

# Chemical dynamics & molecular interaction

overall goal: micro to macro

molecular structure

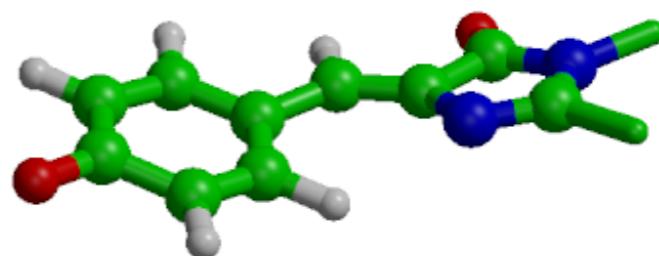
quantum mechanics



molecular interactions

quantum mechanics

molecular dynamics



sampling

configuration space

partition functions

statistical thermodynamics

free energy

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quantum mechanics

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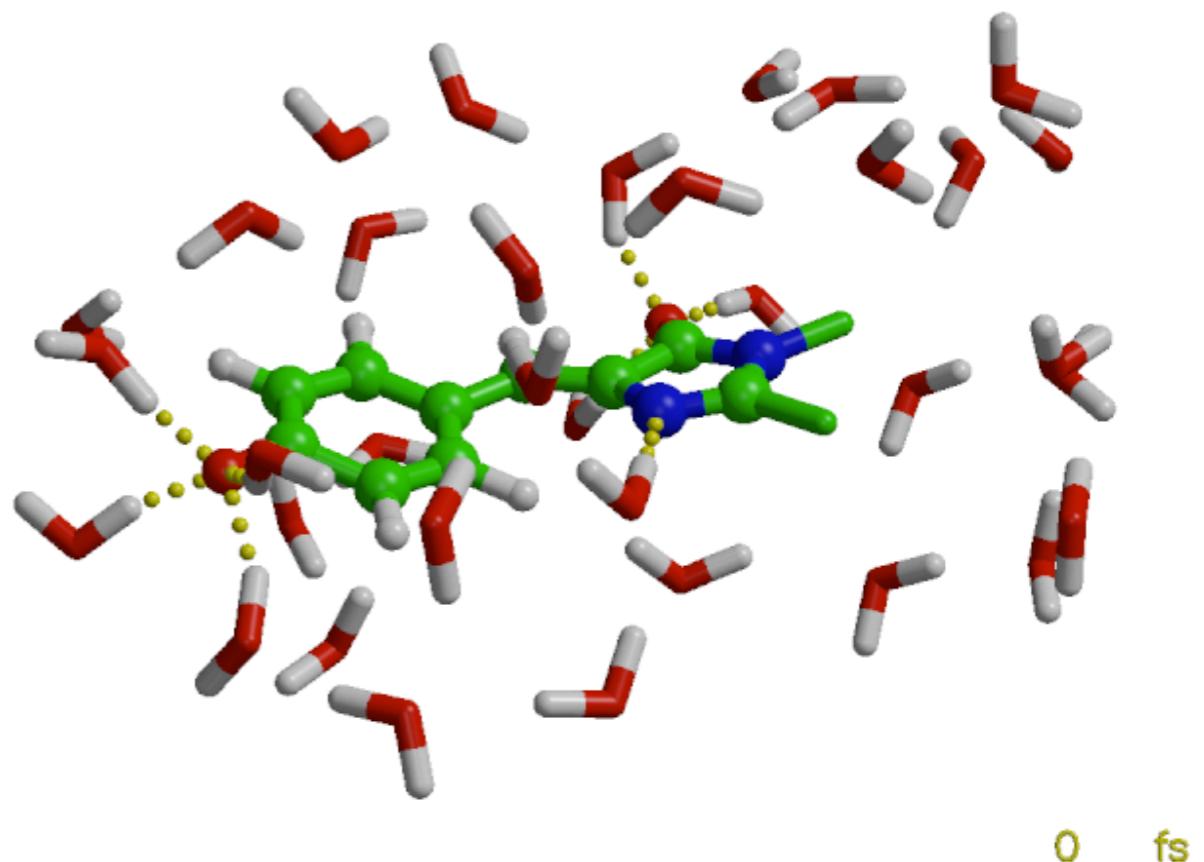
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quantum mechanics

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statistical thermodynamics

free energy

thermodynamics

molecule-free



# Chemical dynamics & molecular interaction

two options

basic: 3 credits

lectures

homework exercises

exam

advanced: 3 additional credits

project

written report

oral presentation

# Chemical dynamics & molecular interaction

## content (could be changed still)

I thermodynamics refresher

equation of state of ideal gas

first & second laws of thermodynamics

Carnot engine

'discovery' of entropy

demonstration (maybe)

efficiency of steam engine

molecule-free

# Chemical dynamics & molecular interaction

content (could be changed still)

## 2 statistical mechanics/thermodynamics

from micro (molecules) to macro (bulk)

micro state

macro state

statistical weight

Boltzman definition of entropy

partition function

free energy

ensembles

micro-canonical

canonical

grand-canonical

# Chemical dynamics & molecular interaction

content (could be changed still)

## 3. molecular interactions

intramolecular interactions

intermolecular interactions

electrostatic

dispersion

hydrogen bonds

evaluating intermolecular interactions

Ewald summation: energy of crystal

partition function

classical statistics

phase space

# Quantum Mechanics (KEMS406)

## lecture 3:

Dirac quantum conditions

Poisson bracket

free energy

equilibrium constant

rates

reaction coordinates

Arrhenius' law

Eyring's transition state theory

Krames' theory

# Chemical dynamics & molecular interaction

## content (could be changed still)

### 5. difficult stuff

quantum statistics

black body radiation

hydrophobic effect

self-aggregation

fluctuations & non-equilibrium processes

jarzynski/Crooks theorema

....

# Thermodynamics

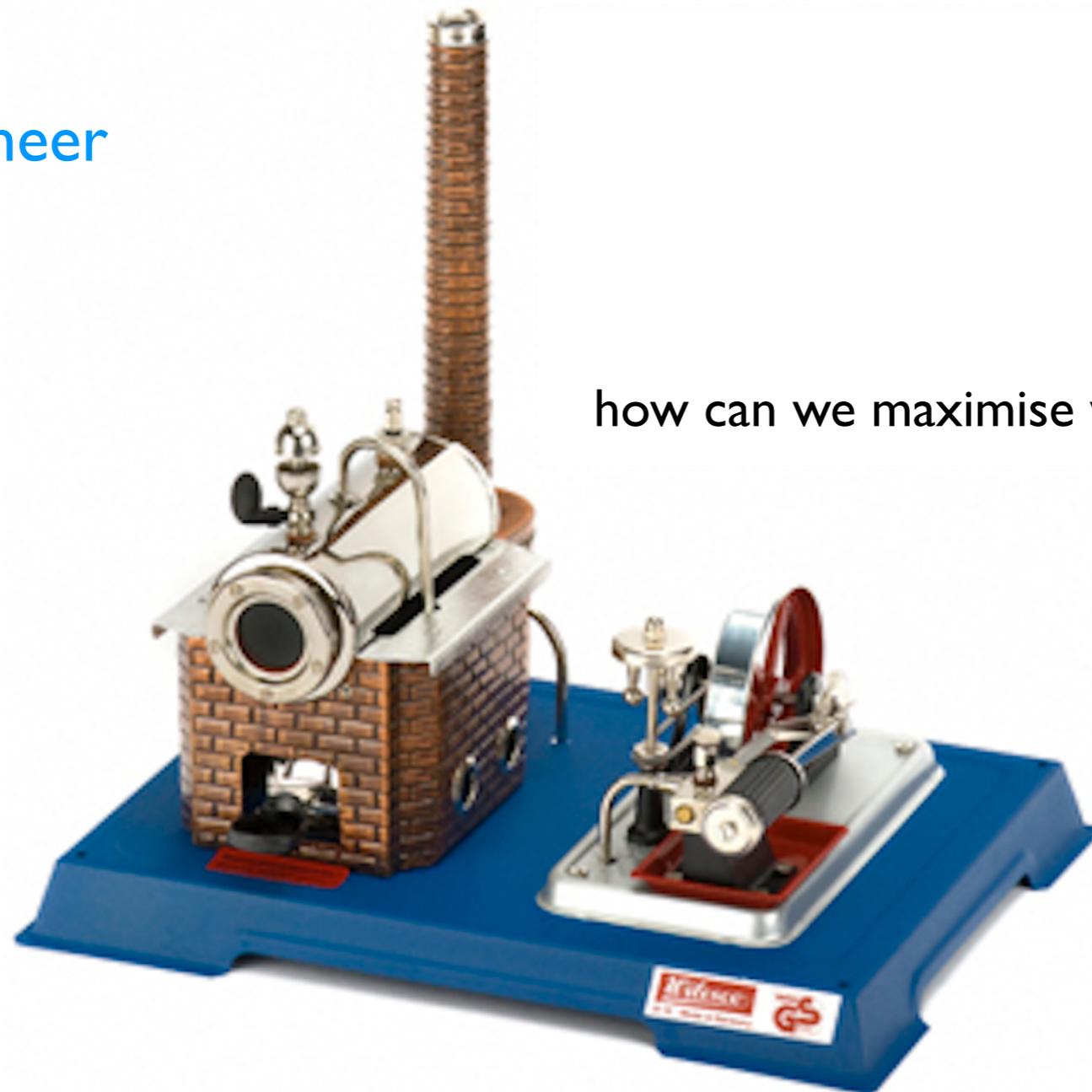
first law: conservation of energy

second law: direction of spontaneous change

important

if you're an engineer

how can we maximise work?



$$(-W_u) \leq -\Delta A = -[\Delta U - T\Delta S]$$

# Thermodynamics

Helmholtz free energy

internal energy

entropy

$$A = U - TS$$

extensive properties

# Thermodynamics

Helmholtz free energy

internal energy

entropy

$$A = U - TS$$

extensive properties

chemical/physical change at constant temperature

$$\Delta A = \Delta U - T\Delta S$$

$$\Delta A = -T\Delta S^{\text{tot}}$$

spontaneous

$$\Delta A < 0$$

equilibrium

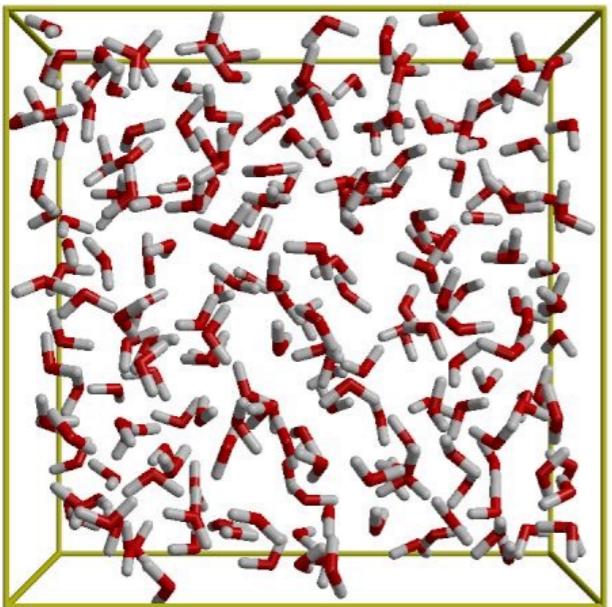
$$\Delta A = 0$$

# Thermodynamics

entropy of isolated system

micro-states (realisations)

box with 216 waters:



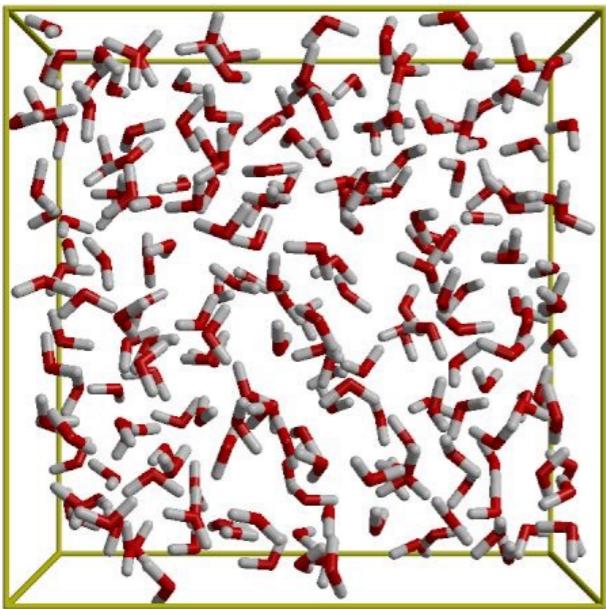
microstate 1

# Thermodynamics

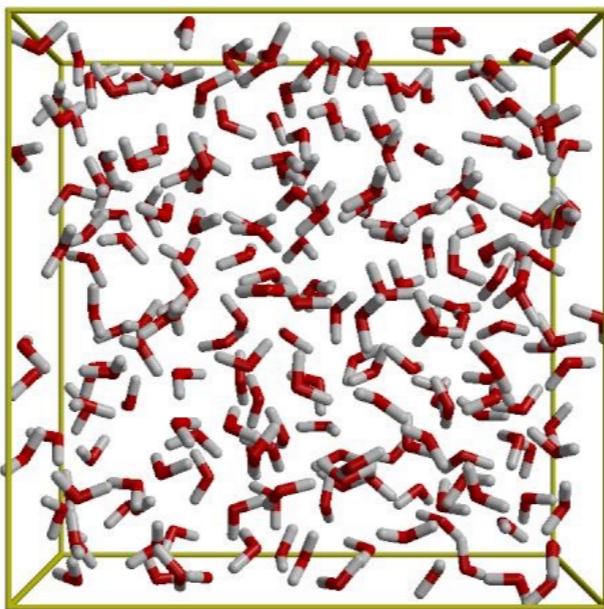
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box with 216 waters:



microstate 1



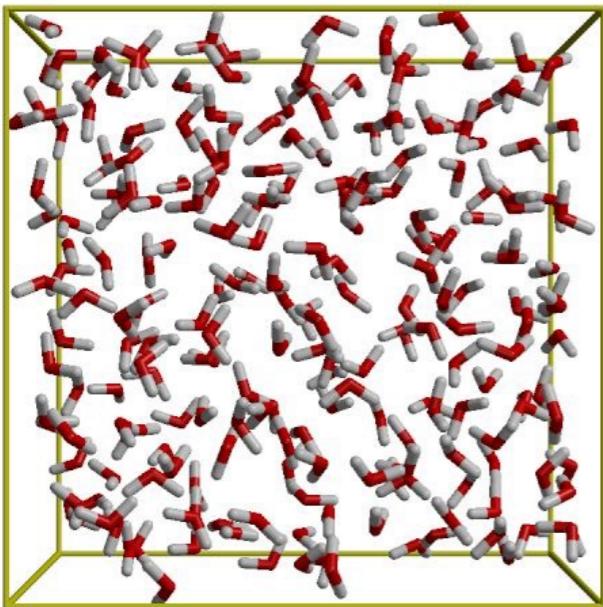
microstate 2

# Thermodynamics

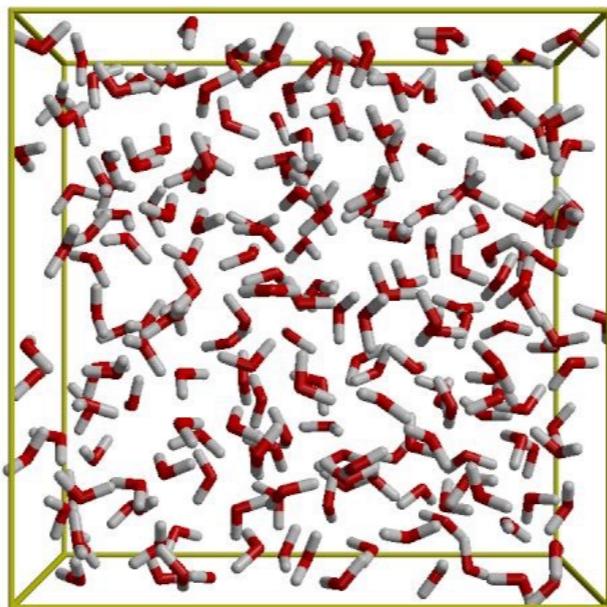
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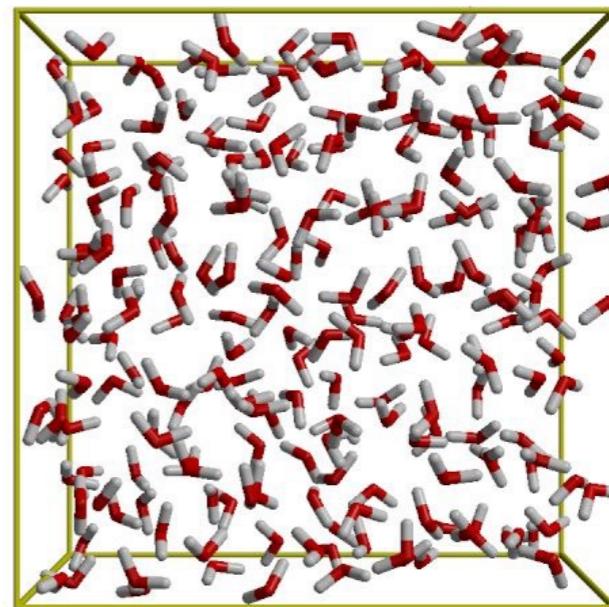
box with 216 waters:



microstate 1



microstate 2



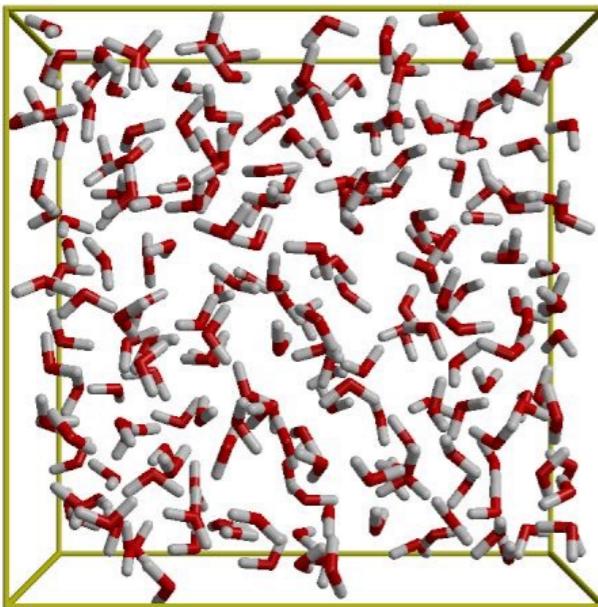
microstate 3

# Thermodynamics

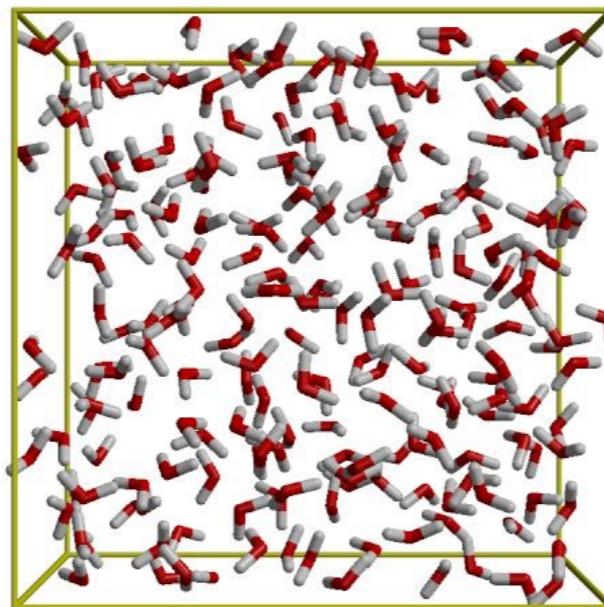
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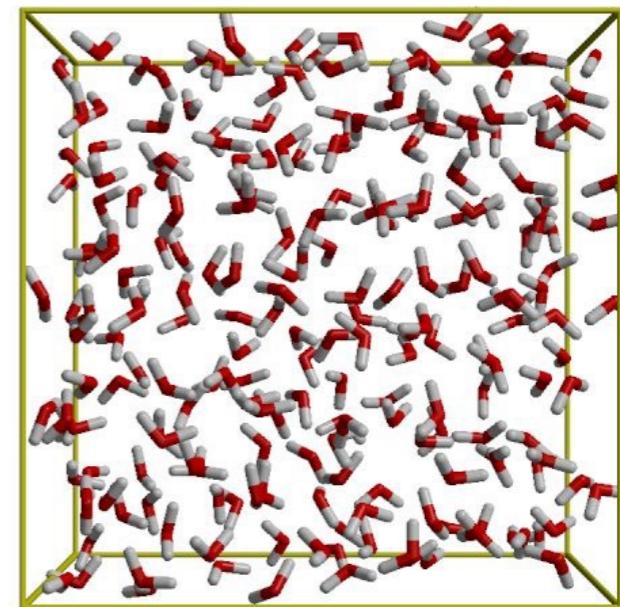
box with 216 waters:



microstate 1



microstate 2



microstate 3

total number of micro-states (realisations)

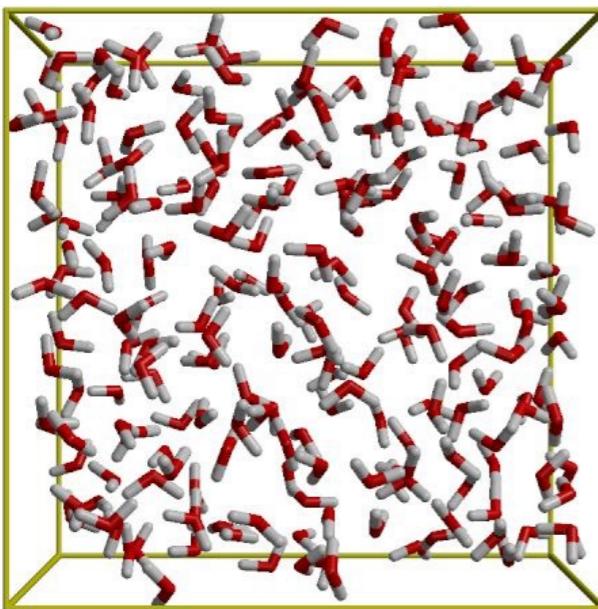
$$\Omega$$

# Thermodynamics

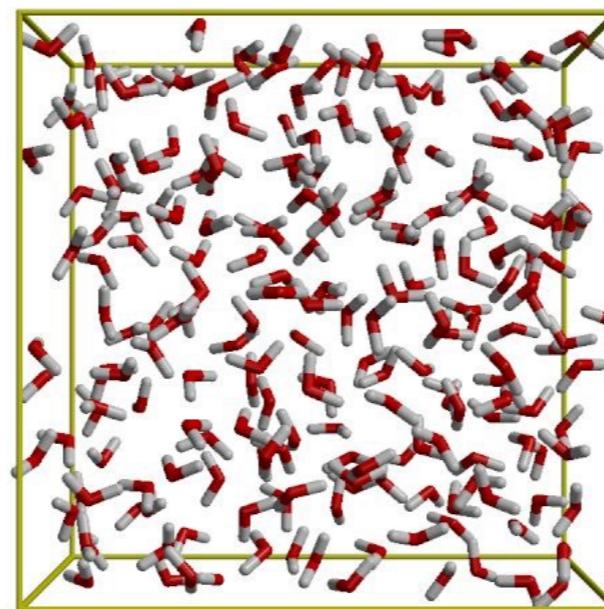
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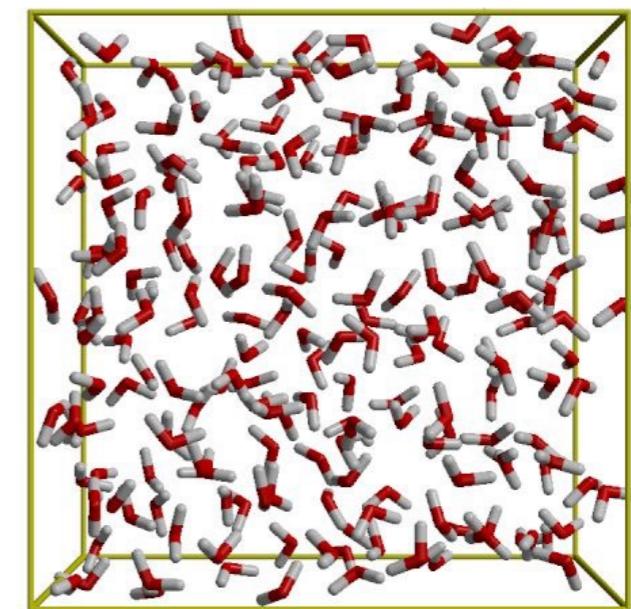
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total number of micro-states (realisations)

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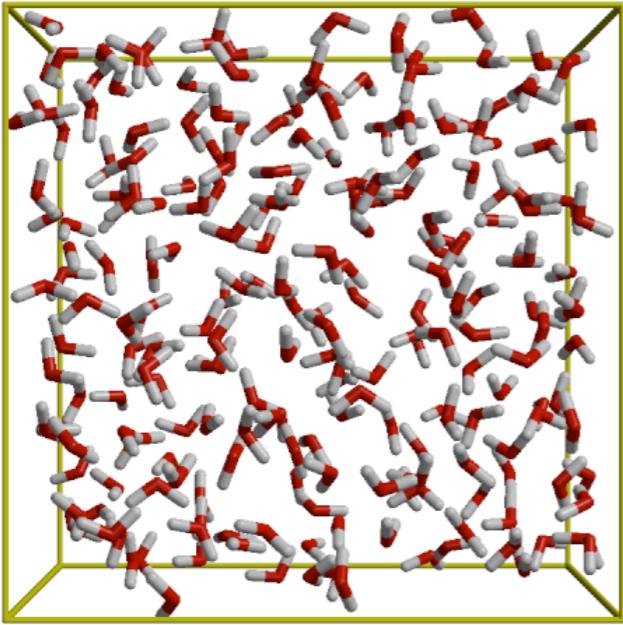
if you know how many, you pass the course today!

