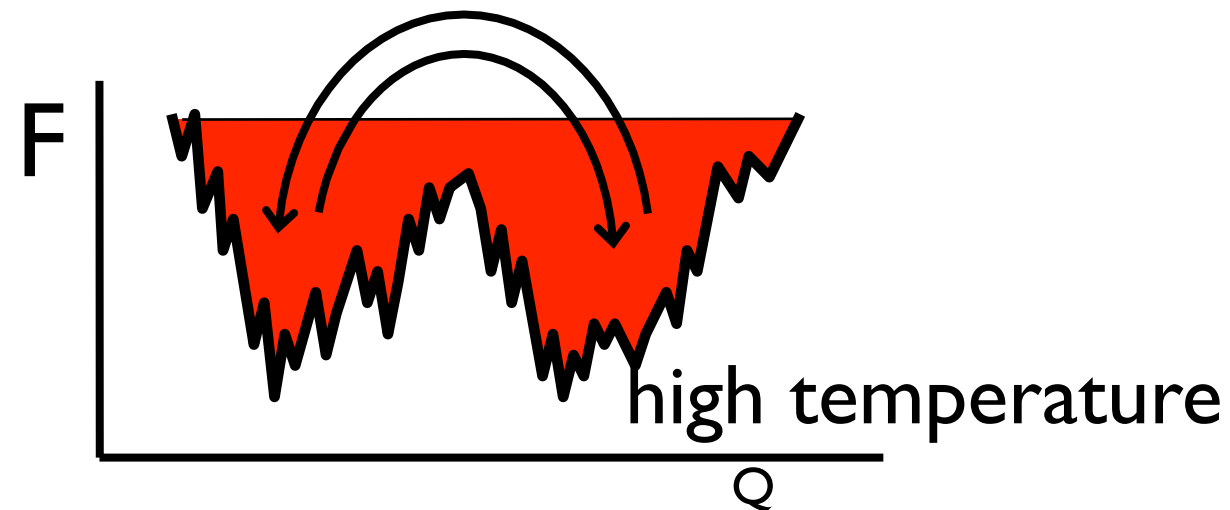
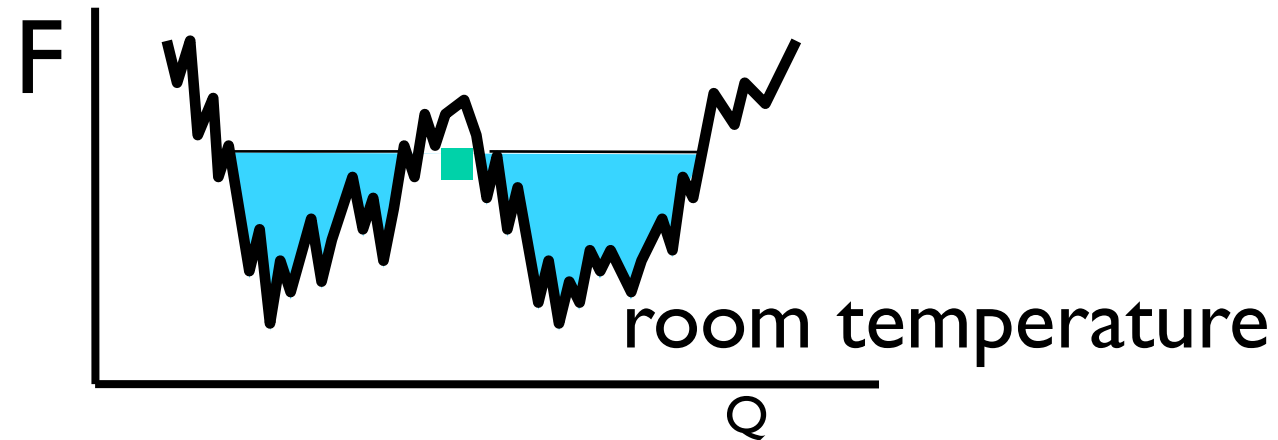
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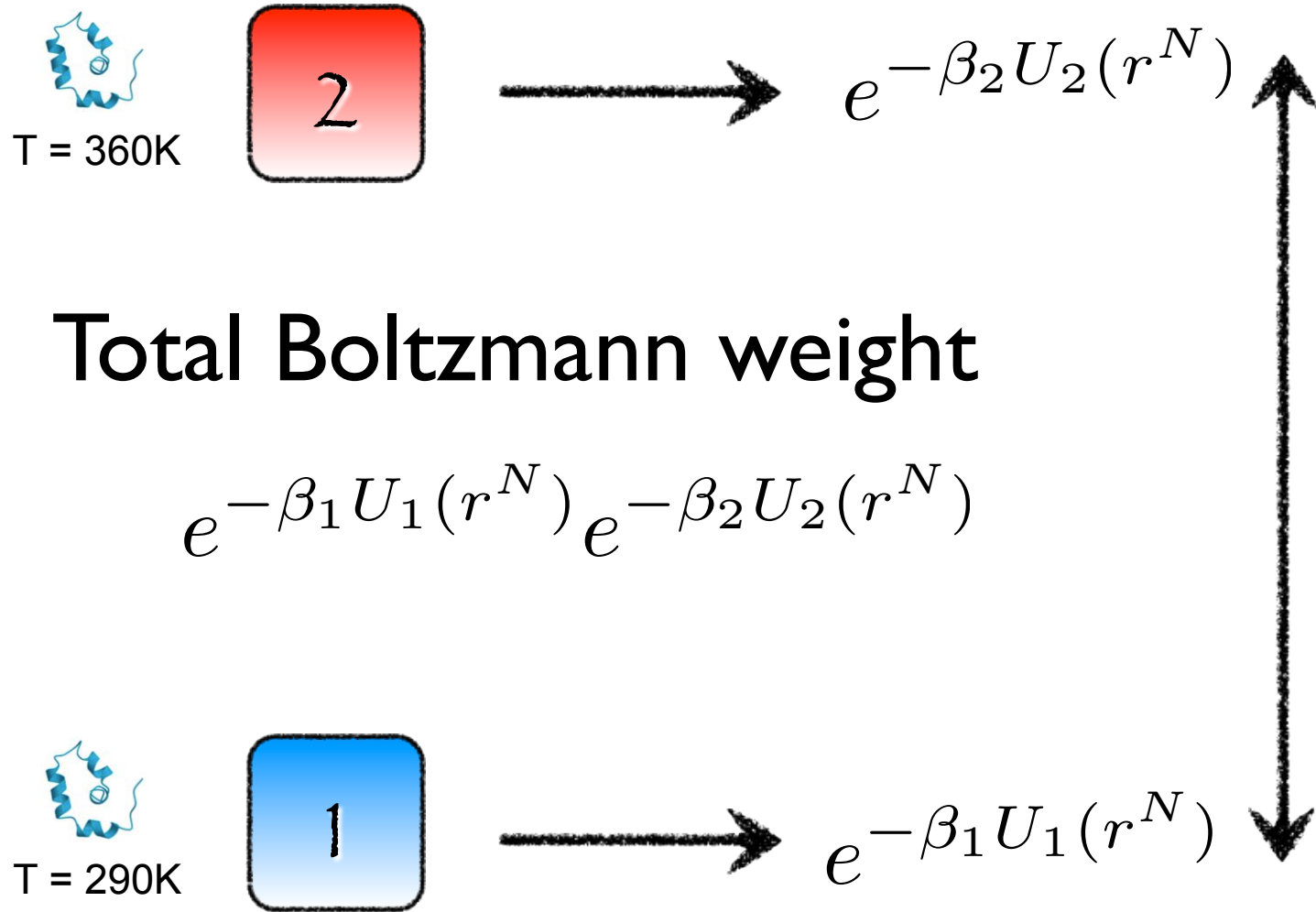
Free energy barriers in complex systems

- Straightforward MD or MC and then use $\beta F(q) = -\ln \langle \delta(q(r) - q) \rangle$ is highly inefficient for high barriers
- Many “tricks” have been proposed to overcome and sample barriers
 - Temperature enhanced sampling: simulated tempering, **parallel tempering**, Temperature accelerated molecular dynamics ...)
 - Constraint dynamics: thermodynamic integration, blue moon sampling....
 - Flat histogram sampling: **umbrella sampling**, hyperdynamics,....
 - history dependent search: Wang-Landau, adaptive biasing force, **metadynamics**,...
 - non-equilibrium methods: steered MD, targeted MD,....
 - trajectory-based methods: **nudged elastic band**, action minimization, string method, **transition path sampling**, forward flux sampling,....

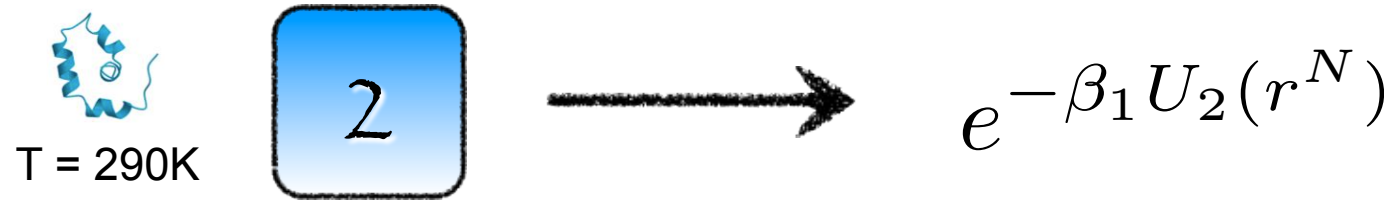
Replica exchange/parallel tempering



Two replicas



Switching temperatures



Total Boltzmann weight

$$e^{-\beta_1 U_2(r^N)} e^{-\beta_2 U_1(r^N)}$$



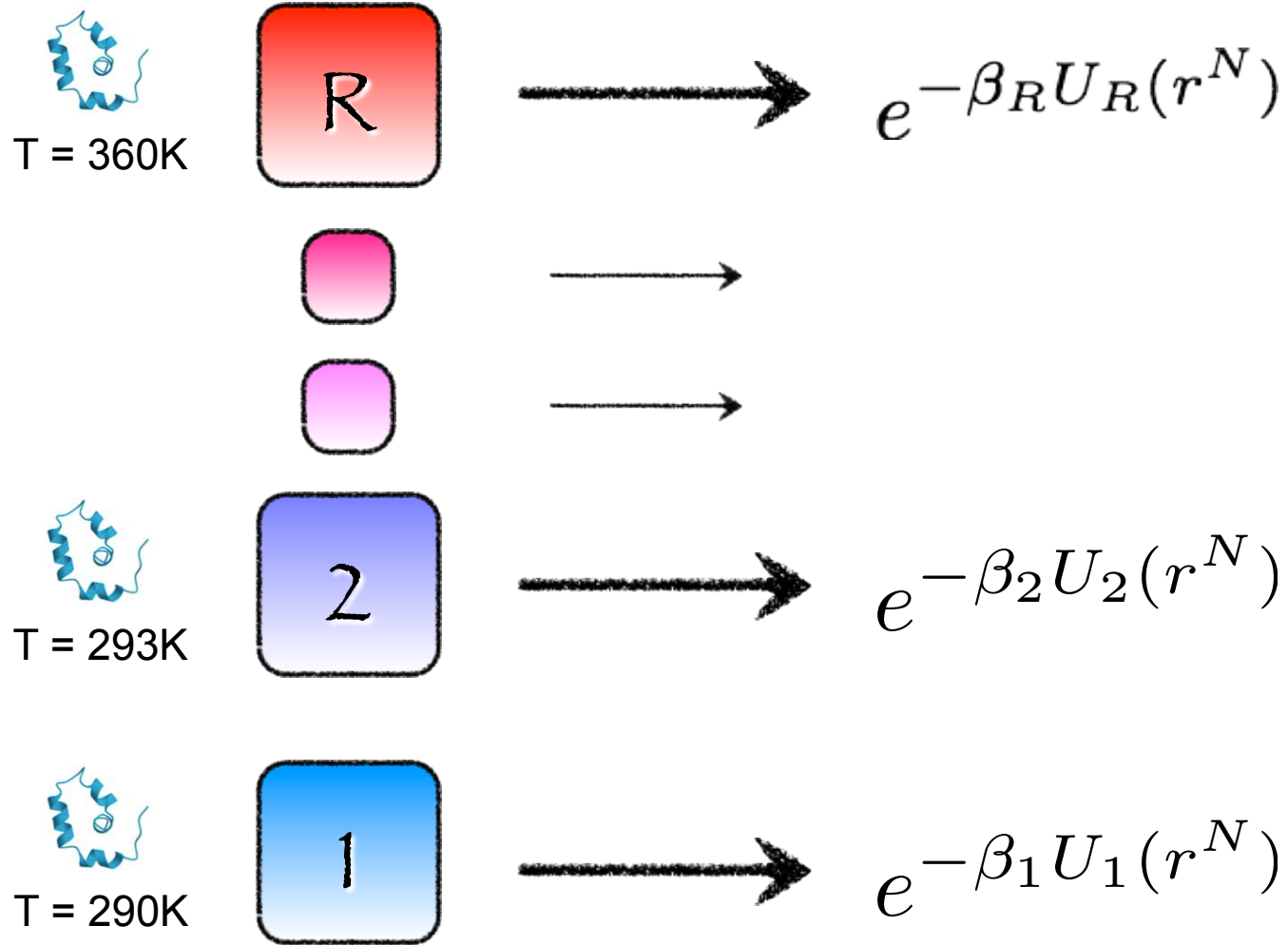
The ratio of the new Boltzmann factor over the old one is:

$$\frac{\mathcal{N}(n)}{\mathcal{N}(o)} = e^{(\beta_2 - \beta_1)[U_2(r^N) - U_1(r^N)]}$$

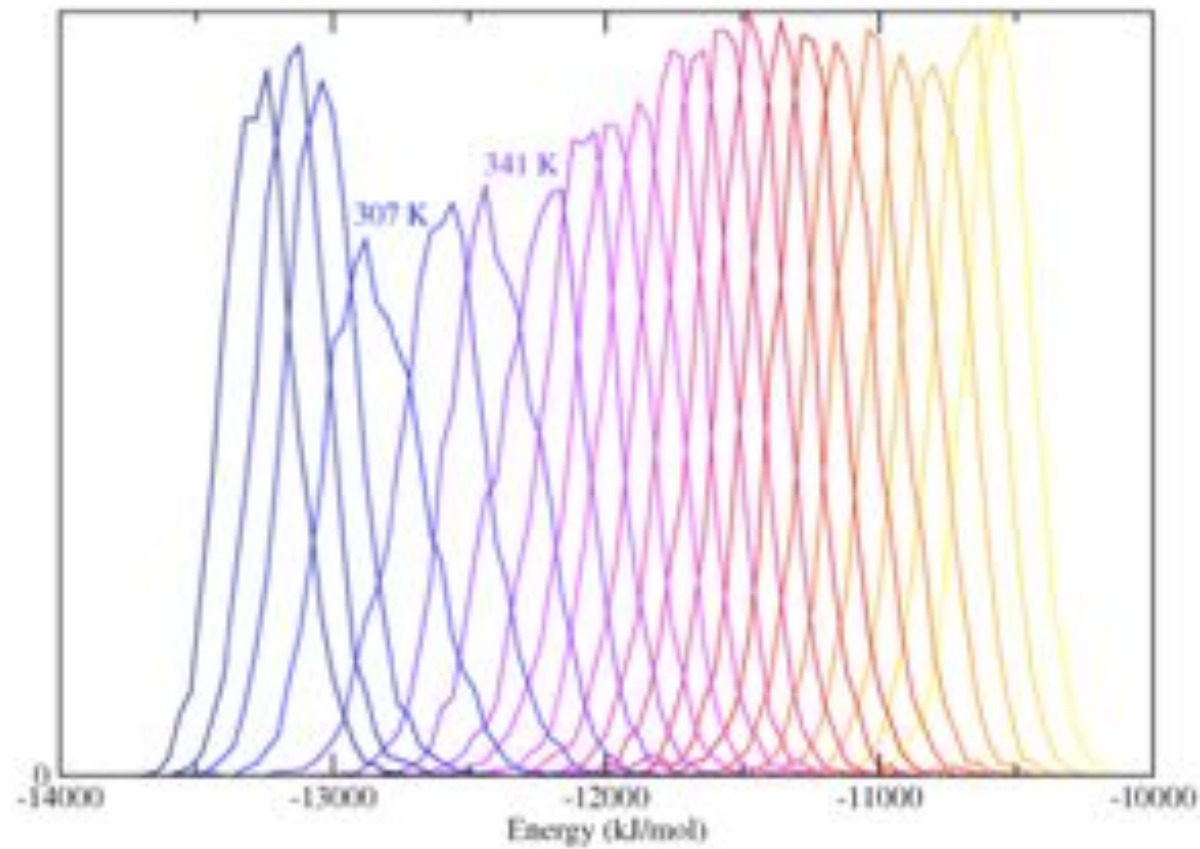
the rule for switching temperatures should obey detailed balance
Metropolis Monte Carlo scheme

$$\text{acc}(1 \leftrightarrow 2) = \min \left(1, e^{(\beta_2 - \beta_1)[U_2(r^N) - U_1(r^N)]} \right)$$

