

Simulations with MM Force Fields

Monte Carlo (MC)
and
Molecular Dynamics (MD)
Video II.vi

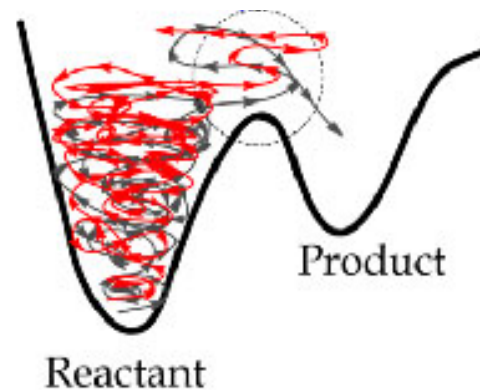
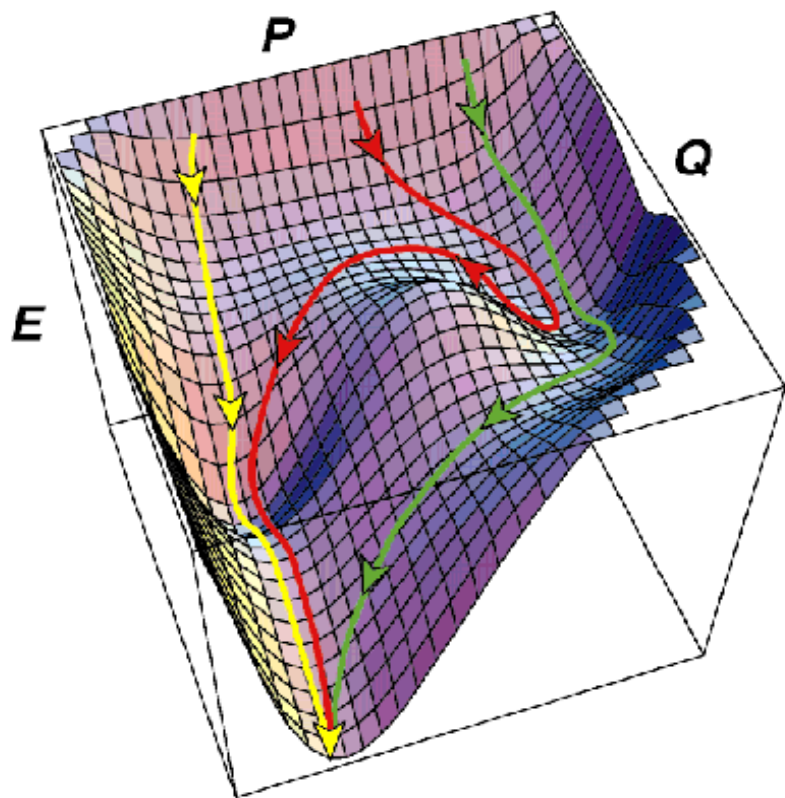
Some slides taken with permission from

Howard R. Mayne

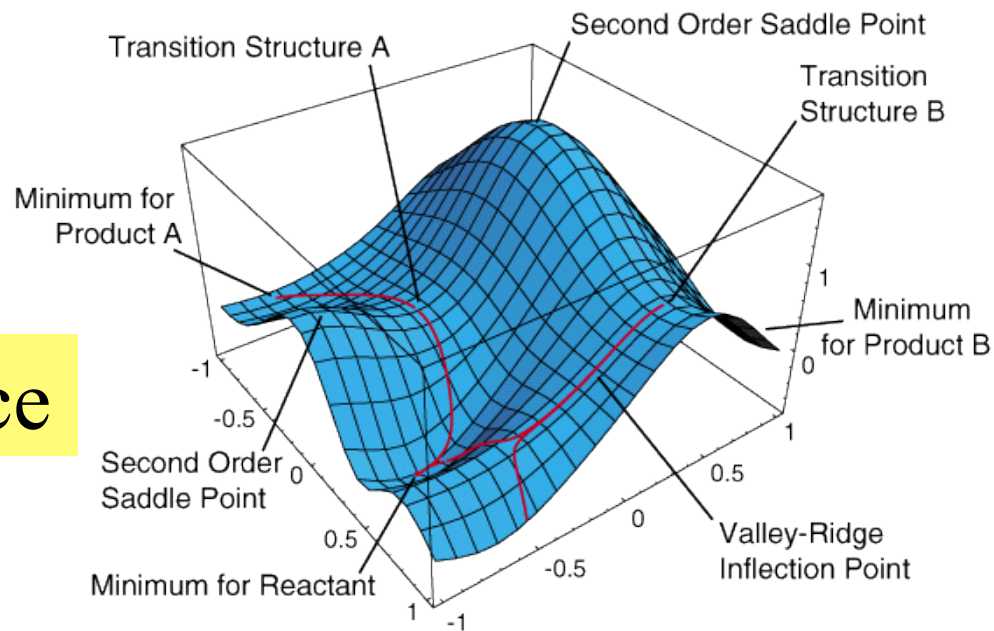
Department of Chemistry

University of New Hampshire

We often draw in 1D,
but we're hiding a lot.



Walking on the Surface

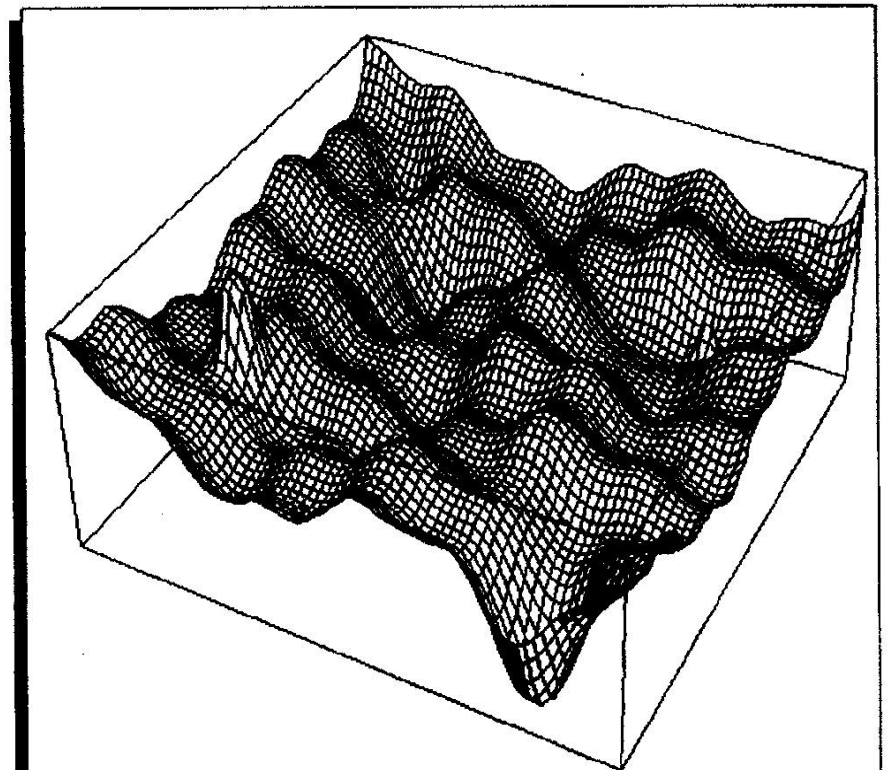


“Finding a Needle in a Haystack”

The lowest point on
The Energy Landscape
is the most stable point
(Global Minimum)

At Absolute Zero
a system in thermal equilibrium
must be at its global minimum

Increasing the efficiency of
searching for the global
minimum is an active area of
research



Some Common Search Strategies (Optimization Techniques)

1. **Systematically search all coordinates.**

IMPOSSIBLE! $\sim N^{100}$ (or so).