# Thermodynamics

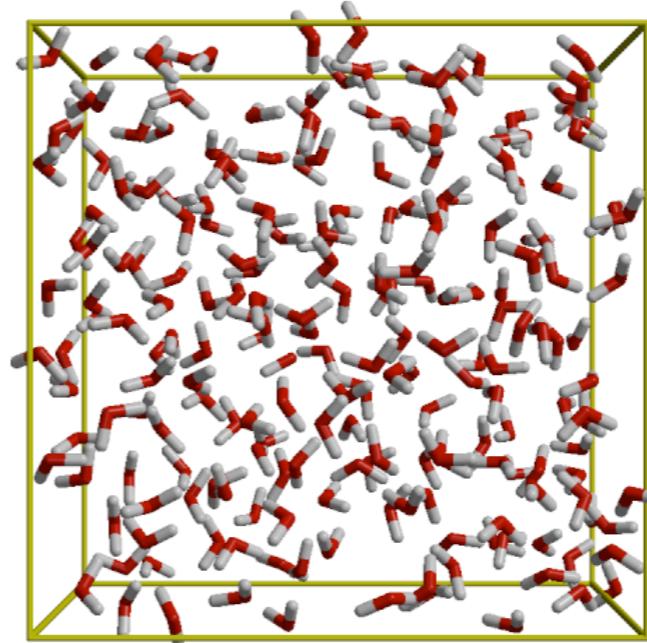
entropy of isolated system

micro-states (realisations)

two boxes of water:



box 1



box 2

total number of micro states (realisations)

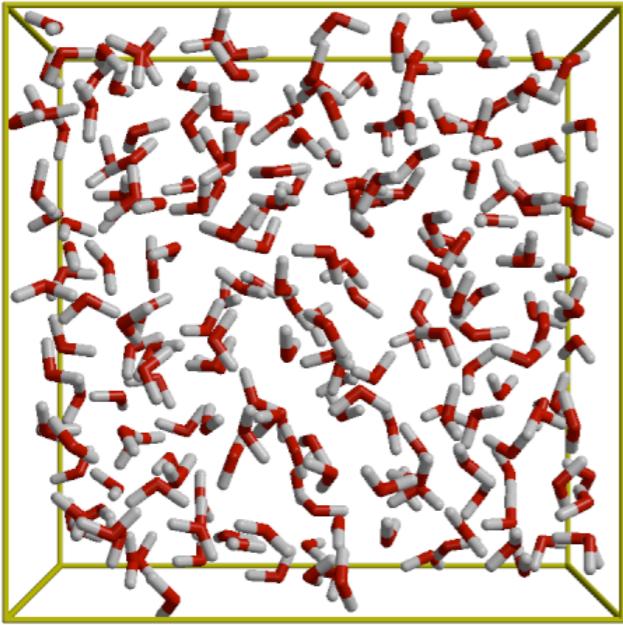
$$\Omega^{\text{tot}} =$$

# Thermodynamics

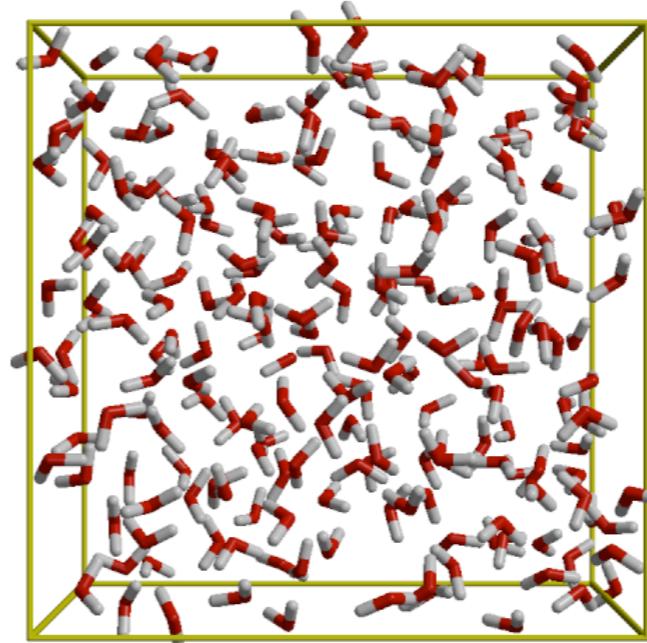
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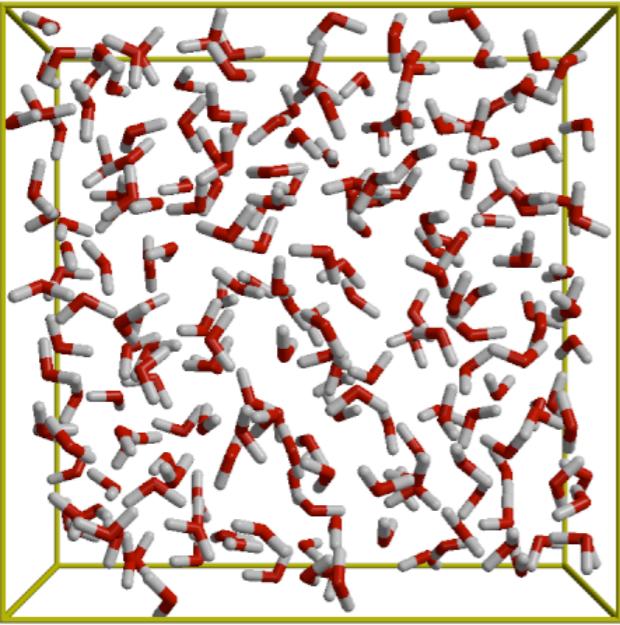
$$\Omega^{\text{tot}} = \Omega_1 \cdot \Omega_2$$

# Thermodynamics

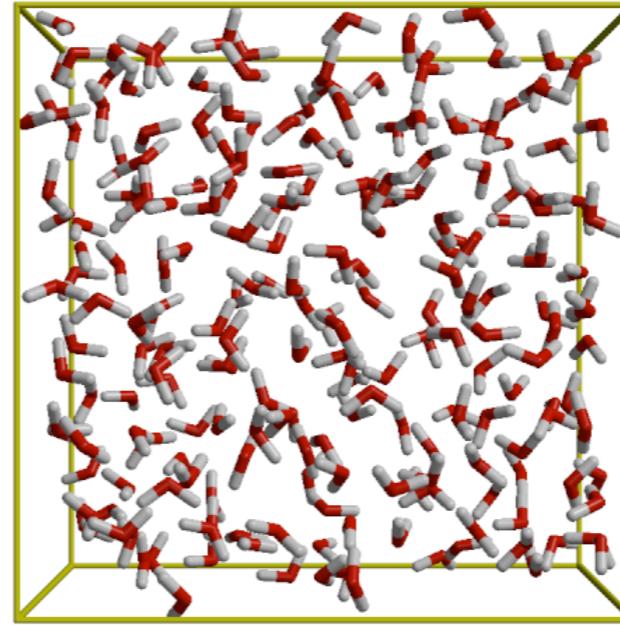
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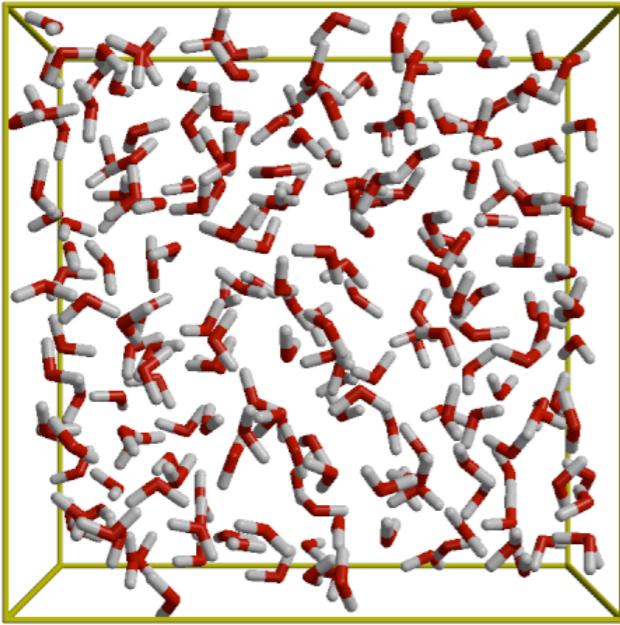
entropy is extensive, so should be sum:

# Thermodynamics

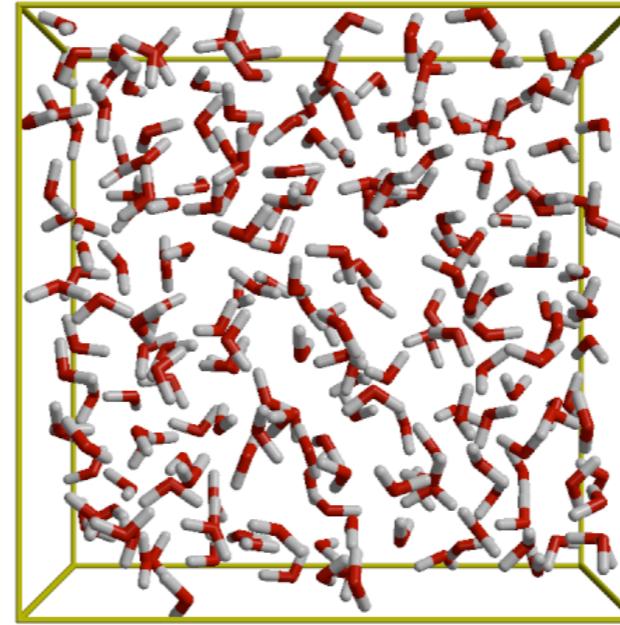
entropy of isolated system

micro-states (realisations)

two boxes of water:



box 1



box 2

total number of micro states (realisations)

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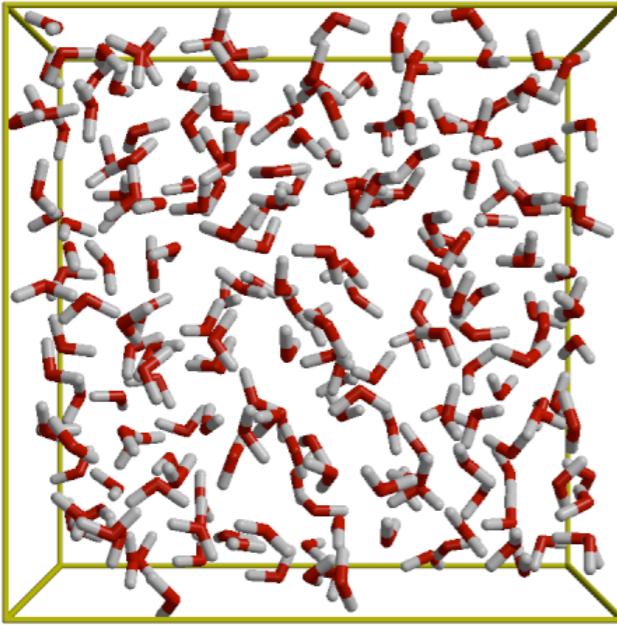
$$S = k \ln \Omega$$

# Thermodynamics

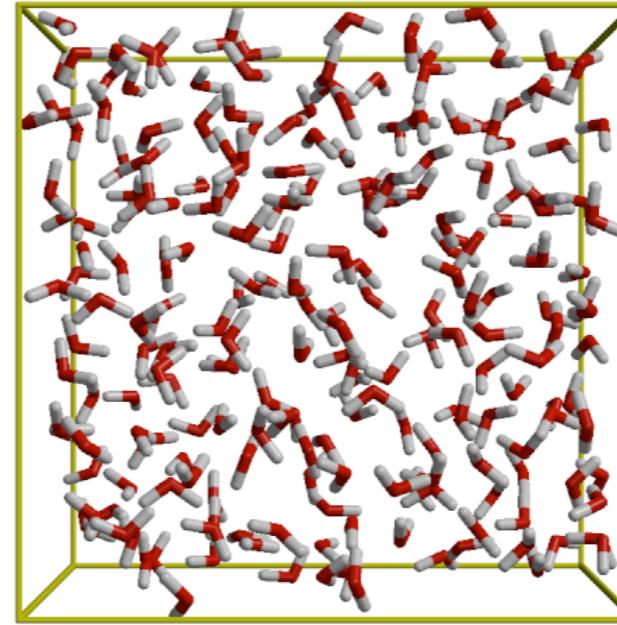
entropy of isolated system

micro-states (realisations)

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box 2

total number of micro states (realisations)

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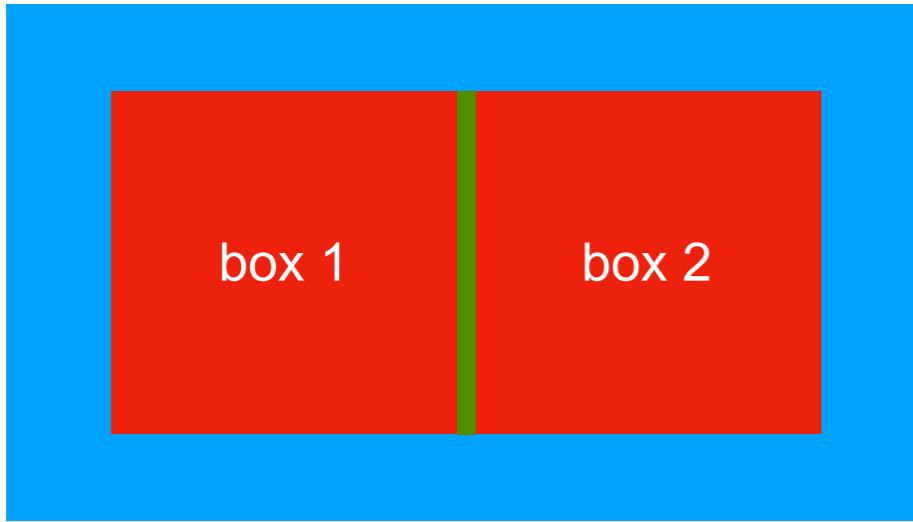
entropy is extensive, so should be sum:

$$S^{\text{tot}} = k \ln[\Omega_1 \cdot \Omega_2] = k \ln \Omega_1 + k \ln \Omega_2 = S_1 + S_2$$

# Thermodynamics

two systems in thermal equilibrium, isolated from world

diathermic walls (only energy can transfer)



$$N_1 + N_2 = N$$

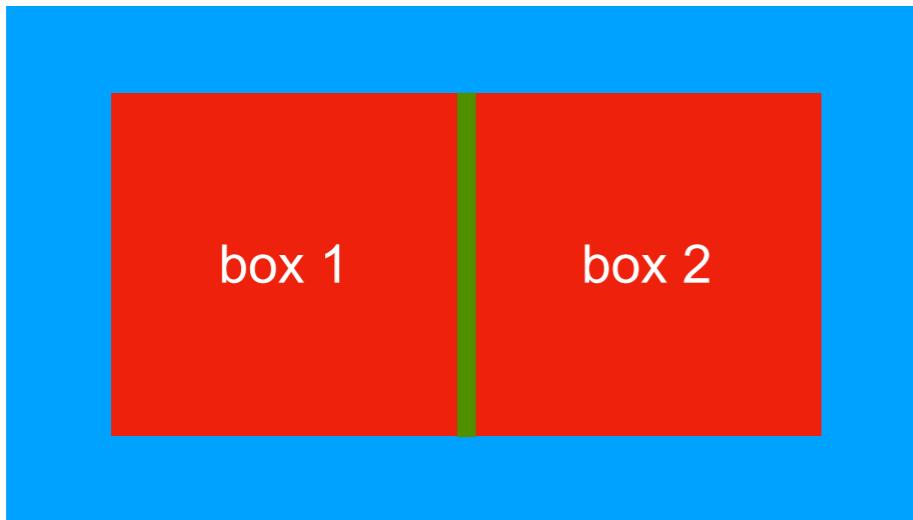
$$E_1 + E_2 = E$$

$$\frac{dE_2}{dE_1} = -1$$

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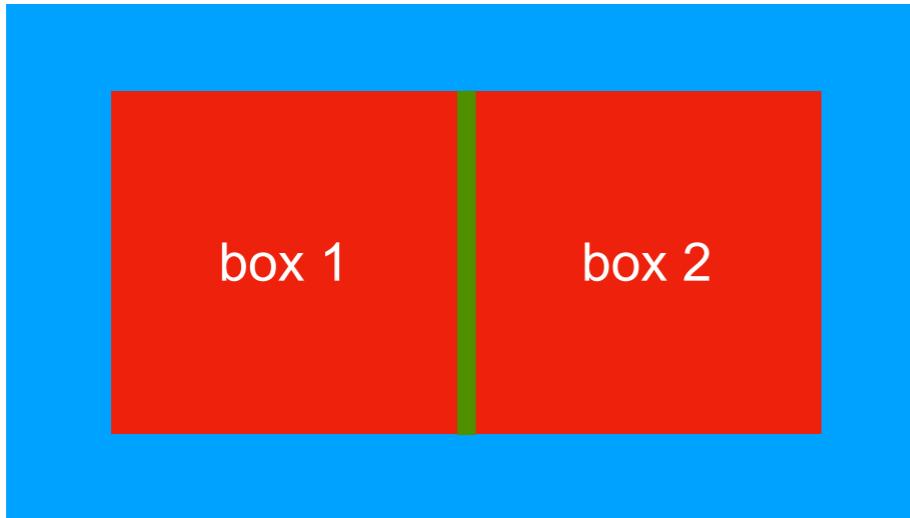
equilibrium: no net changes in total entropy

$$\frac{\partial S^{\text{tot}}}{\partial E_1} = \frac{\partial S_1}{\partial E_1} + \frac{\partial S_2}{\partial E_2} \frac{dE_2}{dE_1} = 0$$

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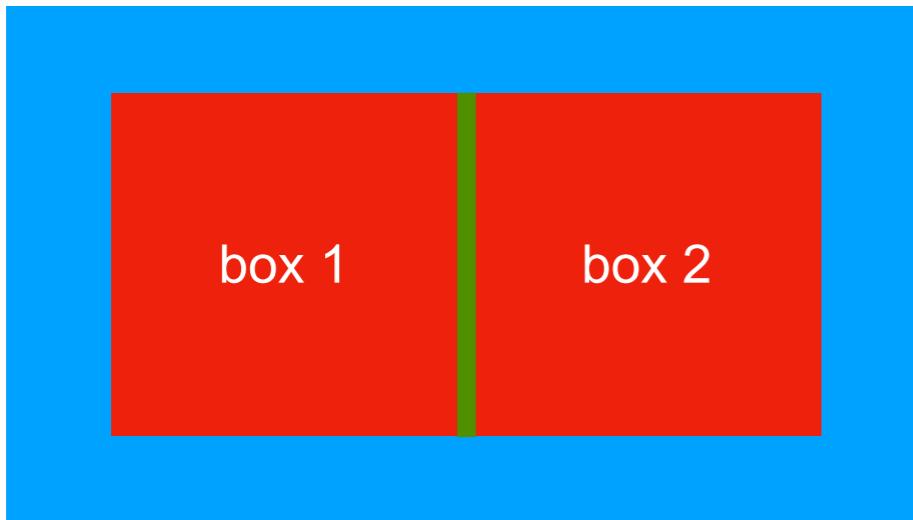
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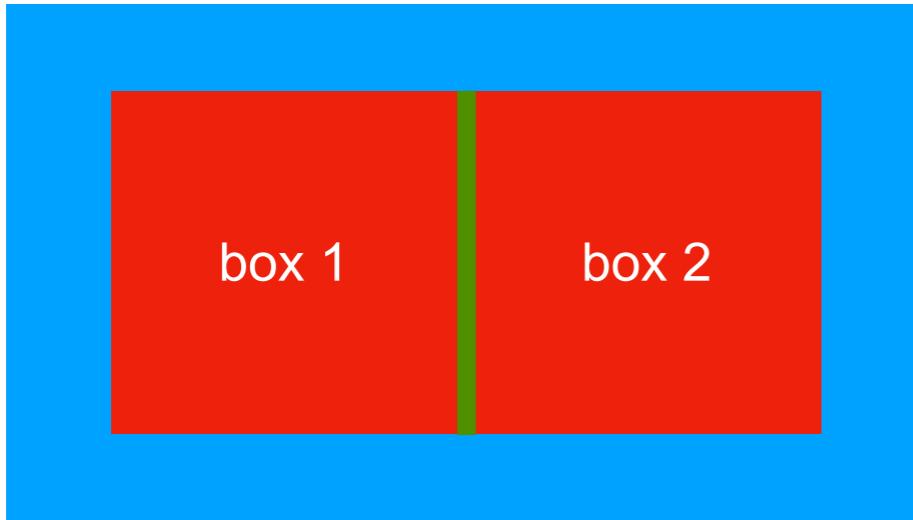
definition of temperature:

$$\frac{\partial S_1}{\partial E_1} = \frac{1}{T_1}$$

# Thermodynamics

two systems in thermal equilibrium, isolated from world

diathermic walls (only energy can transfer)



$$N_1 + N_2 = N$$

$$E_1 + E_2 = E$$

no equilibrium: total entropy must increase

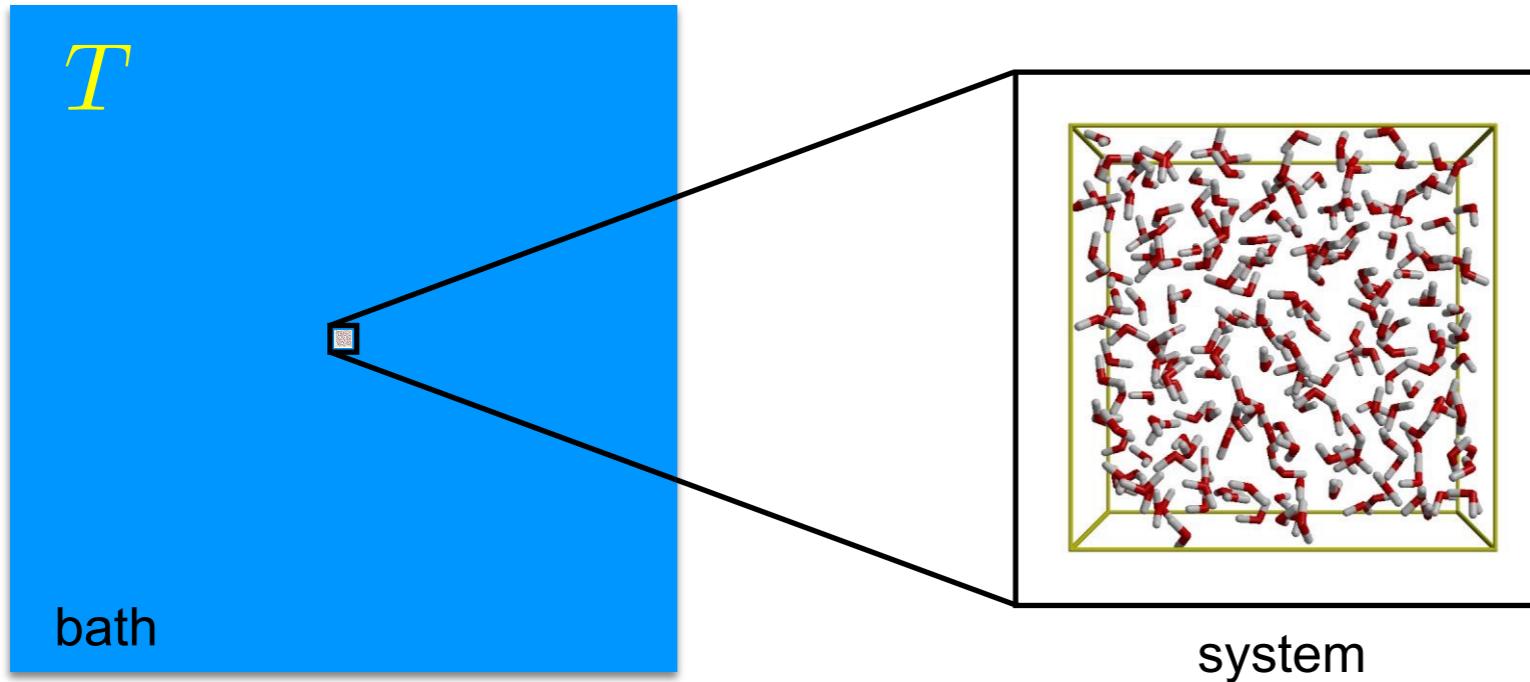
$$\frac{dS^{\text{tot}}}{dt} = \left( \frac{1}{T_1} - \frac{1}{T_2} \right) \frac{dE_1}{dt} > 0$$