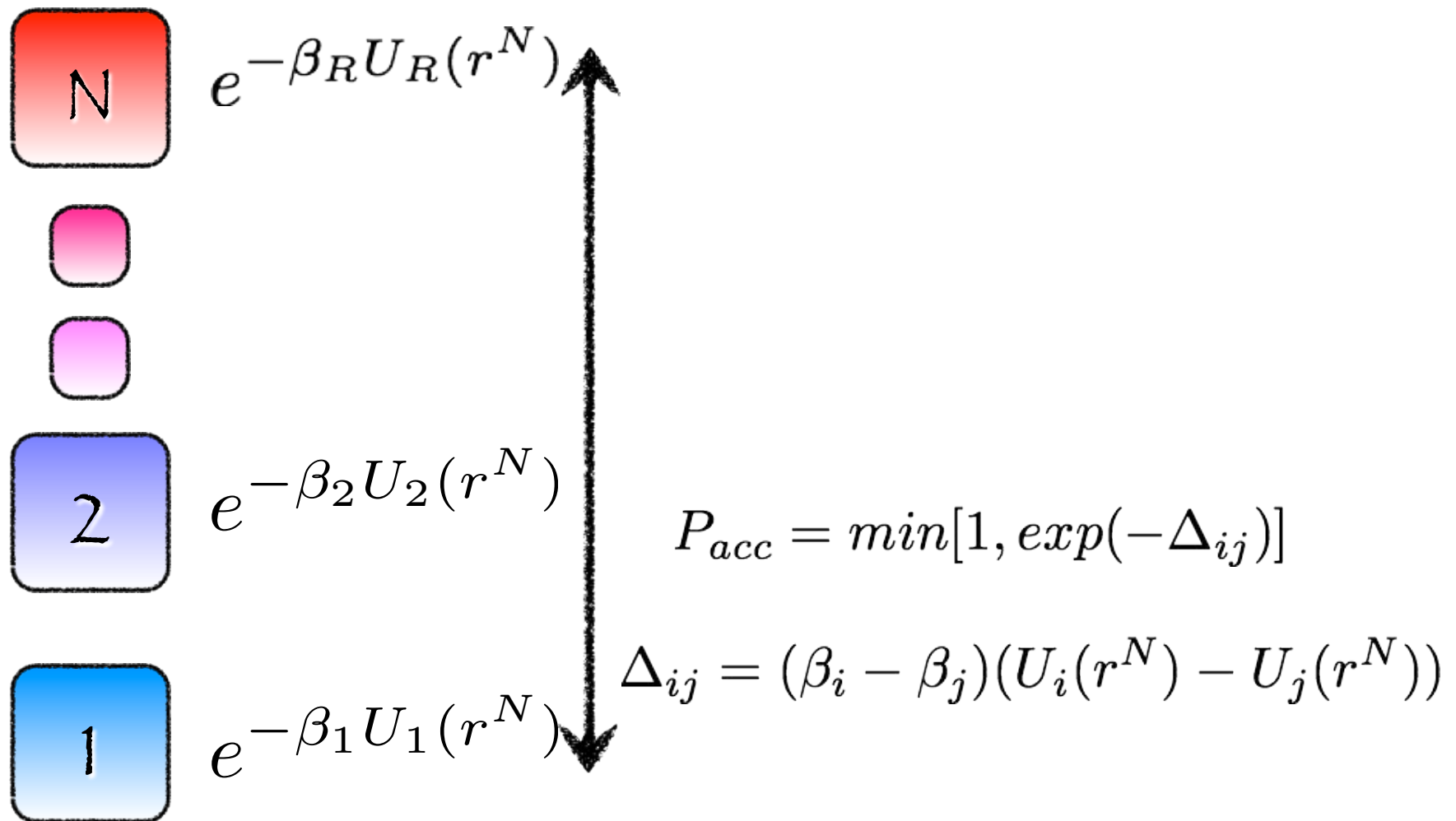
Set of replicas



Overlap in potential energy



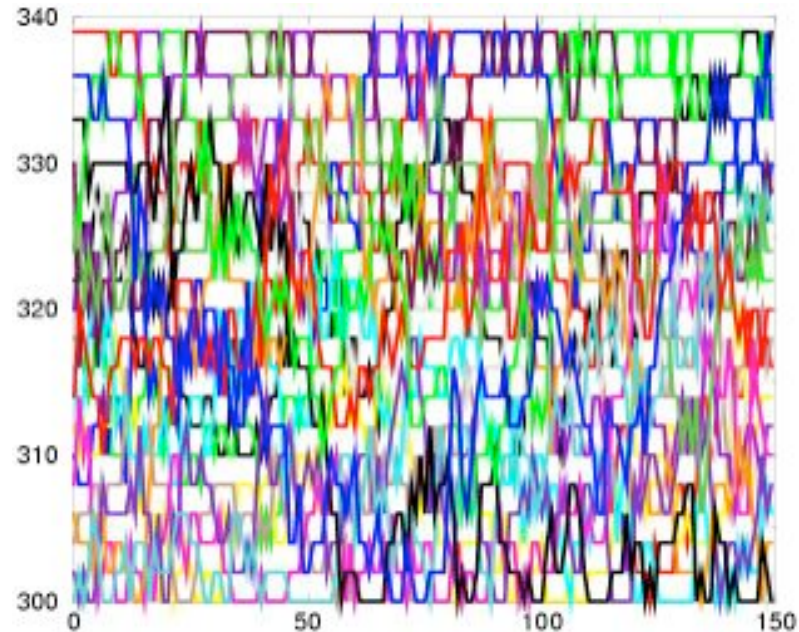
Replica Exchange MD (REMD)



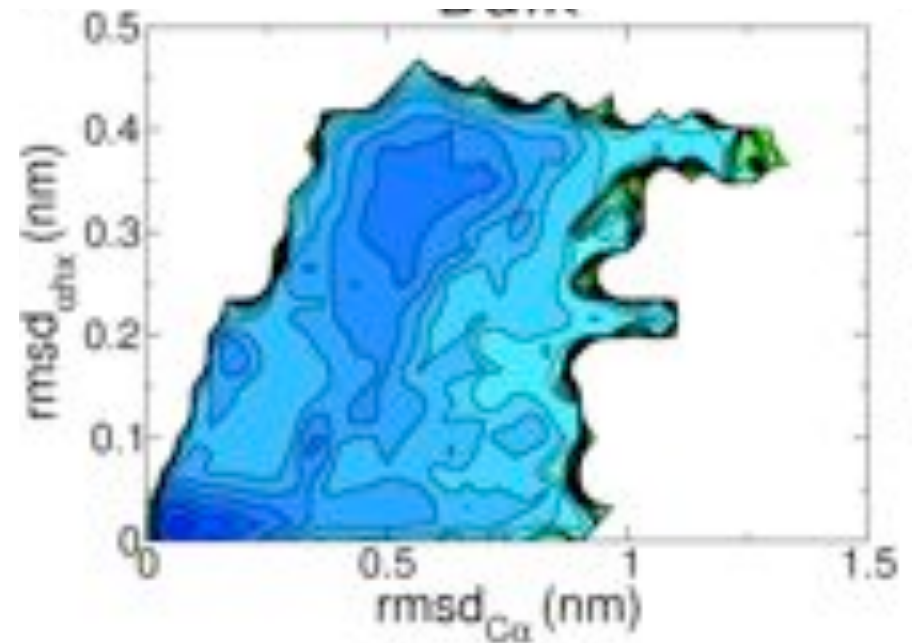
Hansmann Chem Phys Lett 1997

Sugita & Okamoto Chem Phys Lett 1999

Replica Exchange



Exchange as a function of time.



Free energy follows from

$$\beta F(x, y) = -\ln P(x, y)$$

Advantage: no order parameters needed

Disadvantage: convergence of free energy landscape can be still slow, especially around phase transition: many replicas needed.

Metadynamics

- method to obtain free energy in a single simulation
- similar idea as Wang Landau sampling: add history dependent biasing potential to forcefield

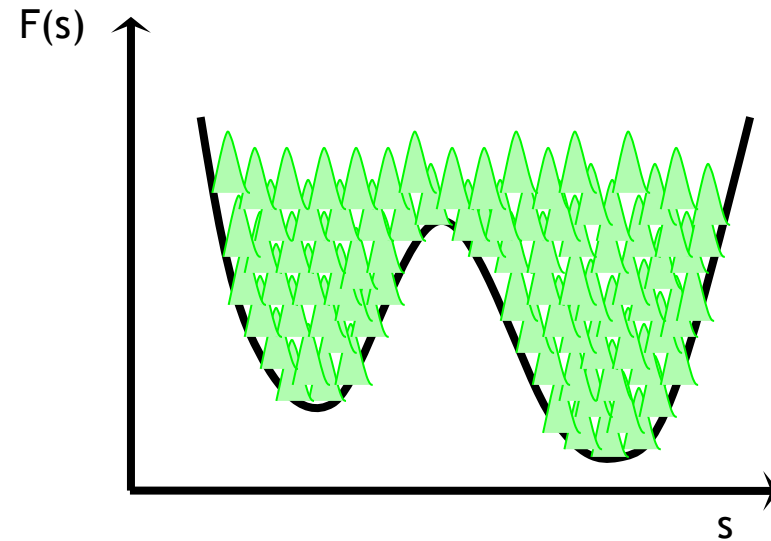
$$V(s; t) = w \sum_{t' < t} e^{-\frac{(s - s(x(t')))^2}{2\sigma^2}}$$

Laio and Parrinello, PNAS (2002)

- s = predefined order parameters
- w = height of hills
- σ = width of gaussians
- w is reduced every cycle

$$F(s) = - \lim_{t \rightarrow \infty} V(s; t)$$

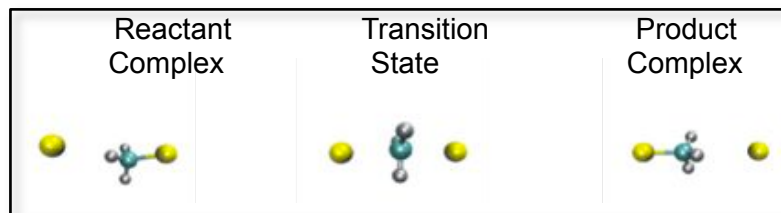
- more controlled version: well tempered MetaD
Barducci, Bussi, Parrinello, PRL, (2008).



Link to bernds animation

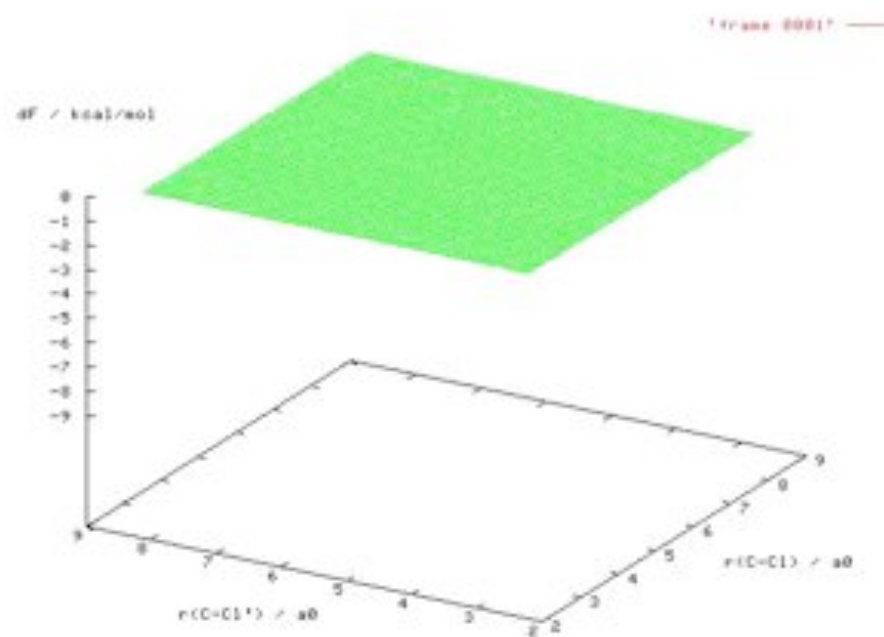
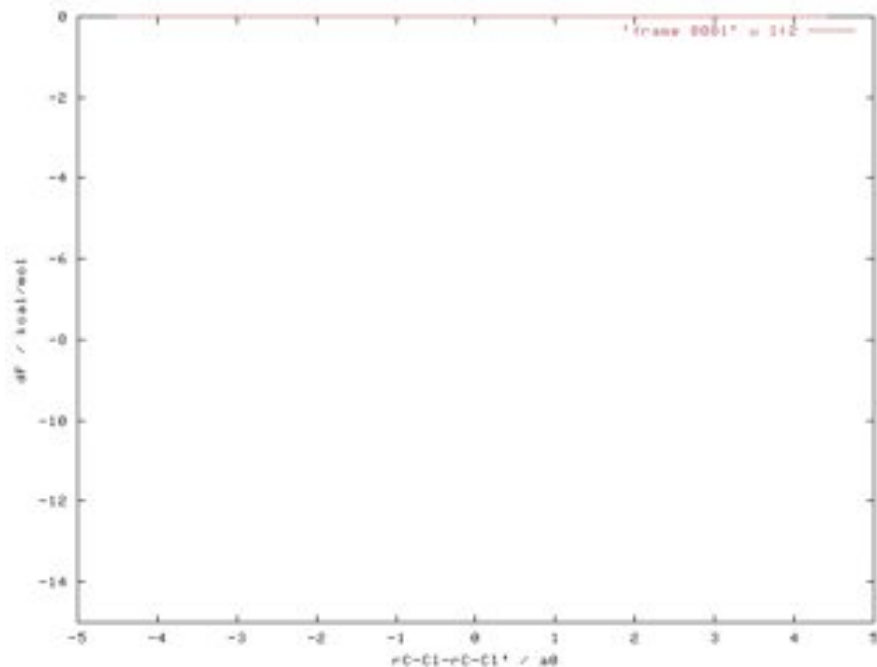
S_N2 reaction between Cl^- and CH_3Cl

$$S(R) = r_{C-Cl} - r_{C-Cl'}$$



$$S_1(R) = r_{C-Cl}$$

$$S_2(R) = r_{C-Cl'}$$



Meta-dynamics can relax the requirement of choosing a good reaction coordinate

Bernd Ensing, Alessandro Laio, Michele Parrinello and Michael L. Klein, *J. Phys. Chem. B* **109** (2005), 6676-6687

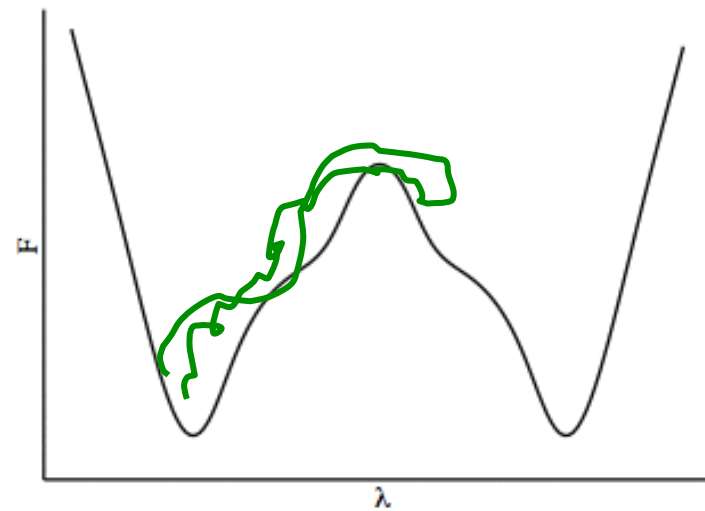
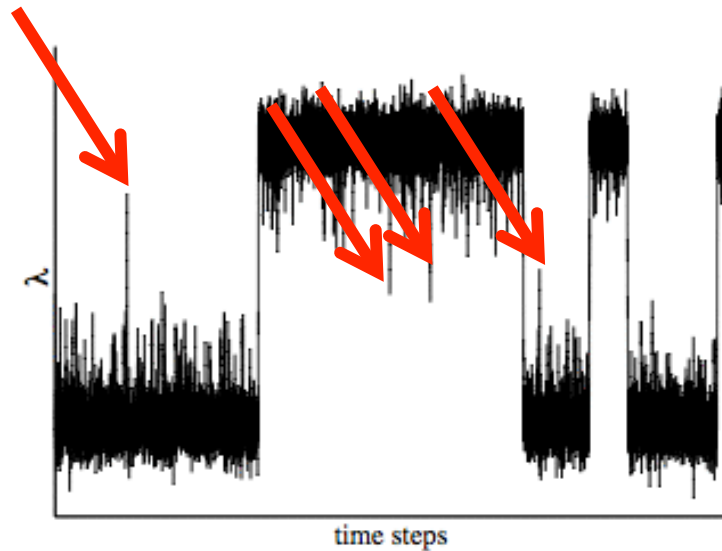
Outline

- Part 1
 - Rare event and reaction kinetics
 - Linear Response theory
 - Transition state theory
 - Free energy methods
 - **Bennet Chandler approach**
 - Example zeolites
- Part 2
 - Two ended methods
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 - Rate constants
 - Reaction coordinate analysis
 - Application to biomolecules

Problem with TST

There are recrossings that cause overestimation of the rate constant

trajectories that seem to overcome the barrier but in fact bounce back



Bennett-Chandler approach

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q^*) \theta(q(t) - q^*) \rangle}{\langle \delta(q(0) - q^*) \rangle} \times \frac{\langle \delta(q(0) - q^*) \rangle}{\langle \theta(q^* - q) \rangle}$$

Computational scheme:

1. Determine the probability from the free energy using MC or MD, e.g. by umbrella sampling, thermodynamic integration or other free energy methods
2. Compute the conditional average from a MD simulation

Bennett-Chandler approach

$$k_{A \rightarrow B}^{TST}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q_1) \theta(\dot{q}) \rangle}{\langle \delta(q(0) - q_1) \rangle} \times \frac{\langle \delta(q(0) - q_1) \rangle}{\langle \theta(q_1 - q) \rangle}$$

$$k_{A \rightarrow B}(t) = \frac{\langle \dot{q}(0) \delta(q(0) - q_1) \theta(q(t) - q_1) \rangle}{\langle \delta(q(0) - q_1) \rangle} \times \frac{\langle \delta(q(0) - q_1) \rangle}{\langle \theta(q_1 - q) \rangle}$$

Transmission coefficient

$$\kappa(t) \equiv \frac{k_{A \rightarrow B}(t)}{k_{A \rightarrow B}^{TST}}$$

$$= \frac{\langle \dot{q}(0) \delta(q(0) - q_1) \theta(q(t) - q_1) \rangle}{0.5 |\dot{q}(0)|}$$

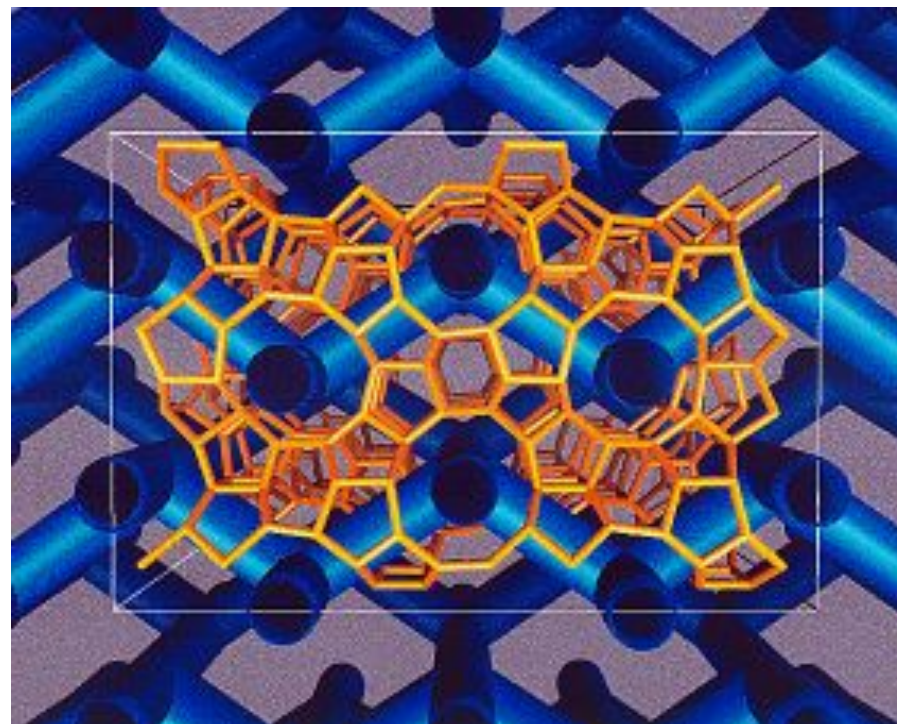
MD simulation to correct the transition state result!