2. **Dynamics + “Quench”**

Roam over the surface, occasionally sliding down to the nearest local minimum.

3. **Simulated Annealing**

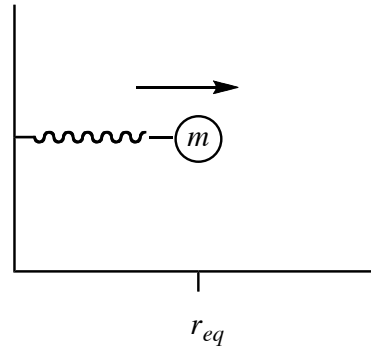
Heat the system up, and cool very slowly.

4. **Evolutionary/Genetic Algorithms**

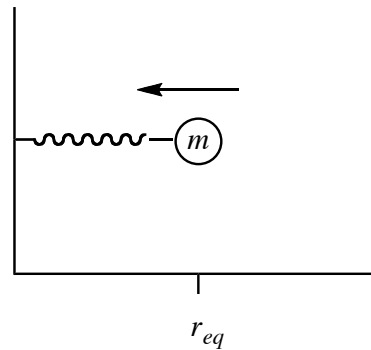
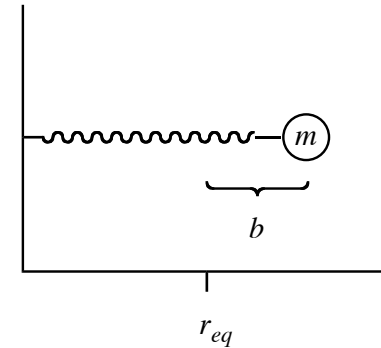
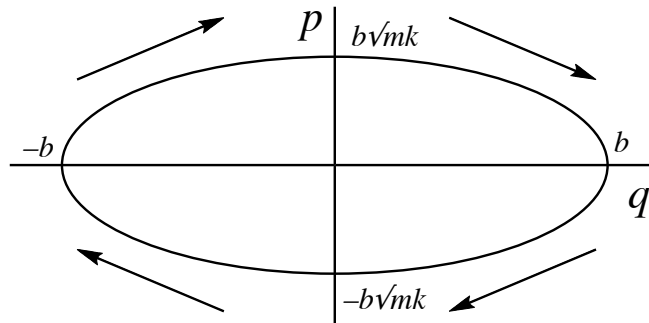
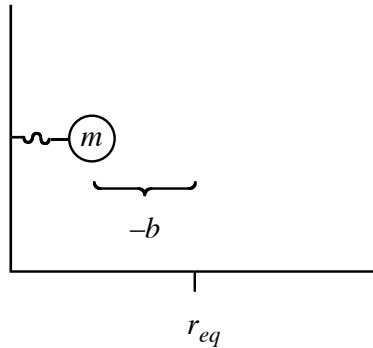
Allow “good” geometries to survive and to share properties, but “bad” ones to die.

#2 and #3 require a discussion of Molecular Dynamics and Metropolis Monte Carlo Techniques

Phase Space — 1D Harmonic Oscillator



No two trajectories in phase space can cross. A system is either periodic or it samples all of phase space in an ergodic fashion.

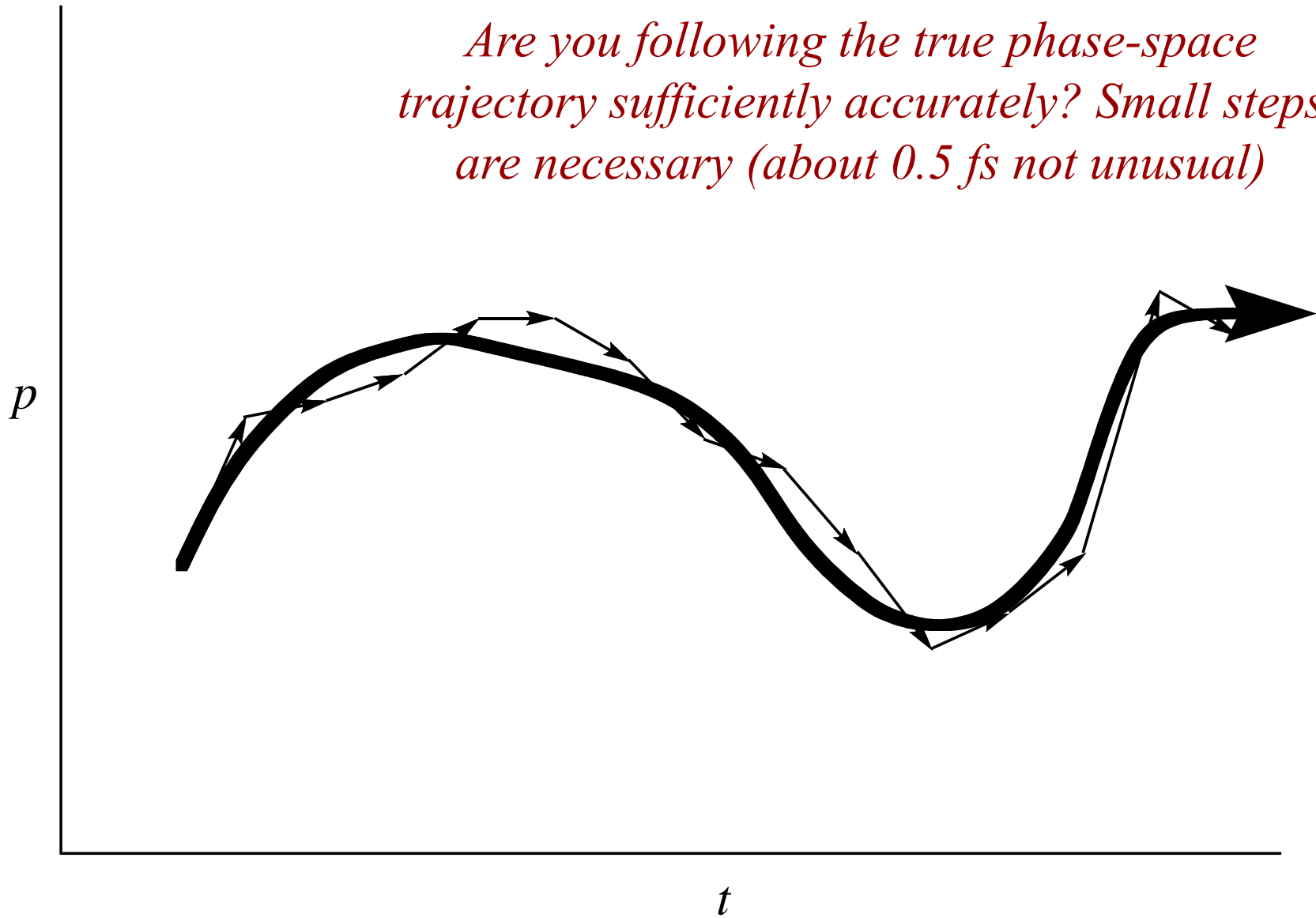


Phase point defined as

$\mathbf{r} = (q, p)$ generalized for N particles as

$\mathbf{r} = (q_{1x}, q_{1y}, q_{1z}, p_{1x}, p_{1y}, p_{1z}, \dots, q_{Nx}, q_{Ny}, q_{Nz}, p_{Nx}, p_{Ny}, p_{Nz})$