energy flows from higher to lower temperature

# Statistical mechanics

## canonical ensemble

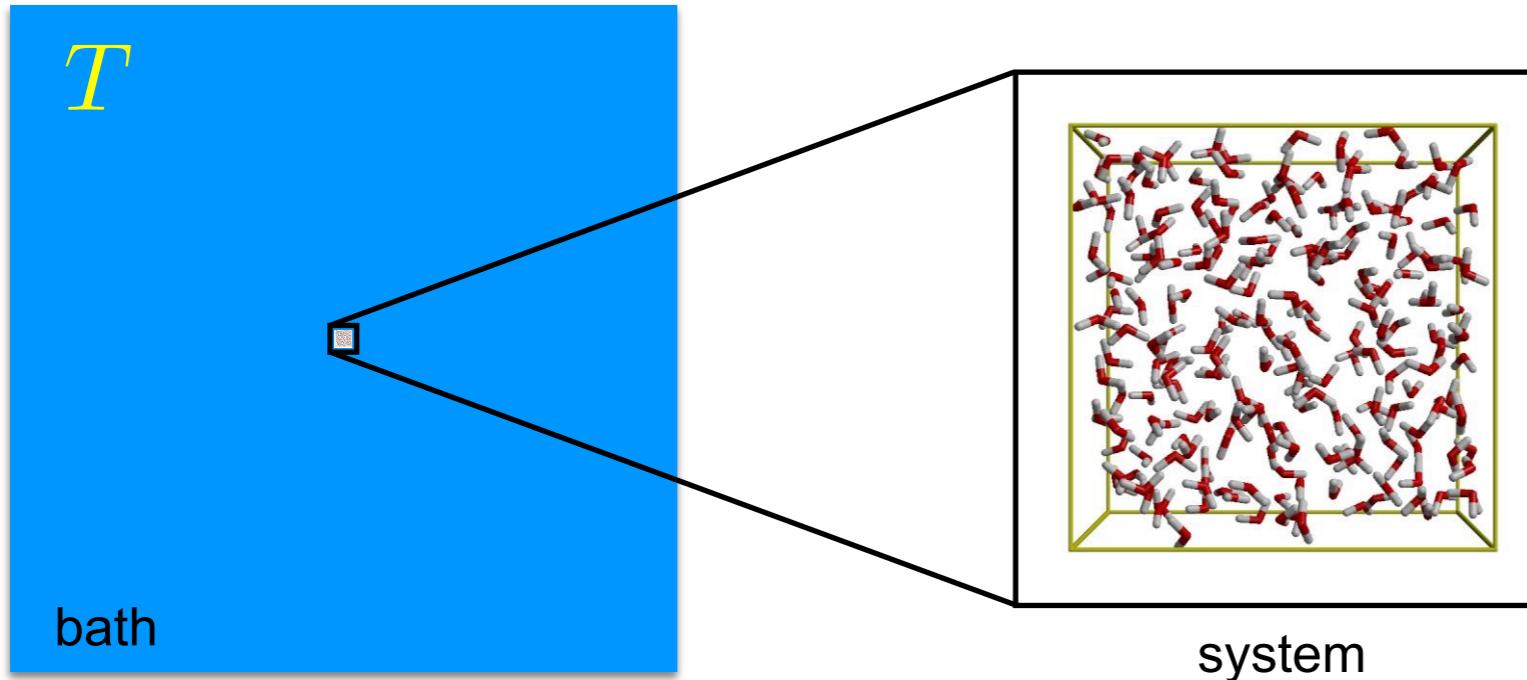
system in thermal equilibrium with bath



# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath



micro-states of system

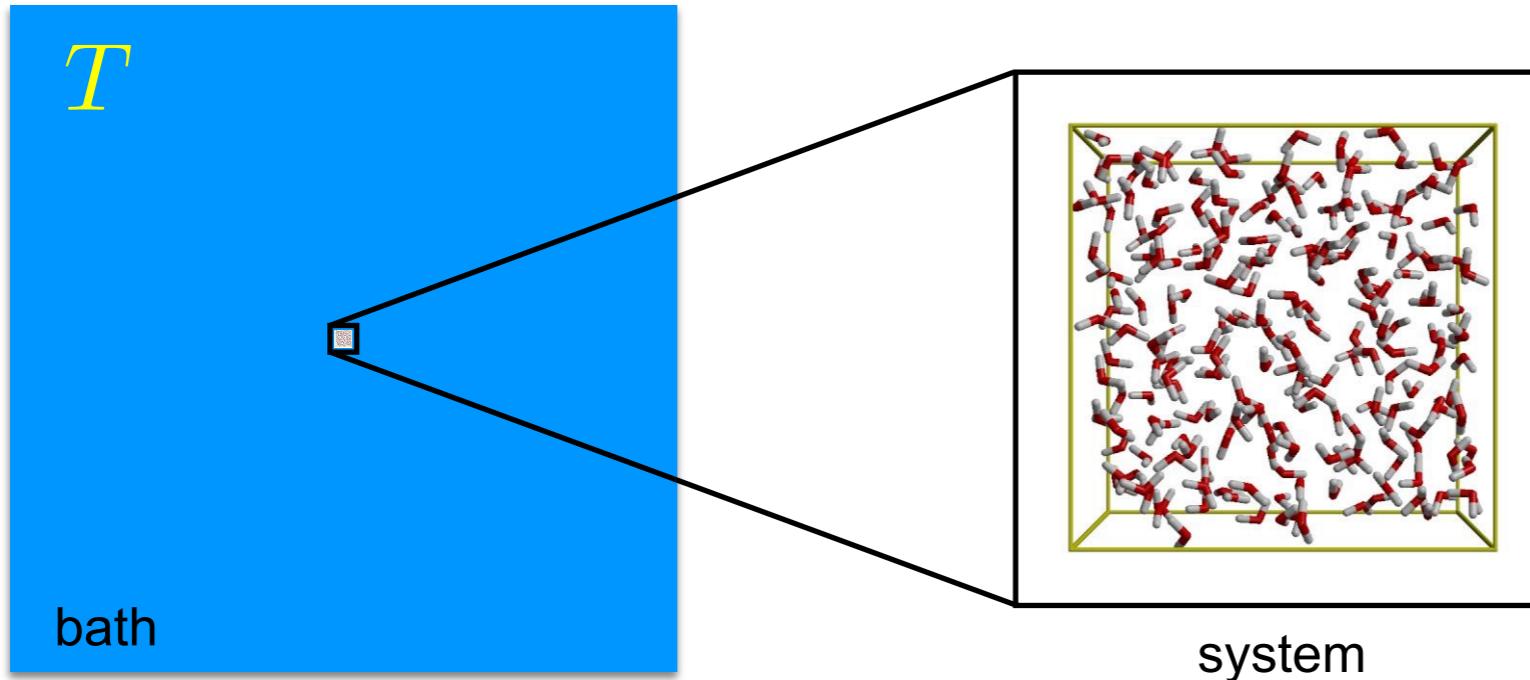
each with different energy

$$E_1 \leq E_2 \leq E_3 \leq \dots \leq E_i \leq \dots$$

# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath



micro-states of system

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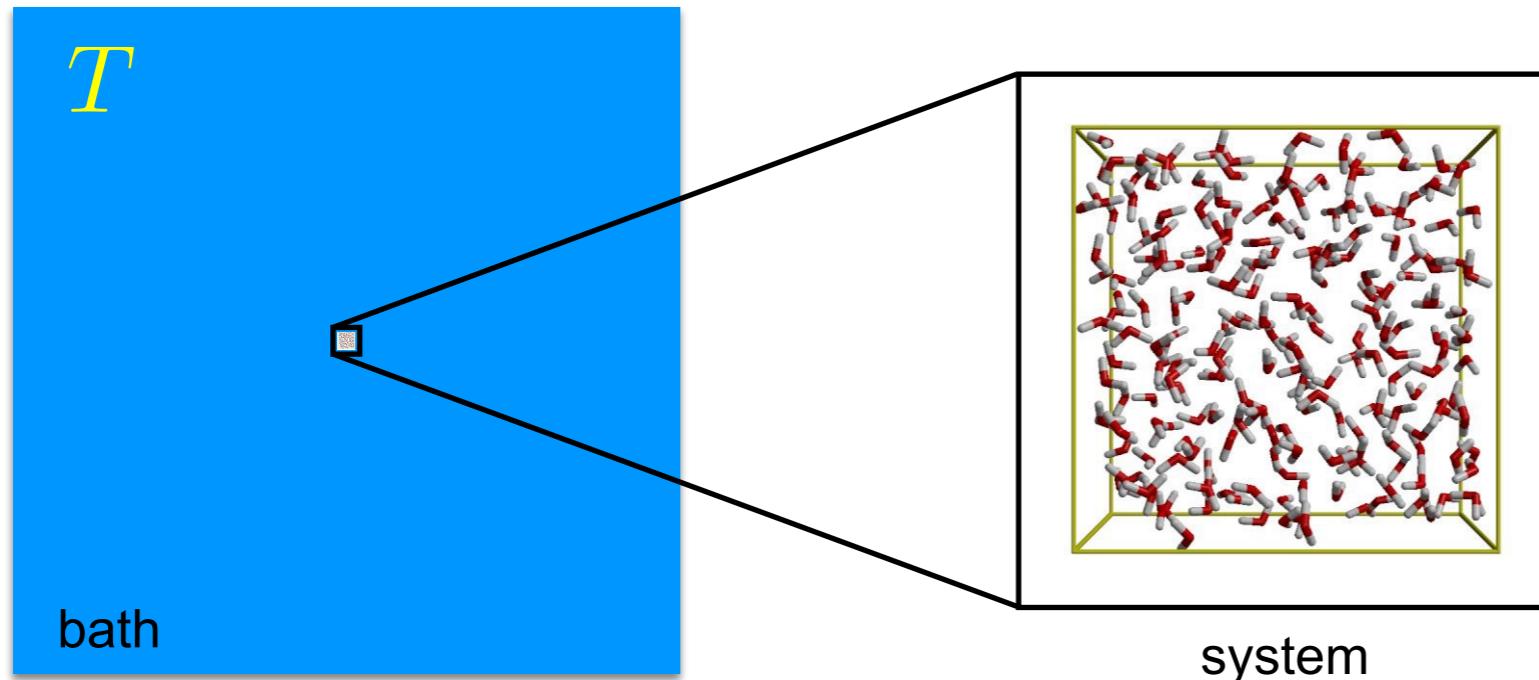
probability of micro state  $i$  proportional to number of micro states of bath

$$p_i = \text{const} \cdot \Omega_{\text{bath}}(E^{\text{tot}} - E_i)$$

# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath



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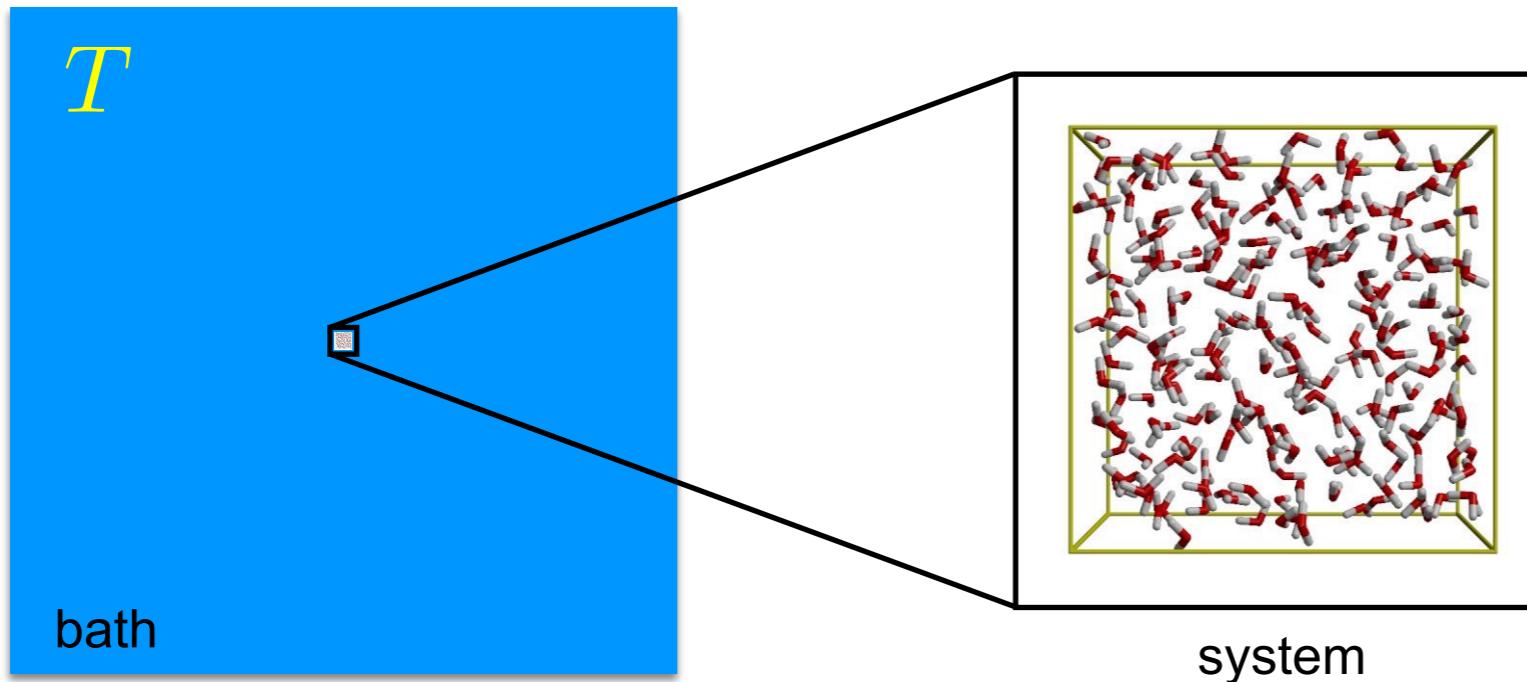
normalisation (const):

$$p_i = \frac{\Omega_{\text{bath}}(E^{\text{tot}} - E_i)}{\sum_i \Omega_{\text{bath}}(E^{\text{tot}} - E_i)}$$

# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath



micro-states of system

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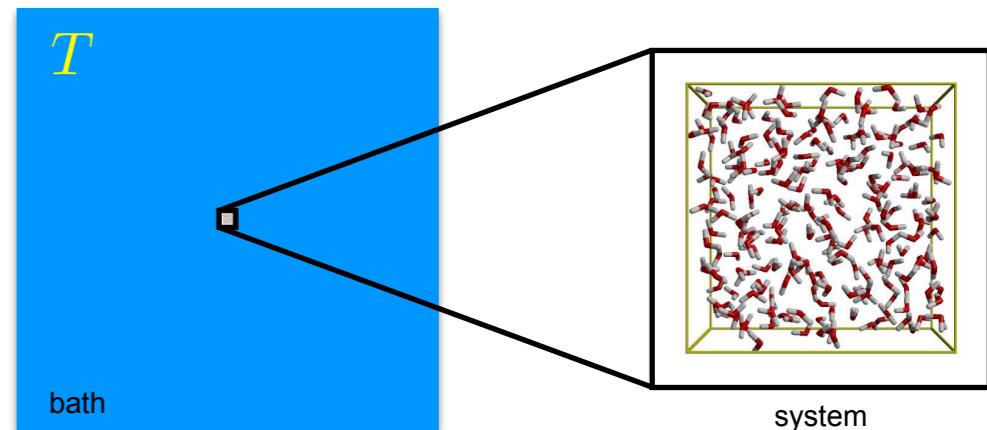
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# Statistical mechanics canonical ensemble

system in thermal equilibrium with bath  
micro-states of system

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# Statistical mechanics canonical ensemble

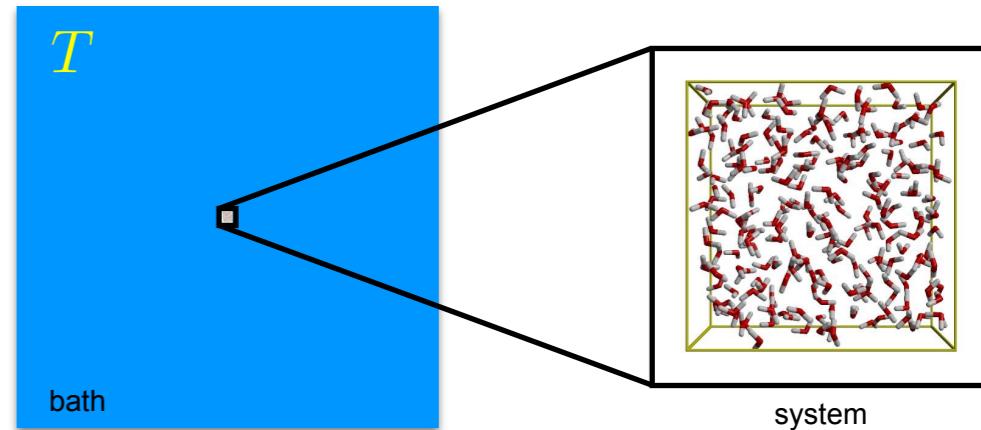
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with definition of entropy:  $S = k \ln \Omega$

$$p_i = \text{const} \cdot \exp[S_{\text{bath}}(E^{\text{tot}} - E_i)/k]$$



# Statistical mechanics canonical ensemble

system in thermal equilibrium with bath  
micro-states of system

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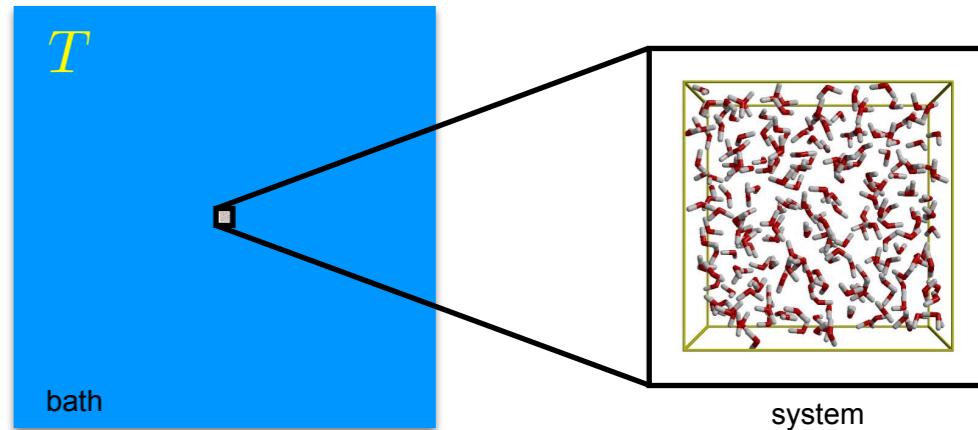
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bath much larger than system:

$$E^{\text{tot}} \gg E_i$$



# Statistical mechanics

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system in thermal equilibrium with bath

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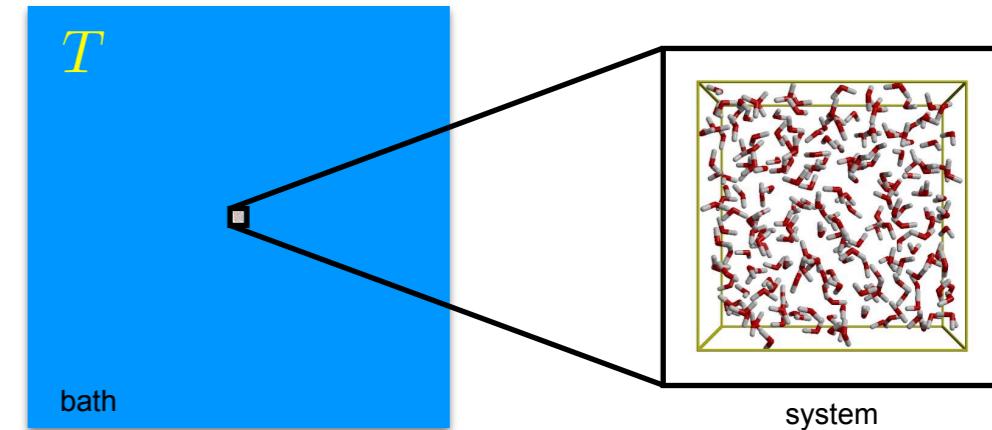
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Taylor expansion of  $S_{\text{bath}}$  around  $E^{\text{tot}}$

$$\frac{1}{k} S_{\text{bath}}(E^{\text{tot}} - E_i) = \frac{1}{k} S_{\text{bath}}(E^{\text{tot}}) - \frac{E_i}{k} \left. \frac{\partial S_{\text{bath}}(E)}{\partial E} \right|_{E=E^{\text{tot}}} + \dots$$



# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath

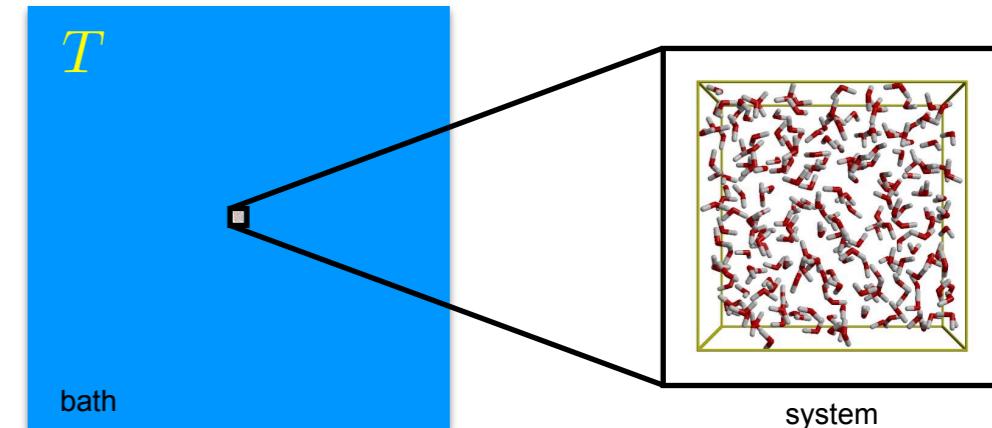
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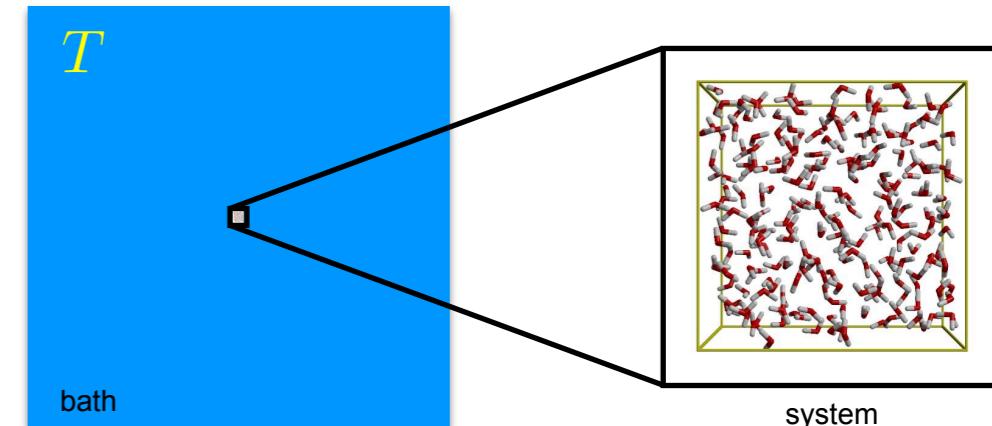
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with definition of temperature

$$\frac{\partial S}{\partial E} = \frac{1}{T}$$

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# Statistical mechanics

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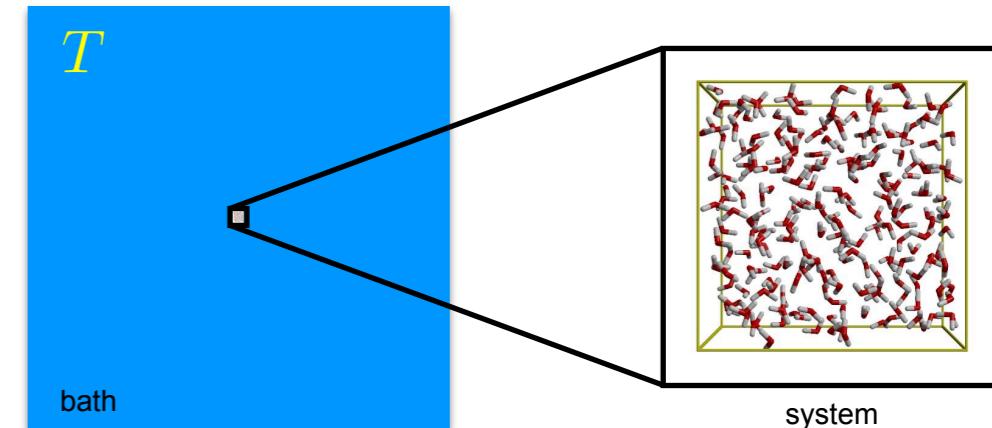
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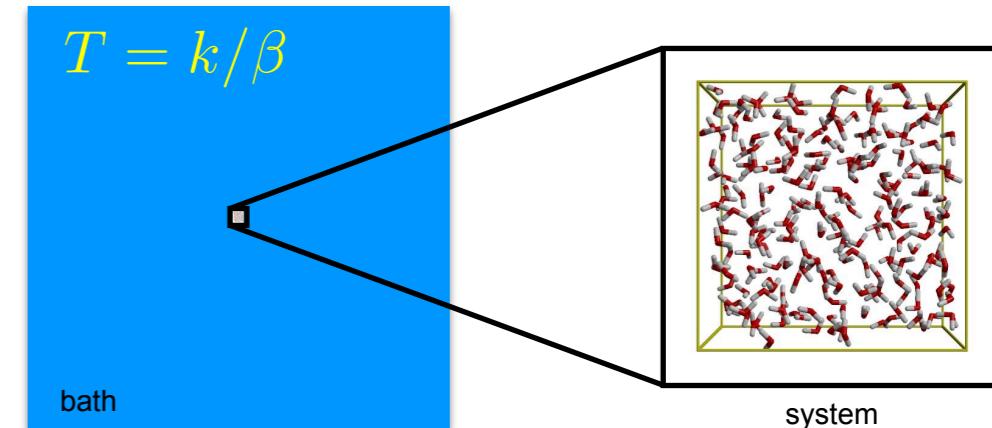
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define

$$\beta \equiv \frac{1}{kT}$$



# Statistical mechanics

## canonical ensemble

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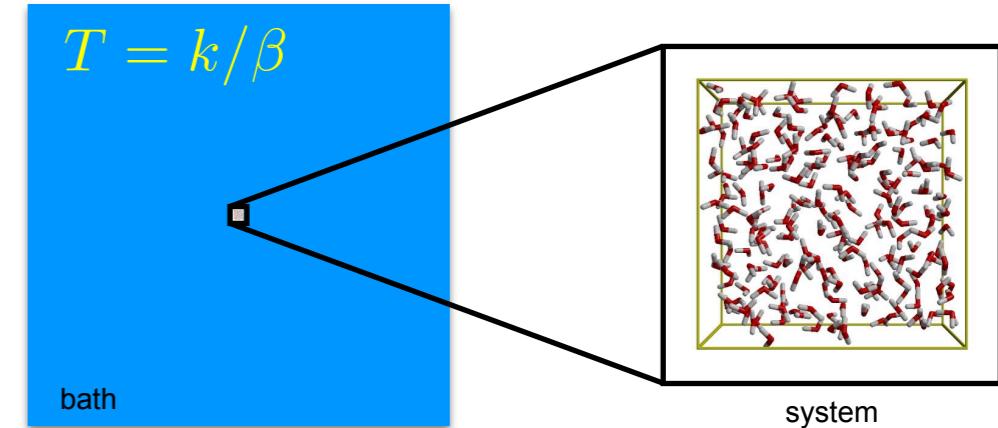
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define

$$\beta \equiv \frac{1}{kT}$$

so that

$$\frac{1}{k}S_{\text{bath}}(E^{\text{tot}} - E_i) = \frac{1}{k}S_{\text{bath}}(E^{\text{tot}}) - \beta E_i$$



# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath

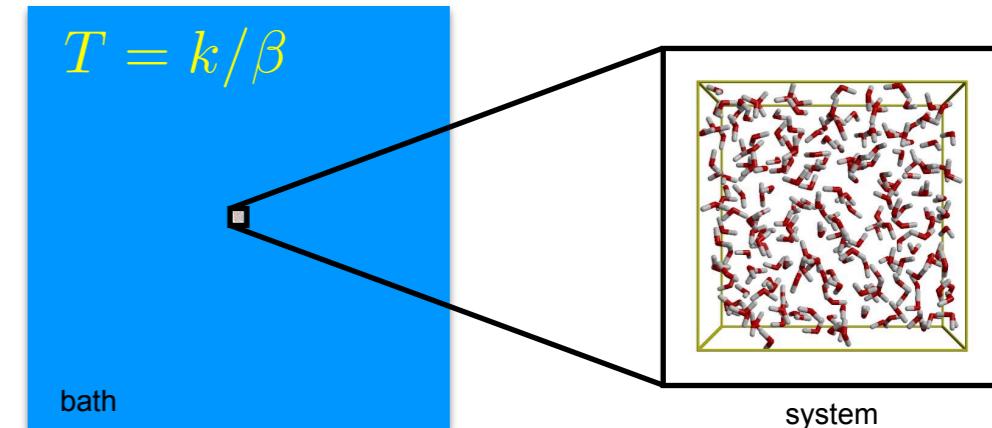
micro-states of system

probability of micro state  $i$  proportional to number of micro-states of bath

$$p_i = \text{const} \cdot \exp[S_{\text{bath}}(E^{\text{tot}} - E_i)/k]$$

Taylor expansion of  $S_{\text{bath}}$  around  $E^{\text{tot}}$

$$\frac{1}{k}S_{\text{bath}}(E^{\text{tot}} - E_i) = \frac{1}{k}S_{\text{bath}}(E^{\text{tot}}) - \beta E_i$$