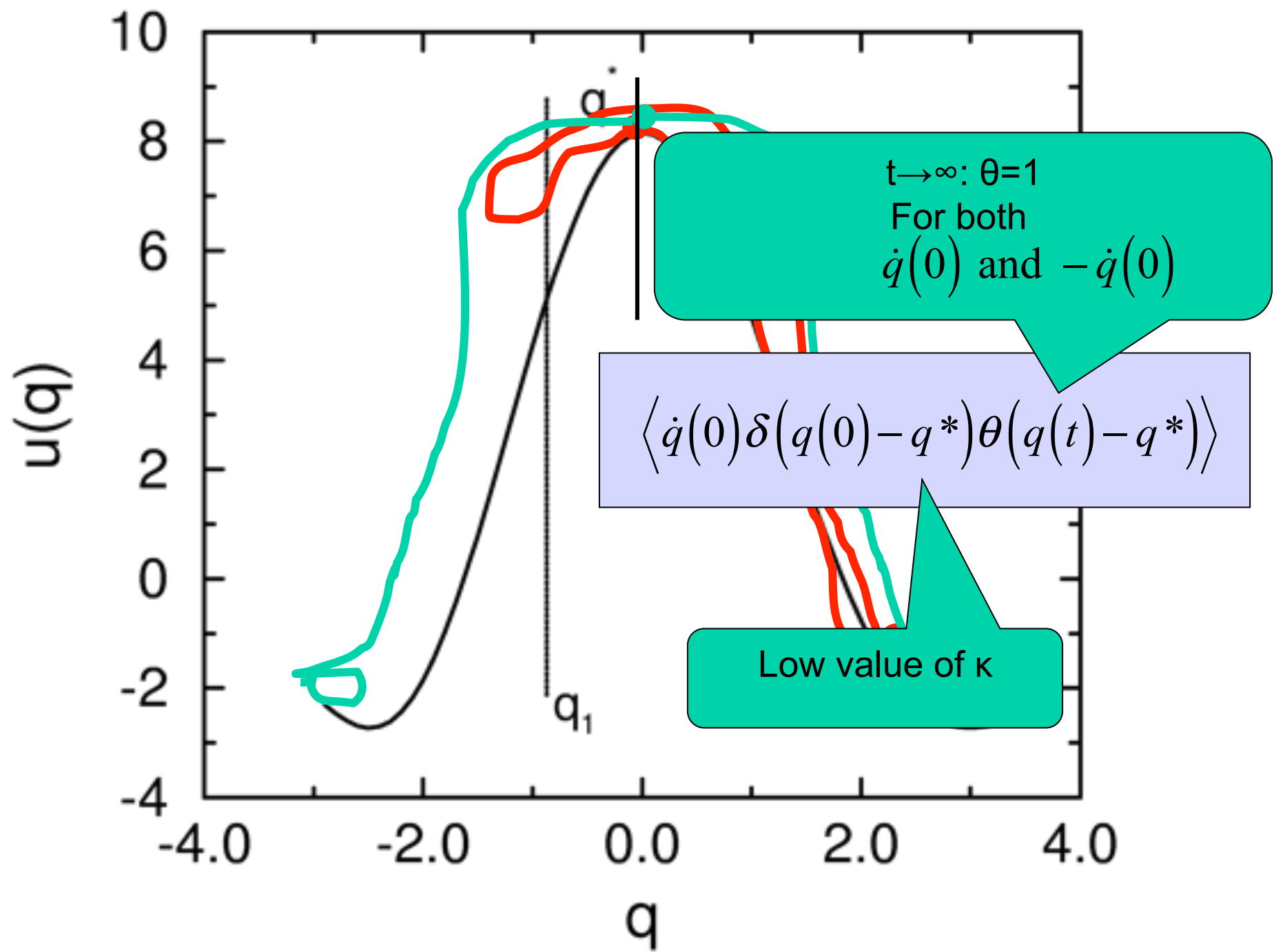
MD simulation:

1. At $t=0$ $q=q_1$
2. Determine fraction at product state weighted with initial velocity

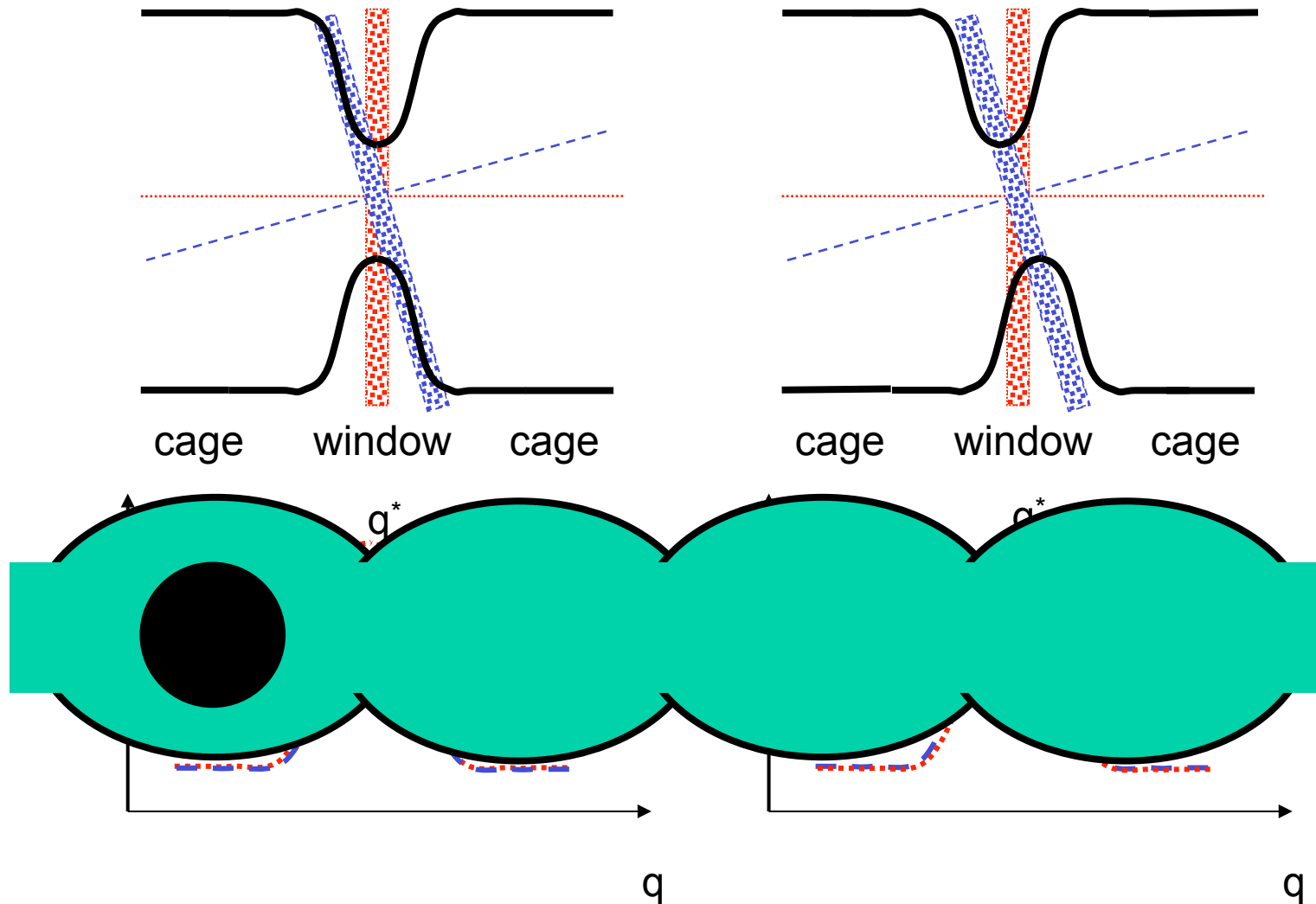
Example diffusion in zeolite

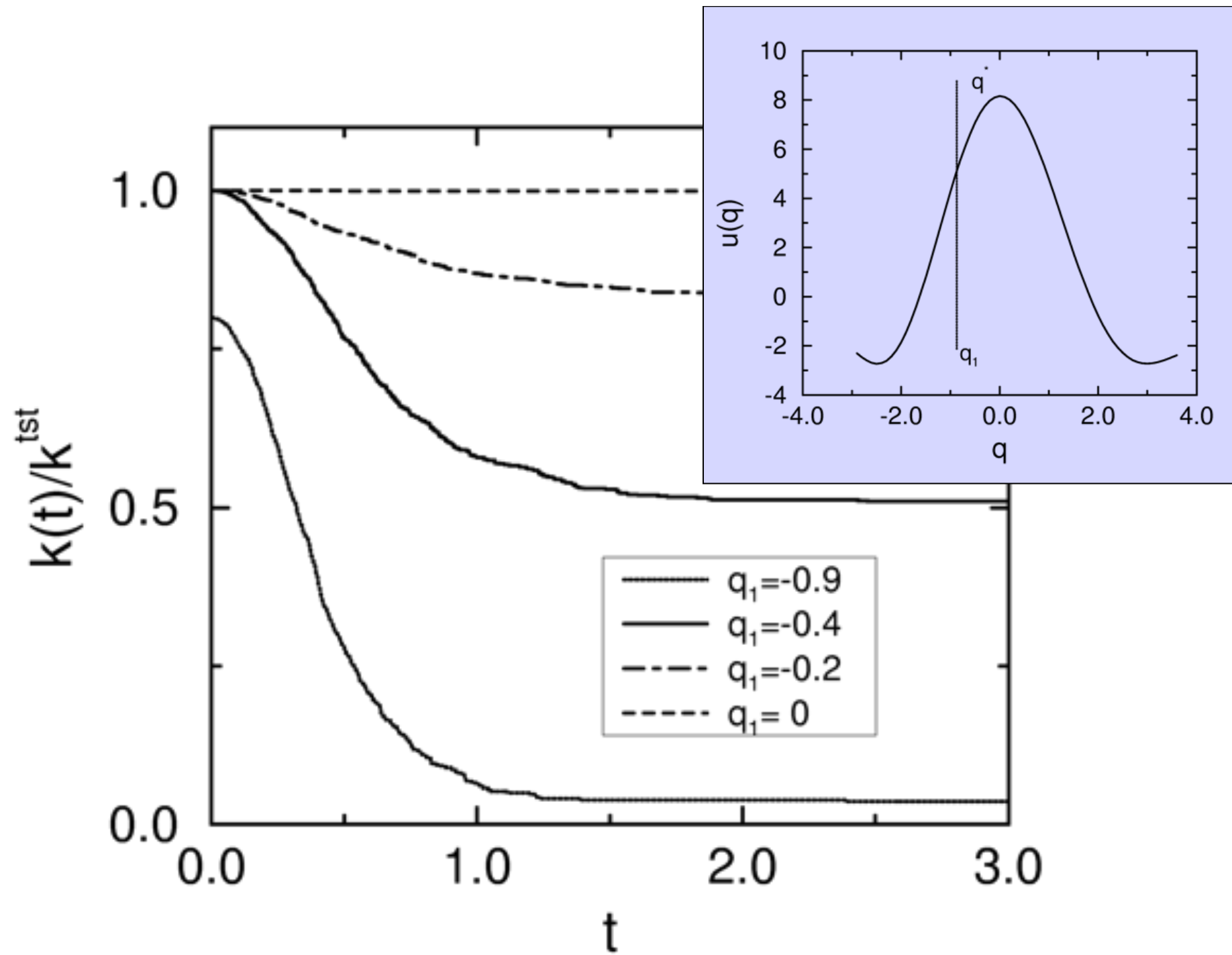
- Zeolites important class of materials
- Diffusion of alkanes in matrix is poorly described
- Approach
 - molecular simulation of alkanes in fixed zeolite frame
 - Unified atom FF by Dubbeldam et al.

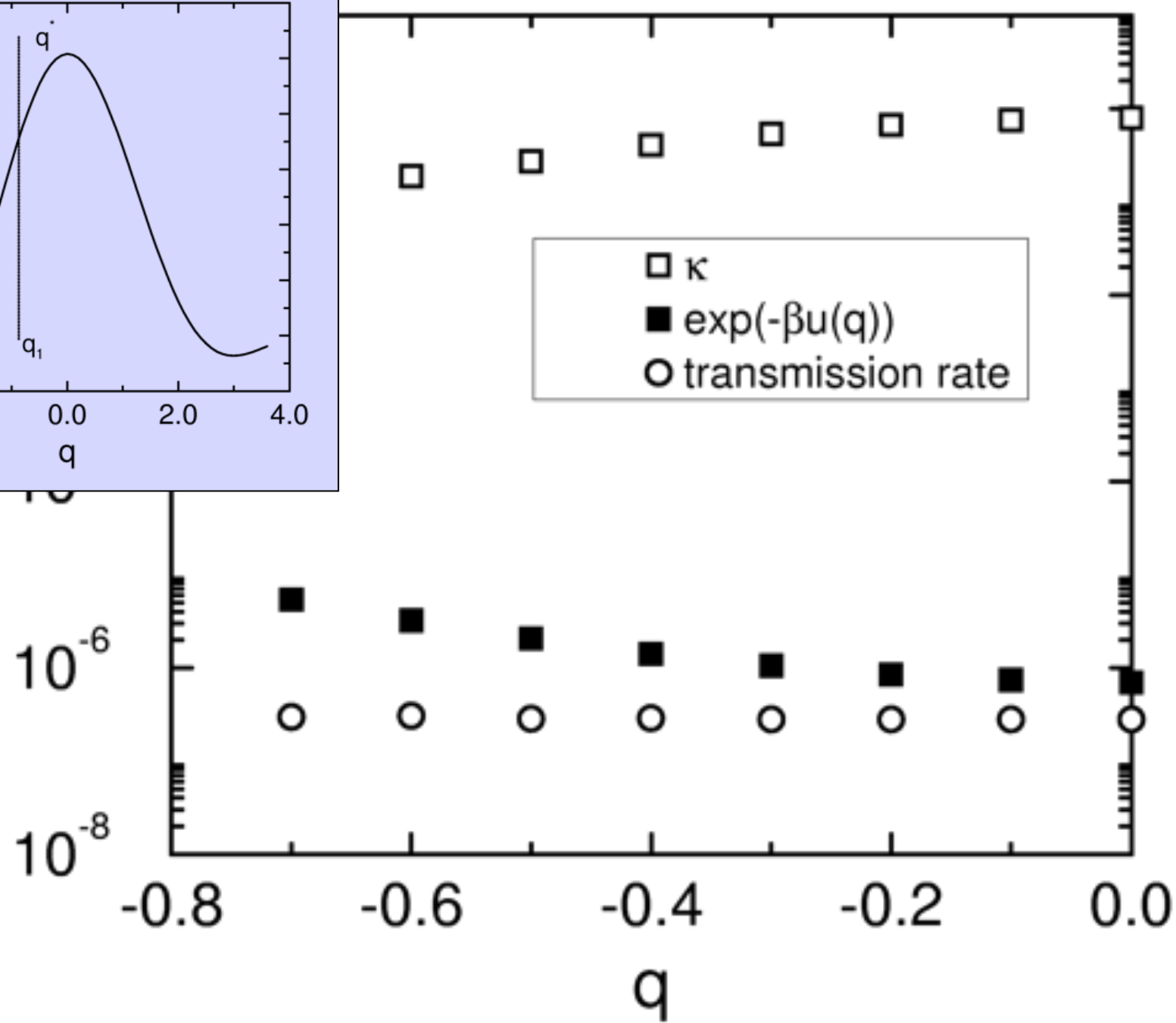
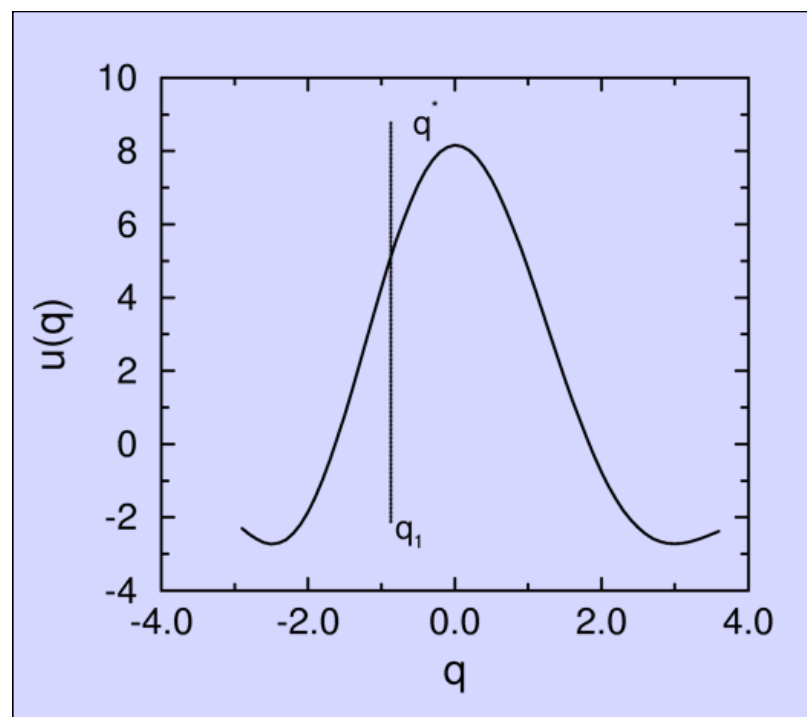




Reaction coordinate





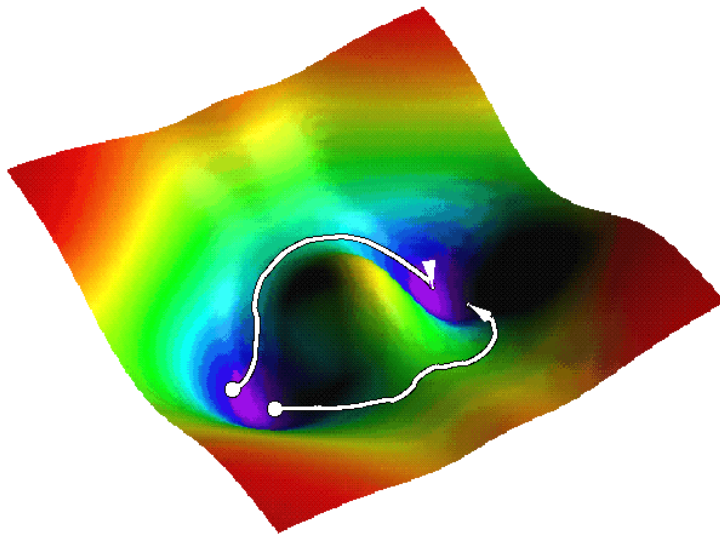


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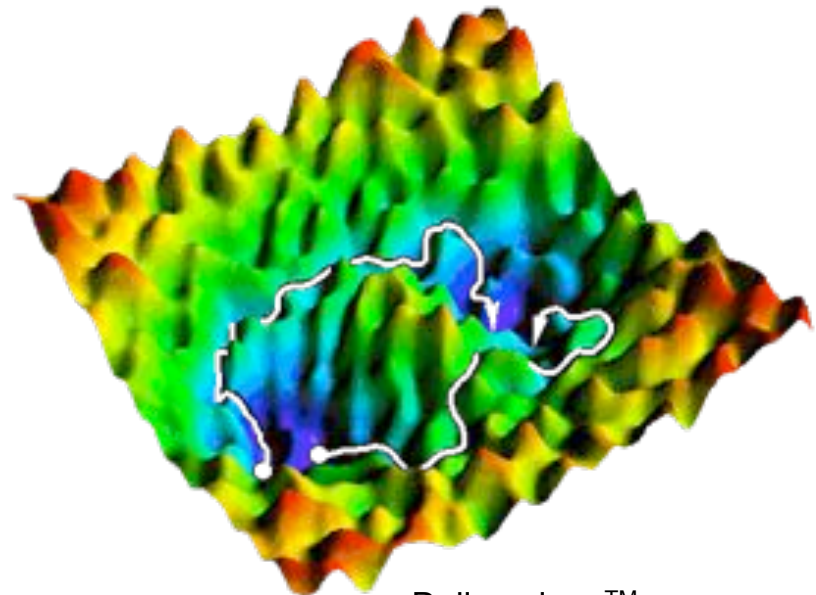
Barriers on smooth and rough energy landscapes

- Clearly, barrier is most important for rare event
- But how to obtain this barrier?
- In multidimensional energy landscapes barrier is saddle point



- # saddle points limited
- determined by potential energy
- use eigenvectors or Hessian to find them