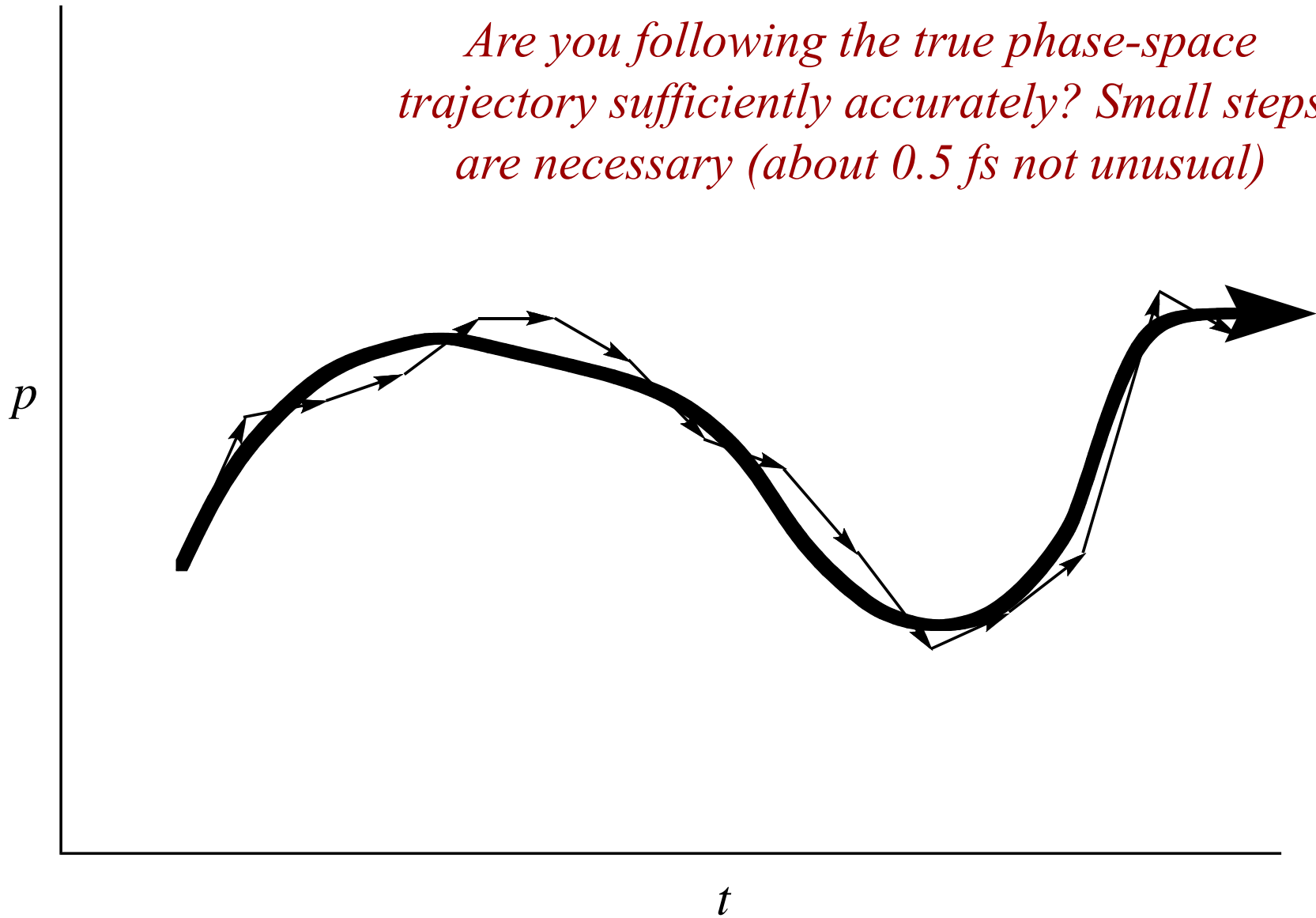
Are you following the true phase-space trajectory sufficiently accurately? Small steps are necessary (about 0.5 fs not unusual)



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Integrating over Phase Space

$$\langle \Xi \rangle = \frac{\int_{\text{PS}} \Xi(\mathbf{r}) P(\mathbf{r}) d\mathbf{r}}{\int_{\text{PS}} P(\mathbf{r}) d\mathbf{r}}$$

Expectation values are dictated by the relative probabilities of being in different regions of phase space

$$P(\mathbf{r}) = e^{-E(\mathbf{q}, \mathbf{p})/k_{\text{B}}T} \quad Q = \int_{\text{PS}} P(\mathbf{r}) d\mathbf{r}$$

Key point: Don't waste time evaluating $\Xi(\mathbf{r})$ if $P(\mathbf{r})$ is zero.

Difficulty: Phase space is $6N$ -dimensional. If you only want to sample all possible combinations of either positive or negative values for each coordinate (i.e., hit every “hyperoctant” in phase space *once*), you need 2^{6N} points!

Metropolis Monte Carlo:

For simplicity we work here with a property independent of momentum, thereby reducing the computational overhead by a factor of 2

Generates a thermal population of geometries

such that $n(\mathbf{r}_1)/n(\mathbf{r}_2) = \exp(-[U(\mathbf{r}_1)-U(\mathbf{r}_2)]/k_B T)$

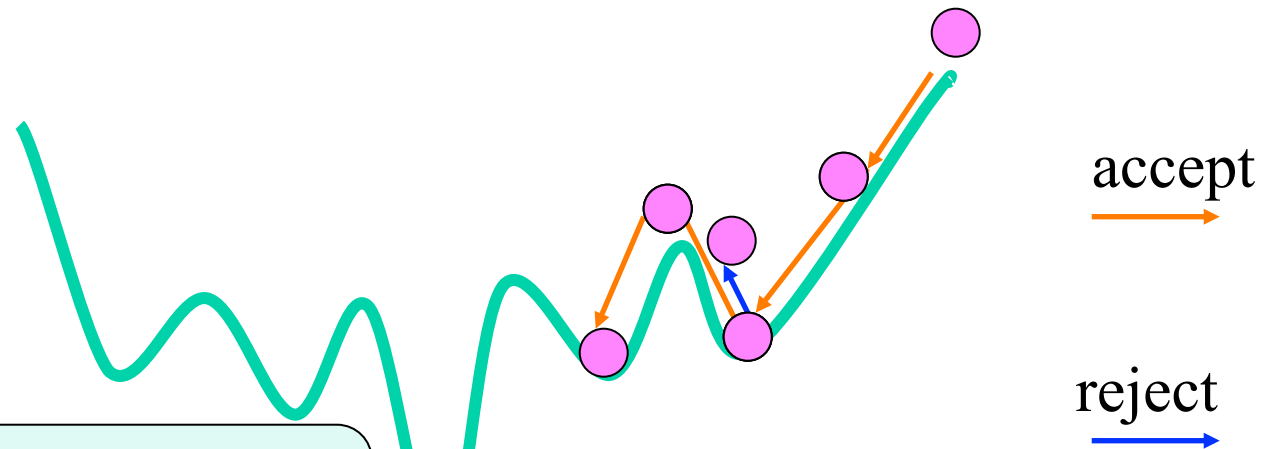
Method.