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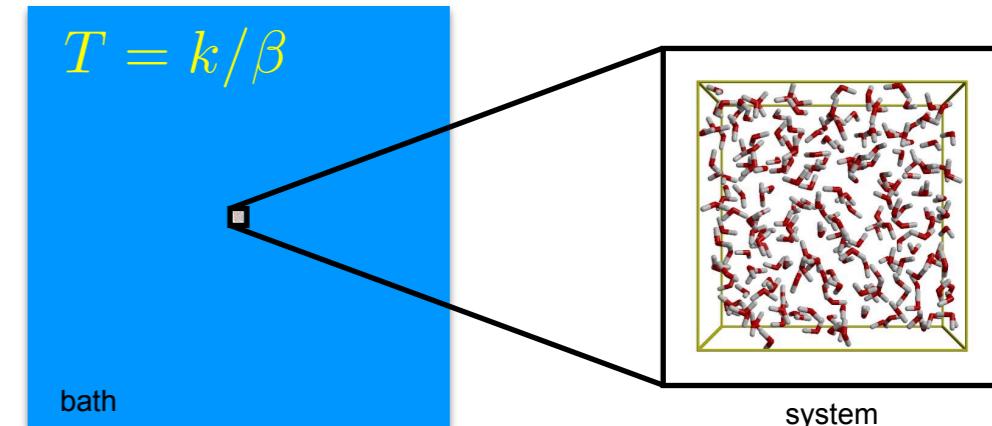
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Boltzmann distribution

$$p_i = \frac{1}{Z} e^{-\beta E_i}$$



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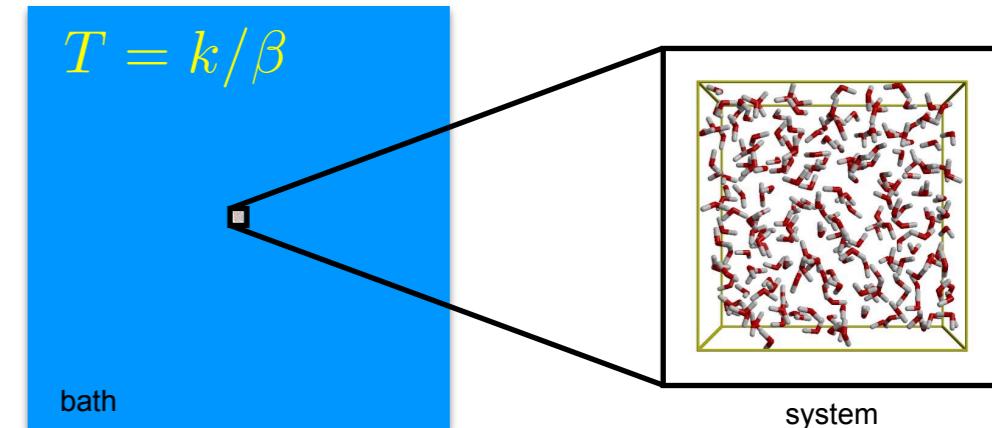
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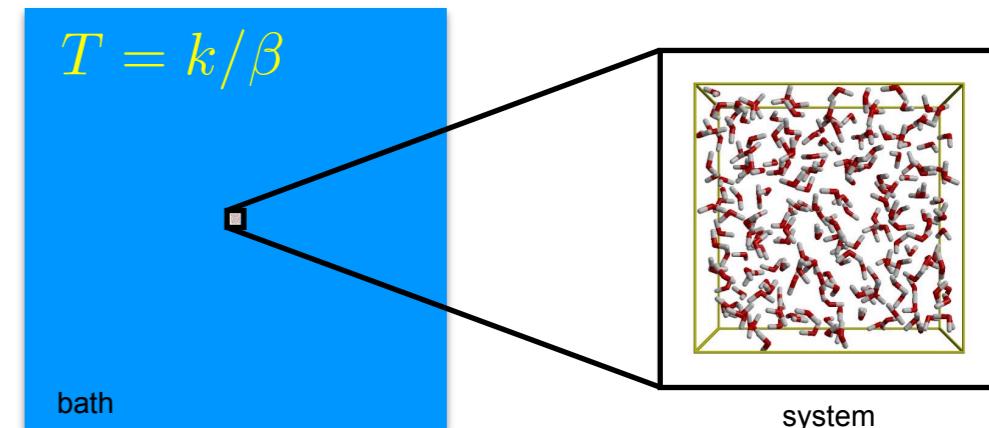
Boltzmann distribution

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partition function

$$Z = \sum_i e^{-\beta E_i}$$

from microscopic to macroscopic with partition function

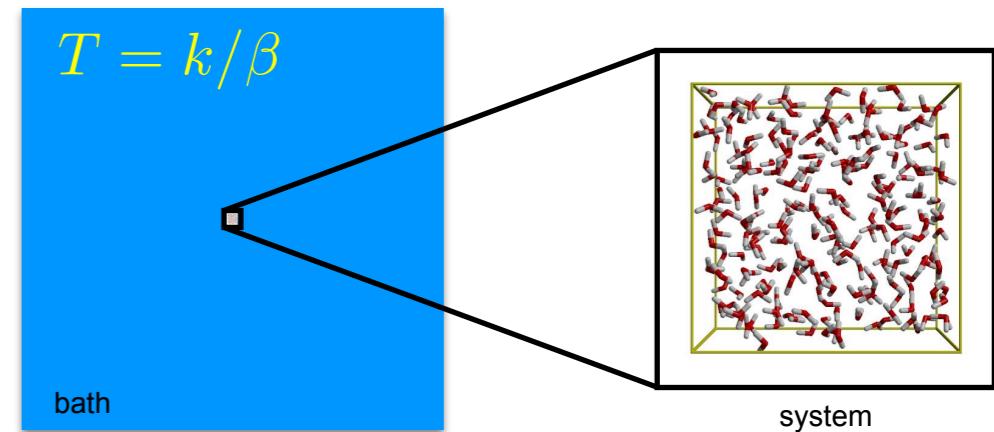


# Statistical mechanics canonical ensemble

system in thermal equilibrium with bath  
entropy of system

probability of micro-state  $i$

$$p_i = \frac{1}{Z} e^{-\beta E_i} \quad Z = \sum_i e^{-\beta E_i}$$



# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath

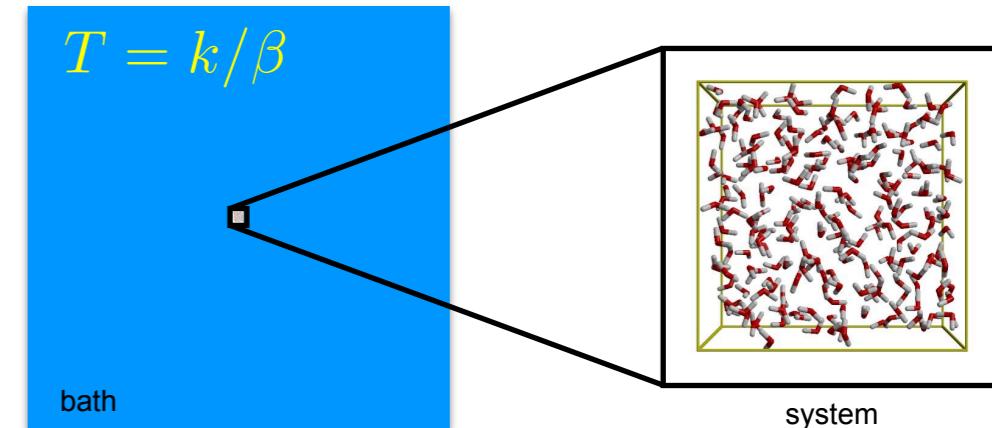
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average energy of system

$$\langle E \rangle =$$



# Statistical mechanics

## canonical ensemble

system in thermal equilibrium with bath

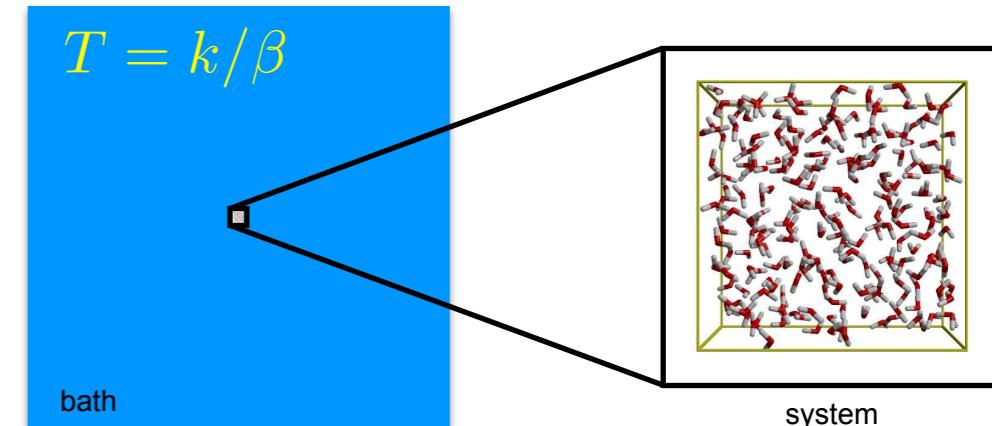
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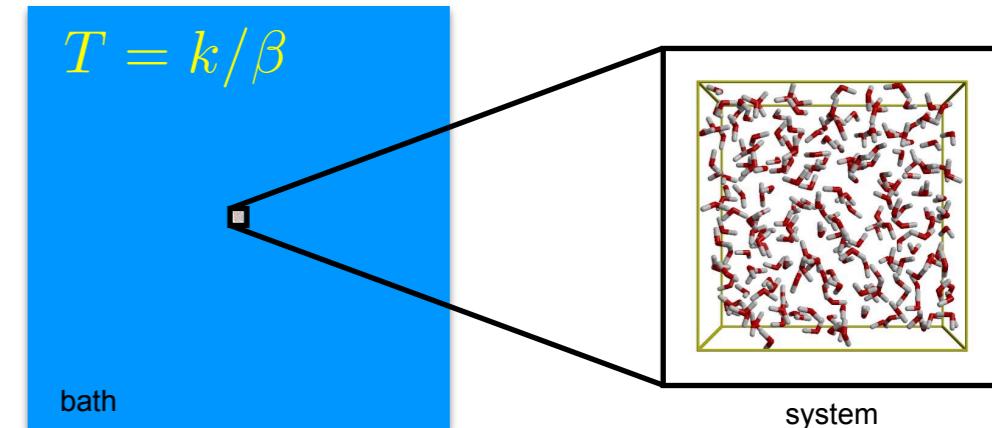
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$$\langle E \rangle = \sum_i p_i E_i = \frac{\sum_i E_i e^{-\beta E_i}}{\sum_i e^{-\beta E_i}}$$



# Statistical mechanics canonical ensemble

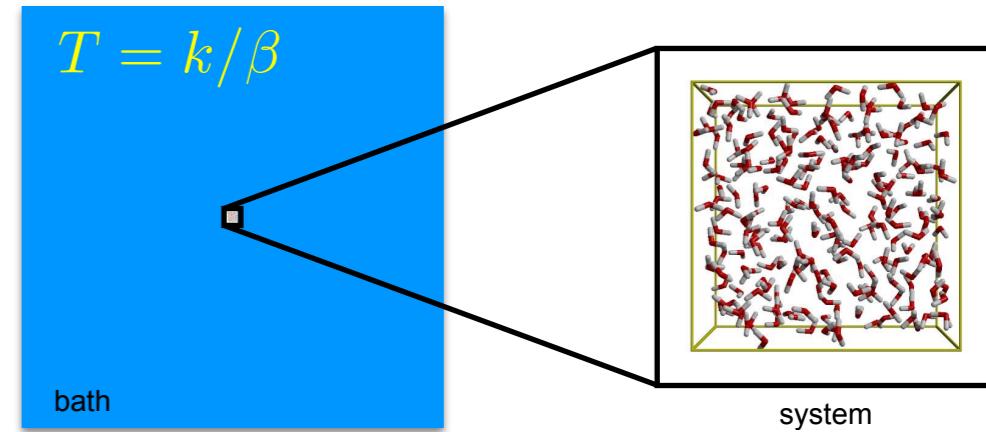
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average energy of system

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# Statistical mechanics canonical ensemble

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entropy of system

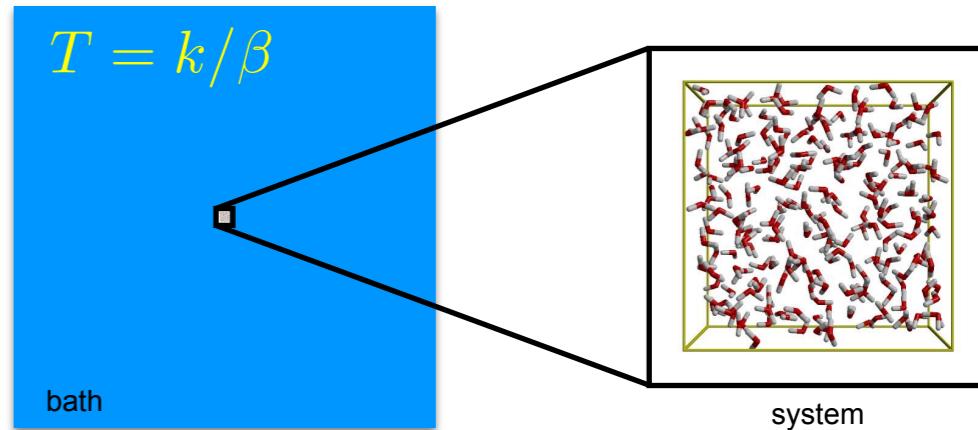
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what about entropy?



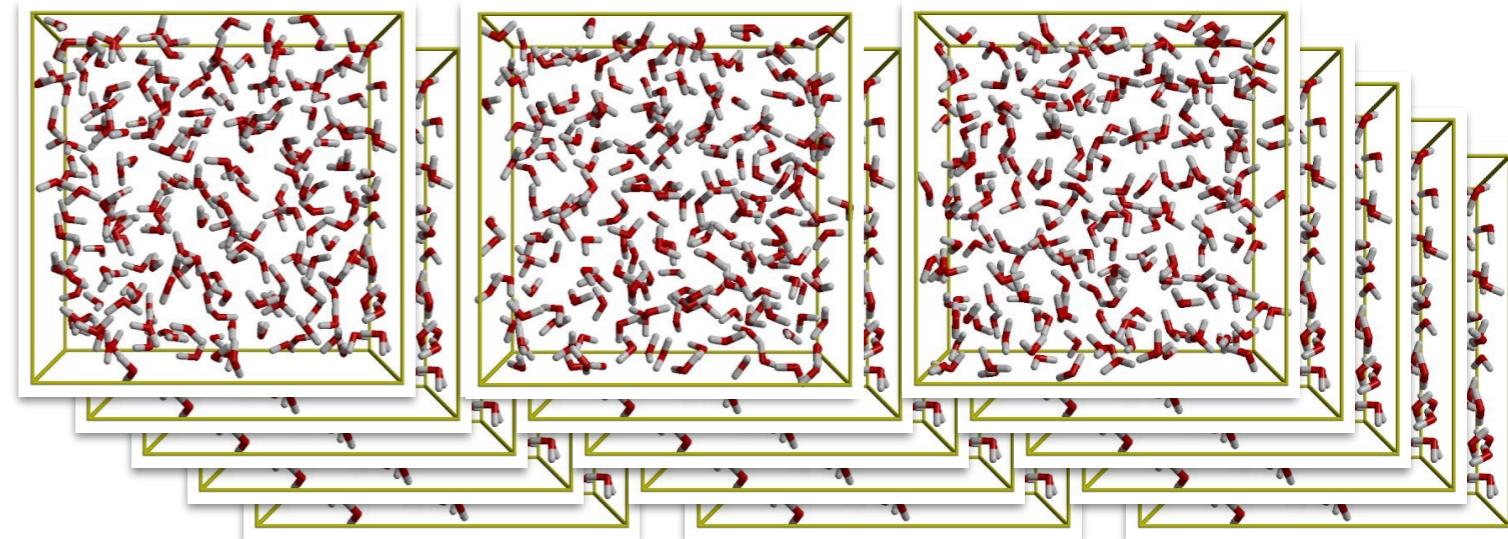
# Statistical mechanics

entropy

general ensemble

replicate many time

ensemble of  $N$  replicas



# Statistical mechanics

entropy

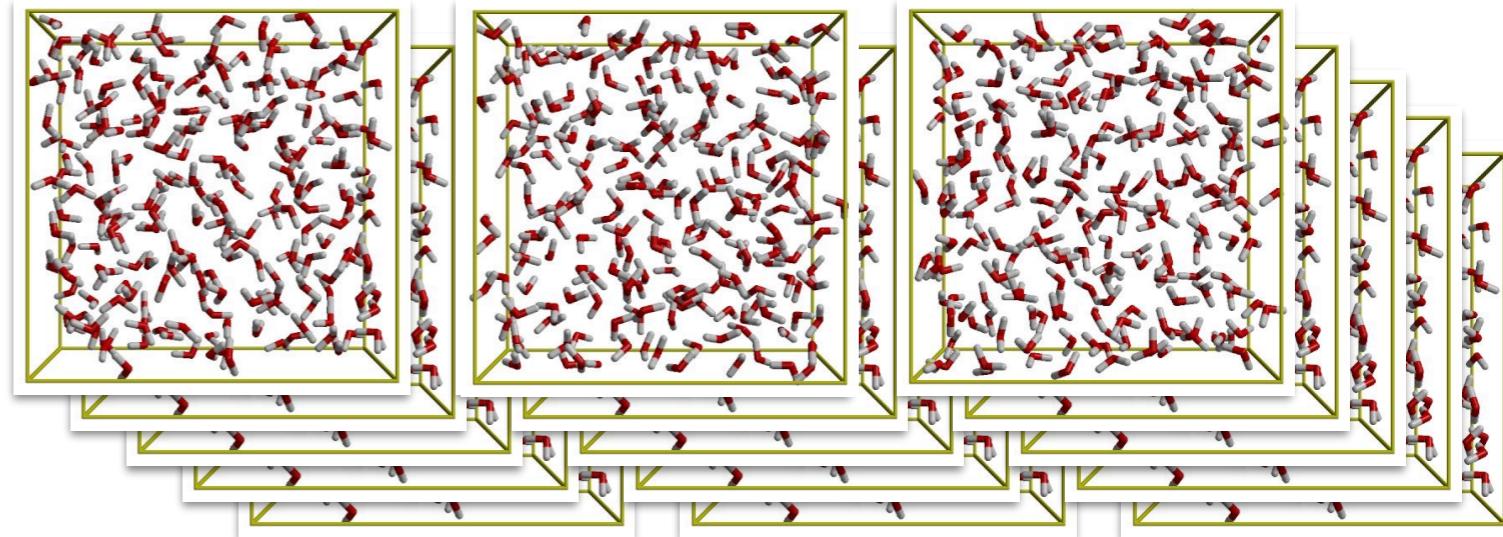
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number of replicas in micro-state  $i$

$$n_i = N p_i \quad \sum_i p_i = 1$$



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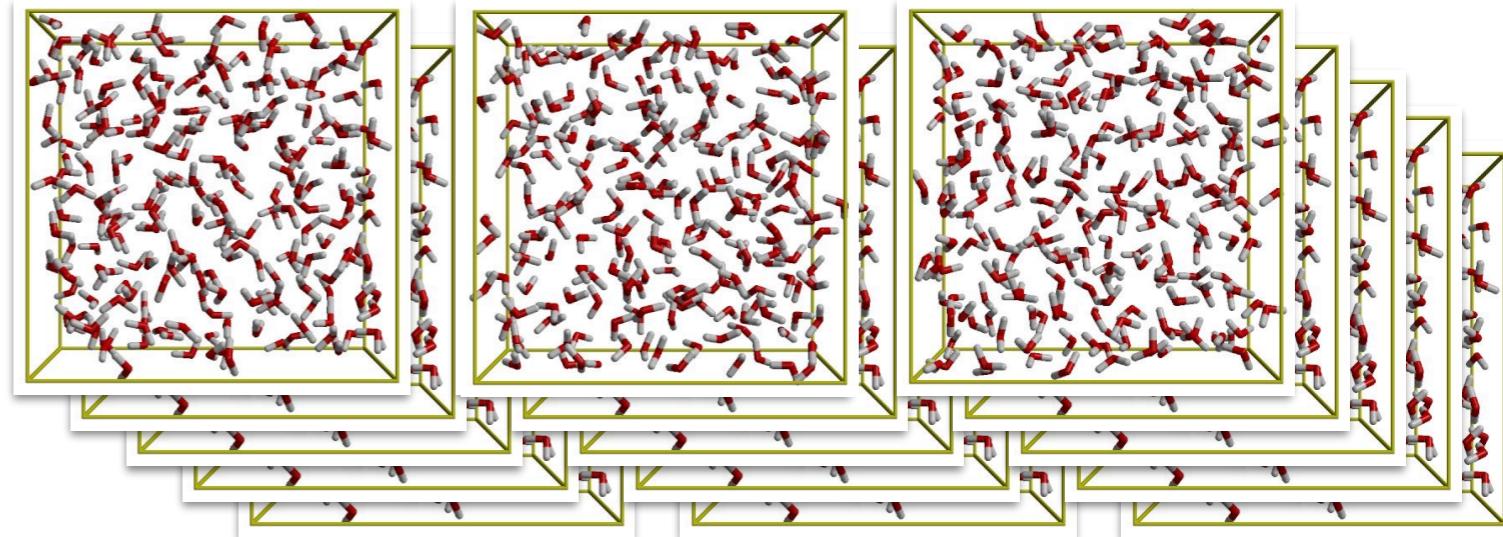
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total number of micro-states

$$\Omega_N = \frac{N!}{n_1! n_2! \dots n_i! \dots}$$



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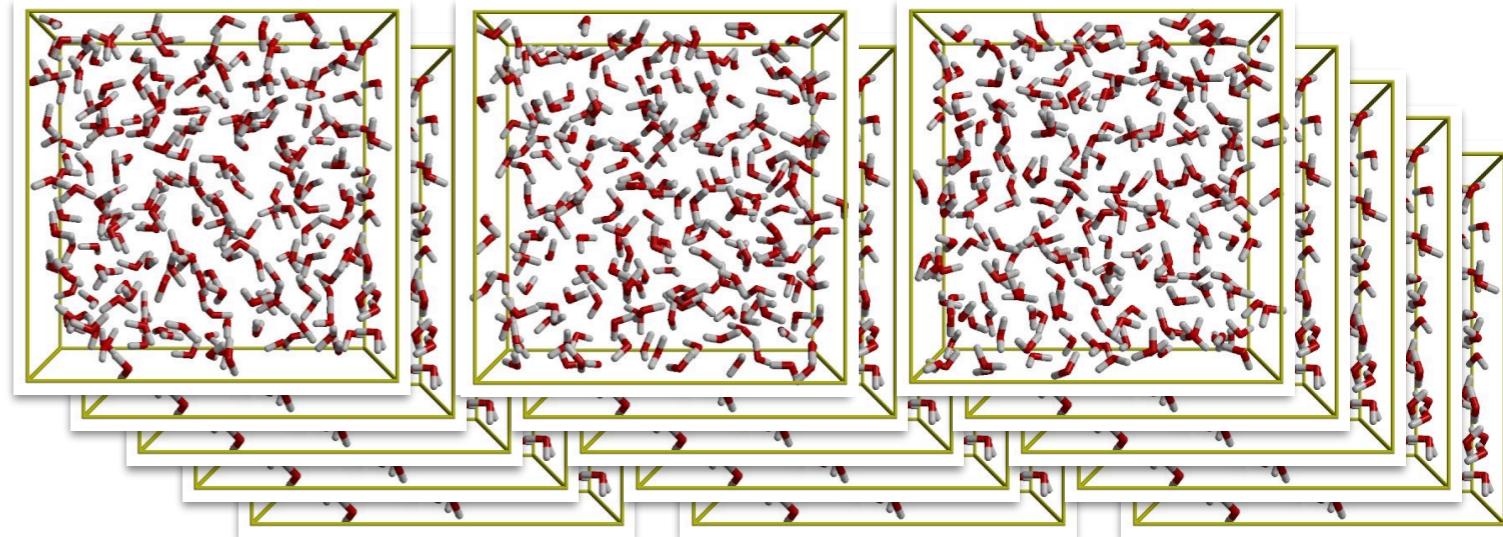
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entropy of ensemble

$$S_N = k \ln \Omega_N = k \ln \left[ \frac{N!}{n_1! n_2! \dots n_i! \dots} \right]$$



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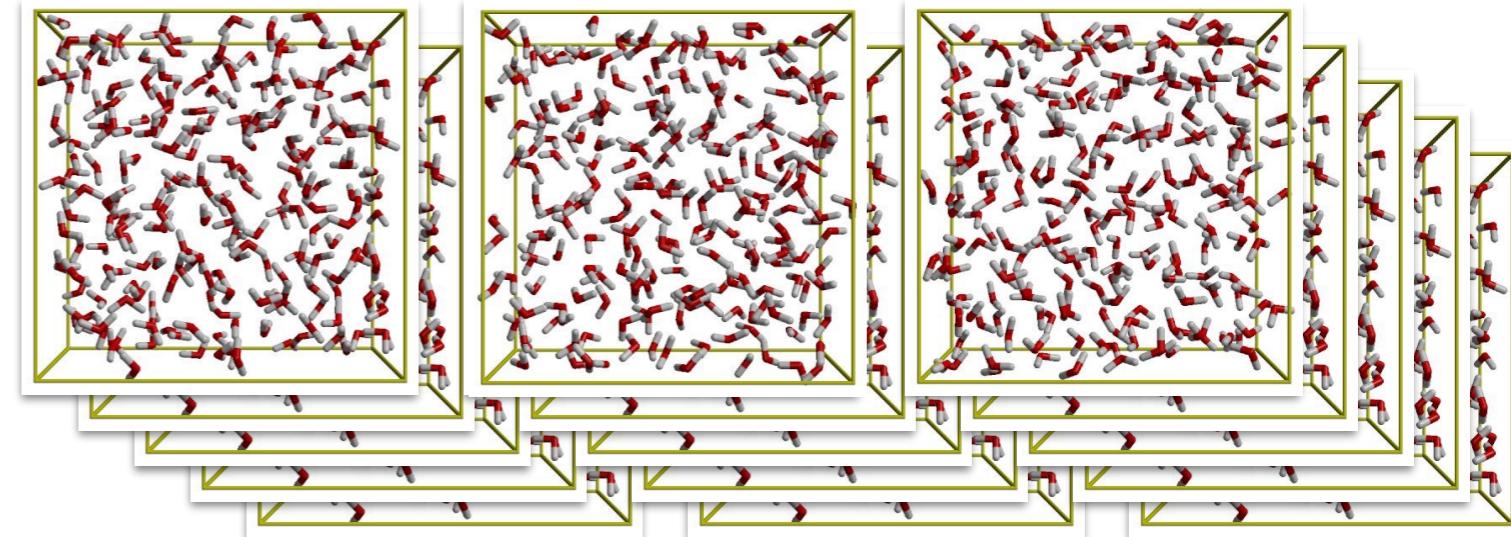
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entropy of ensemble

$$S_N = k \ln \Omega_N = k \ln \left[ \frac{N!}{n_1! n_2! \dots n_i! \dots} \right]$$