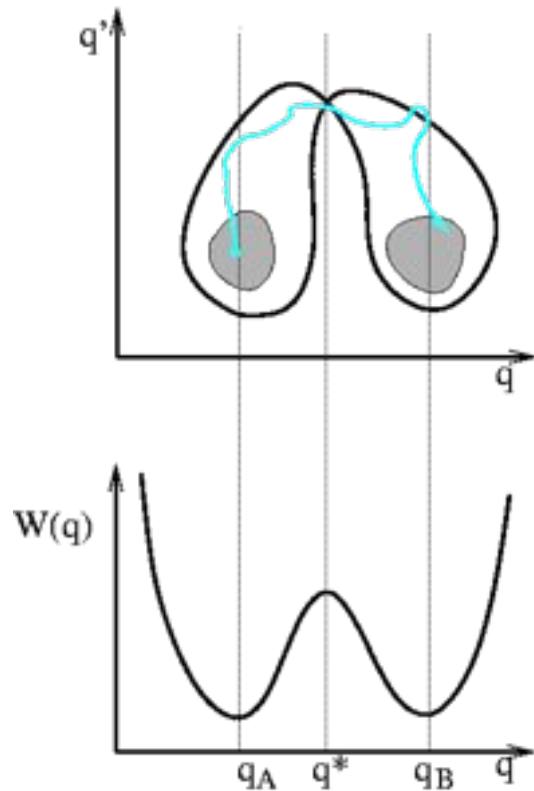
- # saddle points uncountable
- entropy important, many pathways
- determined by free energy
- exploring requires sampling schemes



Dellago logo™

Breakdown of BC approach

κ can become immeasurably low if the reaction coordinate is at the wrong value the reaction coordinate is wrongly chosen

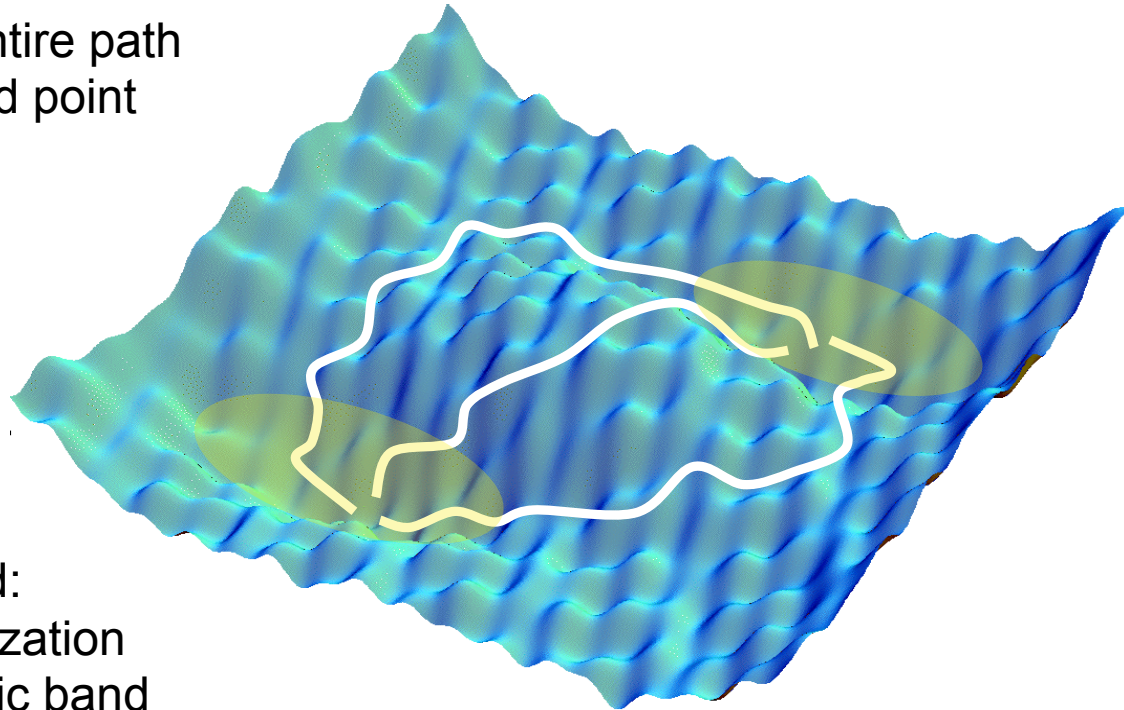


$$W(q) = -kT \ln \int dq' \exp \{-\beta E(q, q')\}$$

If the reaction coordinate is not known, the wrong order parameter can lead to wrong transition states, mechanism and rates

Two ended methods

Methods that take the entire path
and fix the begin and end point

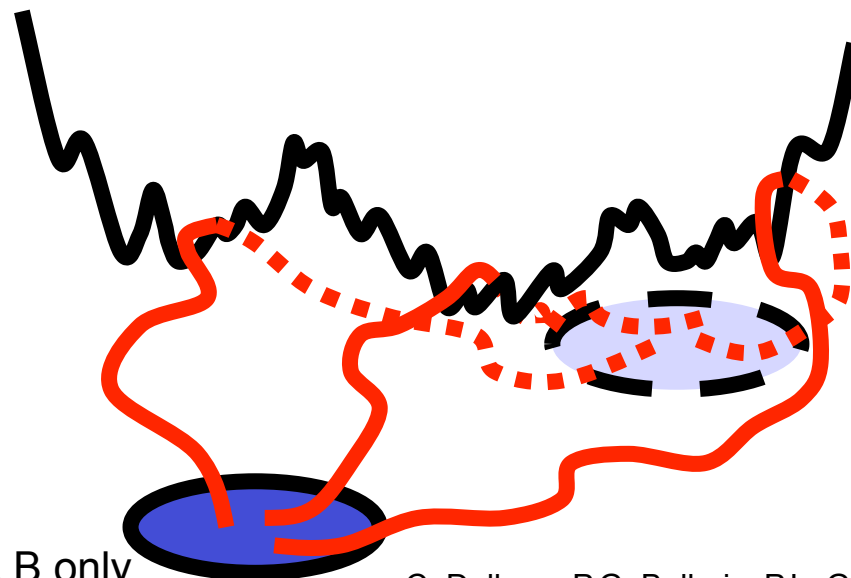


Many methods proposed:

- Action minimization
- Nudged elastic band
- String method
- Path metadynamics
- Milestoning
- Transition path sampling
-

Transition path sampling

Samples the path ensemble:
all trajectories that lead over barrier



- Sampling by Monte Carlo
- Requires definition of stable states A,B only
- Results in ensemble of pathways
- Reaction coordinate is a result of simulation not an input
- Allows for calculation of rate constants

C. Dellago, P.G. Bolhuis, P.L. Geissler
Adv. Chem. Phys. **123**, 1 2002

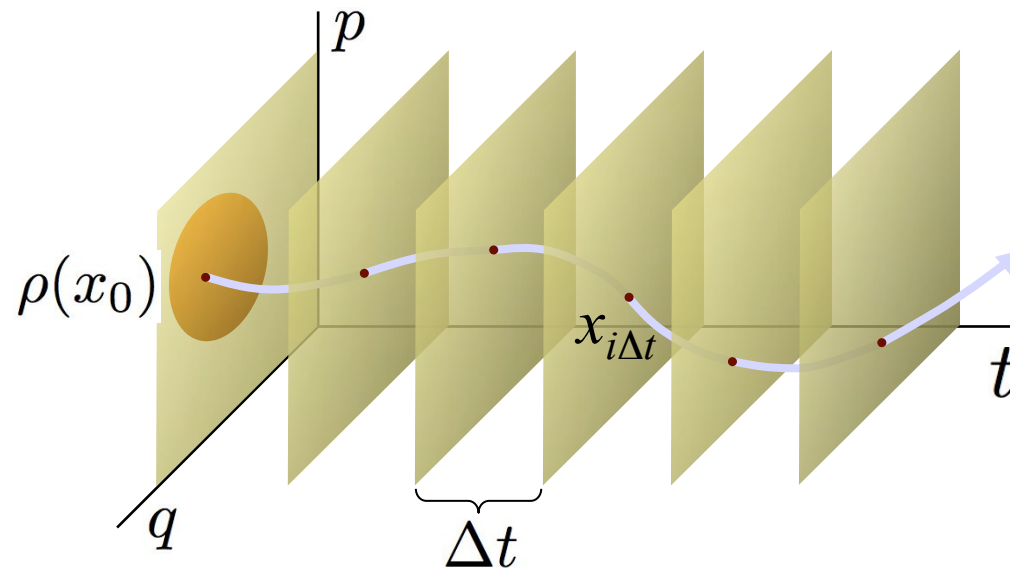
Apply when process of interest

- is a rare event
- is complex and reaction coordinate is not known

Examples: nucleation, reactions in solution, protein folding

Path probability density

$x(\mathcal{T}) \equiv \{x_0, x_{\Delta t}, x_{2\Delta t}, \dots, x_{\mathcal{T}}\}$ Path = Sequence of states



$$\mathcal{P}[x(\mathcal{T})] = \rho(x_0) \prod_{i=0}^{\mathcal{T}/\Delta t - 1} p(x_{i\Delta t} \rightarrow x_{(i+1)\Delta t})$$

Transition path ensemble



$$\mathcal{P}_{AB}[x(T)] \equiv h_A(x_0)\mathcal{P}[x(T)]h_B(x_T)/Z_{AB}(T)$$

$$Z_{AB}(T) \equiv \int \mathcal{D}x(T) h_A(x_0)\mathcal{P}[x(T)]h_B(x_T)$$

$$\int \mathcal{D}x(T) \equiv \int \cdots \int dx_0 dx_{\Delta t} dx_{2\Delta t} \cdots dx_T$$

Metropolis MC of pathways

1. Generate **new** path from **old** one

$$x^{(o)}(T) \longrightarrow x^{(n)}(T)$$



2. Accept **new** path according to **detailed balance**:

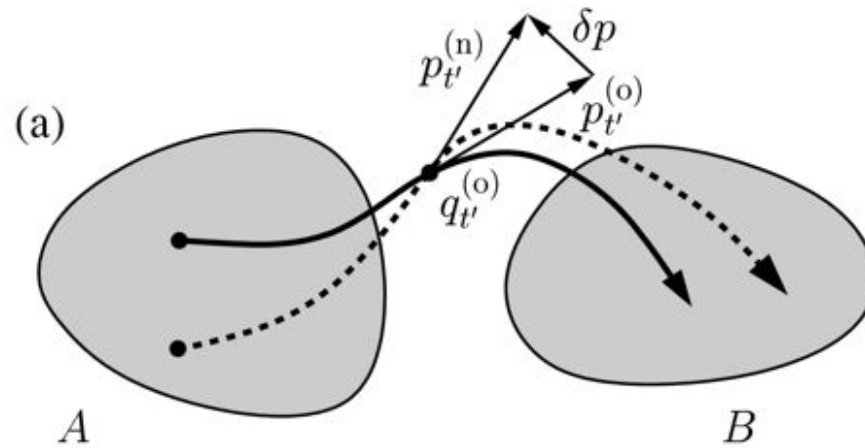
$$\mathcal{P}_{AB}[x^{(o)}(T)]\pi[x^{(o)}(T) \rightarrow x^{(n)}(T)] = \mathcal{P}_{AB}[x^{(n)}(T)]\pi[x^{(n)}(T) \rightarrow x^{(o)}(T)]$$

$$\pi[x^{(o)}(T) \rightarrow x^{(n)}(T)] = P_{\text{gen}}[x^{(o)}(T) \rightarrow x^{(n)}(T)] \times P_{\text{acc}}[x^{(o)}(T) \rightarrow x^{(n)}(T)]$$

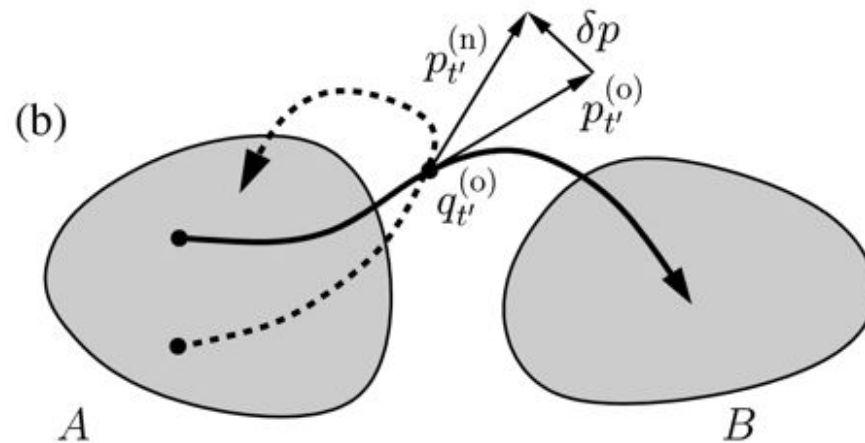
3. Satisfy detailed balance with the **Metropolis rule**:

$$P_{\text{acc}}[x^{(o)}(T) \rightarrow x^{(n)}(T)] = h_A[x_0^{(n)}]h_B[x_T^{(n)}] \min \left\{ 1, \frac{\mathcal{P}[x^{(n)}(T)]P_{\text{gen}}[x^{(n)}(T) \rightarrow x^{(o)}(T)]}{\mathcal{P}[x^{(o)}(T)]P_{\text{gen}}[x^{(o)}(T) \rightarrow x^{(n)}(T)]} \right\}$$

Shooting moves



accept



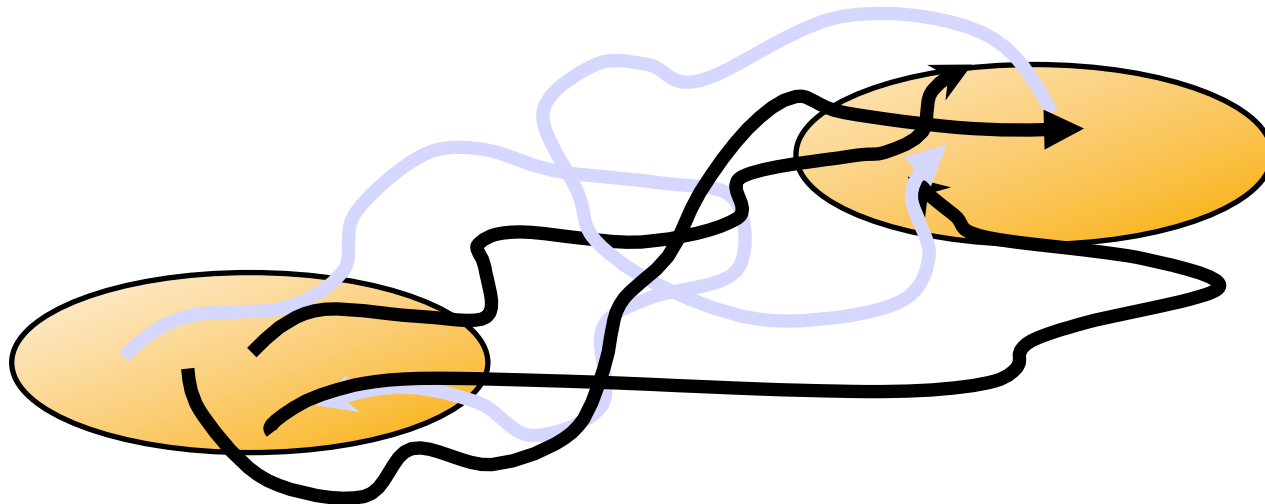
reject

$$P_{acc}[x^{(o)}(T) \rightarrow x^{(n)}(T)] = h_A(x_0^{(n)})h_B(x_T^{(n)})$$

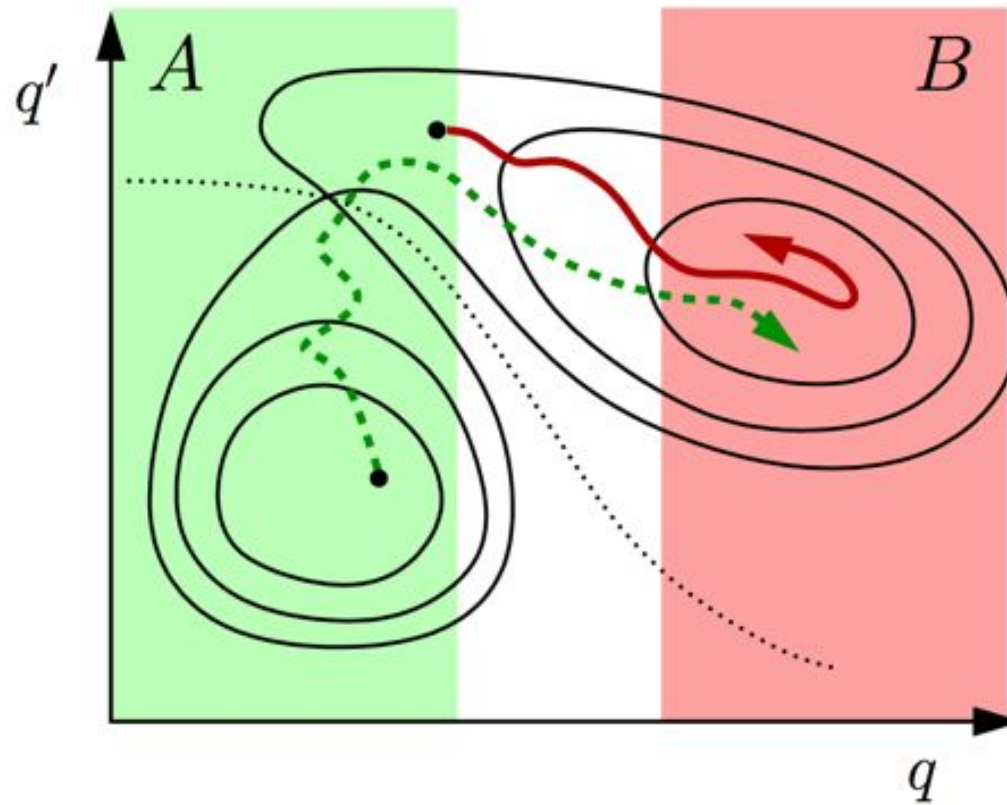
$$h_A(t) = \begin{cases} 1 & \text{if } x_t \in A \\ 0 & \text{if } x_t \notin A \end{cases}$$

Standard TPS algorithm

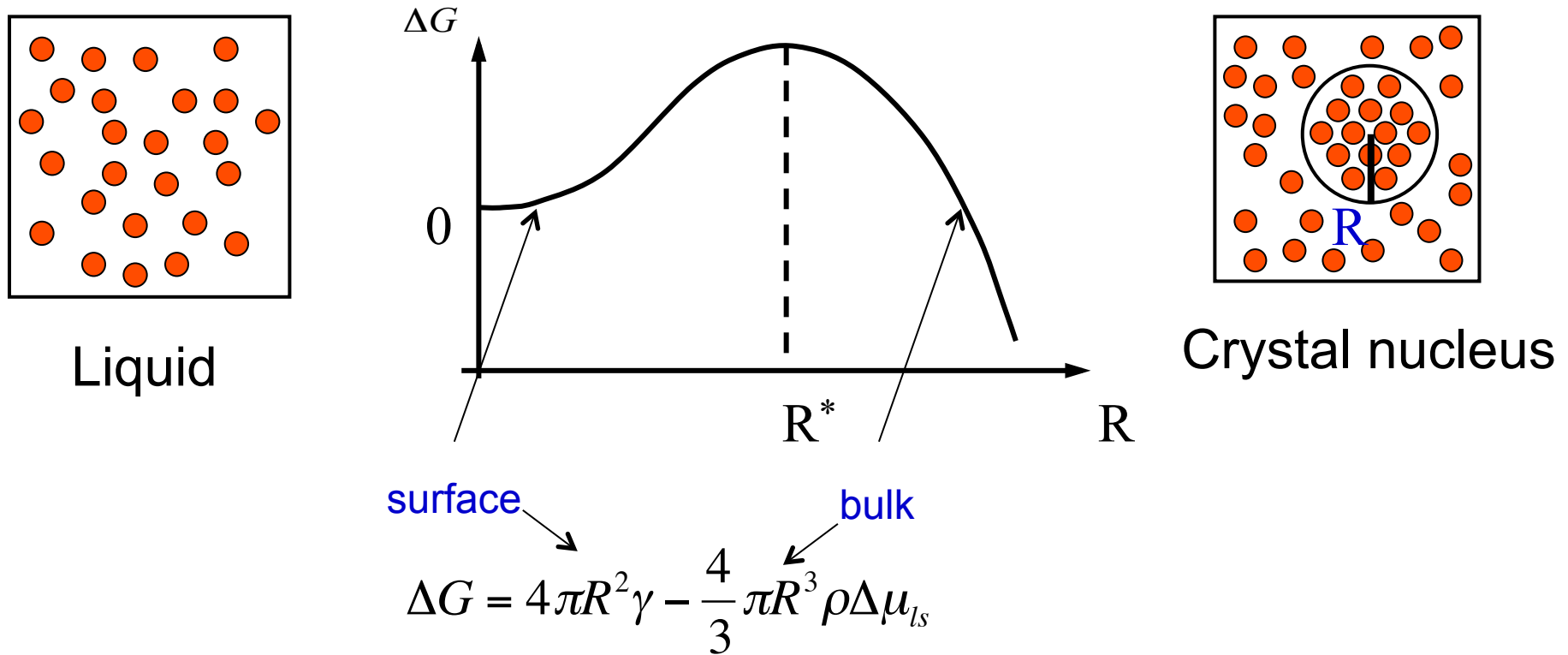
- take existing path
- choose random time slice t
- change momenta slightly at t
- integrate forward and backward in time to create new path of length L
- accept if A and B are connected, otherwise reject and retain old path
- calculate averages
- repeat