1. Propose “move” $\mathbf{r}_1 \rightarrow \mathbf{r}_2$
2. “Accept” move if (i) $U(\mathbf{r}_1) < U(\mathbf{r}_2)$

(ii) $\exp[-(U(\mathbf{r}_1)-U(\mathbf{r}_2))/k_B T] > \text{random } \# \epsilon[0,1]$

3. Else “reject”

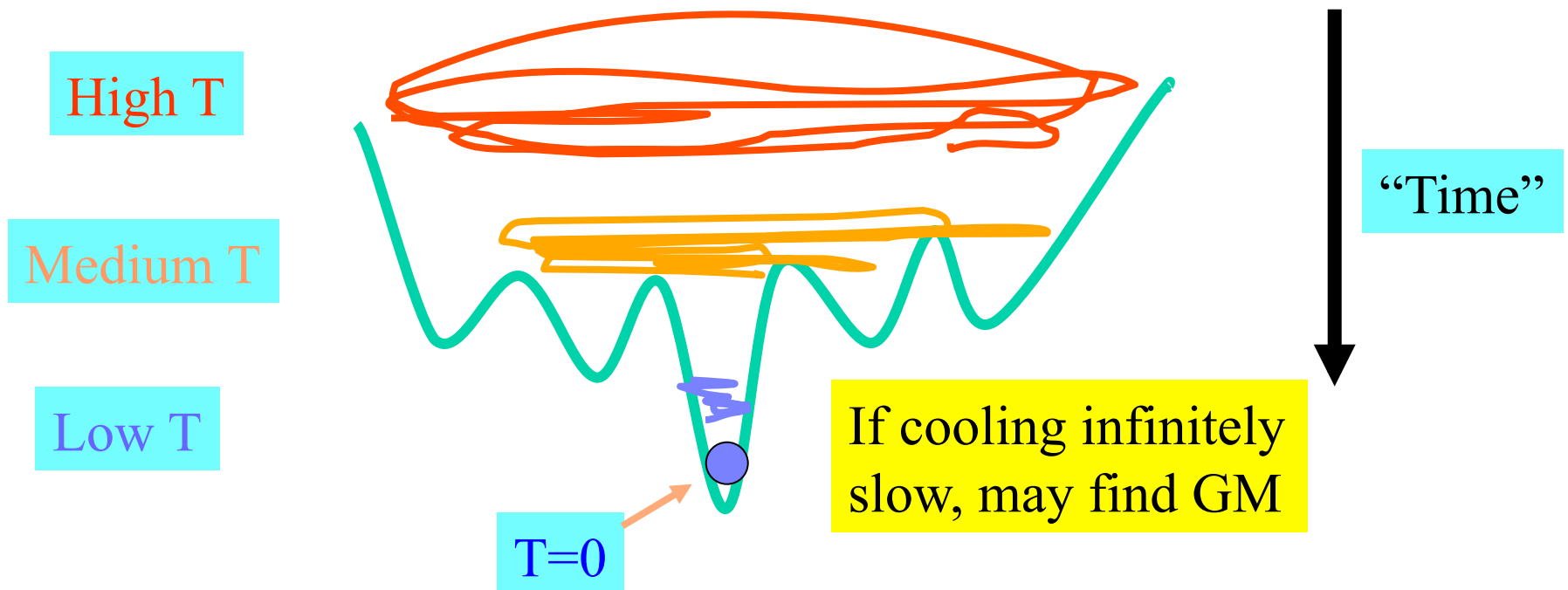
**Boltzmann
Distribution**



So, now $\langle \Xi \rangle = \frac{1}{M} \sum_{i=1}^M \Xi_i(\mathbf{r}_i)$

Simulated Annealing

Start at high temperature, then decrease temperature slowly with time.



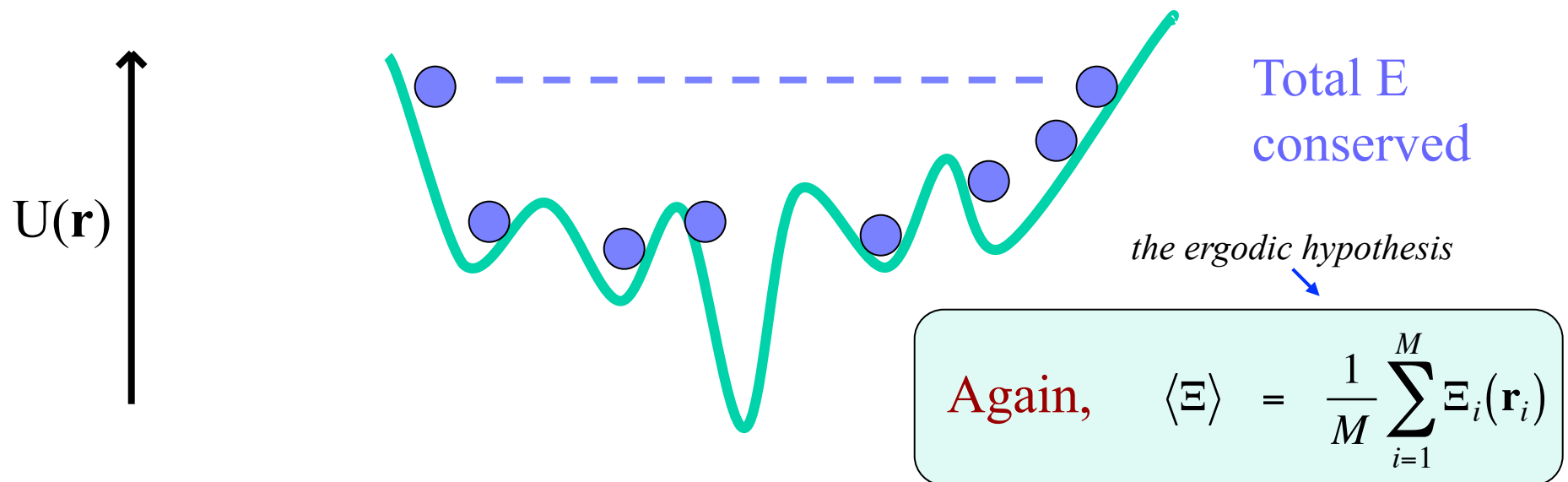
Molecular Dynamics (MD)

Solve classical equations of motion from
some initial geometry and velocity

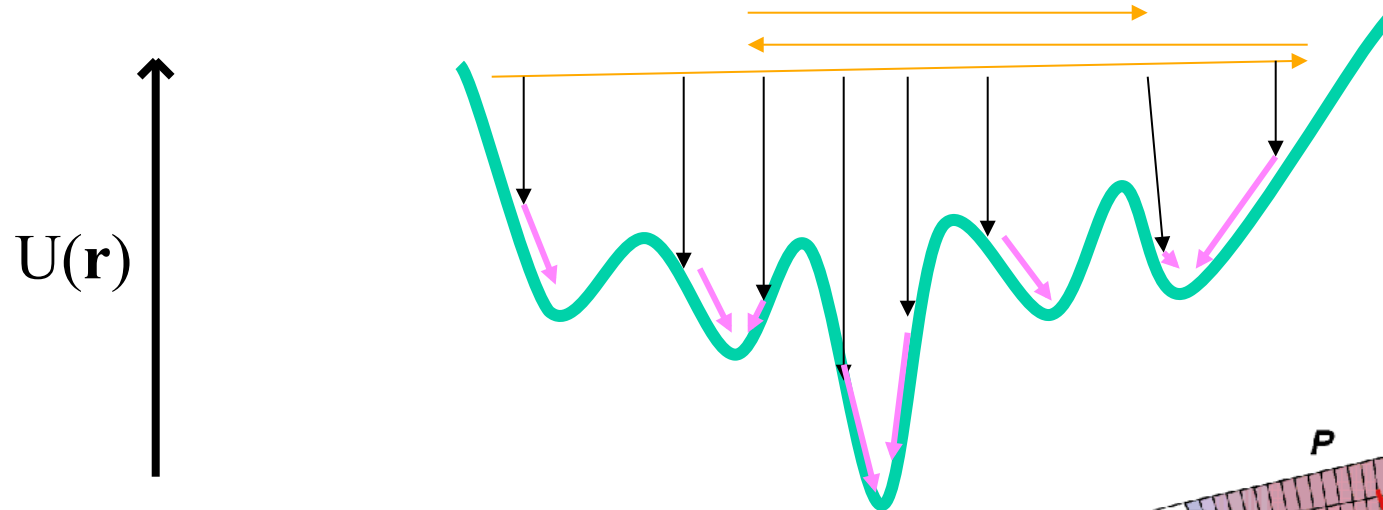
$$\mathbf{r}(0) \rightarrow \mathbf{r}(t) ; \mathbf{v}(0) \rightarrow \mathbf{v}(t)$$