Stirling approximation:

$$\lim_{x \rightarrow \infty} \ln x! = x \ln x - x$$



# Statistical mechanics

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general ensemble

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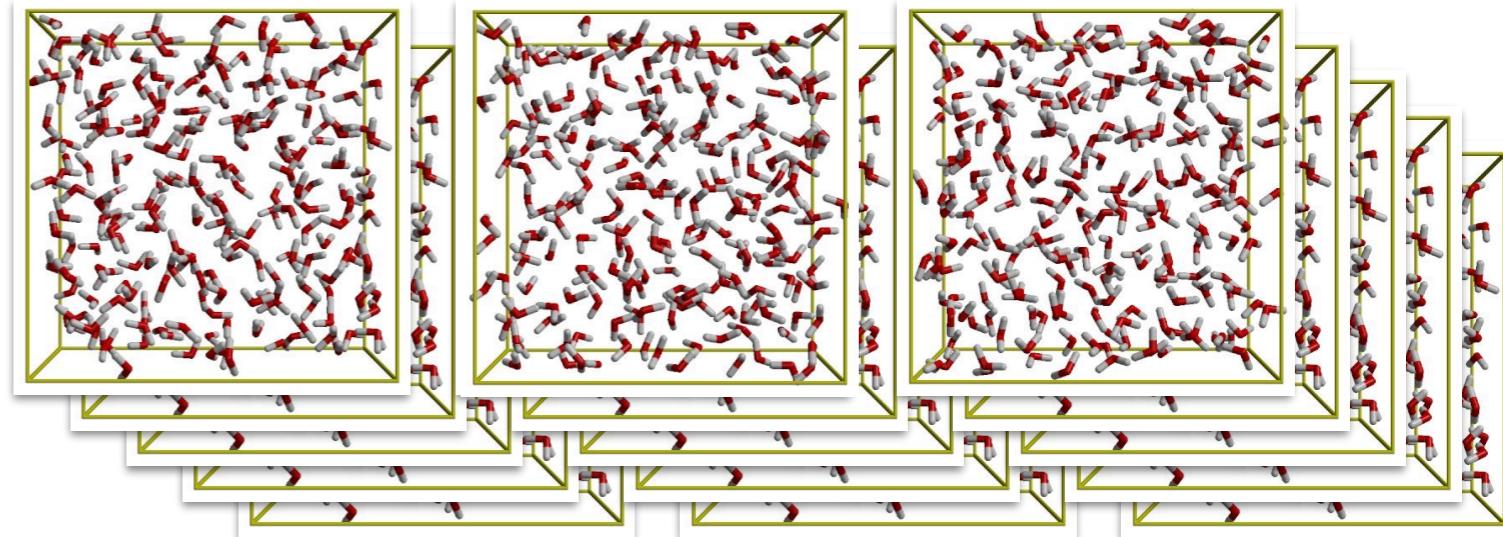
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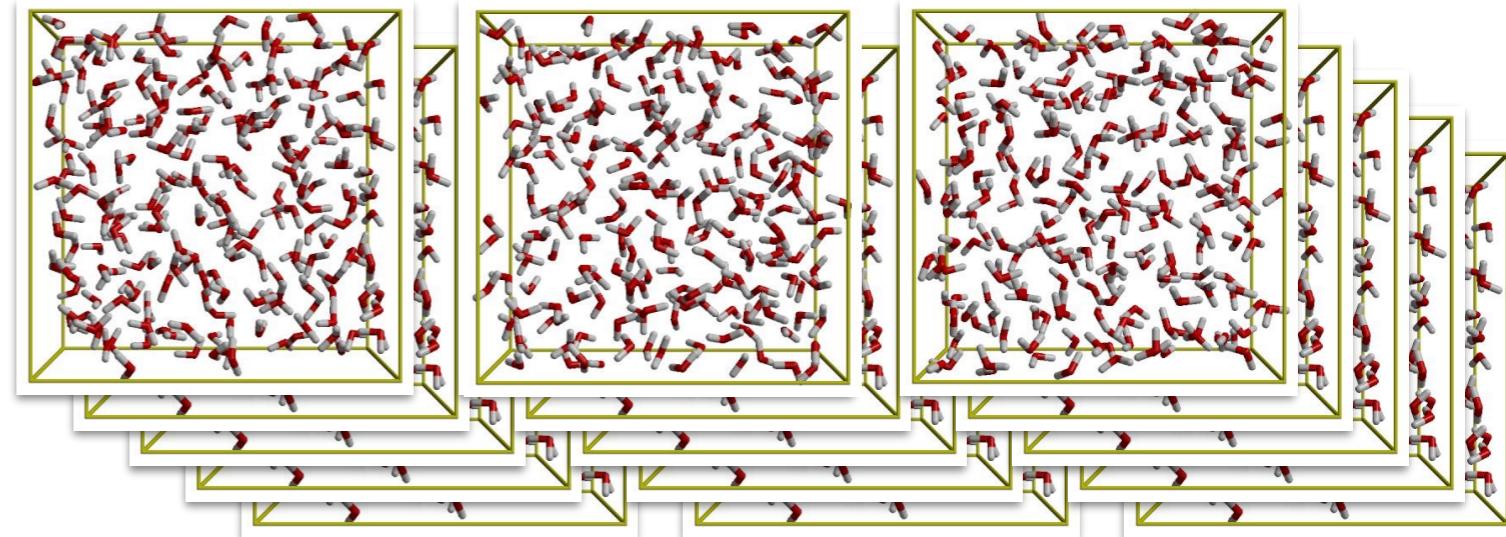
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$$S_N = k \left[ N \ln N - N - \sum_i (n_i \ln n_i - n_i) \right]$$



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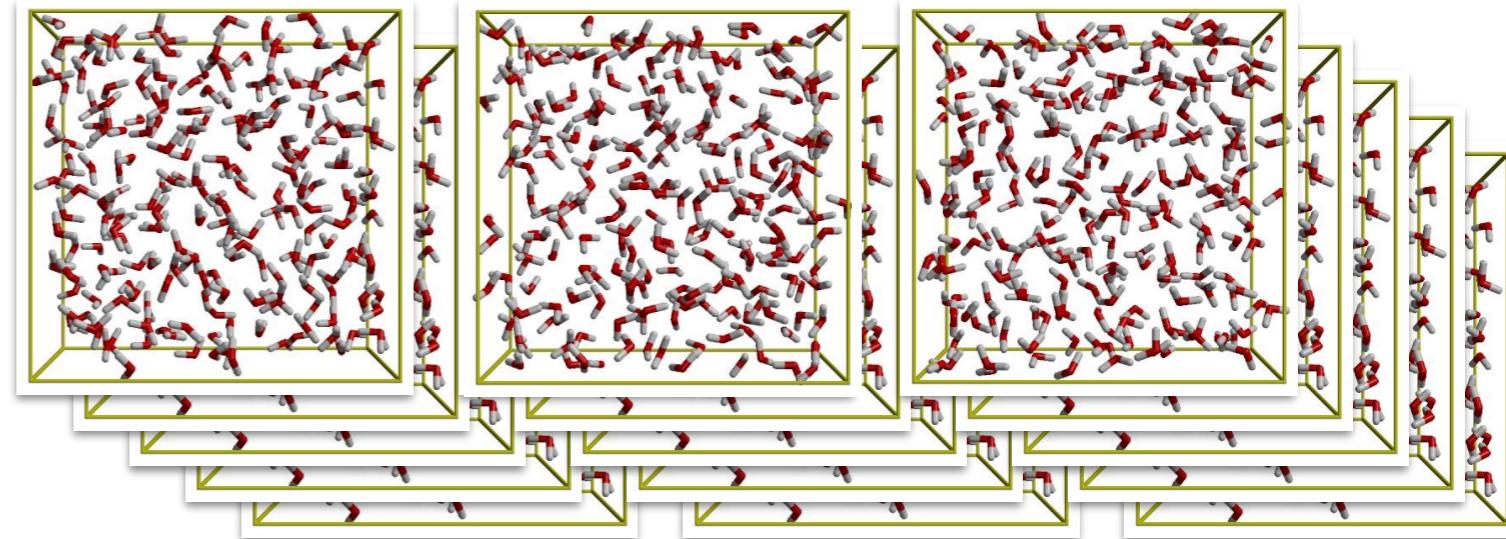
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$$S_N = k \left[ N \ln N - N - \sum_i (n_i \ln n_i - n_i) \right]$$

$$S_N = k \left[ N \ln N - N - N \sum_i (p_i \ln [N p_i] - p_i) \right]$$



# Statistical mechanics

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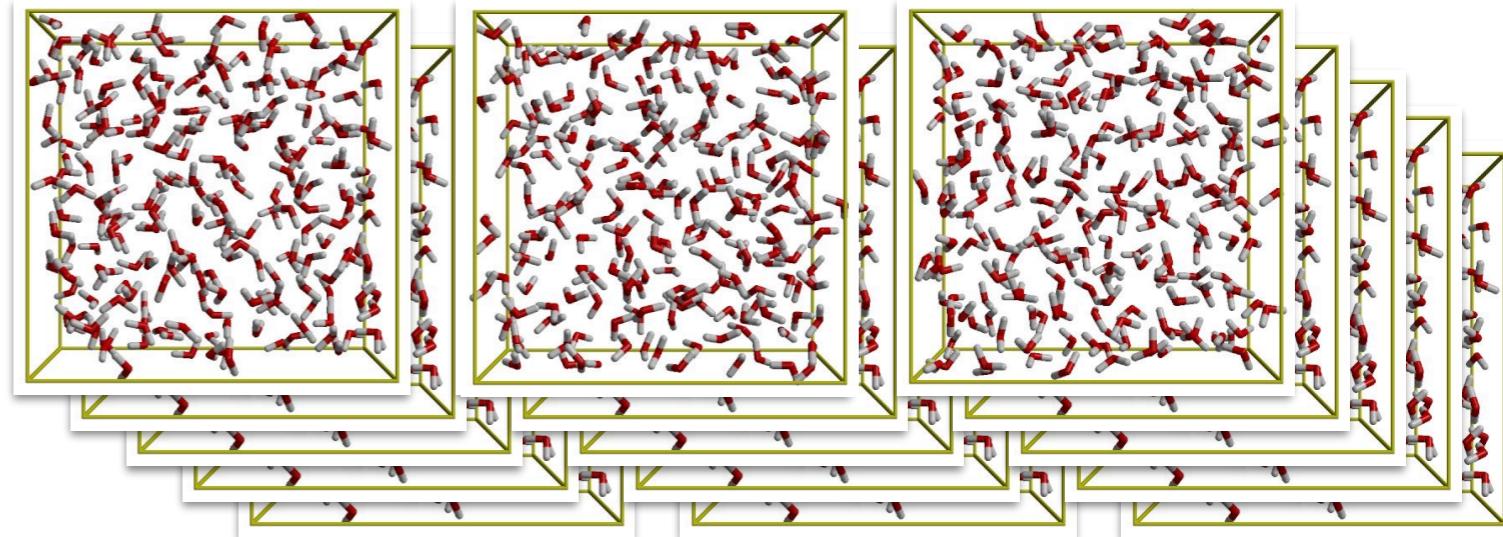
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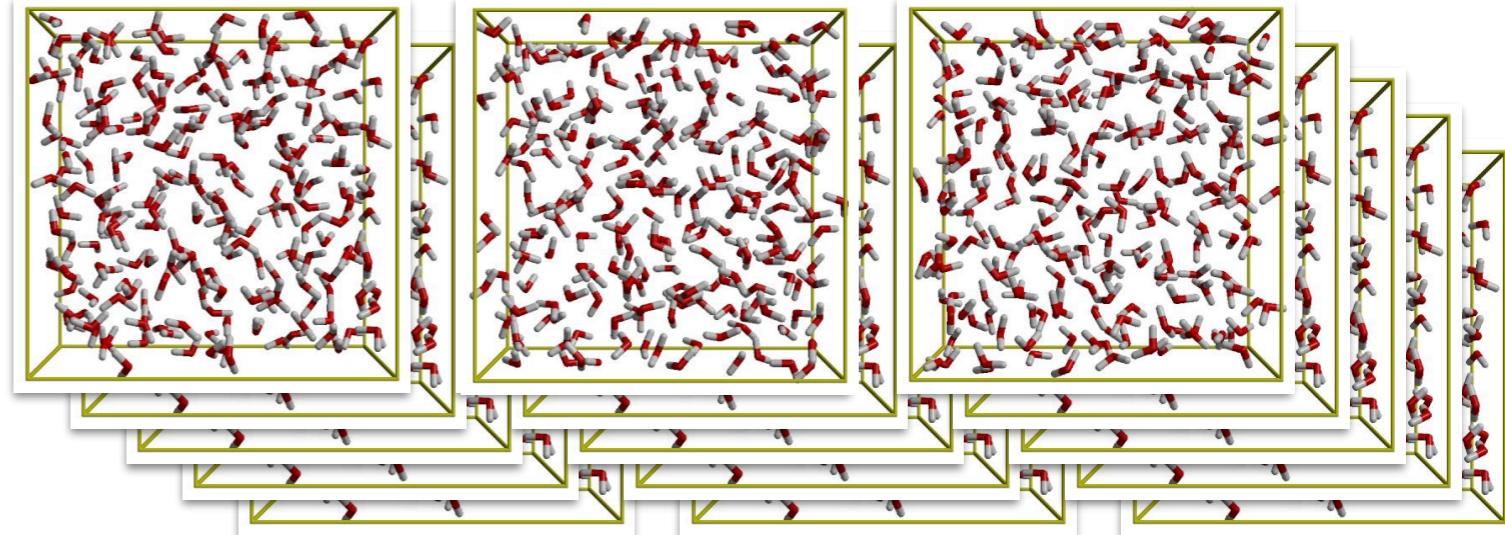
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# Statistical mechanics

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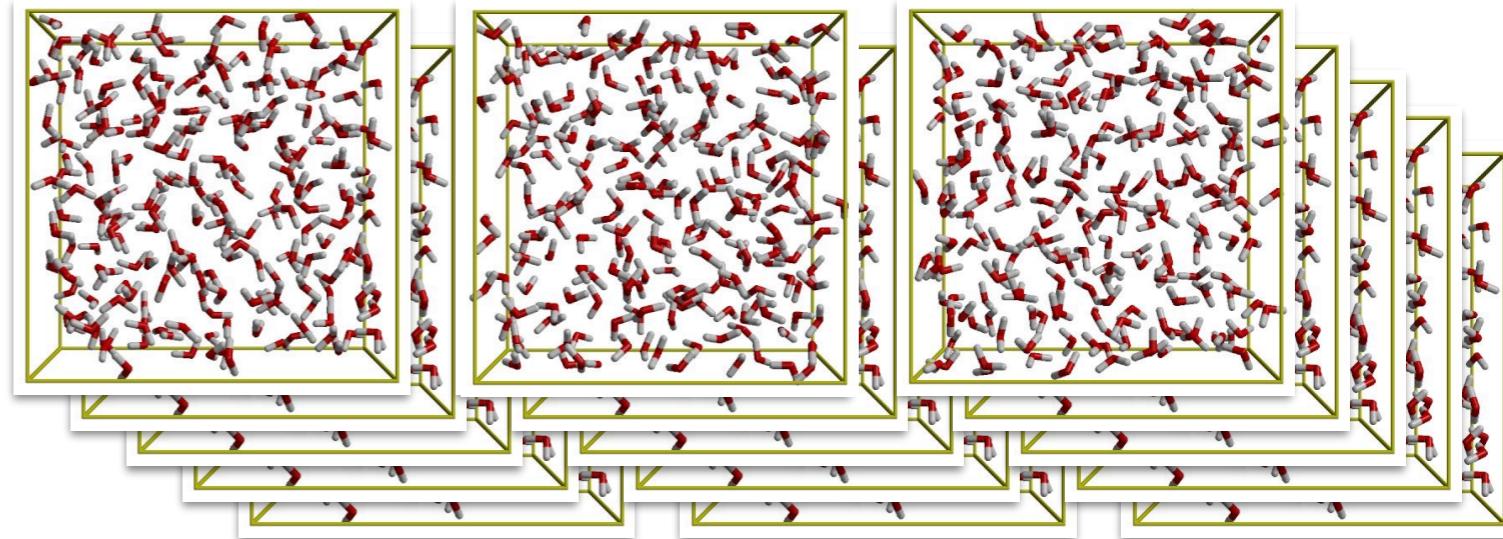
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entropy of ensemble

$$S_N = k \left[ N \ln N - N - N \sum_i (p_i \ln [N p_i] - p_i) \right]$$

$$S_N = k \left[ \cancel{N \ln N} - \cancel{N} - \cancel{N \ln N} - N \sum_i p_i \ln p_i - \cancel{N} \right]$$

$$S_N = -Nk \sum_i p_i \ln p_i$$



# Statistical mechanics

entropy

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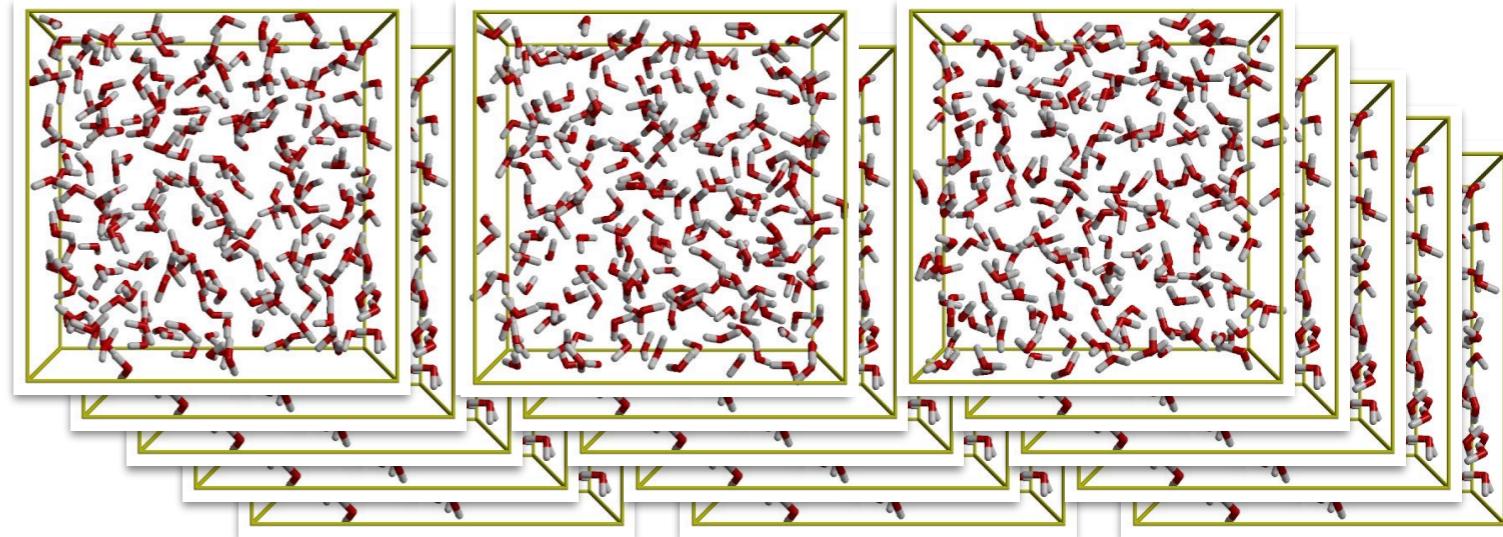
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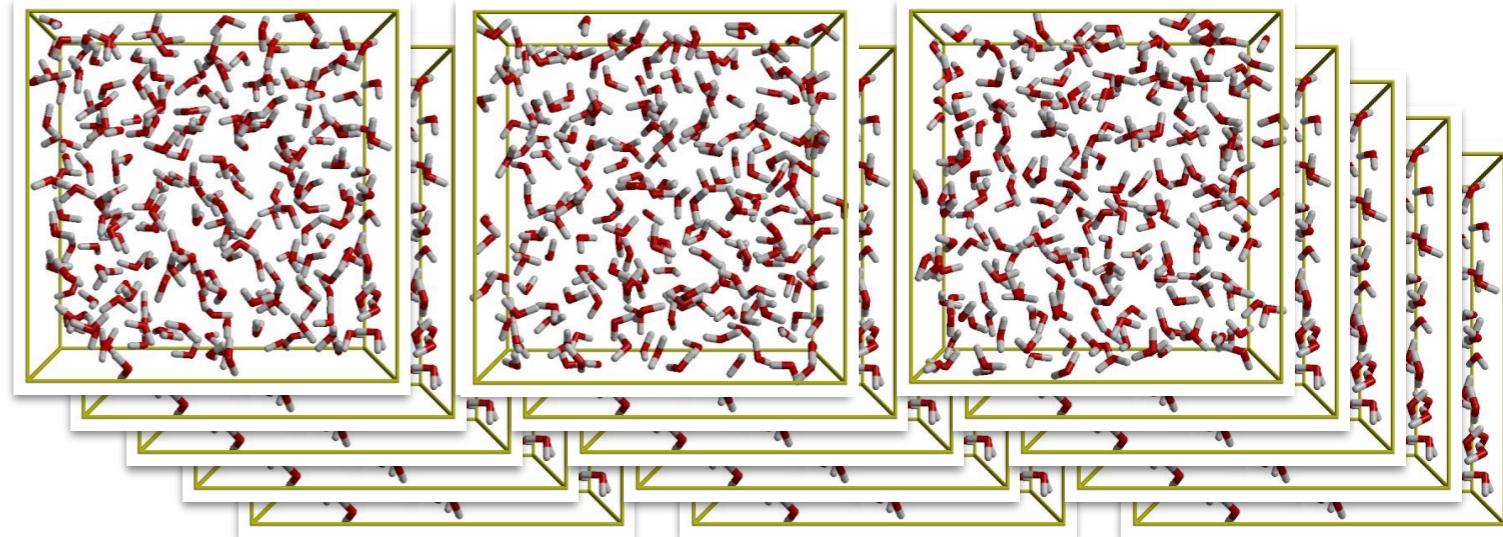
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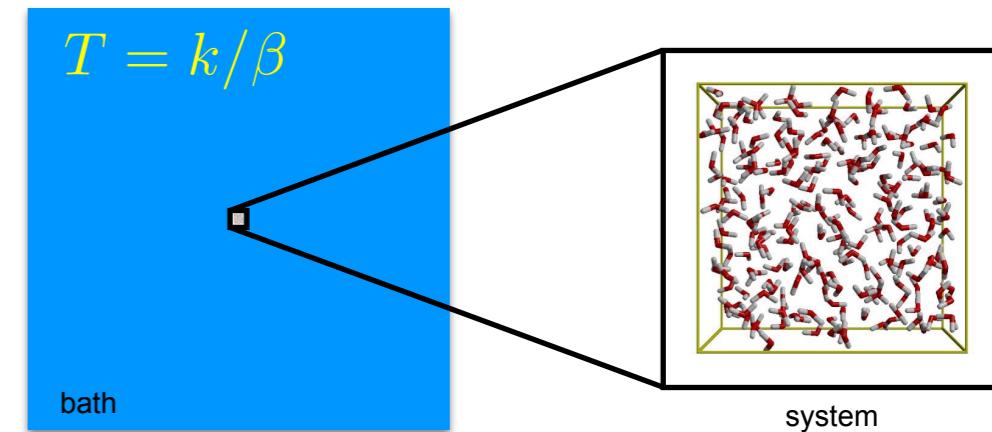
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# Statistical mechanics canonical ensemble

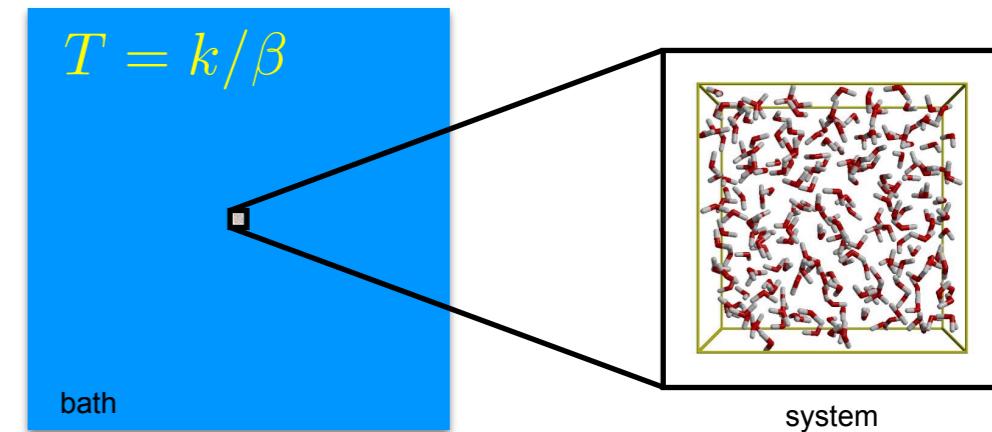
system in thermal equilibrium with bath  
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# Statistical mechanics canonical ensemble

system in thermal equilibrium with bath  
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Boltzmann distribution

$$p_i = \frac{1}{Z} e^{-\beta E_i} \quad Z = \sum_i e^{-\beta E_i} \quad \beta \equiv \frac{1}{kT}$$

# Statistical mechanics

## canonical ensemble

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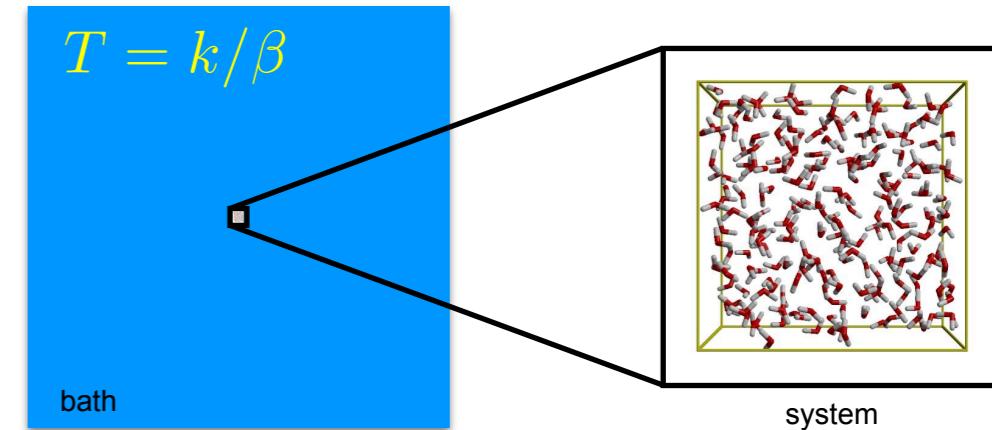
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substituting and rearranging

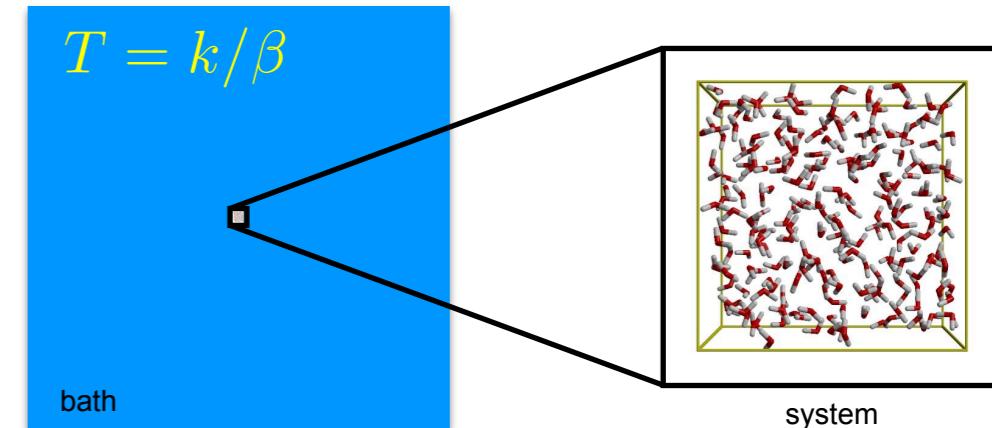
$$S = \frac{k}{Z} \sum_i e^{-\beta E_i} \beta E_i + \frac{k}{Z} \sum_i e^{-\beta E_i} \ln Z$$



# Statistical mechanics

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an almost familiar expression