Definition of the stable states



Classical nucleation (1926)



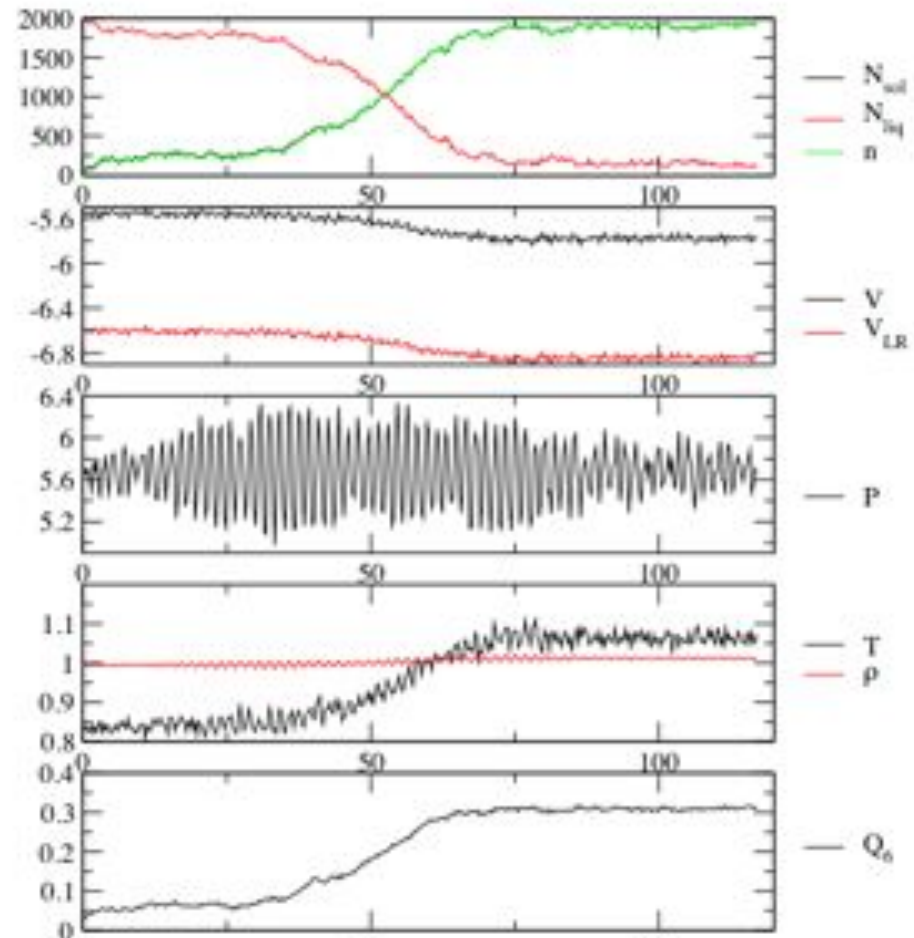
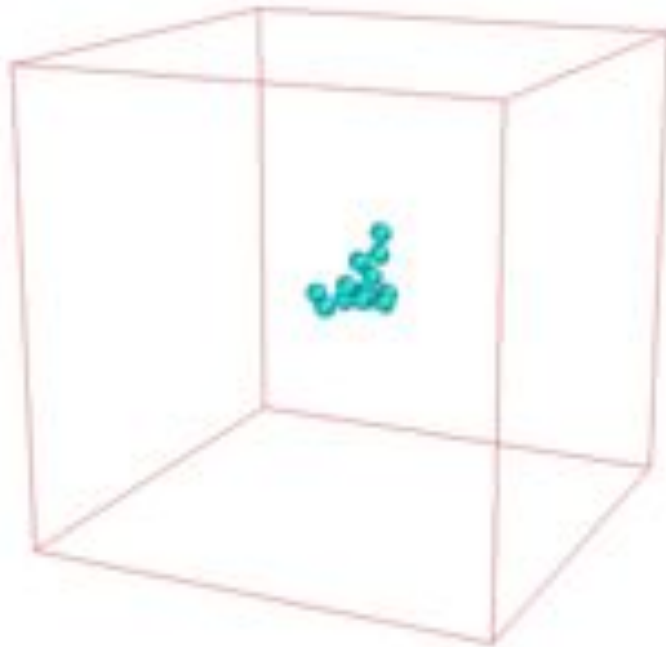
- How does the crystal form?
- What is the structure of the critical nucleus
- Is classical nucleation theory correct?
 - What is the barrier?
 - Rate constant

γ : surface tension
 $\Delta \mu$: chem. pot difference
 ρ : density

Path sampling of nucleation

TIS in NPH ensemble, as density and temperature change

$N=10000$, $P=5.68$ $H=1.41$ (25 % undercooling)

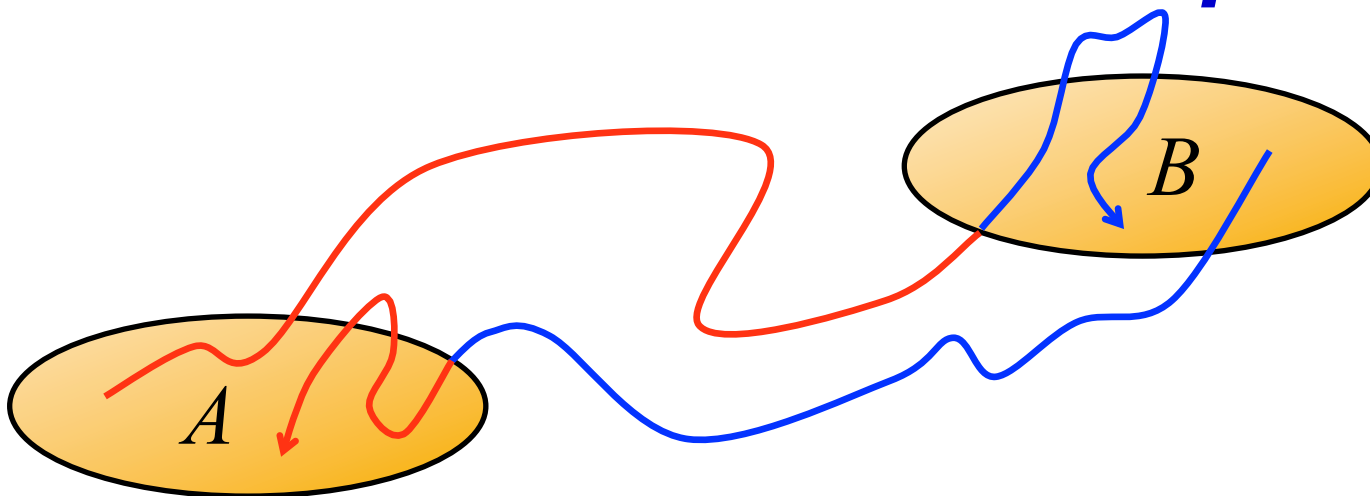


D. Moroni, P. R. ten Wolde, and P. G. Bolhuis, *Phys. Rev. Lett.* **94**, 235703 (2005)

Sampling paths is only the beginning

- *Eugene Wigner: "It is nice to know that the computer understands the problem. But I would like to understand it too."*
- Path ensemble needs to be further explored to obtain:
 - Rate constants
 - Free energy
 - Transition state ensembles
 - Mechanistic picture
 - Reaction coordinate
- Illustrative example: crystal nucleation

Transition interface sampling



Overall states in phase space:

A
B

directly coming from **A**

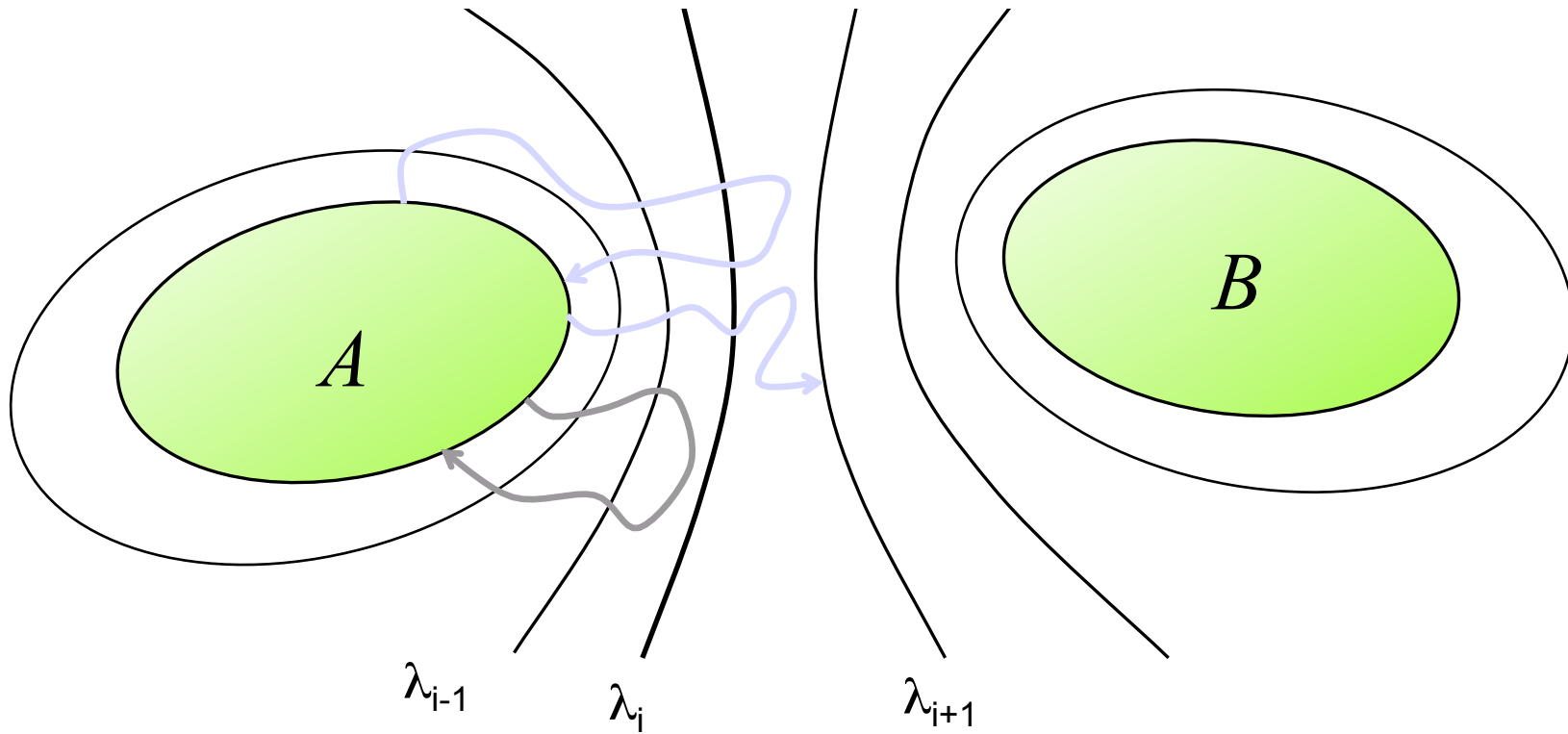
directly coming from **B**

$$C(t) \equiv \frac{\langle h_{\mathcal{A}}(x_0) h_{\mathcal{B}}(x_t) \rangle}{\langle h_{\mathcal{A}} \rangle}$$

$$k_{AB} = \frac{\langle h_{\mathcal{A}}(x_0) \dot{h}_{\mathcal{B}}(x_0) \rangle}{\langle h_{\mathcal{A}} \rangle} = \frac{\langle \phi_{AB} \rangle}{\langle h_{\mathcal{A}} \rangle}$$

T. S. van Erp, D. Moroni and P. G. Bolhuis, *J. Chem. Phys.* **118**, 7762 (2003)

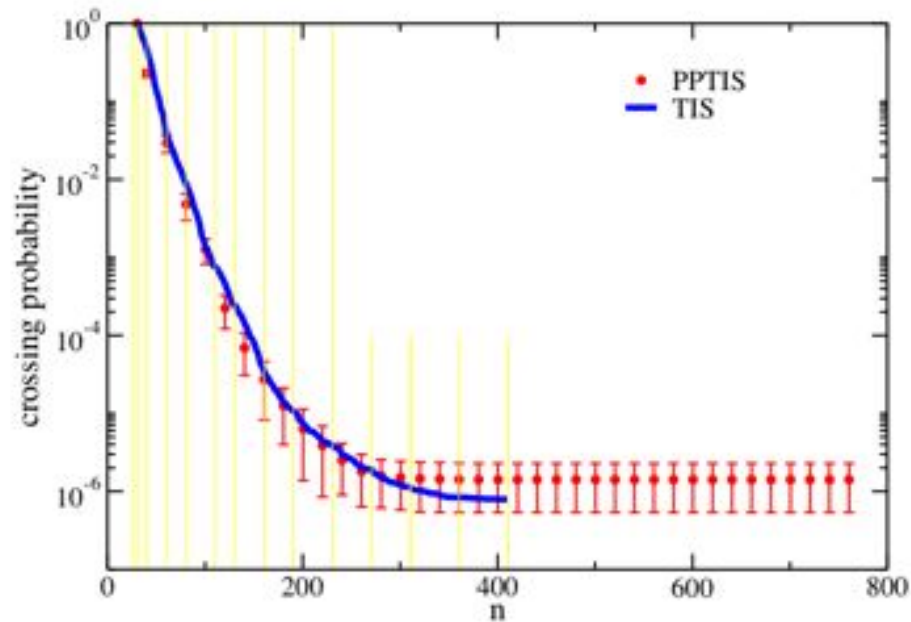
T. S. van Erp and P. G. Bolhuis, *J. Comp. Phys.* **205**, 157 (2005)



$P_A(\lambda_{i+1} | \lambda_i)$ = probability that path crossing i for first time after leaving A reaches $i+1$ before A

$$k_{AB}^{TIS} = \frac{\langle \phi_{AB} \rangle}{\langle h_{\mathcal{A}} \rangle} = \frac{\langle \phi_{AB} \rangle}{\langle h_{\mathcal{A}} \rangle} \prod_{i=1}^{n-1} P_A(\lambda_{i+1} | \lambda_i) = \Phi_A \prod_{i=1}^{n-1} P_A(\lambda_{i+1} | \lambda_i)$$

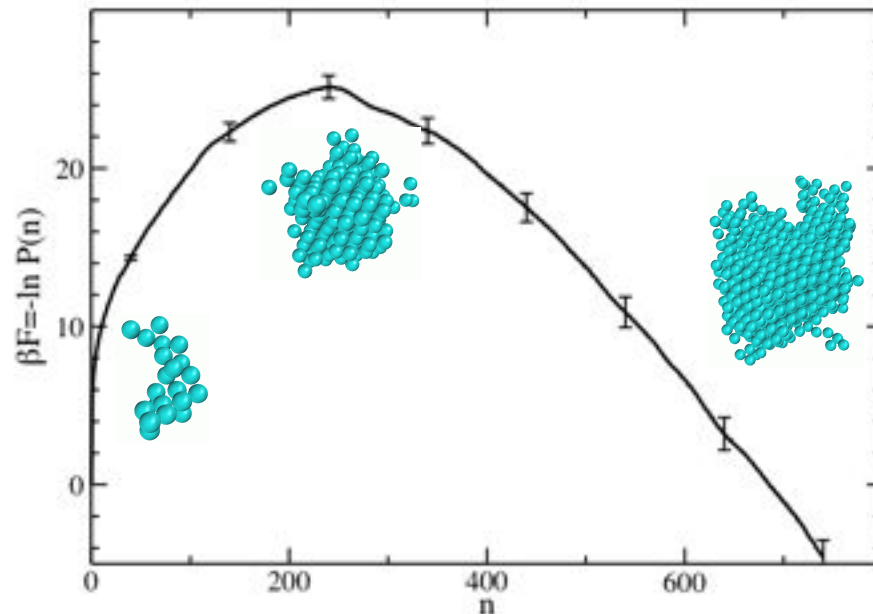
TIS results for nucleation



$$\mathcal{P}_A(B|1) = \prod_{i=1}^{n-1} \mathcal{P}_A(i+1|i) = 8 \times 10^{-7}$$

$$\frac{\langle \phi_{A1} \rangle}{\langle h_A \rangle} = 1.29$$

$$k_{AB} = (1.0 \pm 0.8) \times 10^{-6}$$



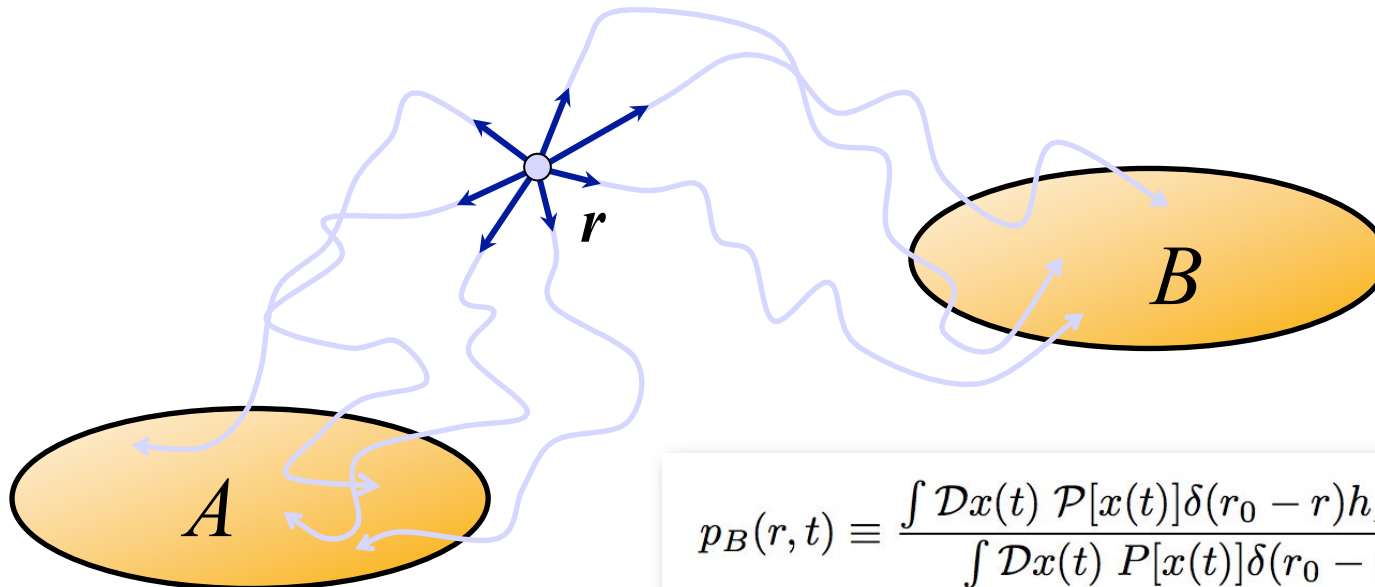
Free energy follows directly
Moroni, van Erp, Bolhuis, PRE, 2005

Structural analysis?