Newton's Law $\mathbf{F} = m\mathbf{a} = -dU(\mathbf{r})/d\mathbf{r}$

Need $\mathbf{r}(0)$, $\mathbf{v}(0)$, $U(\mathbf{r})$, $dU/d\mathbf{r}$ $\mathbf{v}(0)$ from temperature (randomly distributed)
 $\mathbf{r}(t=0)$



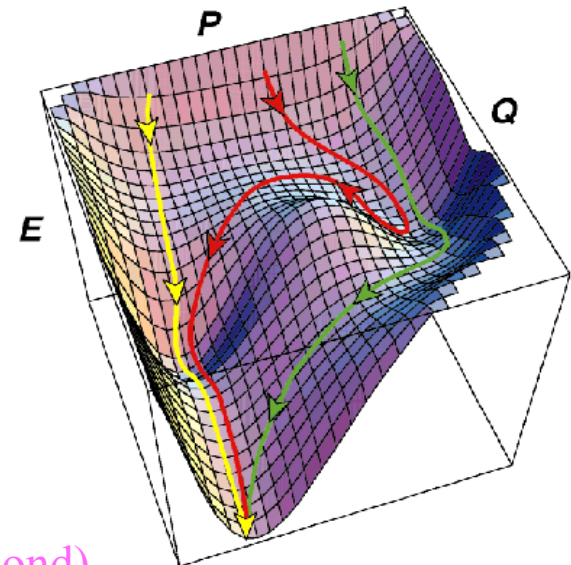
High Energy Dynamics to cross barriers freely



Occasional Quenches

Remove kinetic energy.
Slide from the current geometry
down the steepest slope
(better, conjugate gradient)

Requires first (often second)
derivatives.



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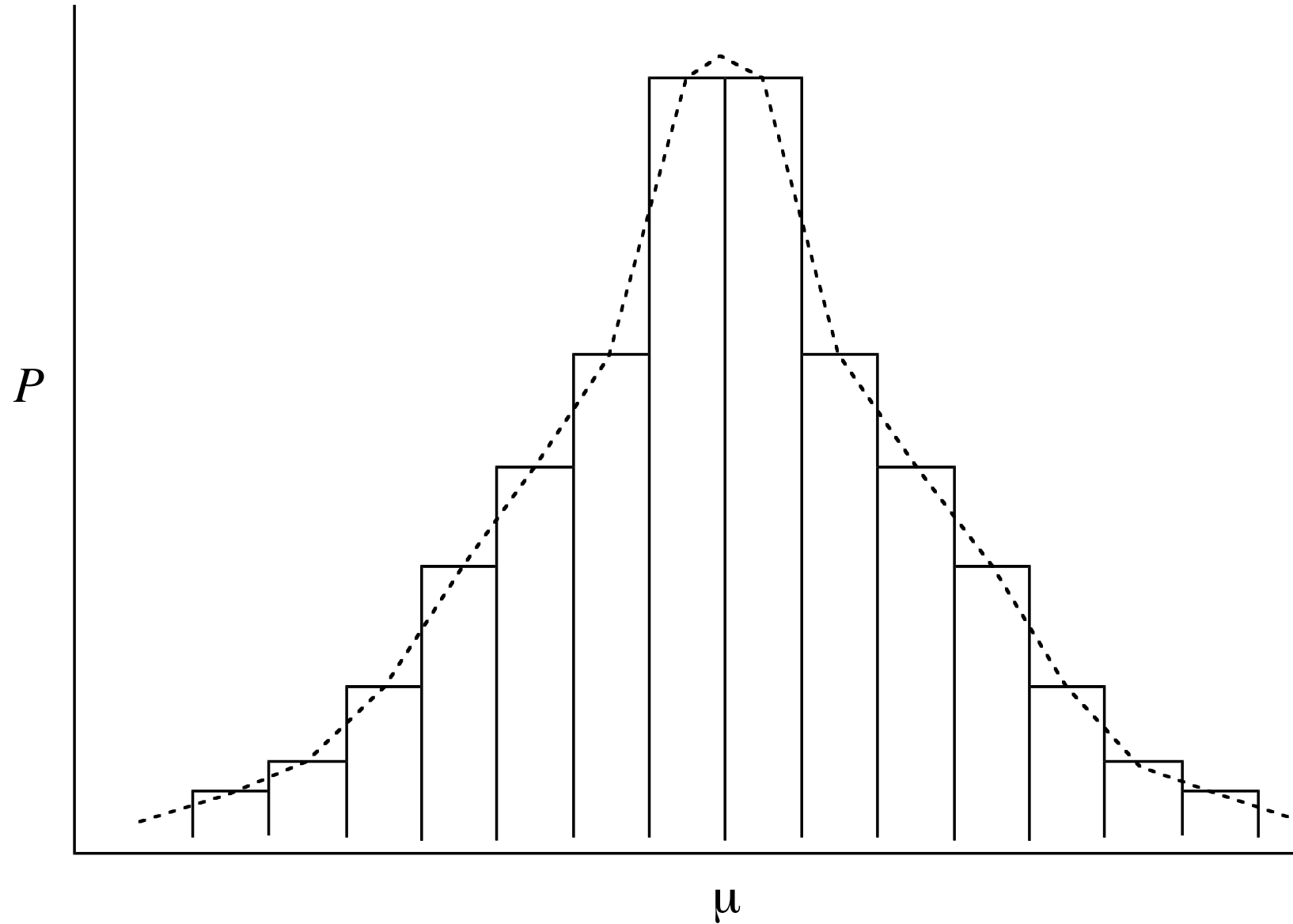
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Nota bene: the standard deviation in an expectation value is not (necessarily) an error, but may instead be a manifestation of dynamical variation



Molecular Dynamics

Simulation yields $\mathbf{r}(t)$, $\mathbf{v}(t)$, $U(\mathbf{r}(t))$,
correlation functions

- Dynamic structure (e.g. does reaction happen?)
- Transport properties
(D , viscosity, etc)

Molecular Dynamics

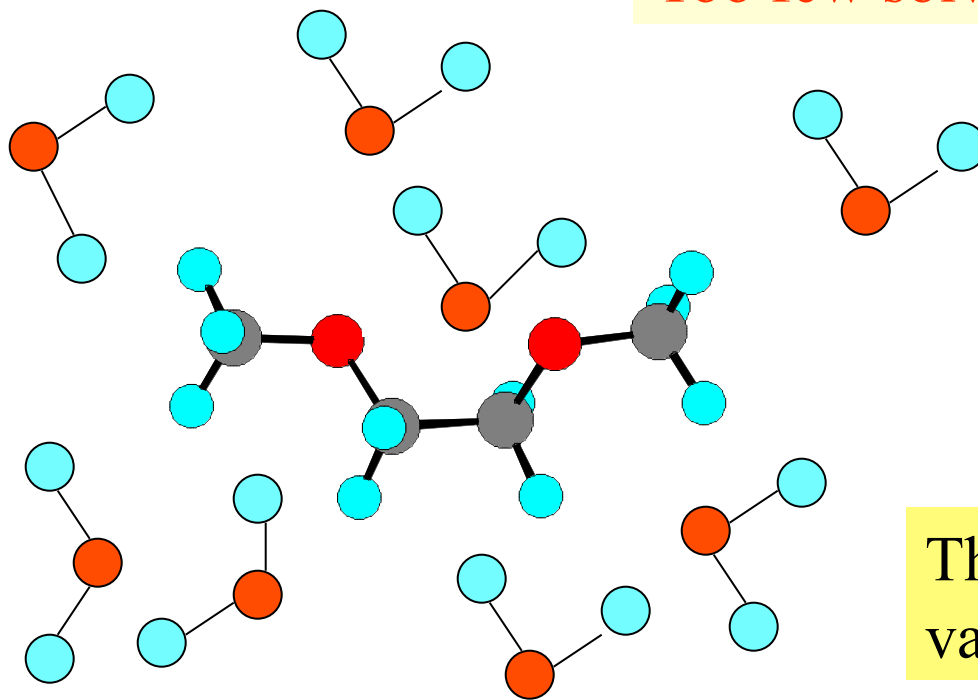
Using “tricks” can be made to run at:

- constant T,
 - constant P,
- or combinations thereof.