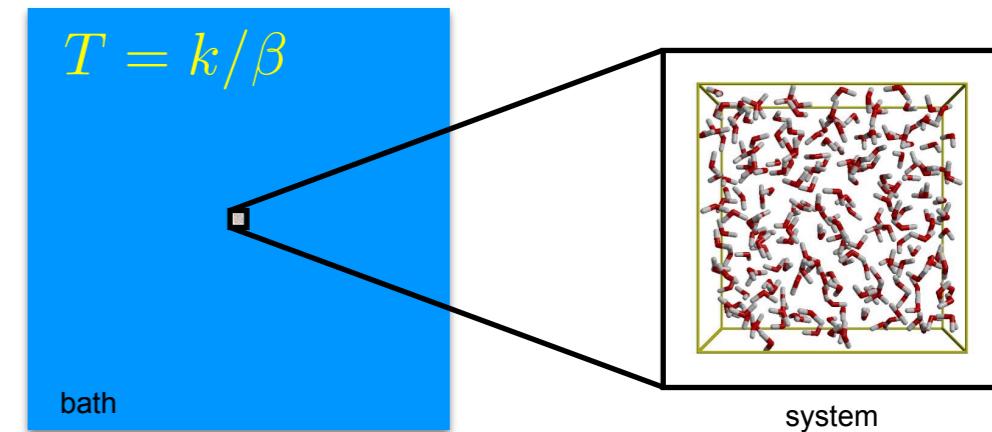
$$S = \frac{1}{T} \langle E \rangle + k \ln Z$$

# Statistical mechanics canonical ensemble

system in thermal equilibrium with bath  
free energy of system

microscopic entropy

$$S = \frac{1}{T} \langle E \rangle + k \ln Z$$



# Statistical mechanics canonical ensemble

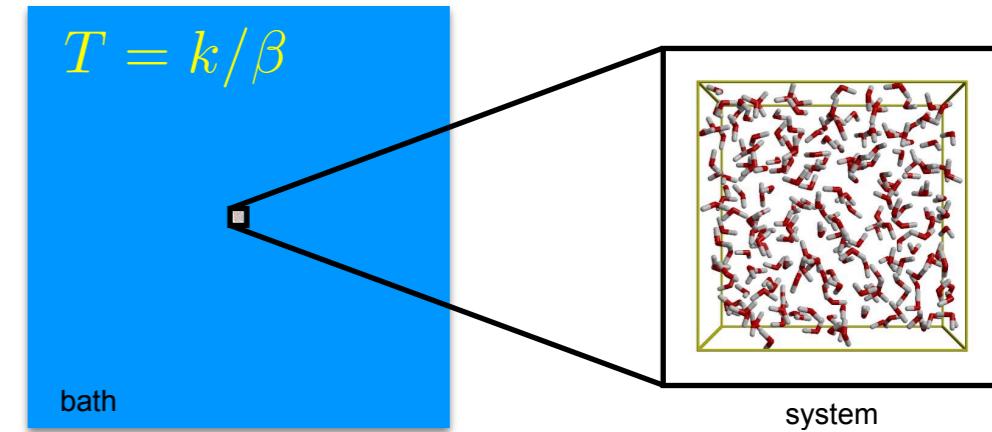
system in thermal equilibrium with bath  
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$$S = \frac{1}{T} \langle E \rangle + k \ln Z$$

microscopic free energy

$$-kT \ln Z = \langle E \rangle - TS$$



# Statistical mechanics canonical ensemble

system in thermal equilibrium with bath  
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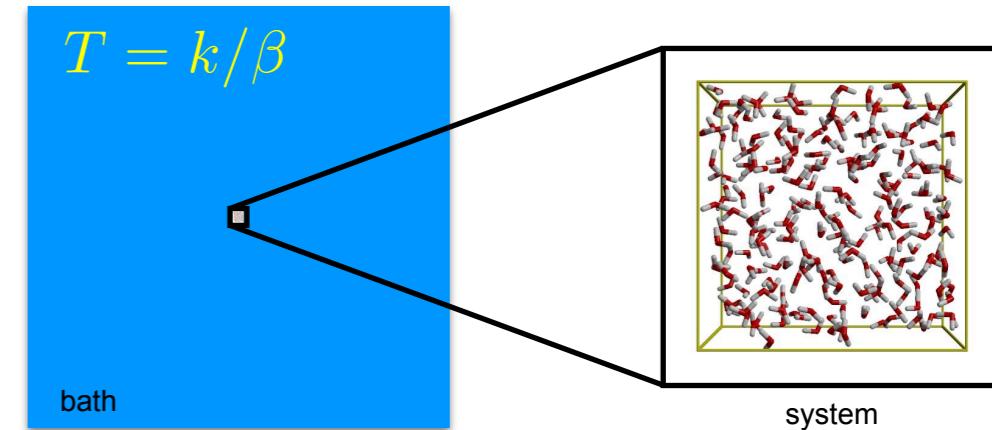
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$$A = -kT \ln Z$$



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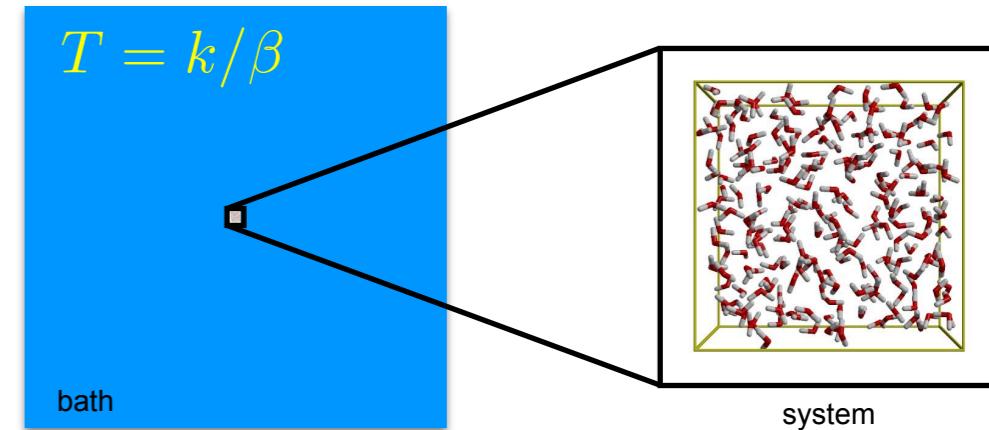
microscopic free energy

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macroscopic free energy

$$A = U - TS$$



# Statistical mechanics

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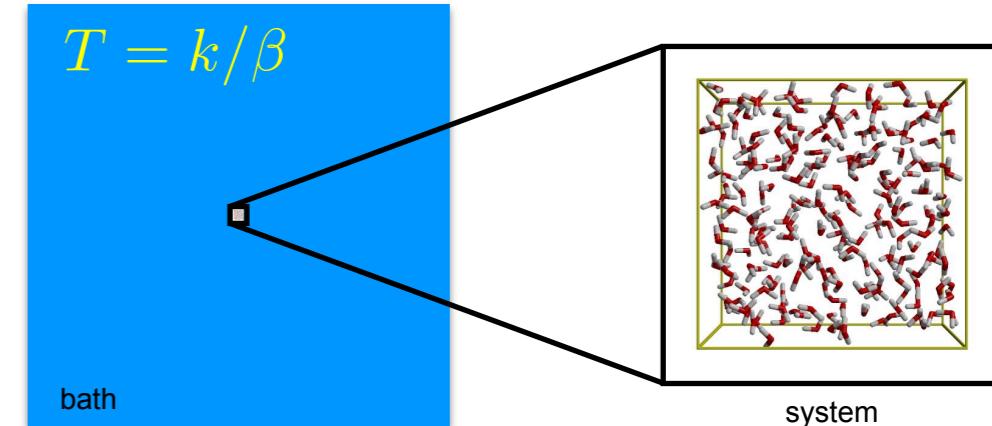
macroscopic free energy

$$A = U - TS$$

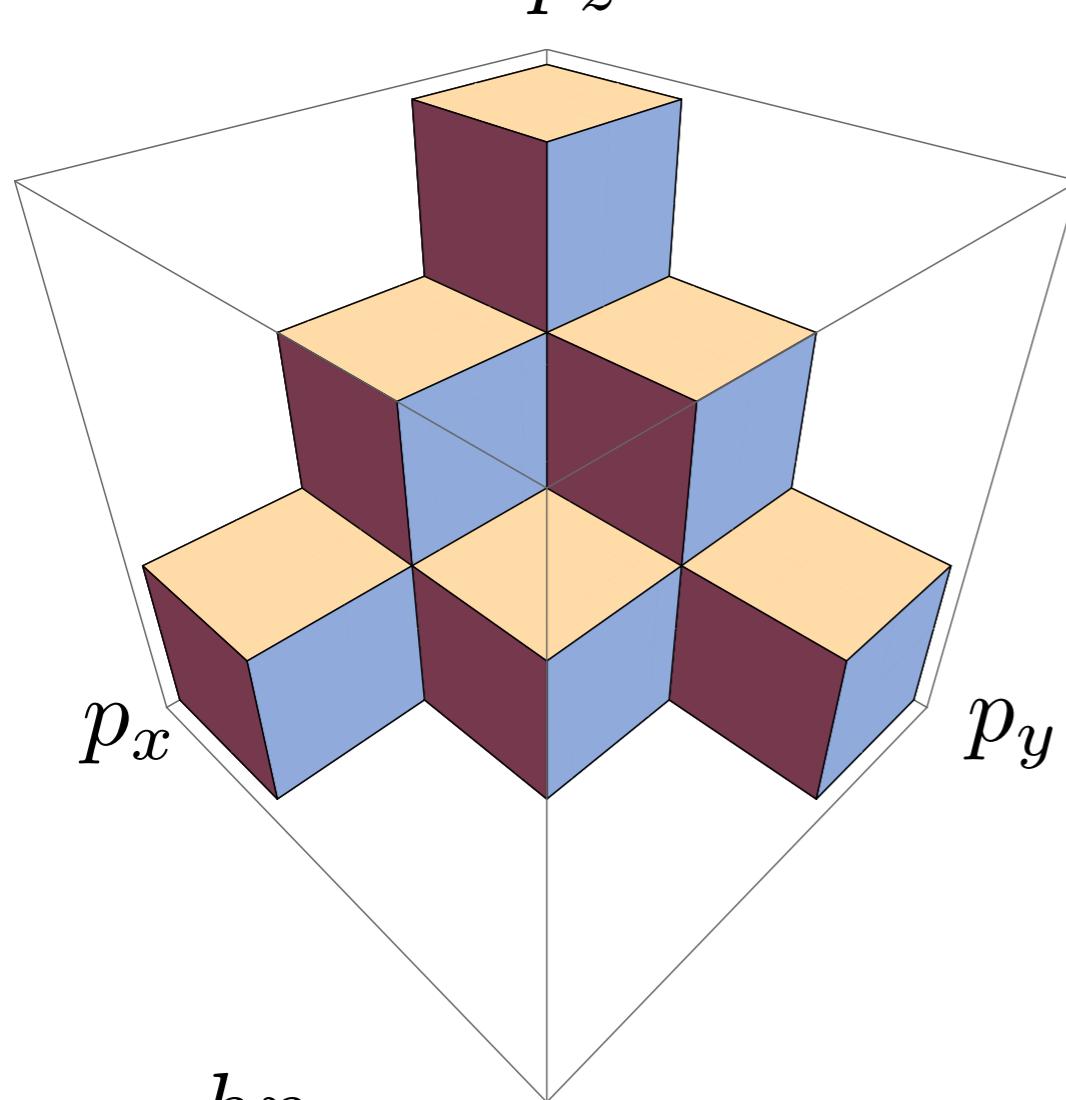
from micro to macro: generate partition function

Monte Carlo

molecular dynamics simulations



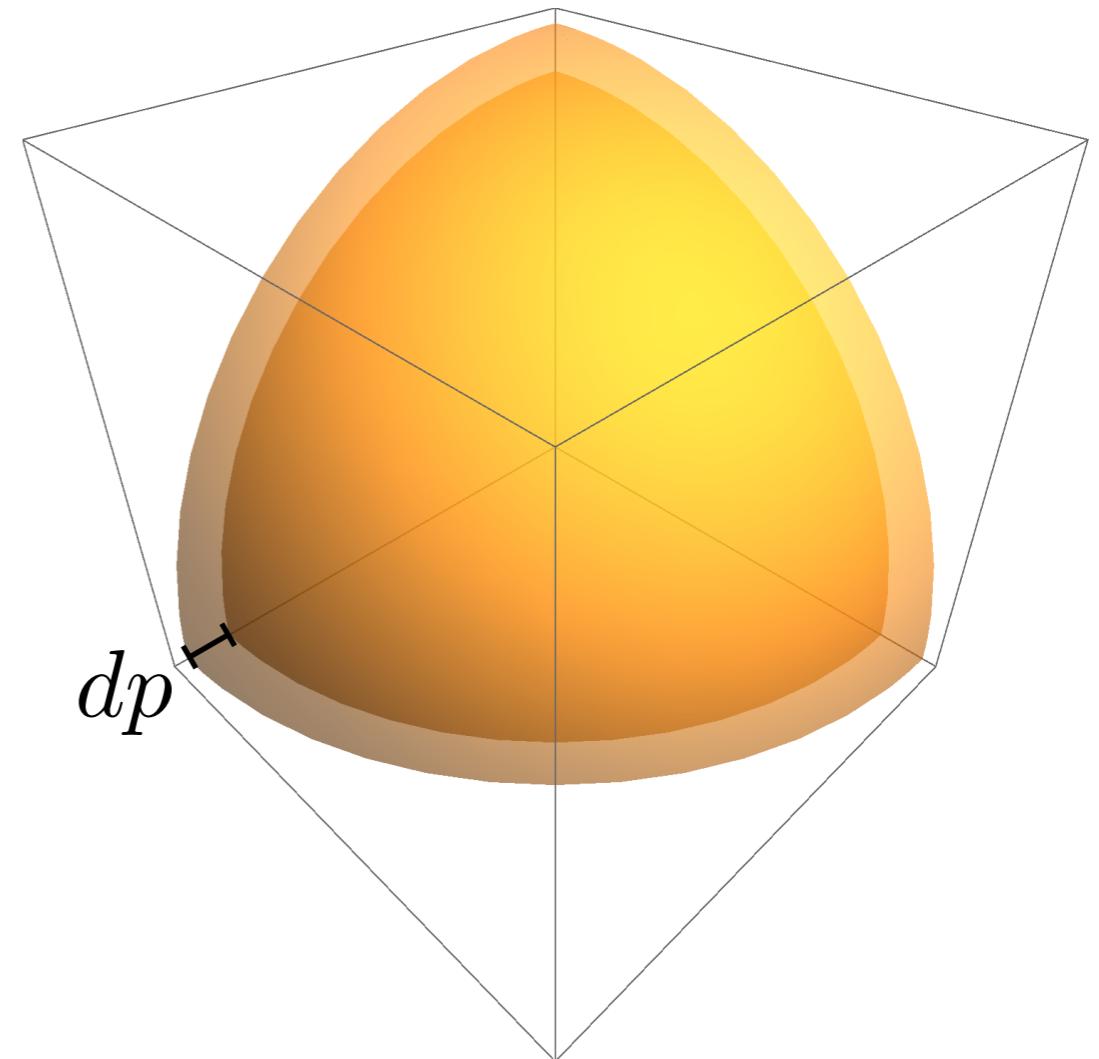
$$A = 4\pi p^2$$



$$p_x = \frac{hn_x}{2L}$$

$$p_y = \frac{hn_y}{2L}$$

$$p_z = \frac{hn_z}{2L} \quad n_x, n_y, n_z = 1, 2, 3, \dots$$



$$V(p + \delta p) = 4\pi p^2 dp$$

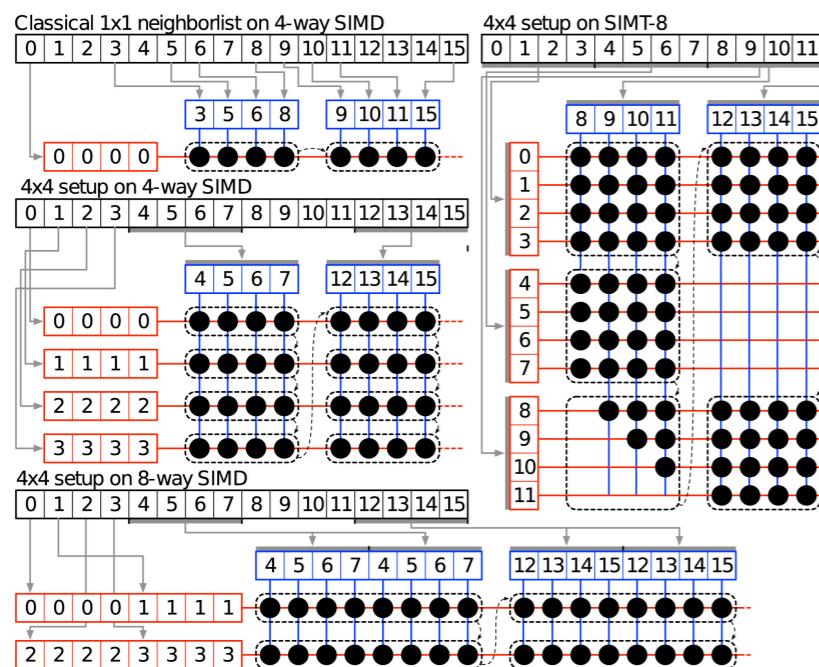
# Statistical mechanics on a computer

modern computer hardware

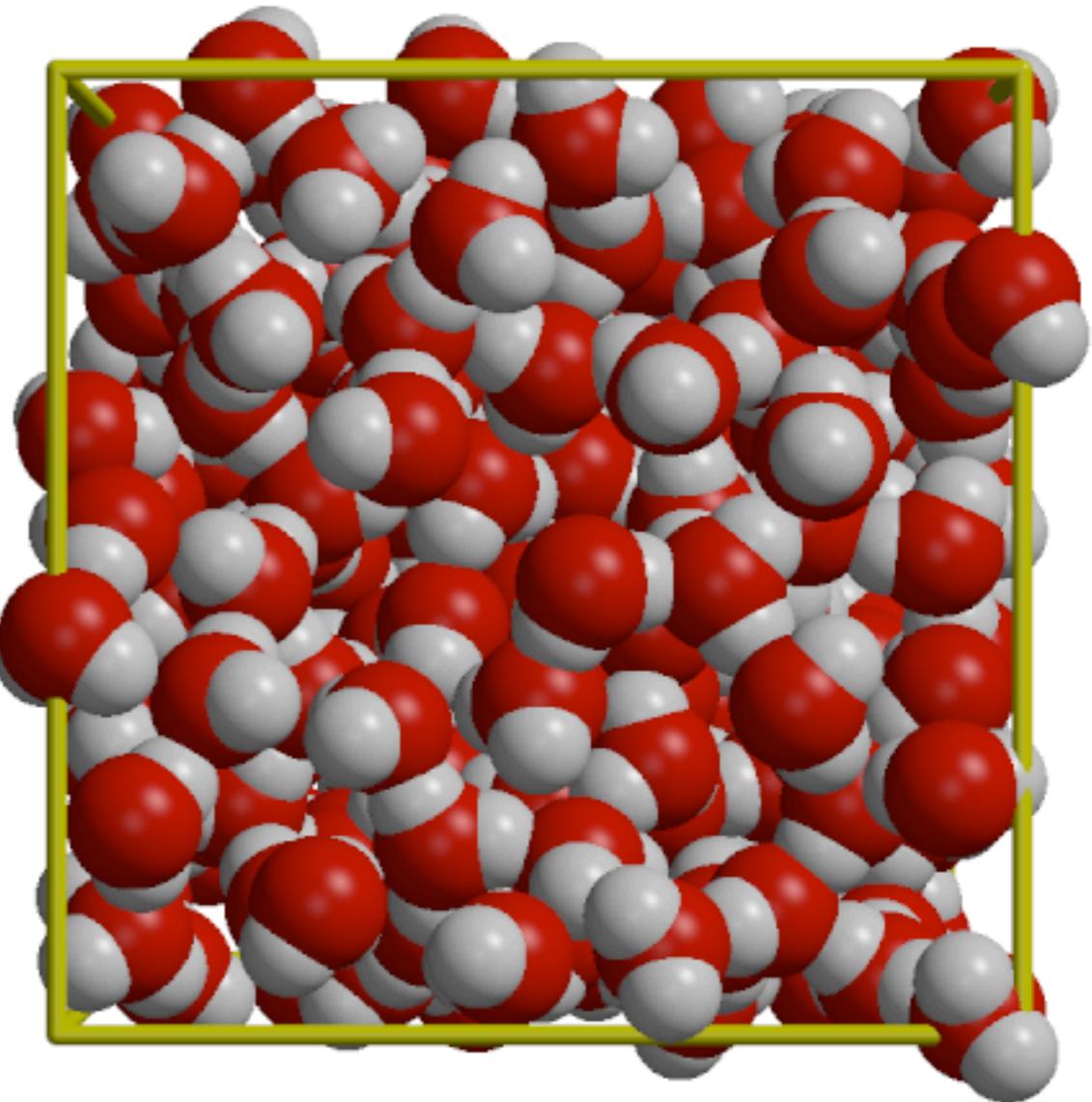


modern software

Gromacs



[www.gromacs.org](http://www.gromacs.org)



some water

10,000,000,000,000 X ►►

approximations

cannot be derived from first-principles

compare with experiment instead

# The very basics

molecules & matter

electrons (-e), protons (e) & neutrons



Ernest Rutherford Niels Bohr

# The very basics

molecules & matter

electrons (-e), protons (e) & neutrons

Coulomb interaction

keeps molecules together

$$V(\mathbf{r}_1, \mathbf{r}_2) = \frac{1}{4\pi\epsilon_0} \frac{q_1 q_2}{|\mathbf{r}_2 - \mathbf{r}_1|}$$



Ernest Rutherford Niels Bohr



Charles de Coulomb

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Quantum mechanics

non-relativistic time-dependent Schrödinger equation (1926)

$$i\hbar \frac{\partial}{\partial t} \Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots) = \hat{H} \Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots)$$



Ernest Rutherford Niels Bohr



Charles de Coulomb



Erwin Schrödinger

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non-relativistic time-independent Schrödinger equation (1926)

Charles de Coulomb

$$\hat{H}\Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots) = E\Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots)$$



Ernest Rutherford Niels Bohr



Erwin Schrödinger

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electrons (-e), protons (e) & neutrons

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non-relativistic time-independent Schrödinger equation (1926)

Charles de Coulomb

$$\hat{H}\Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots) = E\Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots)$$

Hamilton operator

$$\hat{H} = \hat{T}(\dot{\mathbf{R}}_1, \dot{\mathbf{R}}_2, \dots, \dot{\mathbf{r}}_1, \dot{\mathbf{r}}_2, \dots) + \hat{V}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots)$$

$$= \sum_A \frac{1}{2} m_A \dot{\mathbf{R}}_A^2 + \sum_a \frac{1}{2} m_e \dot{\mathbf{r}}_a^2$$

$$+ \frac{e^2}{4\pi\epsilon_0} \sum_A \sum_B \frac{Z_A Z_B}{|\mathbf{R}_B - \mathbf{R}_A|} - \frac{e^2}{4\pi\epsilon_0} \sum_A \sum_a \frac{Z_A}{|\mathbf{r}_a - \mathbf{R}_A|} + \frac{e^2}{4\pi\epsilon_0} \sum_a \sum_b \frac{1}{|\mathbf{r}_b - \mathbf{r}_a|}$$



Ernest Rutherford Niels Bohr



Erwin Schrödinger

# Approximate methods of applying QM

## Born-Oppenheimer approximation (1927)

separate electronic and nuclear degrees of freedom

$$m_e \ll m_{H^+}$$



Max Born



Robert  
Oppenheimer

$$\Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots) = \Xi(\mathbf{R}_1, \mathbf{R}_2, \dots) \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots)$$

# Approximate methods of applying QM

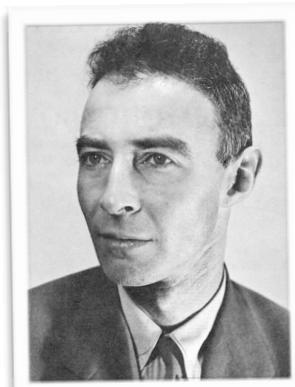
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separate Schrödinger equations for nuclei & electrons

$$\hat{H}_e \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots) = \left[ \hat{T}_e(\dot{\mathbf{r}}_1, \dot{\mathbf{r}}_2, \dots) + \hat{V}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots) \right] \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots)$$

$$= V_e(\mathbf{R}_1, \mathbf{R}_2, \dots) \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots)$$

$$\hat{H} \Xi(\mathbf{R}_1, \mathbf{R}_2, \dots) = \left[ \hat{T}_n(\dot{\mathbf{R}}_1, \dot{\mathbf{R}}_2, \dots) + V_e(\mathbf{R}_1, \mathbf{R}_2, \dots) \right] \Xi(\mathbf{R}_1, \mathbf{R}_2) = E \Xi(\mathbf{R}_1, \mathbf{R}_2)$$