Committor

(aka *p-fold*, *splitting probability*)

$p_B(r, t)$ = Probability that a trajectory initiated at r relaxes into B



$$p_B(r, t) \equiv \frac{\int \mathcal{D}x(t) \mathcal{P}[x(t)] \delta(r_0 - r) h_B(x_t)}{\int \mathcal{D}x(t) \mathcal{P}[x(t)] \delta(r_0 - r)}$$

$$p_B(r, t) \approx \frac{1}{N} \sum_{i=1}^N h_B(x_t^{(i)})$$

$$\sigma = \sqrt{\langle (p_B^{(N)} - p_B)^2 \rangle} = \sqrt{\frac{p_B(1 - p_B)}{N}}$$

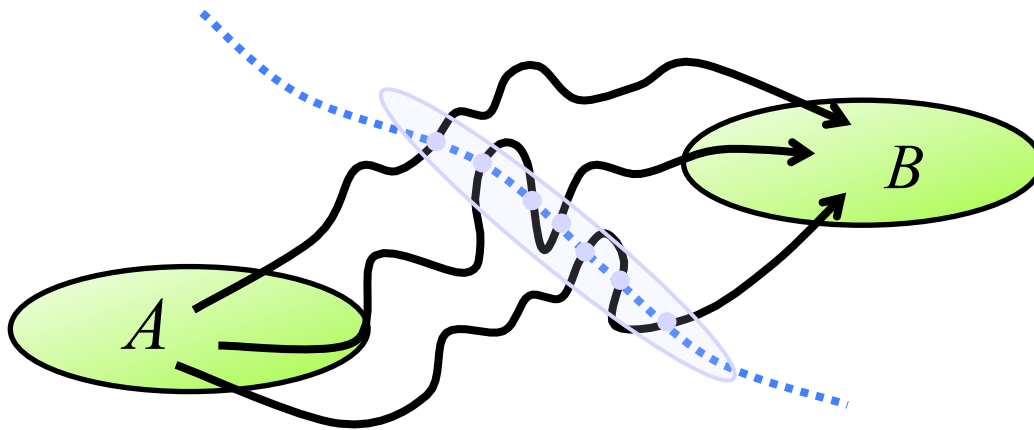
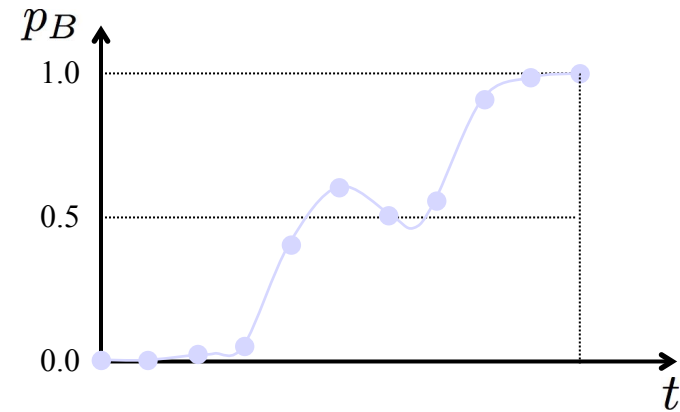
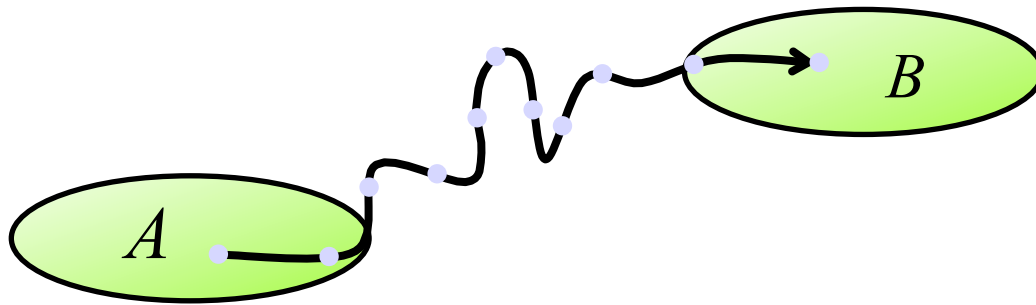
L. Onsager, *Phys. Rev.* **54**, 554 (1938).

M. M. Klosek, B. J. Matkowsky, Z. Schuss, *Ber. Bunsenges. Phys. Chem.* **95**, 331 (1991)

V. Pande, A. Y. Grosberg, T. Tanaka, E. I. Shakhnovich, *J. Chem. Phys.* **108**, 334 (1998)

Transition state ensemble

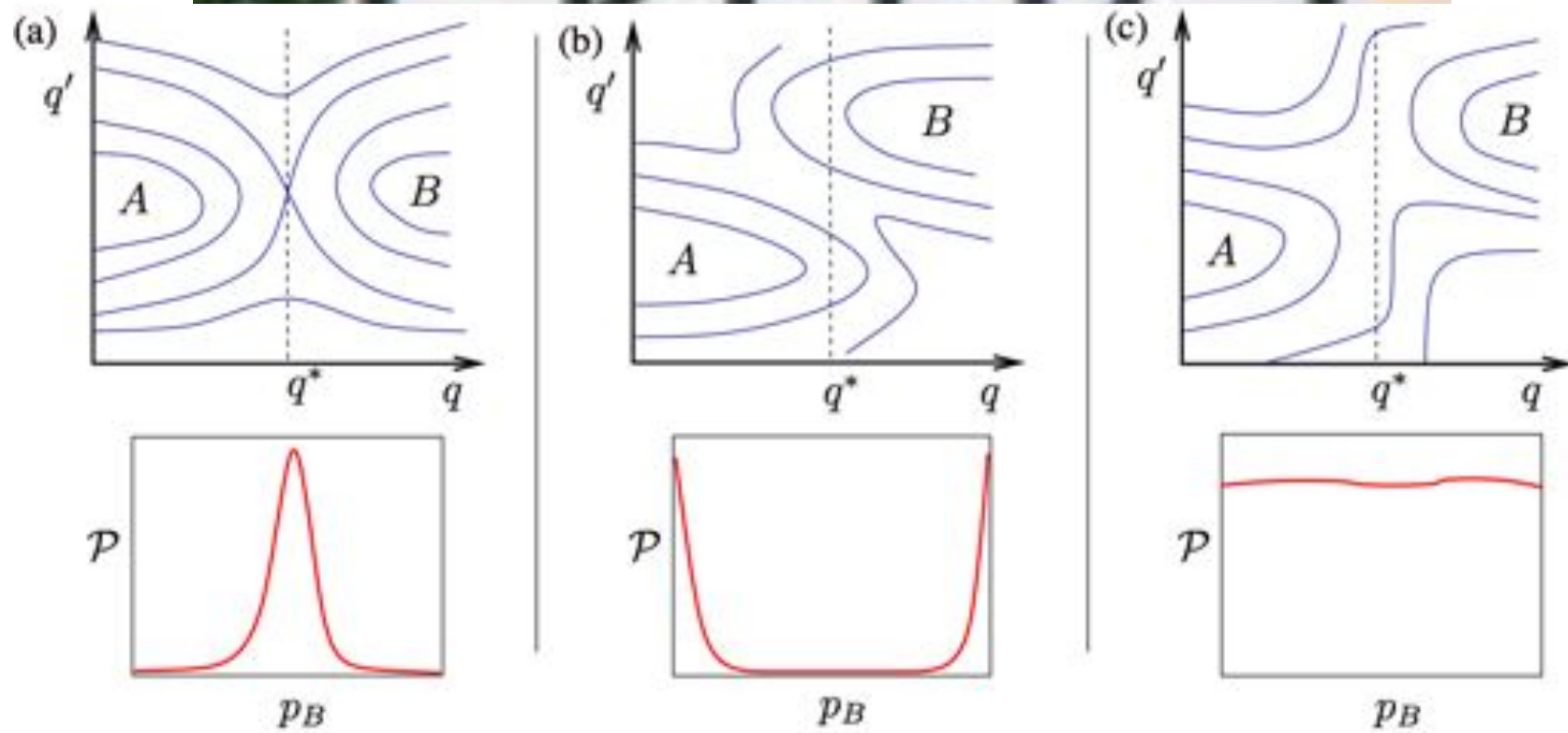
r is a **transition state** (TS) if $p_B(r) = p_A(r) = 0.5$



TSE:

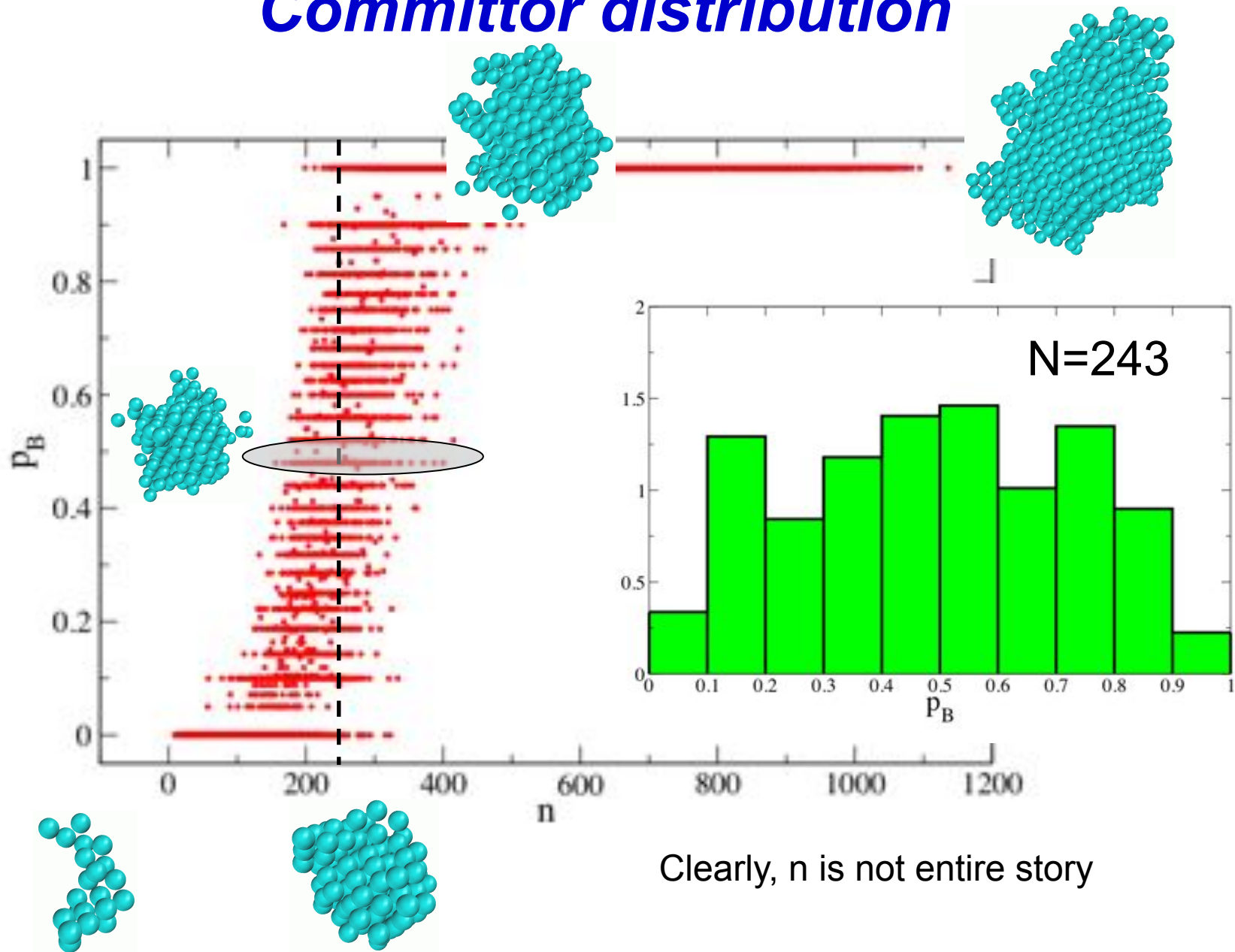
Intersections of transition
pathways with the
 $p_B = 1/2$ surface

Committor distributions



RIGHT

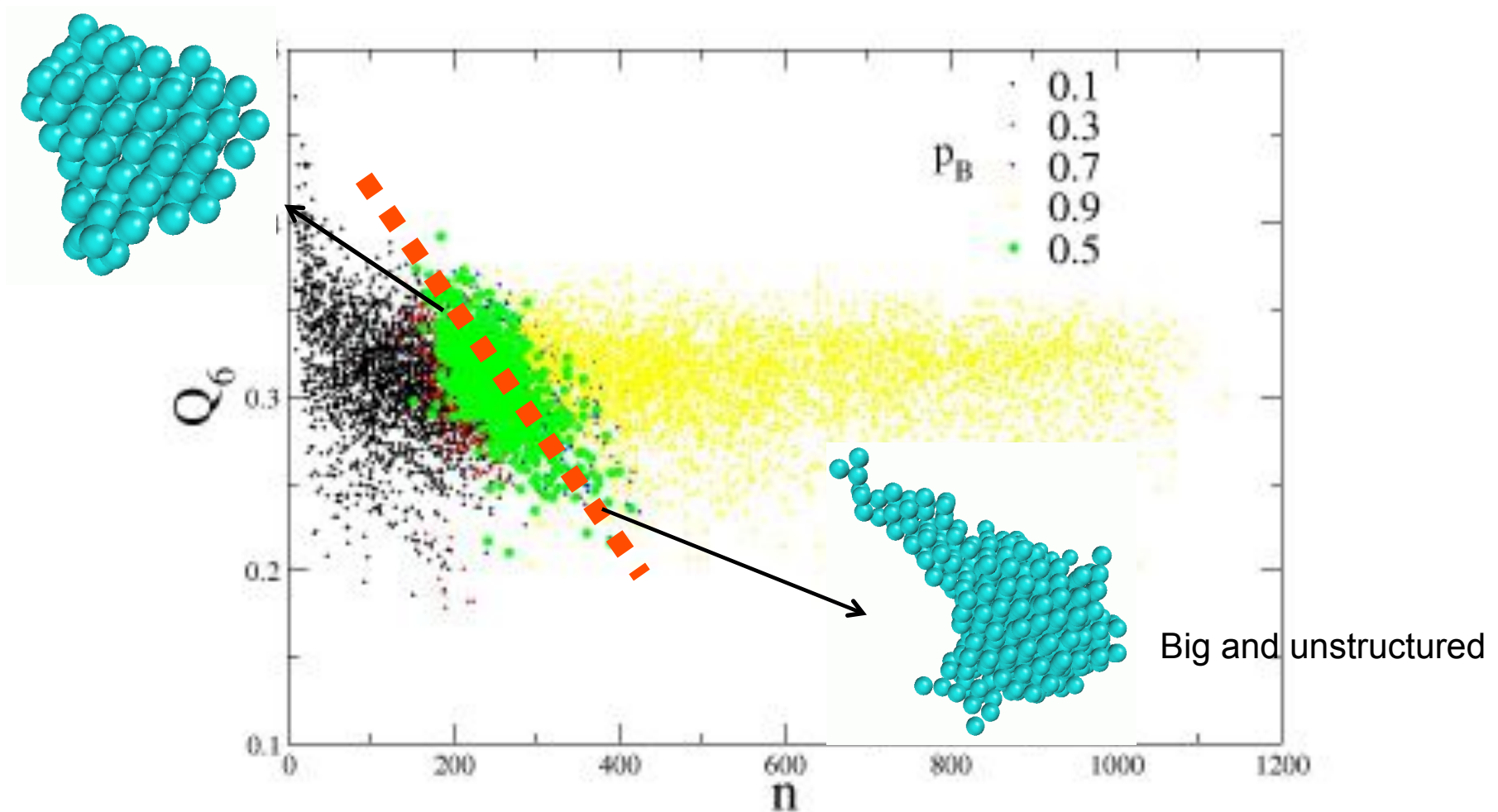
Committer distribution



Clearly, n is not entire story

Structure

Small and structured



Committor analysis gives valuable insight

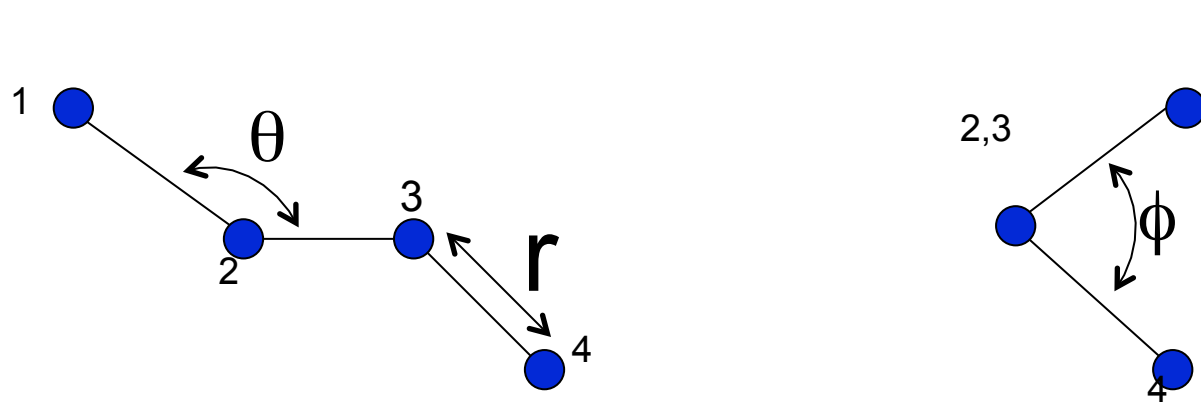
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All-atom force fields for biomolecules

- Potential energy for protein

$$V(\mathbf{r}) = \sum_{\text{bonds}} k_r (r - r_{eq})^2 + \sum_{\text{angles}} k_\theta (\theta - \theta_{eq})^2 + \sum_{\text{dihedrals}} \frac{1}{2} v_n (1 + \cos(n\phi - \phi_0)) \\ + \sum_{i < j} \left(\frac{a_{ij}}{r_{ij}^{12}} - \frac{b_{ij}}{r_{ij}^6} + \frac{q_i q_j}{\epsilon r_{ij}} \right)$$



vdW interactions only between non-bonded $|i-j| > 4$

Currently available empirical force fields

- CHARMM (MacKerrel et al 96)
 - AMBER (Cornell et al. 95)
 - GROMOS (Berendsen et al 87)
 - OPLS-AA (Jorgensen et al 95)
 - ENCAD (Levitt et al 83)
-
- Subtle differences in improper torsions, scale factors 1-4 bonds, united atom rep.
 - Partial charges based on empirical fits to small molecular systems
 - Amber & Charmm also include ab-initio calculations
 - Not clear which FF is best : top 4 mostly used
-
- Water models also included in description
 - TIP3P, TIP4P
 - SPC/E
 - Current limit: 10^6 atoms, microseconds (with Anton ms)



Folding of Trp-cage

20-residue protein NLYIQ WLKDG GPSSG RPPPS

2-state folder, experimental rate 4 μ s

(Andersen et al, Nature 2002, Zhou et al. PNAS 2004, others)

System:

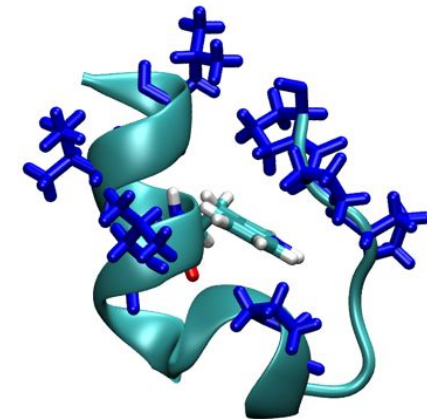
1L2Y in 2800 waters

OPLSAA, PME, Nose-Hoover, GROMACS

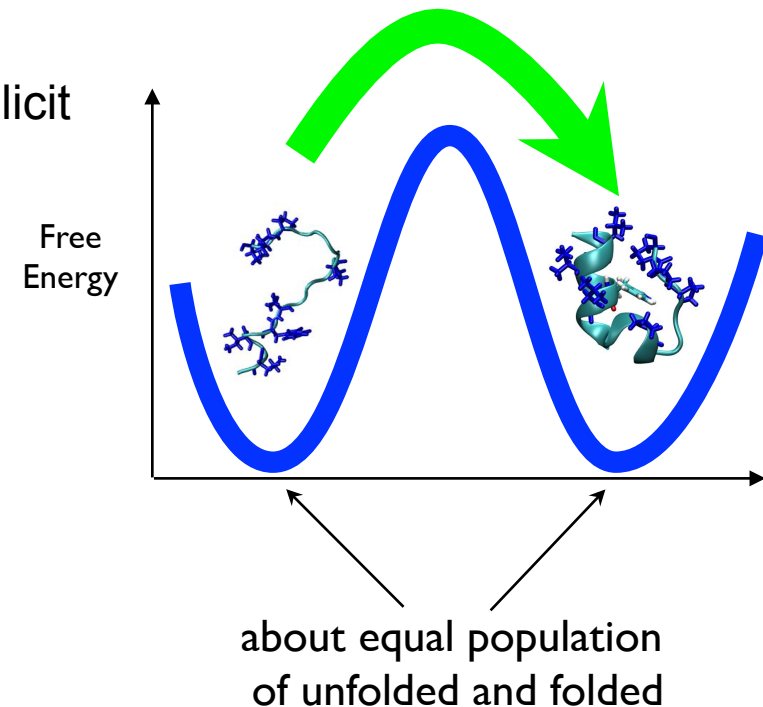
What is folding mechanism and kinetics in explicit water at 300K?