(Keywords: Statistical mechanical ensemble;
heat bath; thermostats; pistons)

“Tricks” in Simulations, continued...

Problem!
Too few solvent molecules!

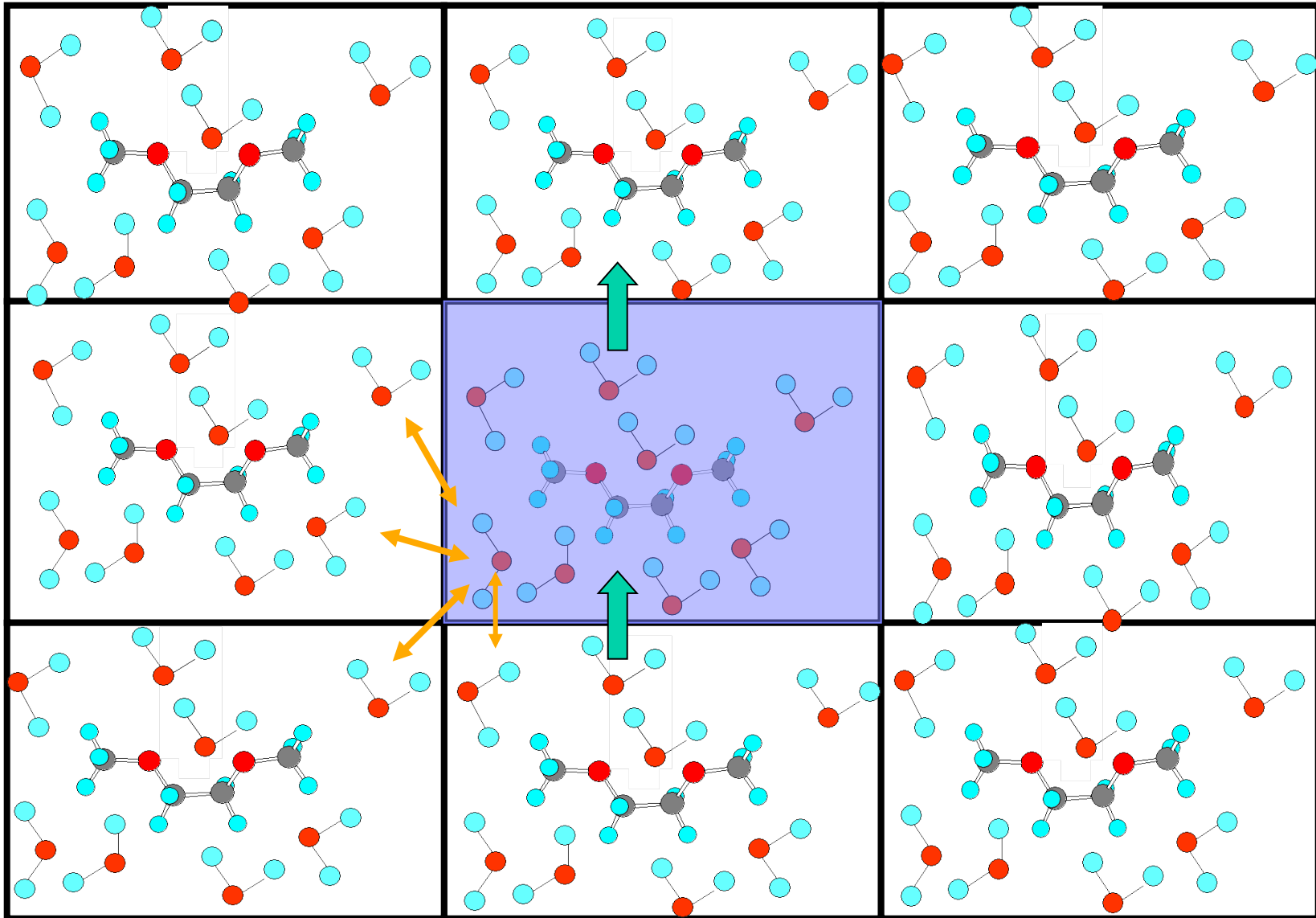


The solvent sees
vacuum, not bulk.

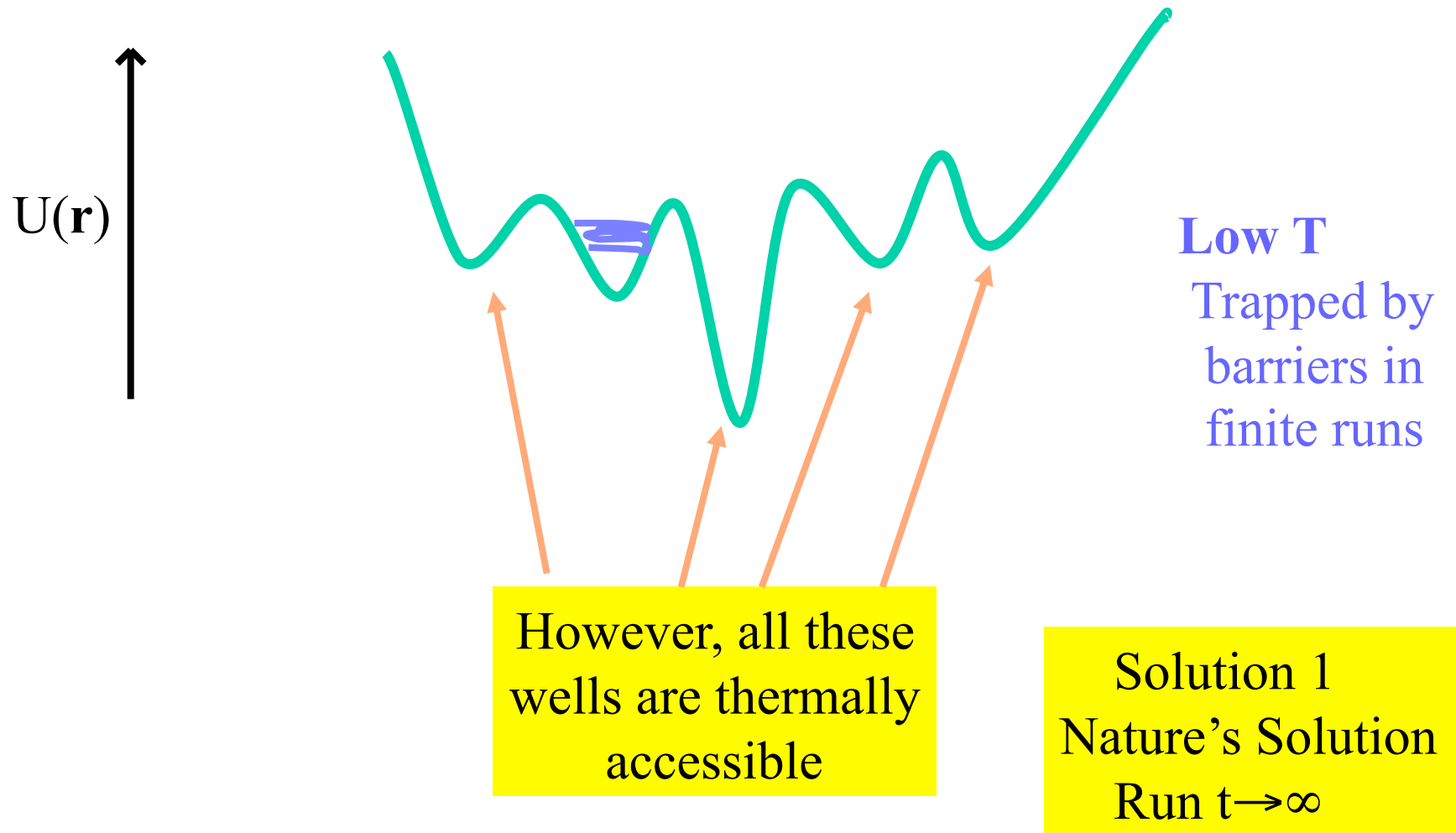
Adding more solvent molecules
increases computational effort!