# Approximate methods of applying QM

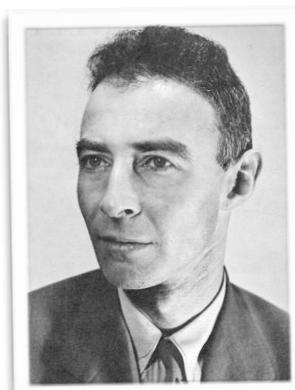
## Born-Oppenheimer approximation (1927)

separate electronic and nuclear degrees of freedom

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Robert  
Oppenheimer

$$\Psi(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots) = \Xi(\mathbf{R}_1, \mathbf{R}_2, \dots) \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots)$$

separate Schrödinger equations for nuclei & electrons

$$\hat{H}_e \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots) = \left[ \hat{T}_e(\dot{\mathbf{r}}_1, \dot{\mathbf{r}}_2, \dots) + \hat{V}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{r}_1, \mathbf{r}_2, \dots) \right] \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots)$$

$$= V_e(\mathbf{R}_1, \mathbf{R}_2, \dots) \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots)$$

$$\hat{H} \Xi(\mathbf{R}_1, \mathbf{R}_2, \dots) = \left[ \hat{T}_n(\dot{\mathbf{R}}_1, \dot{\mathbf{R}}_2, \dots) + V_e(\mathbf{R}_1, \mathbf{R}_2, \dots) \right] \Xi(\mathbf{R}_1, \mathbf{R}_2) = E \Xi(\mathbf{R}_1, \mathbf{R}_2)$$

electronic potential energy surface

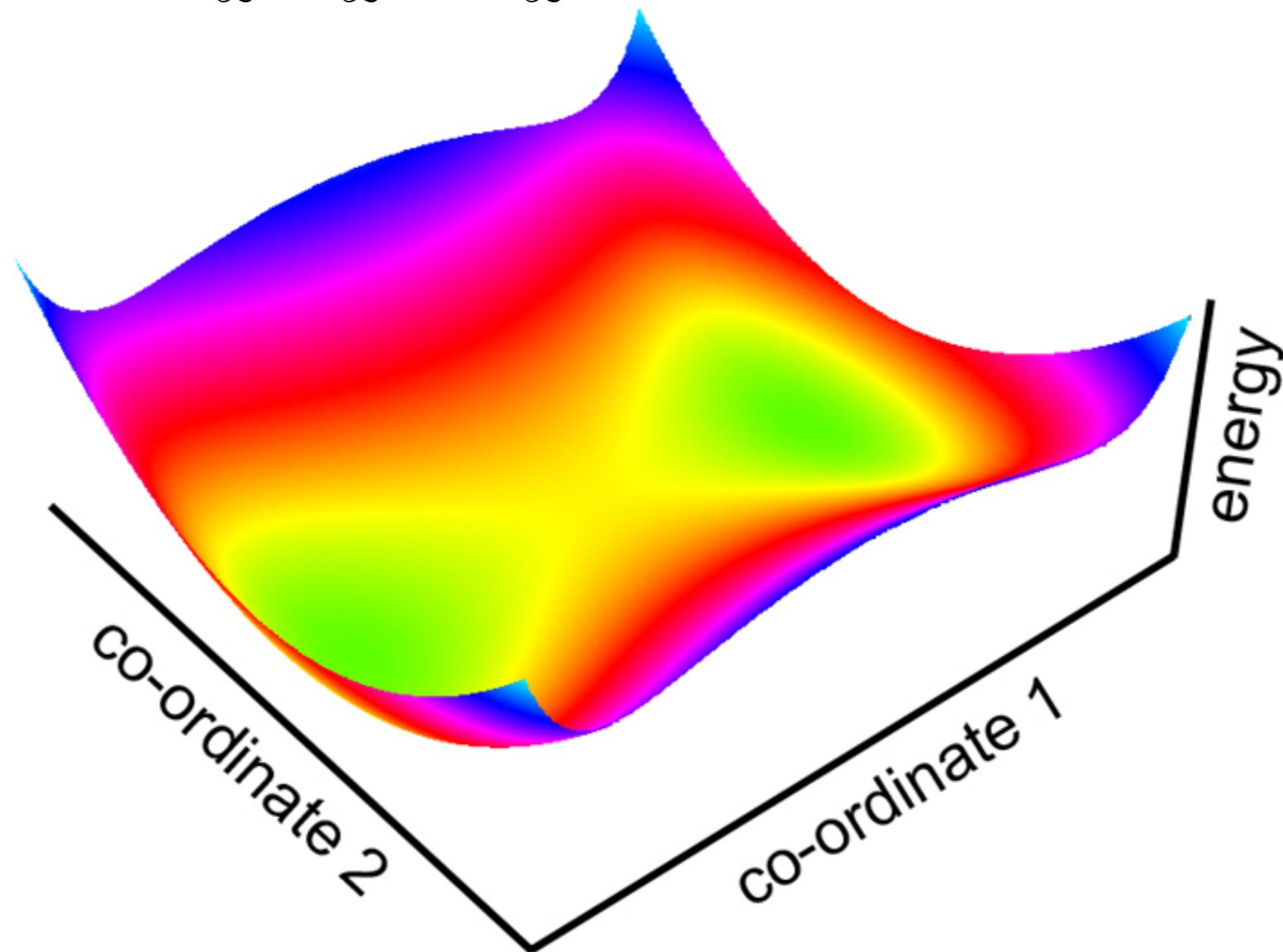
$$V_e(\mathbf{R}_1, \mathbf{R}_2, \dots) = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} \dots \int_{-\infty}^{\infty} \Phi^*(\mathbf{r}_1, \mathbf{r}_2, \dots) \hat{H}_e \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots) d\mathbf{r}_1 d\mathbf{r}_2 \dots d\mathbf{r}_n$$

# Approximate methods of applying QM

Born-Oppenheimer approximation (1927)

potential energy surface on which nuclei move

$$V_e(\mathbf{R}_1, \mathbf{R}_2, \dots) = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} \dots \int_{-\infty}^{\infty} \Phi^*(\mathbf{r}_1, \mathbf{r}_2, \dots) \hat{H}_e \Phi(\mathbf{r}_1, \mathbf{r}_2, \dots) d\mathbf{r}_1 d\mathbf{r}_2 \dots d\mathbf{r}_n$$

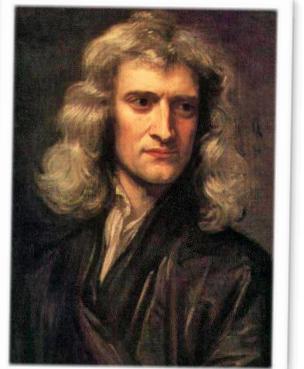


# Approximate methods of applying QM

## classical approximation for nuclei

Newton's equations of motion

$$F_B = m_B \mathbf{a}_B = -\nabla_{\mathbf{R}_B} V_e(\mathbf{R}_1, \mathbf{R}_2, \dots)$$



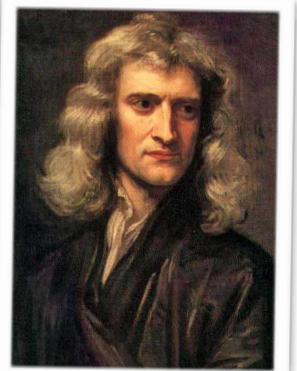
Isaac Newton

# Approximate methods of applying QM

## classical approximation for nuclei

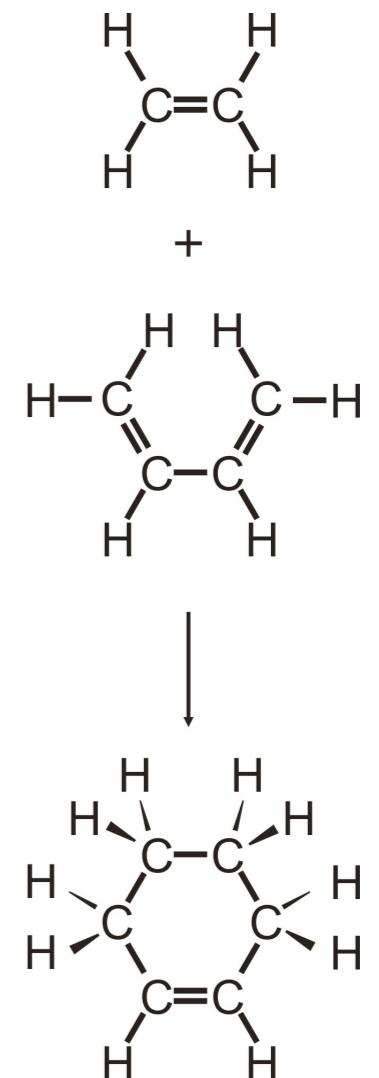
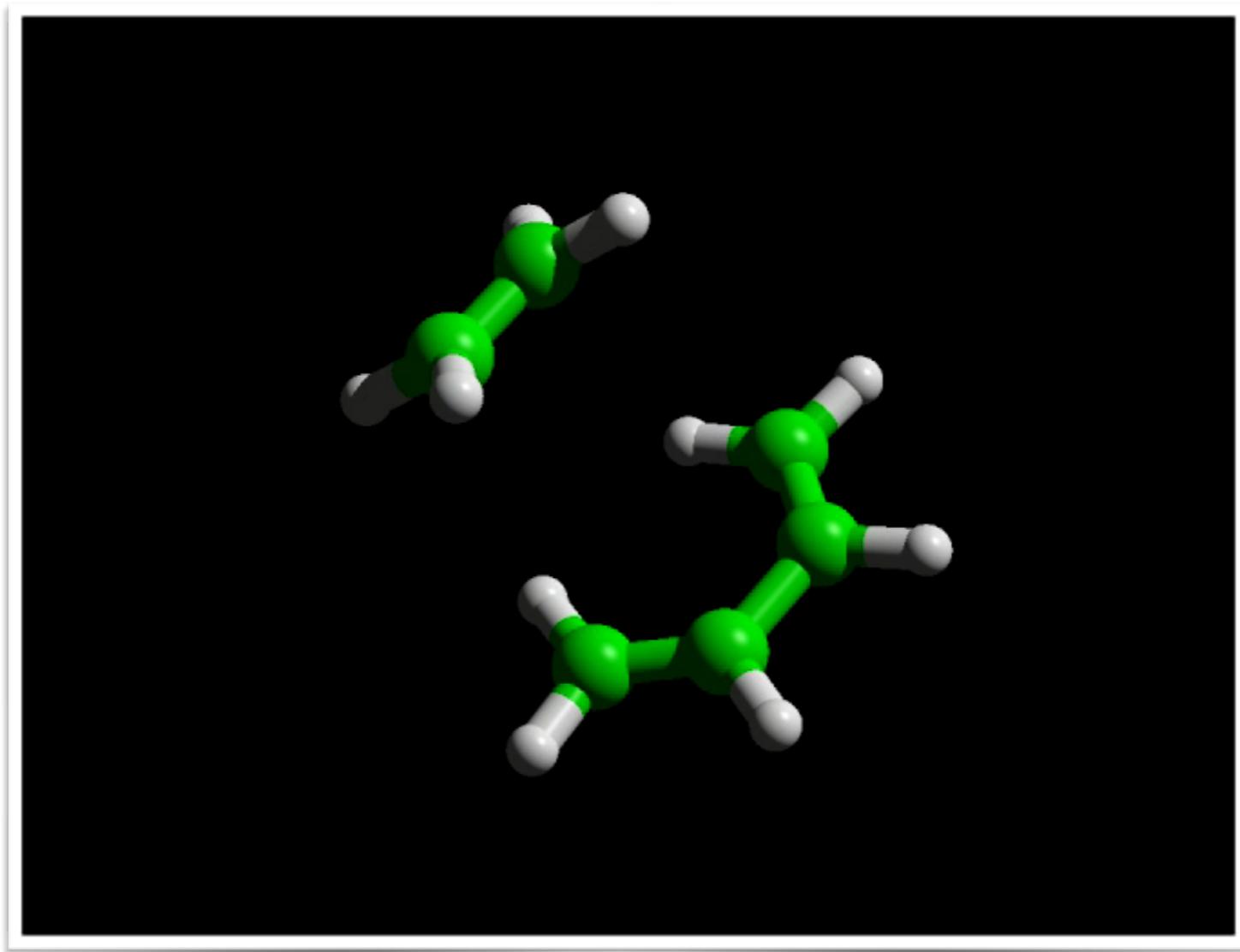
Newton's equations of motion

$$F_B = m_B \mathbf{a}_B = -\nabla_{\mathbf{R}_B} V_e(\mathbf{R}_1, \mathbf{R}_2, \dots)$$



Isaac Newton

example: Diels-Alder reaction



# Approximate methods of applying QM

approximations for electronic wave function

Hartree Fock & beyond (1927)

$$\Phi(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) = \hat{A}\phi_1(\mathbf{r}_1)\phi_2(\mathbf{r}_2)\dots\phi_n(\mathbf{r}_n)$$

3N dimensions

10 - 1000 atoms



Douglas  
Hartree



Vladimir  
Fock



John  
Slater

# Approximate methods of applying QM

## approximations for electronic wave function

Hartree Fock & beyond (1927)

$$\Phi(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) = \hat{A}\phi_1(\mathbf{r}_1)\phi_2(\mathbf{r}_2)\dots\phi_n(\mathbf{r}_n)$$

3N dimensions

10 - 1000 atoms

density functional theory (1964)

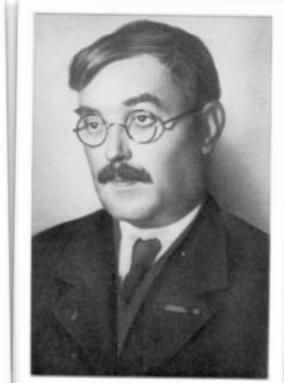
$$\rho(\mathbf{r}) \rightarrow \Phi_0(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n)$$

3 dimensions

100 - 10000 atoms



Douglas  
Hartree



Vladimir  
Fock



John  
Slater



Walter  
Kohn



Pierre  
Hohenberg



Lu  
Sham

# Approximate methods of applying QM

## approximations for electronic wave function

Hartree Fock & beyond (1927)

$$\Phi(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) = \hat{A}\phi_1(\mathbf{r}_1)\phi_2(\mathbf{r}_2)\dots\phi_n(\mathbf{r}_n)$$

3N dimensions

10 - 1000 atoms

density functional theory (1964)

$$\rho(\mathbf{r}) \rightarrow \Phi_0(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n)$$

3 dimensions

100 - 10000 atoms

molecular mechanics force field (1970's)

forget about electrons!!!

low-dimensional functions & parameters

$$V^{\text{MM}}(R_1, R_2, \dots, R_N) = \sum_k v_k(R_i, R_j, R_k, R_l; \{p_k\})$$



Douglas  
Hartree



Vladimir  
Fock



John  
Slater



Walter  
Kohn



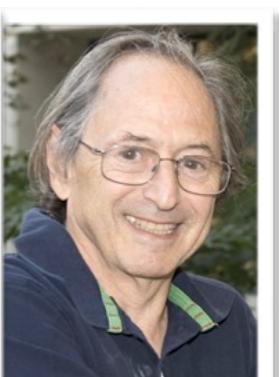
Pierre  
Hohenberg



Lu  
Sham



Martin  
Karplus



Michael  
Levitt



Arieh  
Warshel

# Molecular Mechanics Force Field

throw away the electrons!!!

low-dimensional functions

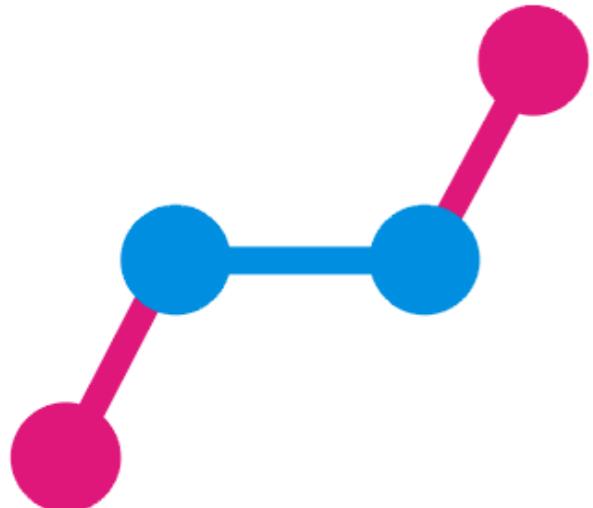
empirical parameters

experimental data & *ab initio* calculations

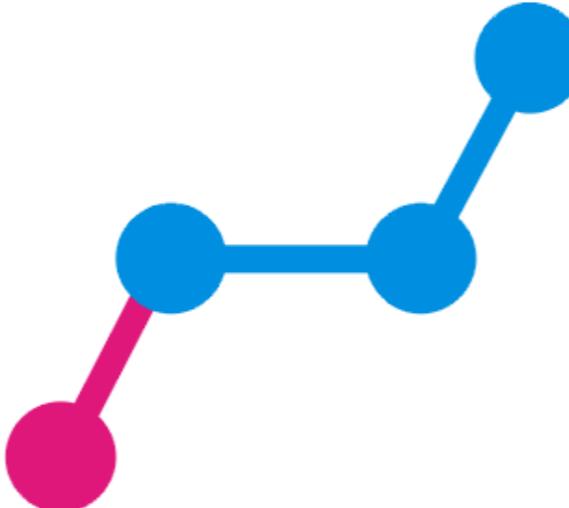
$$V^{\text{MM}}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = \sum_k v_k(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C, \mathbf{R}_D; \mathbf{p}_k)$$

covalent interactions

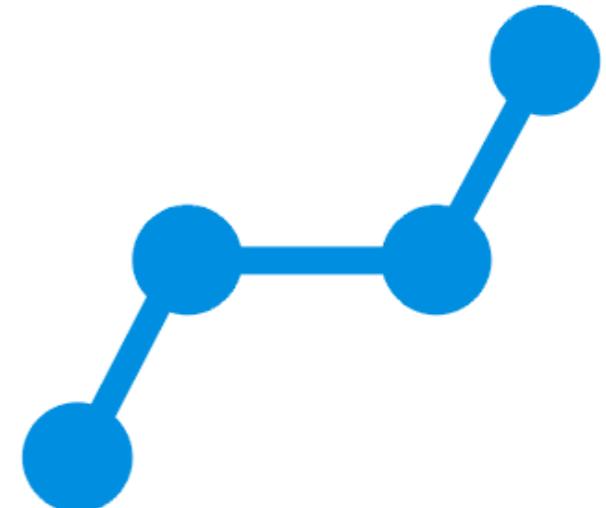
bond



angle



torsion



$$v_b(\mathbf{R}_A, \mathbf{R}_B) = \frac{1}{2} k_b (R_{AB} - r_0)^2 \quad v_a(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C) = \frac{1}{2} k_a (\theta_{ABC} - \theta_0)^2 \quad v_d(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C, \mathbf{R}_D) = \sum_n^5 k_n (\cos(\varphi_{ABCD}))^n$$

# Molecular Mechanics Force Field

throw away the electrons!!!

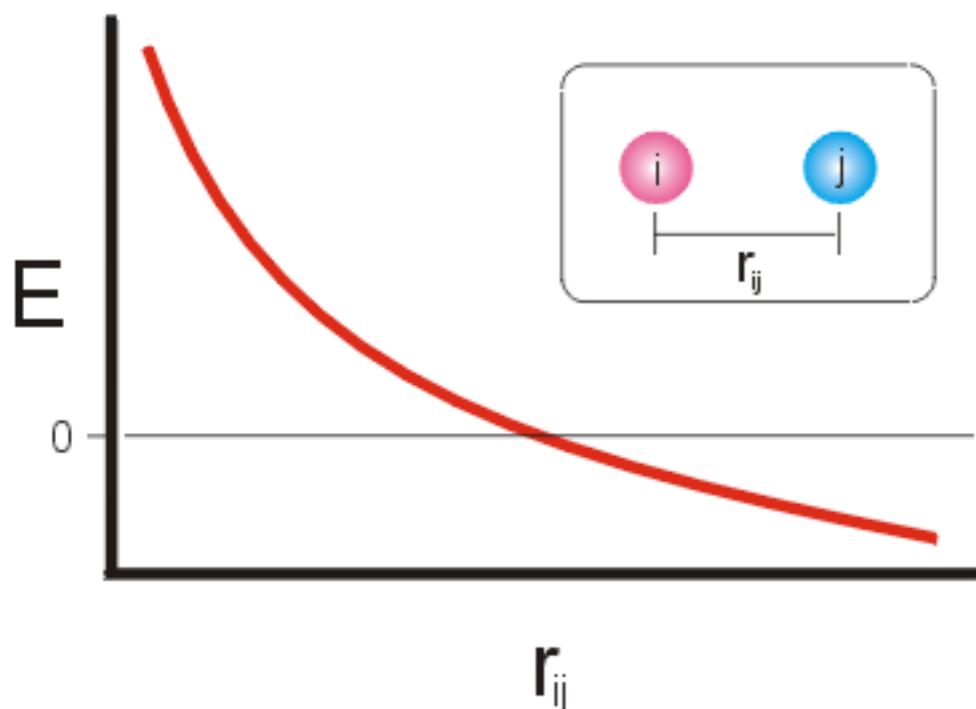
low-dimensional functions

empirical parameters

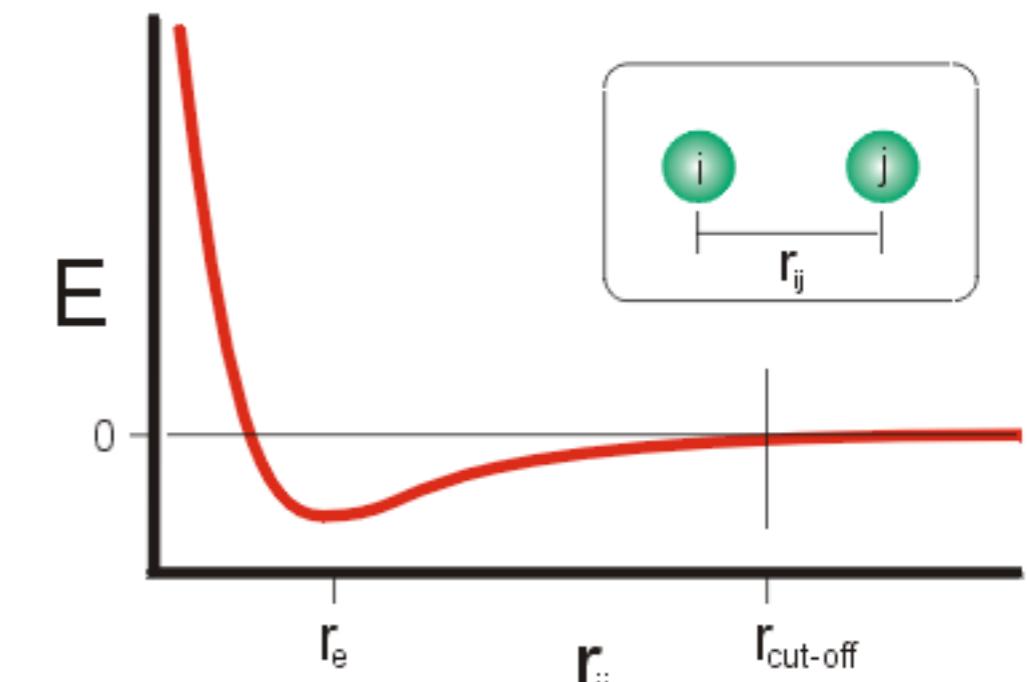
experimental data & *ab initio* calculations

$$V^{\text{MM}}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = \sum_k v_k(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C, \mathbf{R}_D; \mathbf{p}_k)$$

non-covalent interactions



$$v_{\text{Coul}}(\mathbf{R}_A, \mathbf{R}_B) = \frac{e^2 q_A q_B}{4\pi\epsilon_0 R_{AB}}$$

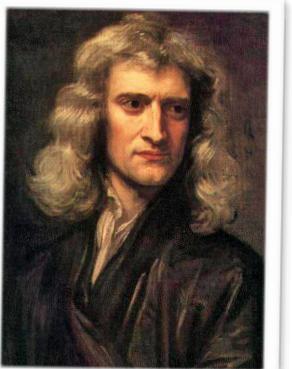


$$v_{\text{LJ}}(\mathbf{R}_A, \mathbf{R}_B) = \frac{C_{AB}^{(12)}}{R_{AB}^{12}} - \frac{C_{AB}^{(6)}}{R_{AB}^6}$$

# Molecular dynamics simulations

## classical nuclei

$$\mathbf{F}_i = -\nabla_{\mathbf{R}_i} V(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = m_i \frac{d^2}{dt^2} \mathbf{R}_i$$

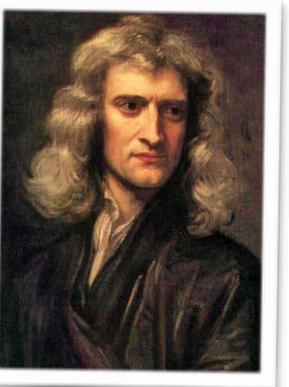


Isaac Newton

# Molecular dynamics simulations

classical nuclei

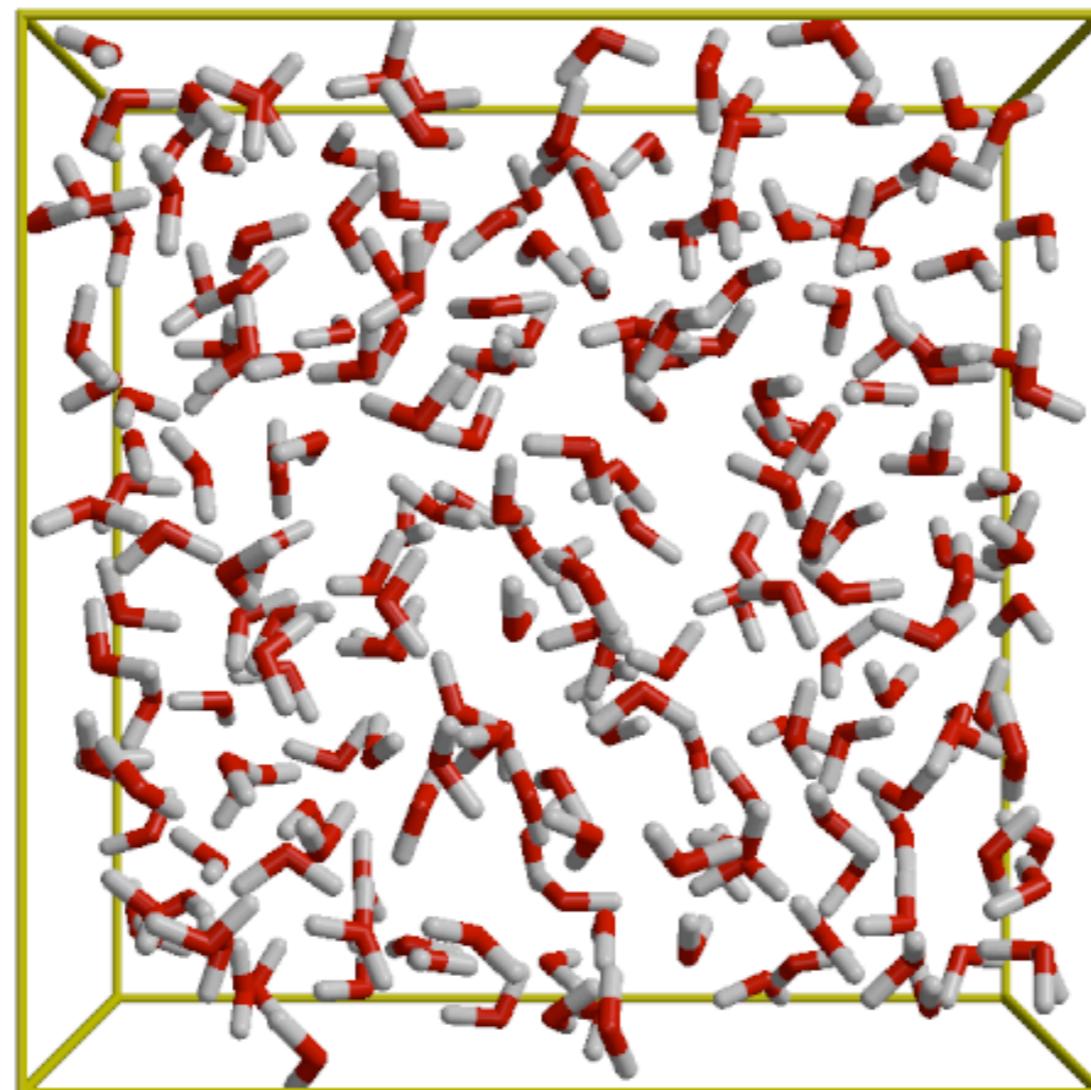
$$\mathbf{F}_i = -\nabla_{\mathbf{R}_i} V(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = m_i \frac{d^2}{dt^2} \mathbf{R}_i$$