Strategy:

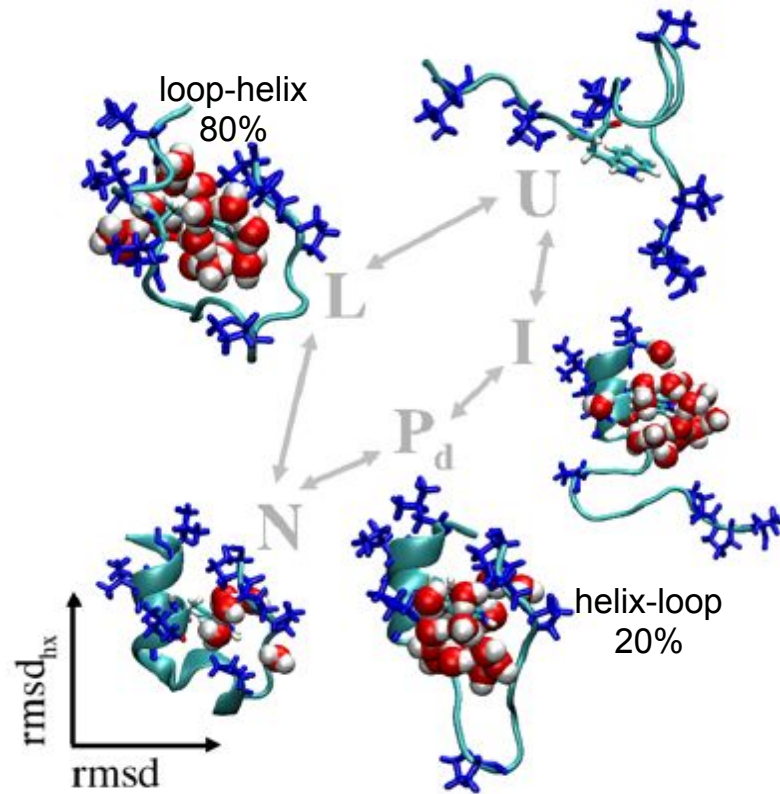
- Stable states by replica exchange MD
- Mechanism by path sampling
- Rate calculation



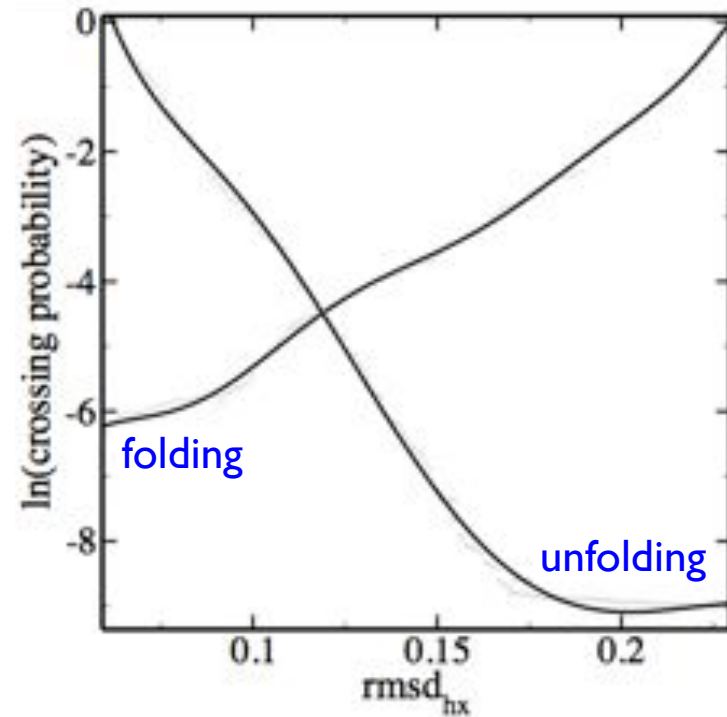
one time per 4 μ s



TPS of Trp-cage folding



Rates by TIS



Rates	TIS	exp
k_{fol}	$0.2 \mu\text{s}^{-1}$	$0.24 \mu\text{s}^{-1}$
k_{unf}	$0.8 \mu\text{s}^{-1}$	$0.08 \mu\text{s}^{-1}$

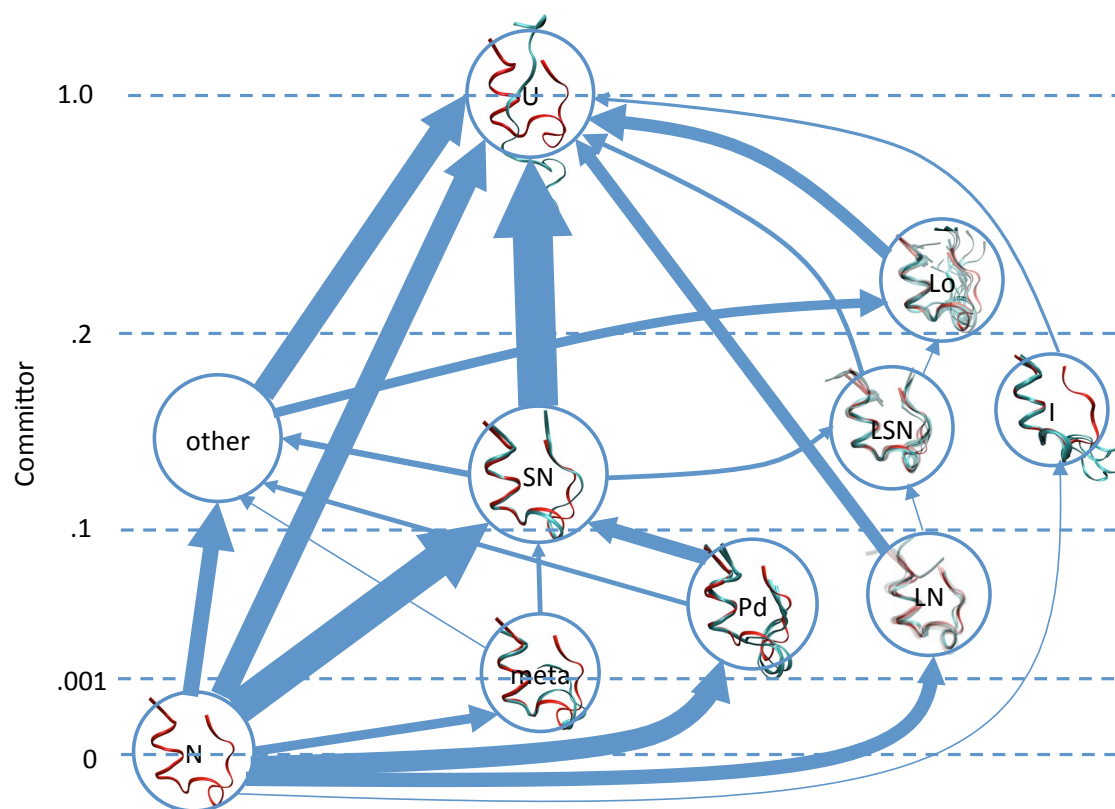


Jarek Juraszek

J. Juraszek, PGB PNAS 2006
Biophys. J. 95 4246 (2008)

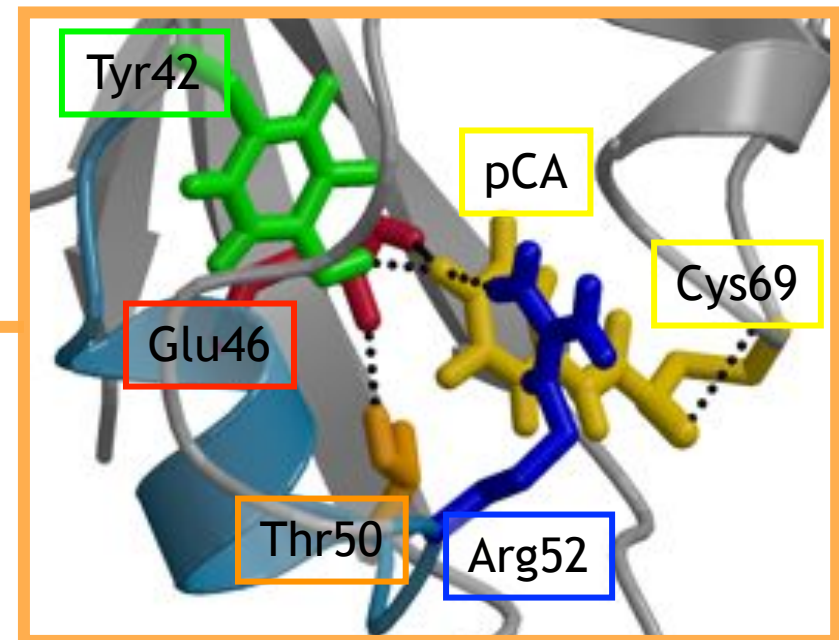
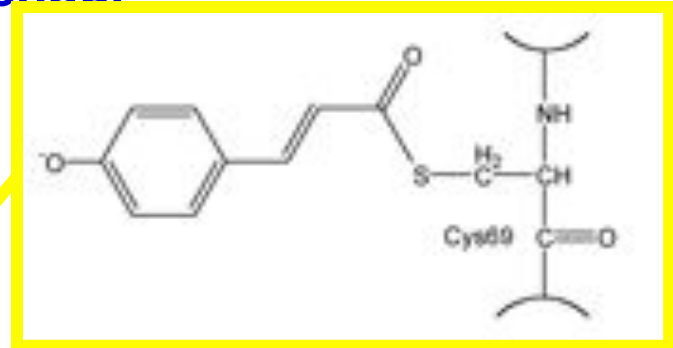
Advanced path sampling results

- Very recent single replica multiple state transition interface sampling revealed much more complex network with many short-lived intermediates



Photoactive Yellow Protein

bacterial blue-light sensor



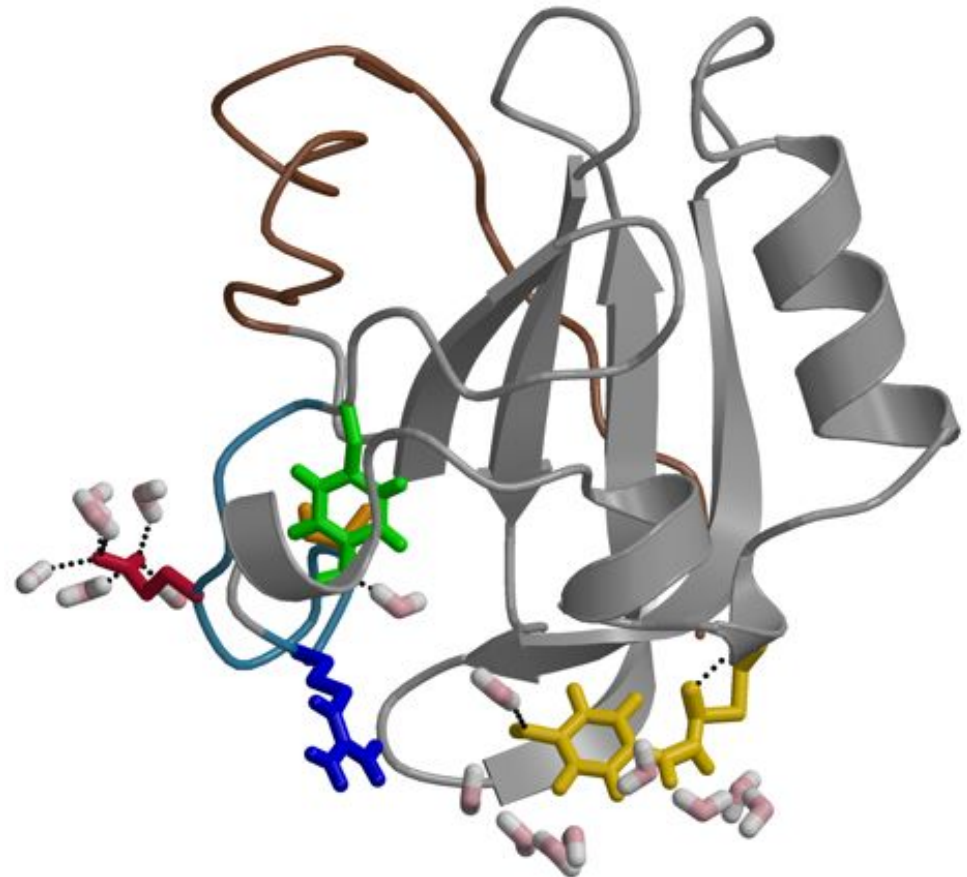
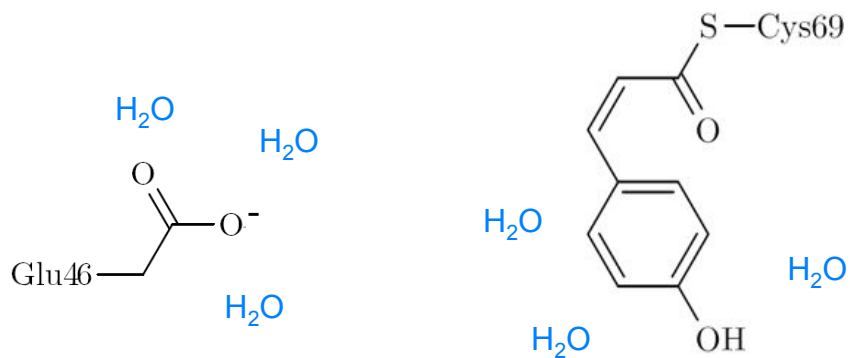
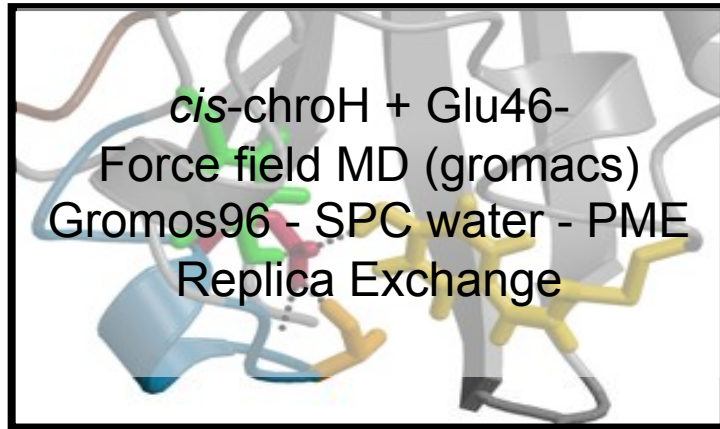
N-terminal domain PAS domain

Absorption of a blue-light photon triggers the photo cycle

J. Vreede et al. Biophys. J. 2005

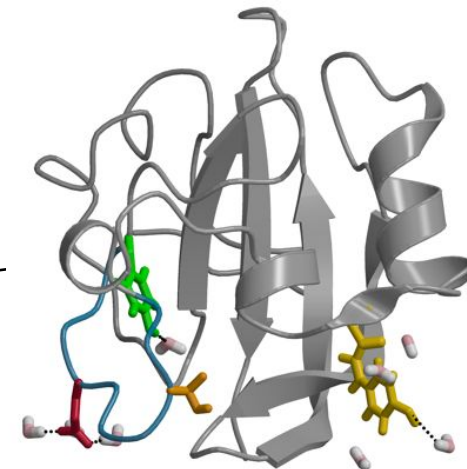
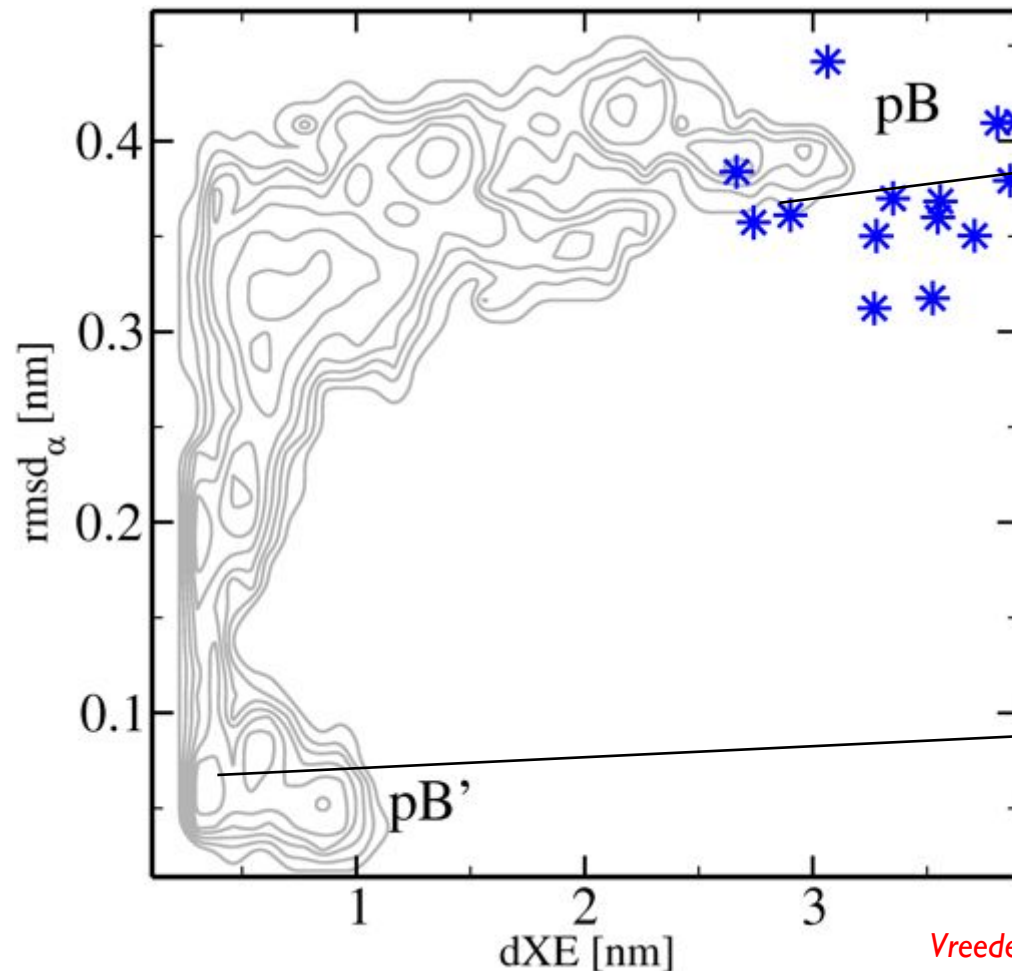
Partial unfolding