Periodic Boundary Conditions

Make the system think it's larger than it really is.



Problem with MD and Monte Carlo
“Quasi-Ergodic” Sampling Problem



What method to use?

MD needs smooth derivatives

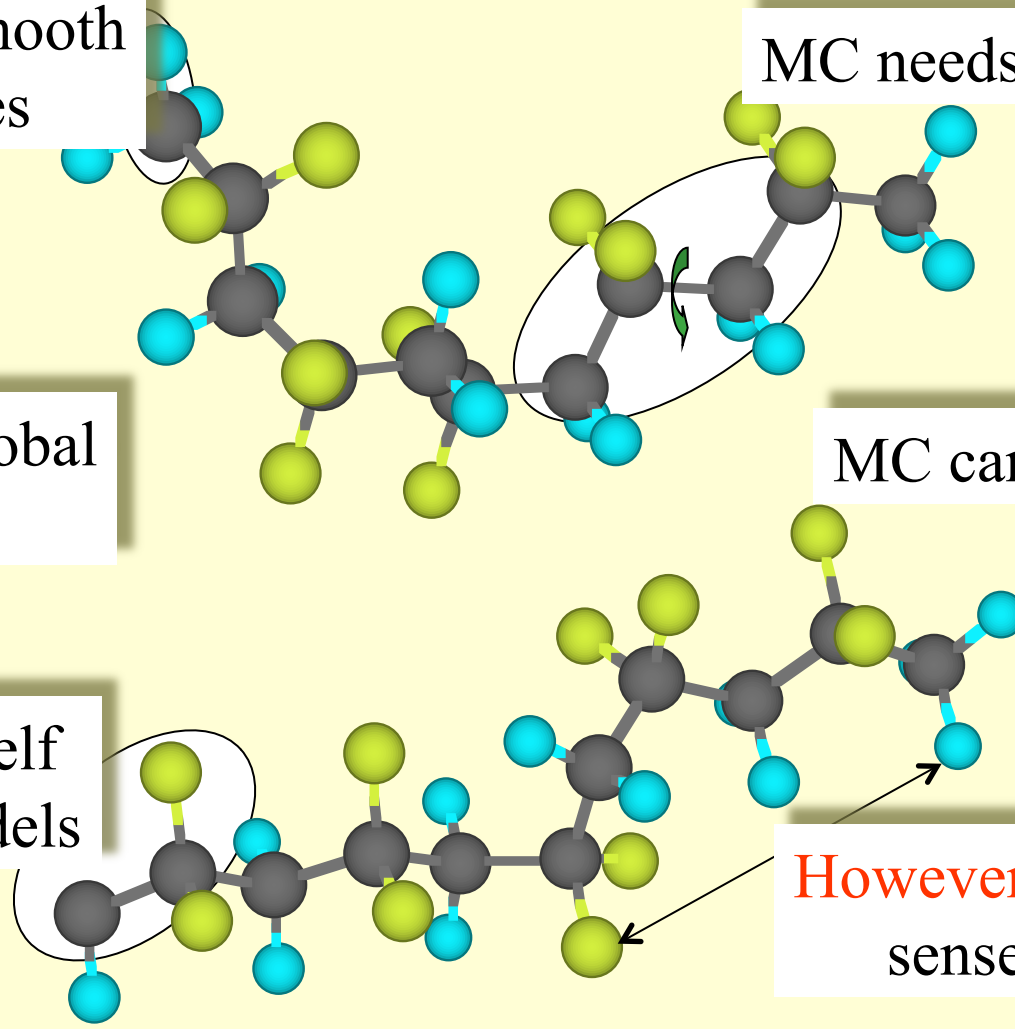
MC needs no derivatives

MD needs global updates

MC can use local updates

MC lends itself to simple models

However, MC has no sense of time!



So, What Method To Use?