- Loss of α -helical structure
- Exposure of hydrophobic groups
- Increased flexibility in parts of the protein backbone

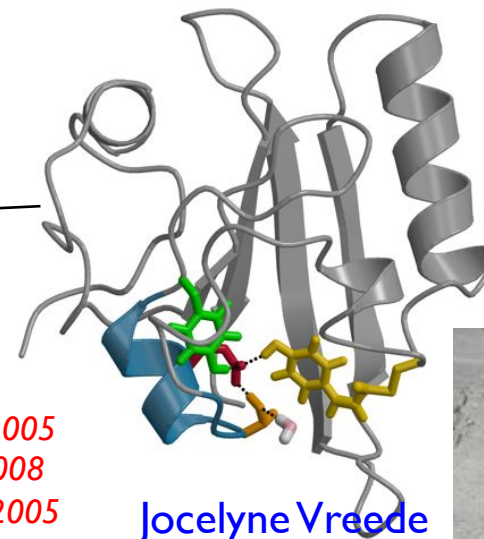


Partial unfolding: REMD free energy

Unfolding happens on millisecond timescale
(1000 times longer than possible by direct MD)



Helix 43-51 unfolded
Chromophore and Glu46 are solvent exp
Agreement with experiment



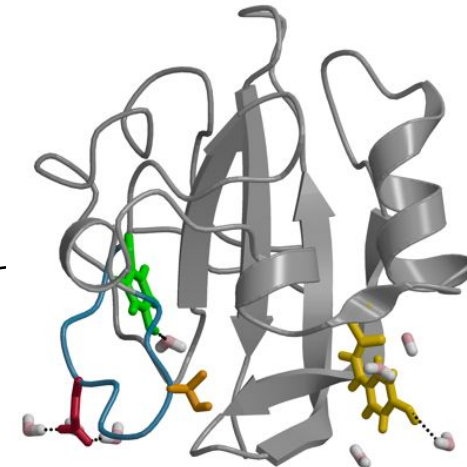
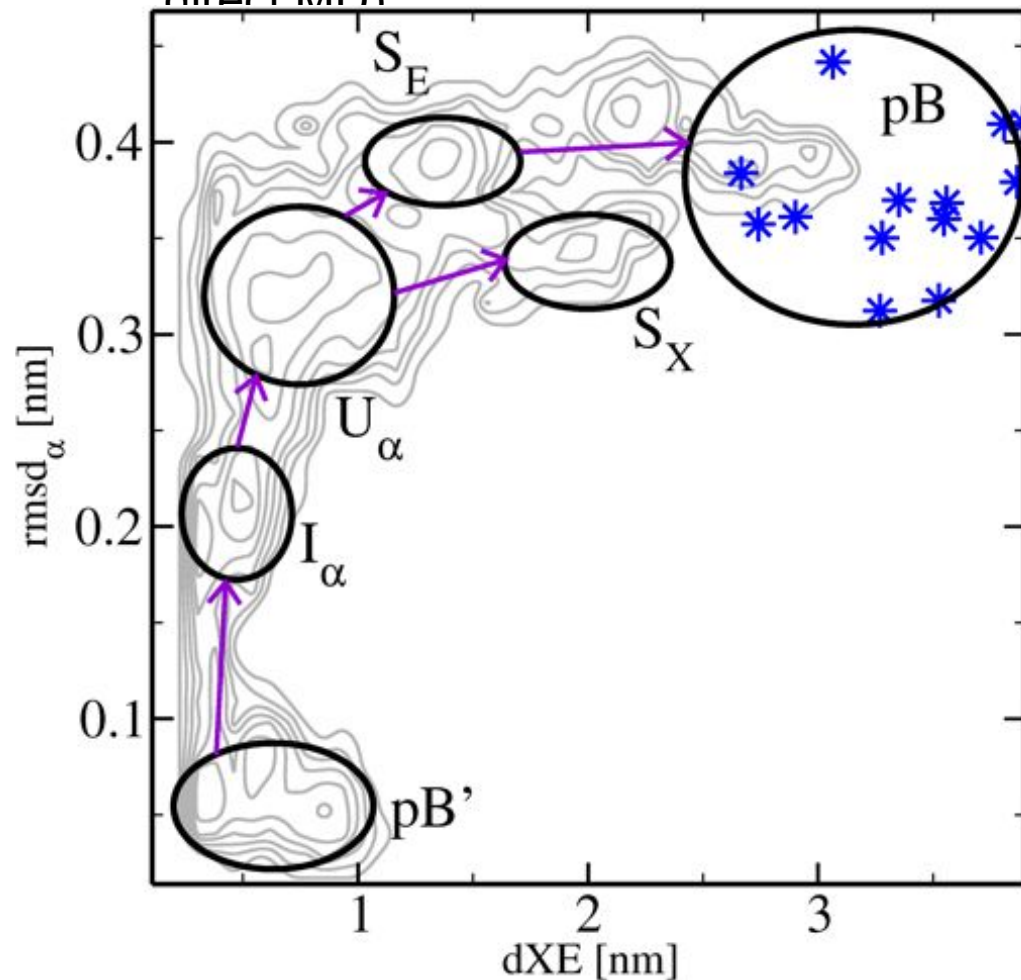
Vreede et al. Biophys. J. 2005
Vreede et al. Proteins 2008
Bernard et al. Structure 2005

Jocelyne Vreede

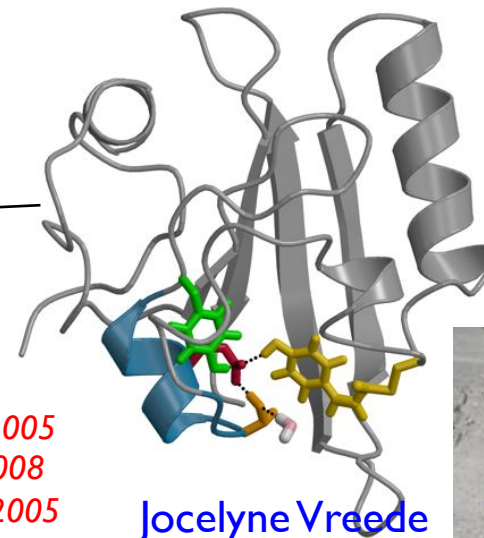


Partial unfolding: REMD free energy

Unfolding happens on sub-millisecond timescale (1000 times longer than possible by direct MD)



Helix 43-51 unfolded
Chromophore and Glu46 are solvent exp
Agreement with experiment

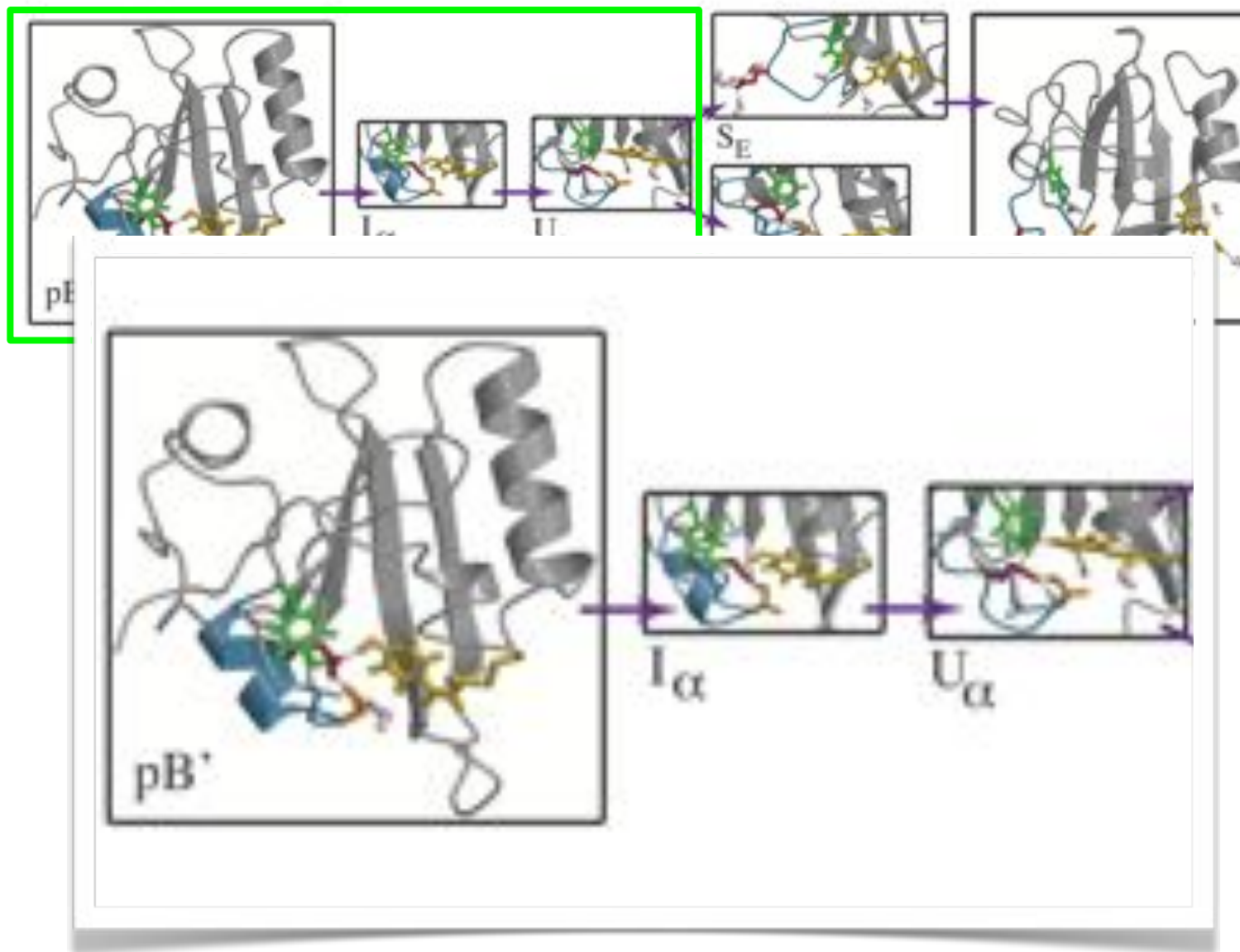


et al. Biophys. J. 2005
Vree de et al. Proteins 2008
Bernard et al. Structure 2005

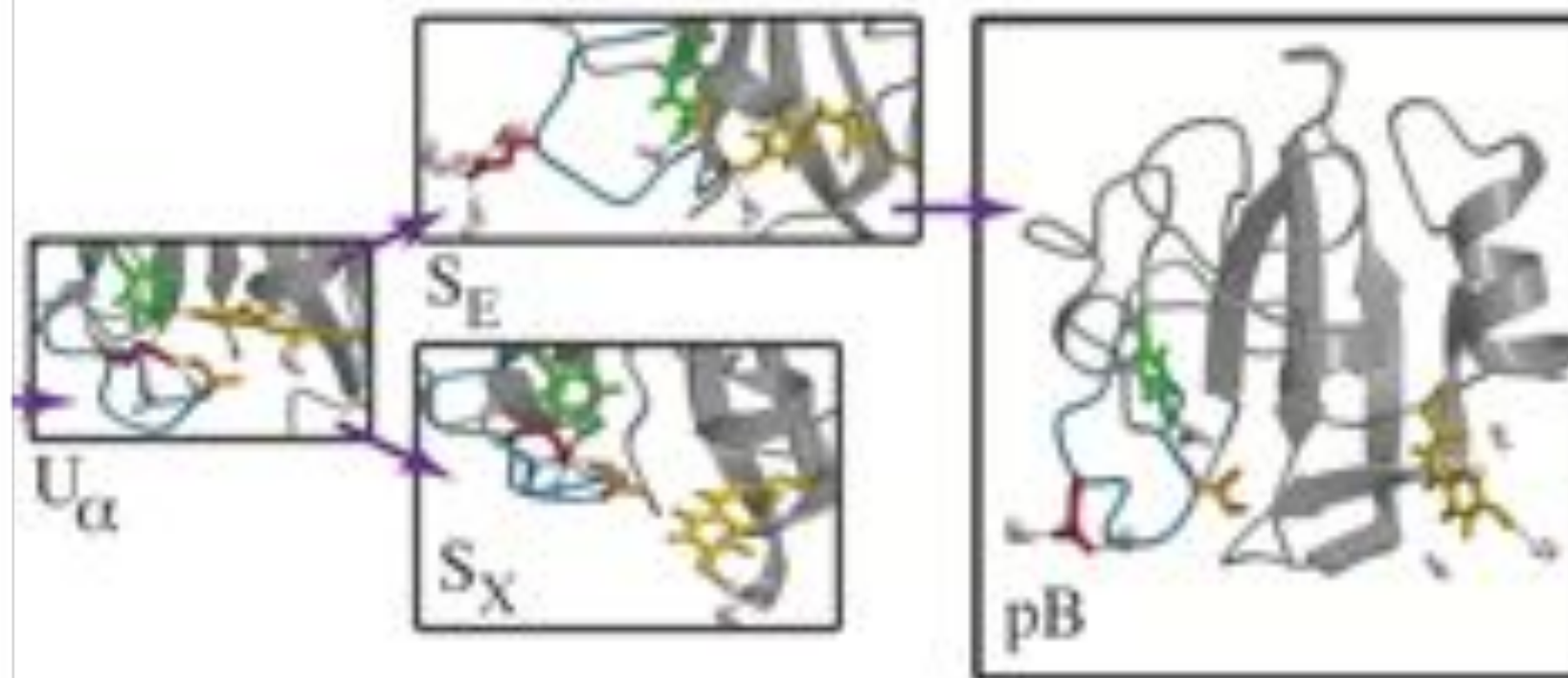
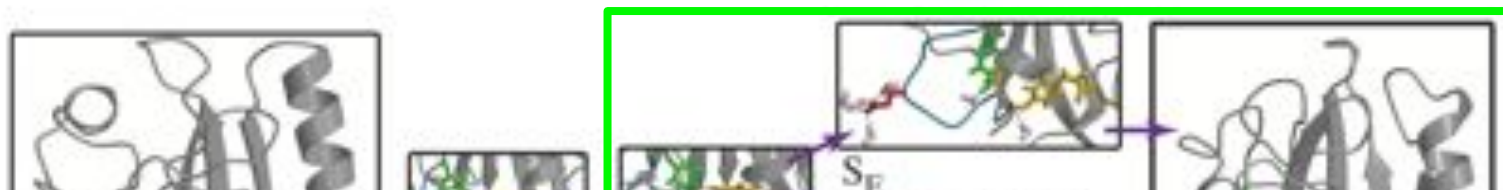
Jocelyne Vree de

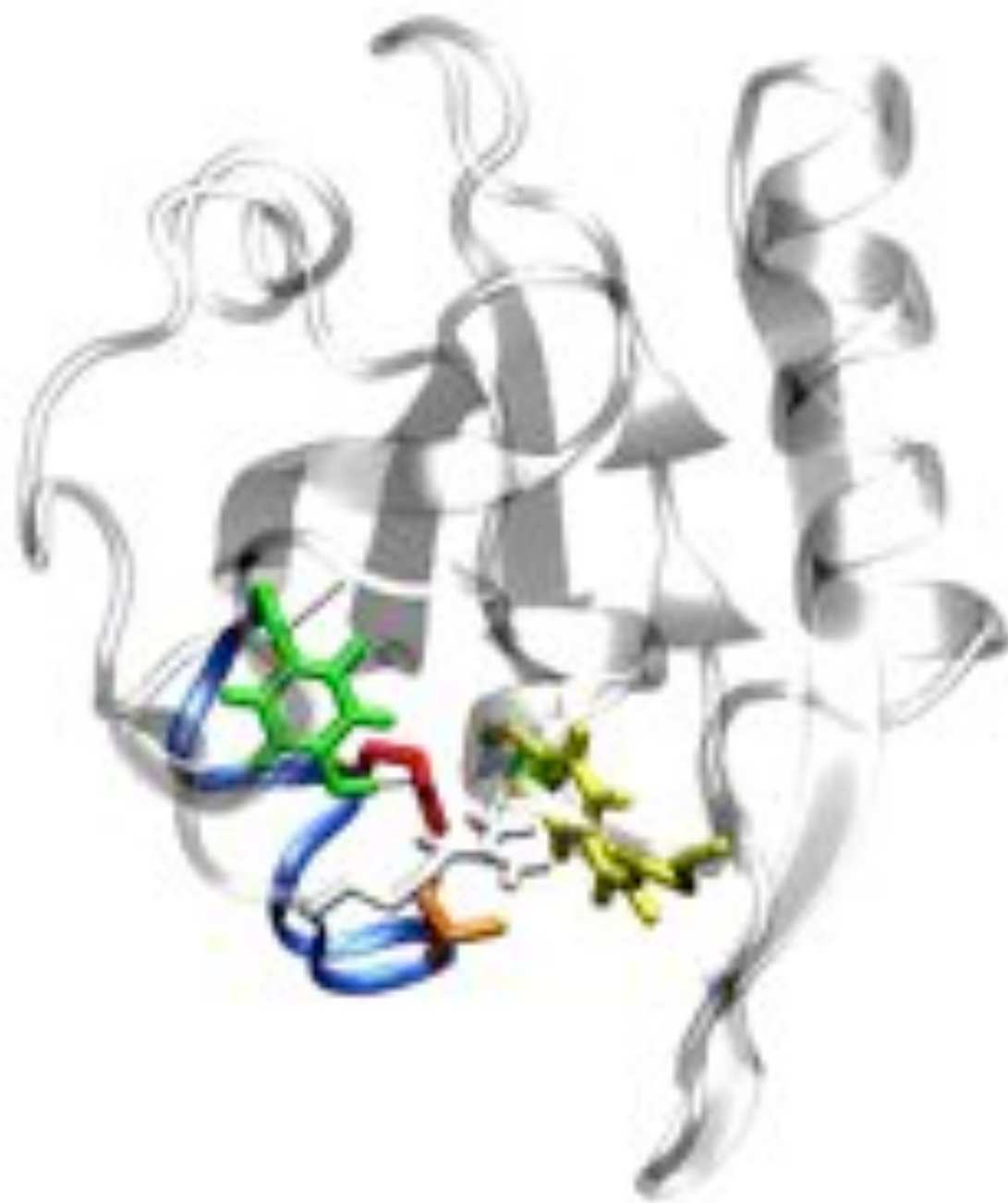


Transitions in the partial unfolding



Solvent exposure transitions





The end



"Mr. Osborne, may I be excused? My brain is full."