For equilibrium problems
Monte Carlo is a
good first pass

Time Scale

10^{-6} S

10^{-8} S

10^{-12} S

10^{-10} m

10^{-8} m

10^{-6} m

10^{-4} m

Length Scale

quantum
chemistry

$$H\psi = E\psi$$

Molecular
Dynamics

$$F = Ma$$

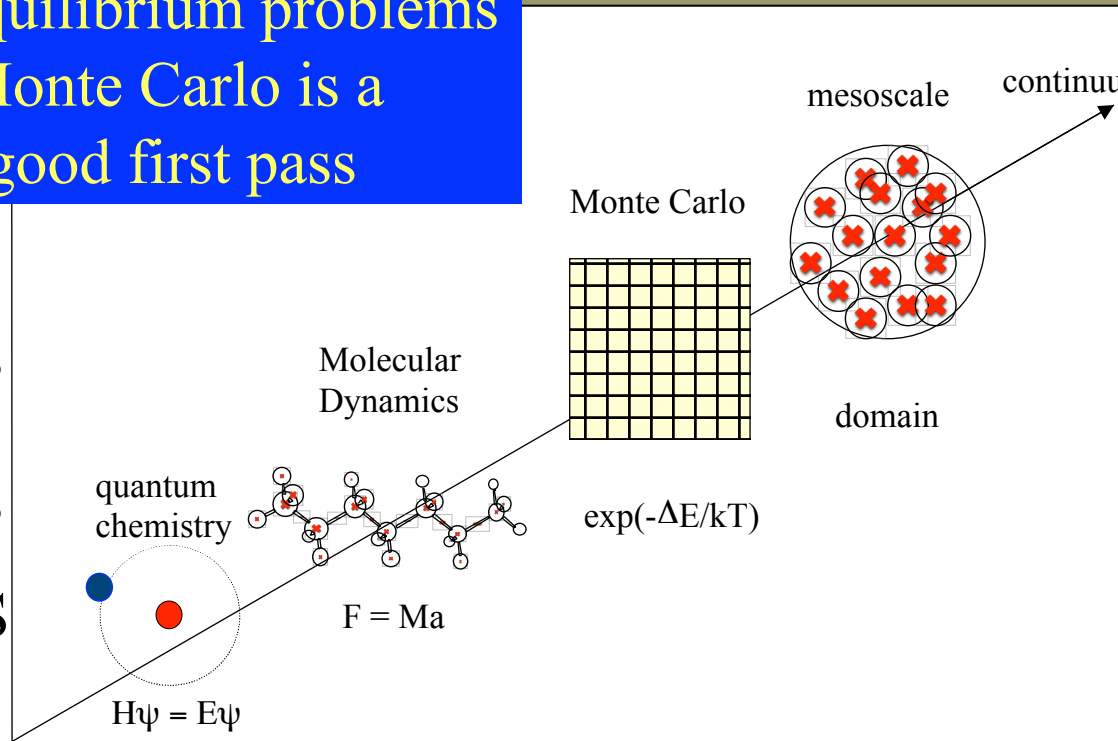
Monte Carlo

$$\exp(-\Delta E/kT)$$

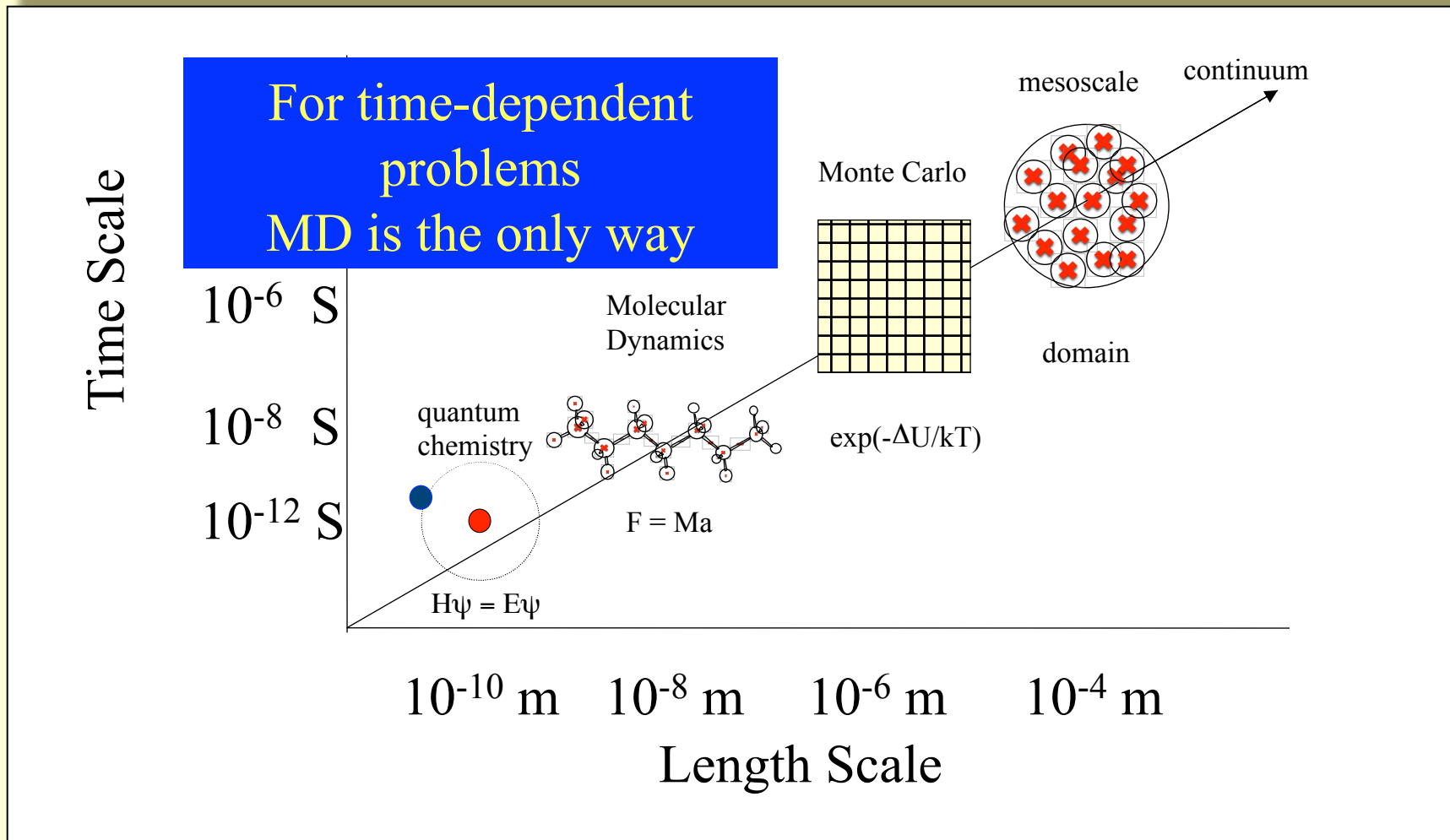
mesoscale

continuum

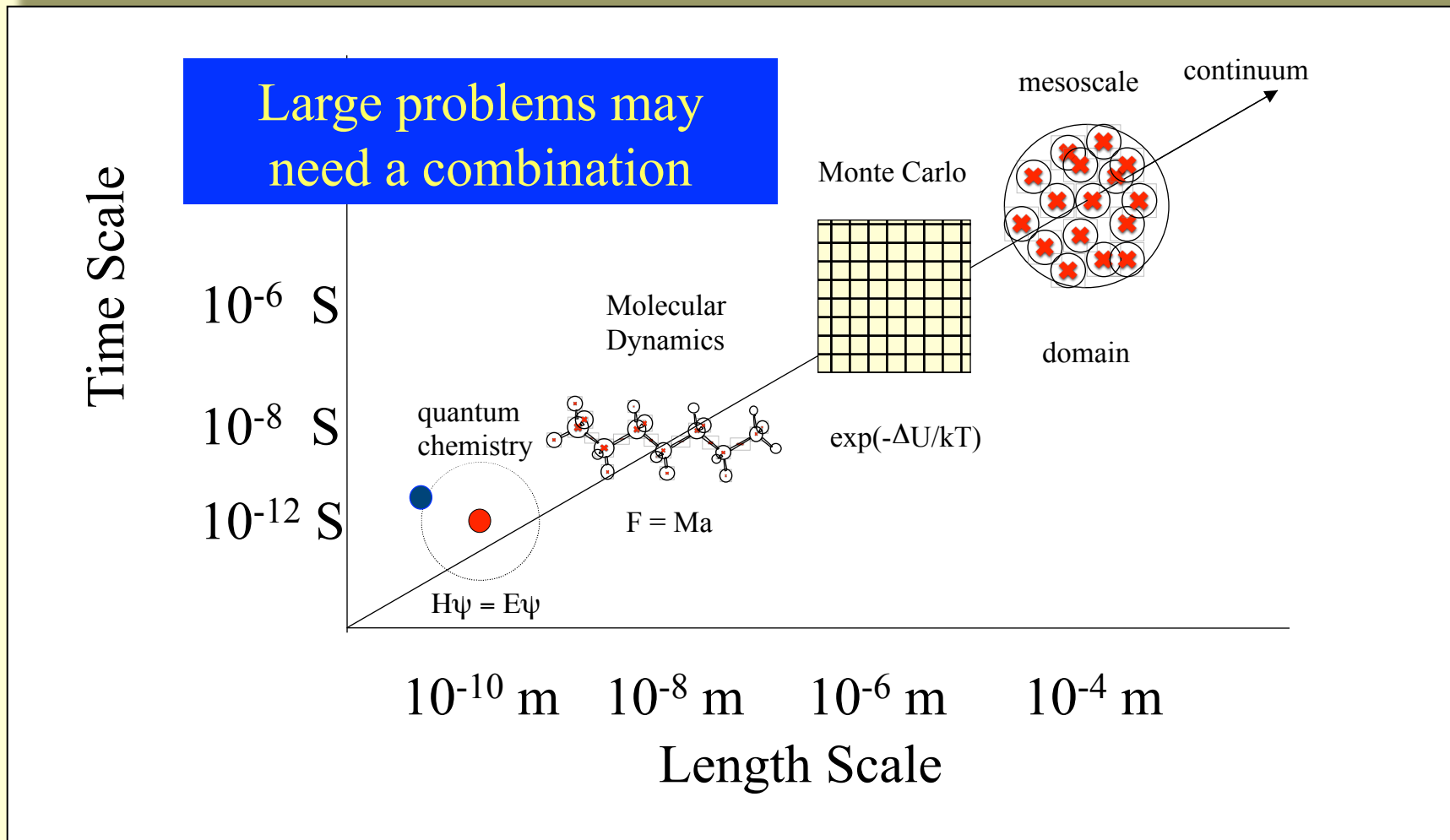
domain



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Key point: Don't waste time evaluating $\Xi(\mathbf{r})$ if $P(\mathbf{r})$ is zero.

$$\text{MC/MD} \quad \langle \Xi \rangle = \frac{1}{M} \sum_{i=1}^M \Xi_i(\mathbf{r}_i)$$