Isaac Newton

trajectory

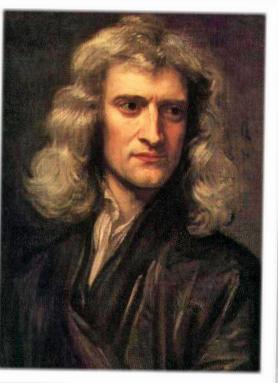
jiggling & wiggling



# Molecular dynamics simulations

classical nuclei

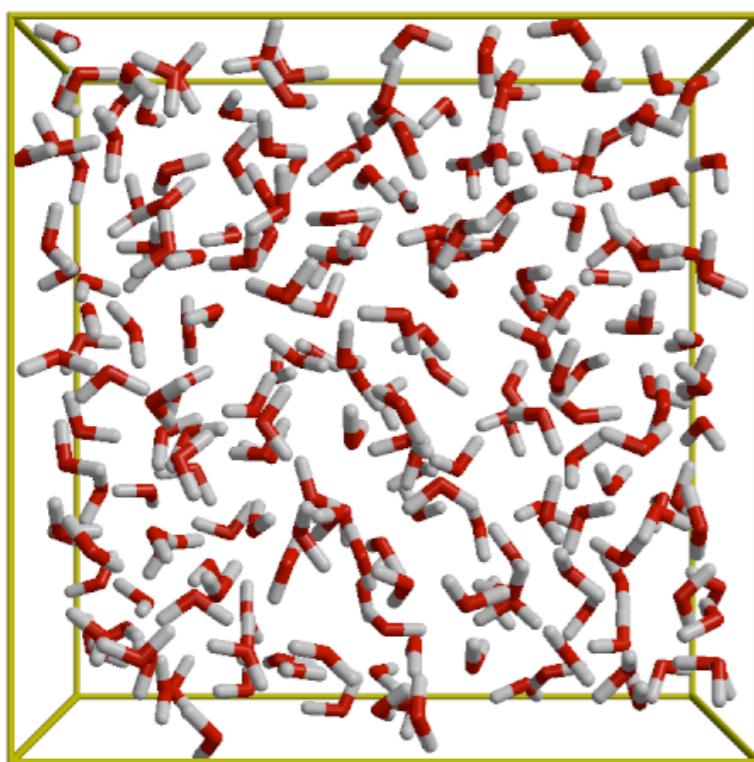
$$\mathbf{F}_i = -\nabla_{\mathbf{R}_i} V(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = m_i \frac{d^2}{dt^2} \mathbf{R}_i$$



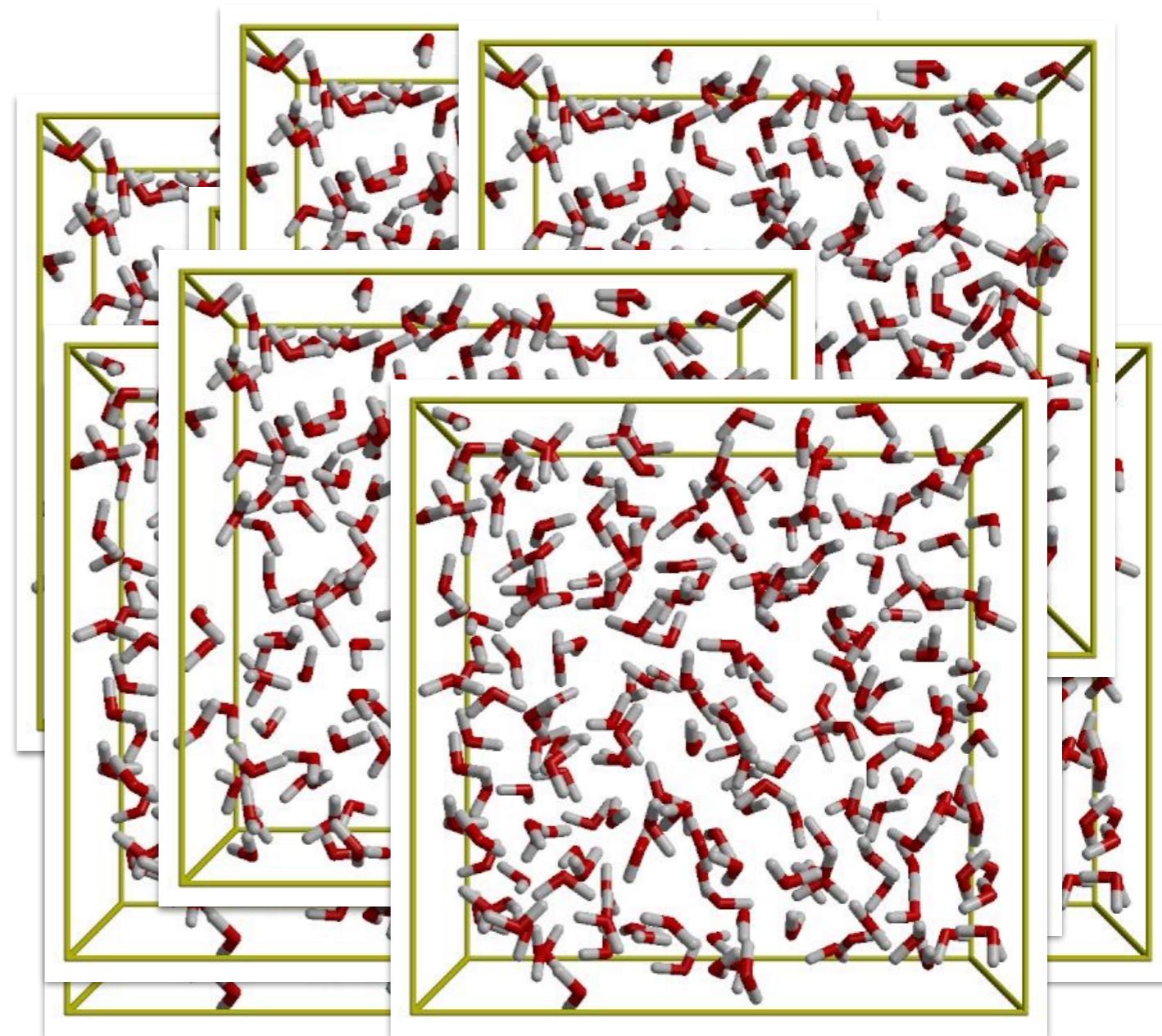
Isaac Newton

trajectory

ergodicity



=



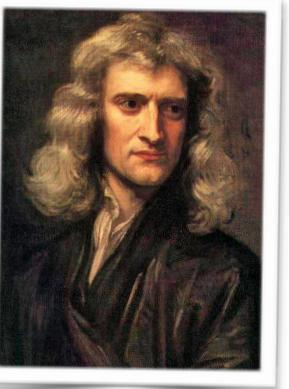
trajectory

ensemble

# Molecular dynamics simulations

classical nuclei

$$\mathbf{F}_i = -\nabla_{\mathbf{R}_i} V(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = m_i \frac{d^2}{dt^2} \mathbf{R}_i$$

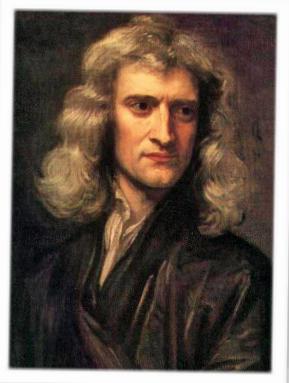


Isaac Newton

potential energy functions

# Molecular dynamics simulations

classical nuclei



Isaac Newton

$$\mathbf{F}_i = -\nabla_{\mathbf{R}_i} V(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = m_i \frac{d^2}{dt^2} \mathbf{R}_i$$

potential energy functions

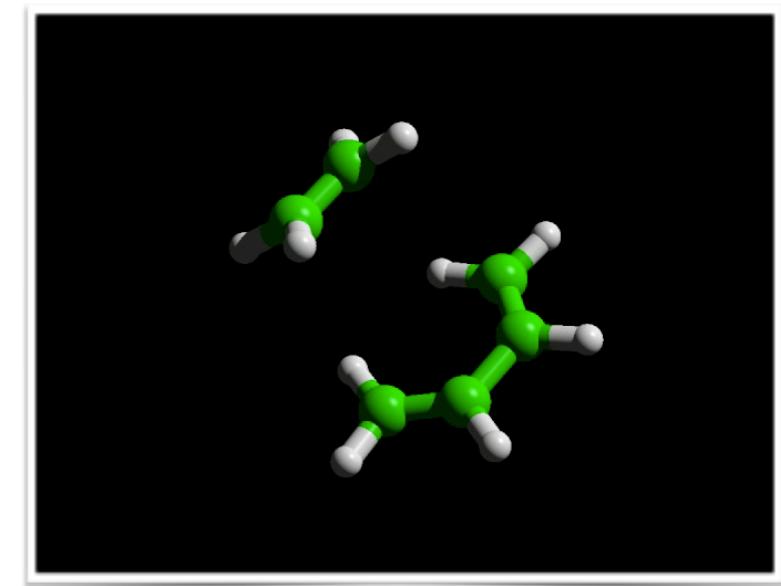
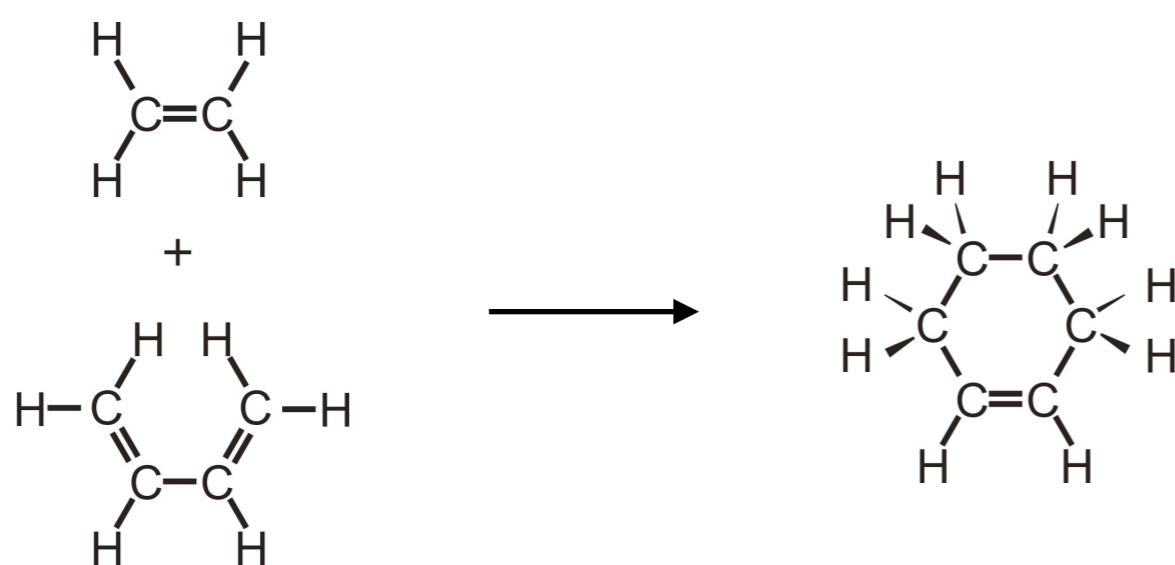


quantum chemistry (QM)

$$V^{\text{QM}}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) =$$

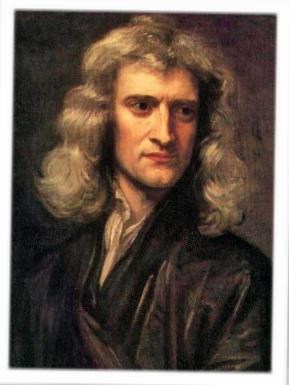
Erwin Schrödinger

$$\langle \Psi_e(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) | \hat{H}_e(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) | \Psi_e(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) \rangle$$



# Molecular dynamics simulations

classical nuclei



Isaac Newton

$$\mathbf{F}_i = -\nabla_{\mathbf{R}_i} V(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = m_i \frac{d^2}{dt^2} \mathbf{R}_i$$

potential energy functions



quantum chemistry (QM)

$$V^{\text{QM}}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) =$$

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$$\langle \Psi_e(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) | \hat{H}_e(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) | \Psi_e(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) \rangle$$

molecular mechanics (MM)

empirical functions with parameters

$$V^{\text{MM}}(R_1, R_2, \dots, R_N) = \sum_k v_k(R_i, R_j, R_k, R_l; \{p_k\})$$

# Molecular Mechanics Force Field

throw away the electrons!!!

low-dimensional functions

empirical parameters

experimental data & *ab initio* calculations

$$V^{\text{MM}}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = \sum_k v_k(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C, \mathbf{R}_D; \mathbf{p}_k)$$

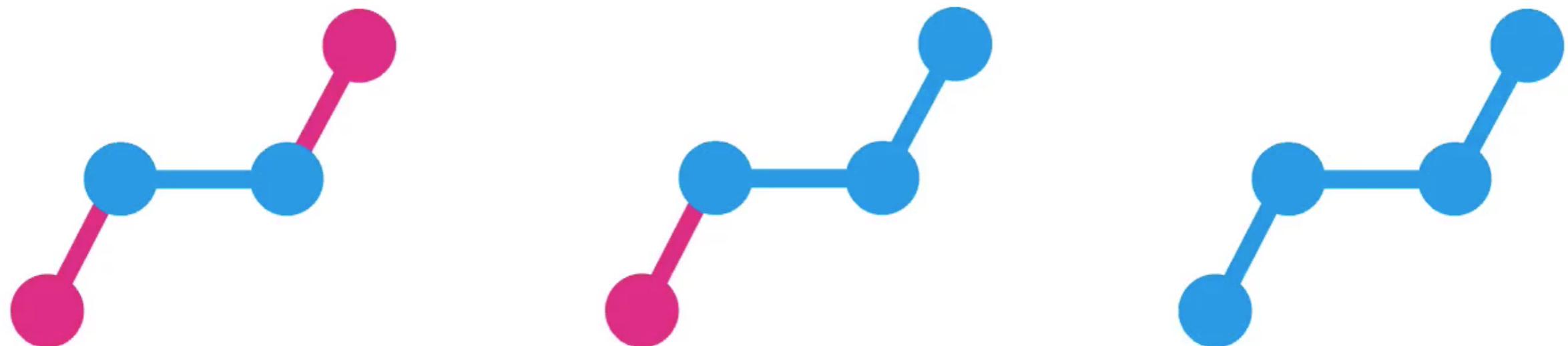
bonded interactions



Martin  
Karplus

Michael  
Levitt

Arieh  
Warshel



$$v_b(\mathbf{R}_A, \mathbf{R}_B) = \frac{1}{2} k_b (R_{AB} - r_0)^2 \quad v_a(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C) = \frac{1}{2} k_a (\theta_{ABC} - \theta_0)^2 \quad v_d(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C, \mathbf{R}_D) = \sum_n^5 k_n (\cos(\varphi_{ABCD}))^n$$

# Molecular Mechanics Force Field

throw away the electrons!!!

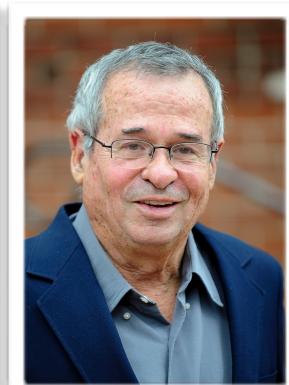
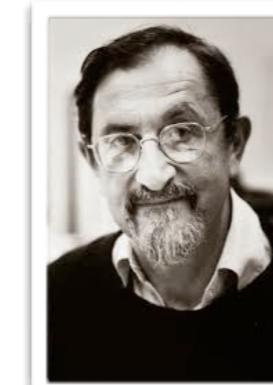
low-dimensional functions

empirical parameters

experimental data & *ab initio* calculations

$$V^{\text{MM}}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = \sum_k v_k(\mathbf{R}_A, \mathbf{R}_B, \mathbf{R}_C, \mathbf{R}_D; \mathbf{p}_k)$$

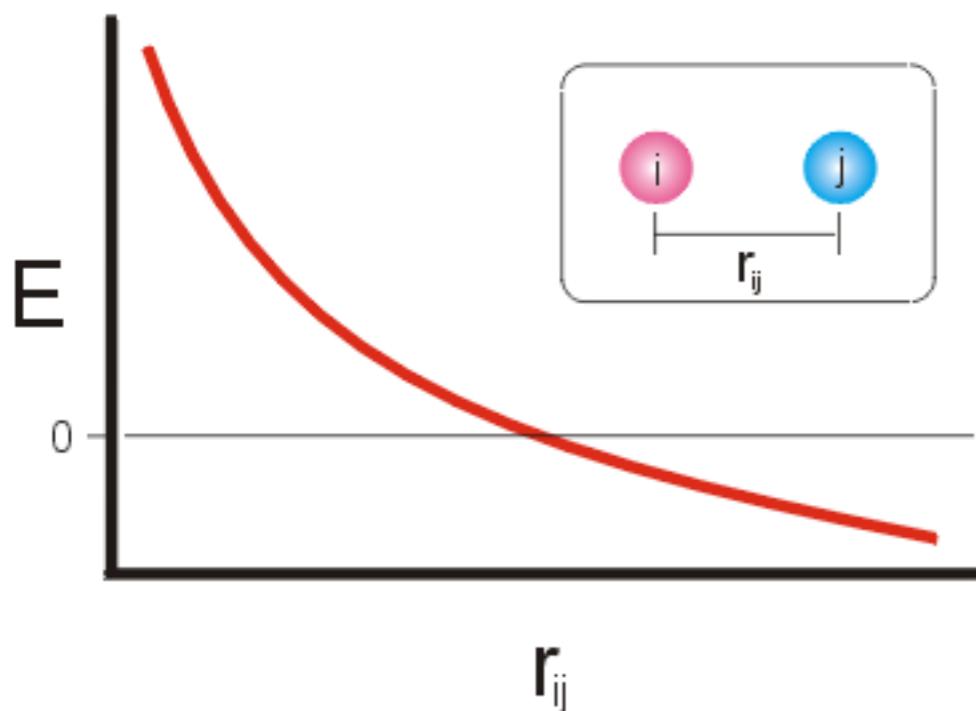
bonded interactions



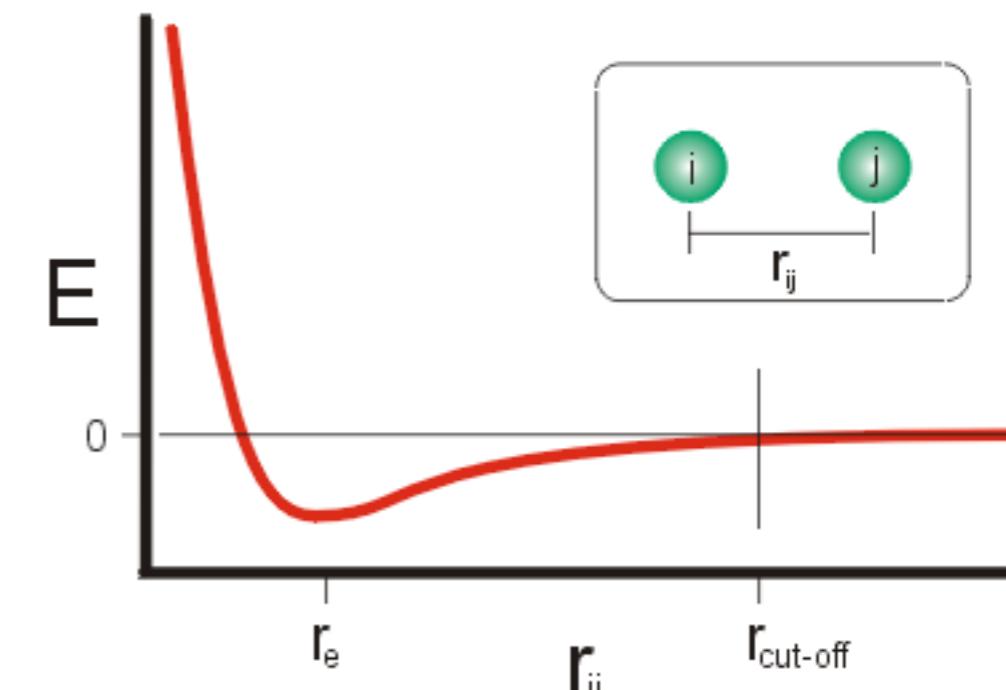
Martin  
Karplus

Michael  
Levitt

Arieh  
Warshel



$$v_{\text{Coul}}(\mathbf{R}_A, \mathbf{R}_B) = \frac{e^2 q_A q_B}{4\pi\epsilon_0 R_{AB}}$$

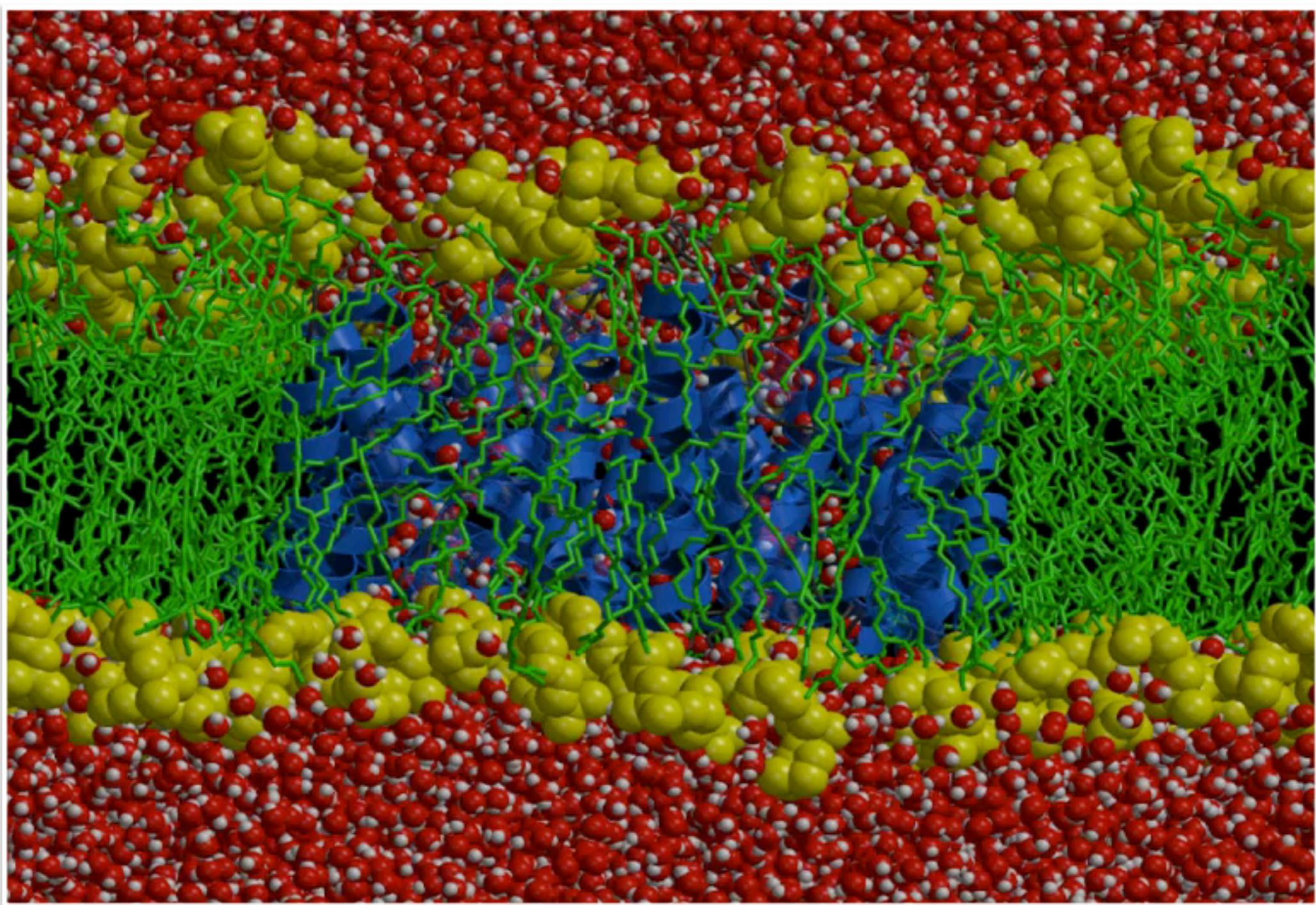


$$v_{\text{LJ}}(\mathbf{R}_A, \mathbf{R}_B) = \frac{C_{AB}^{(12)}}{R_{AB}^{12}} - \frac{C_{AB}^{(6)}}{R_{AB}^6}$$

# Chemistry without test-tubes

observe jiggling and wiggling

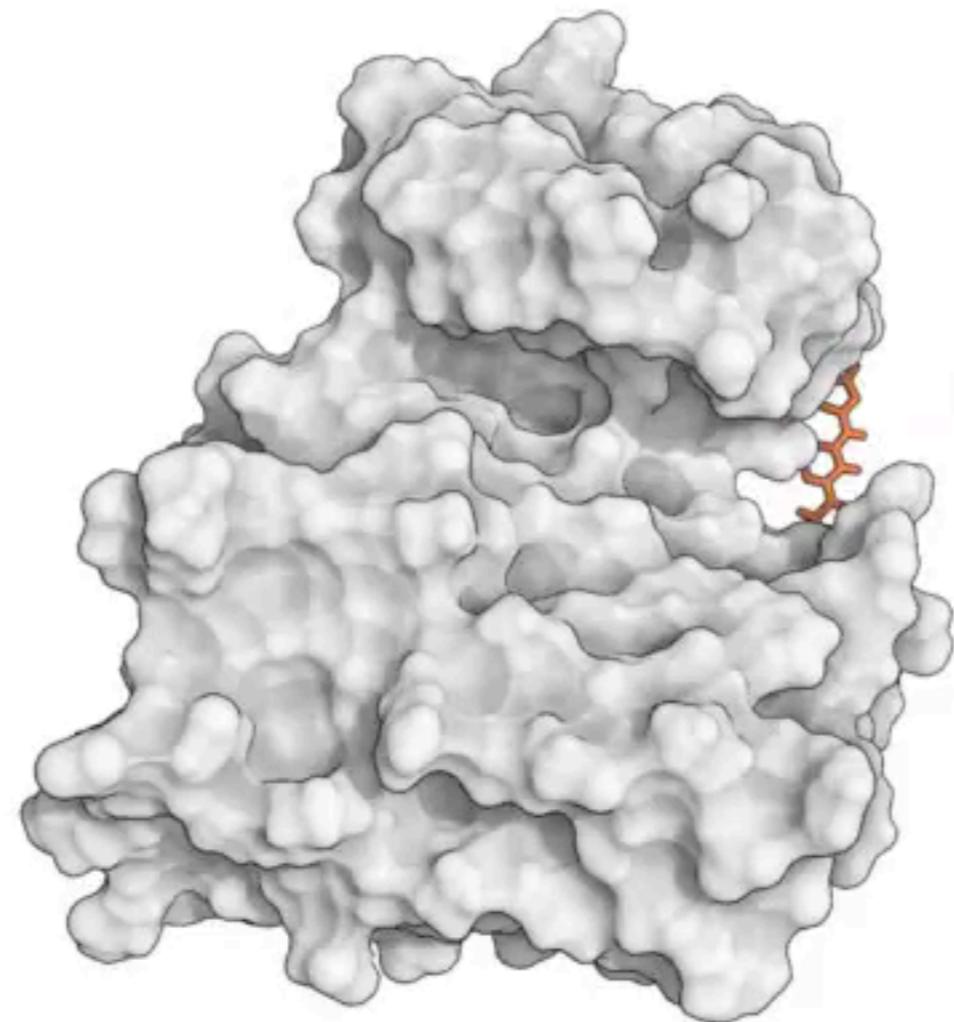
MD simulation of aqua-porin water channel



# Chemistry without test-tubes

how drugs bind their targets

all-atom simulations of 2.3  $\mu$ s (in total 35  $\mu$ s)

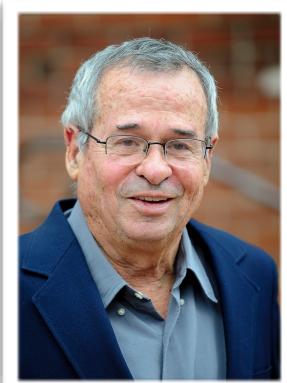


# Chemistry without test-tubes

hybrid quantum mechanics /molecular mechanics

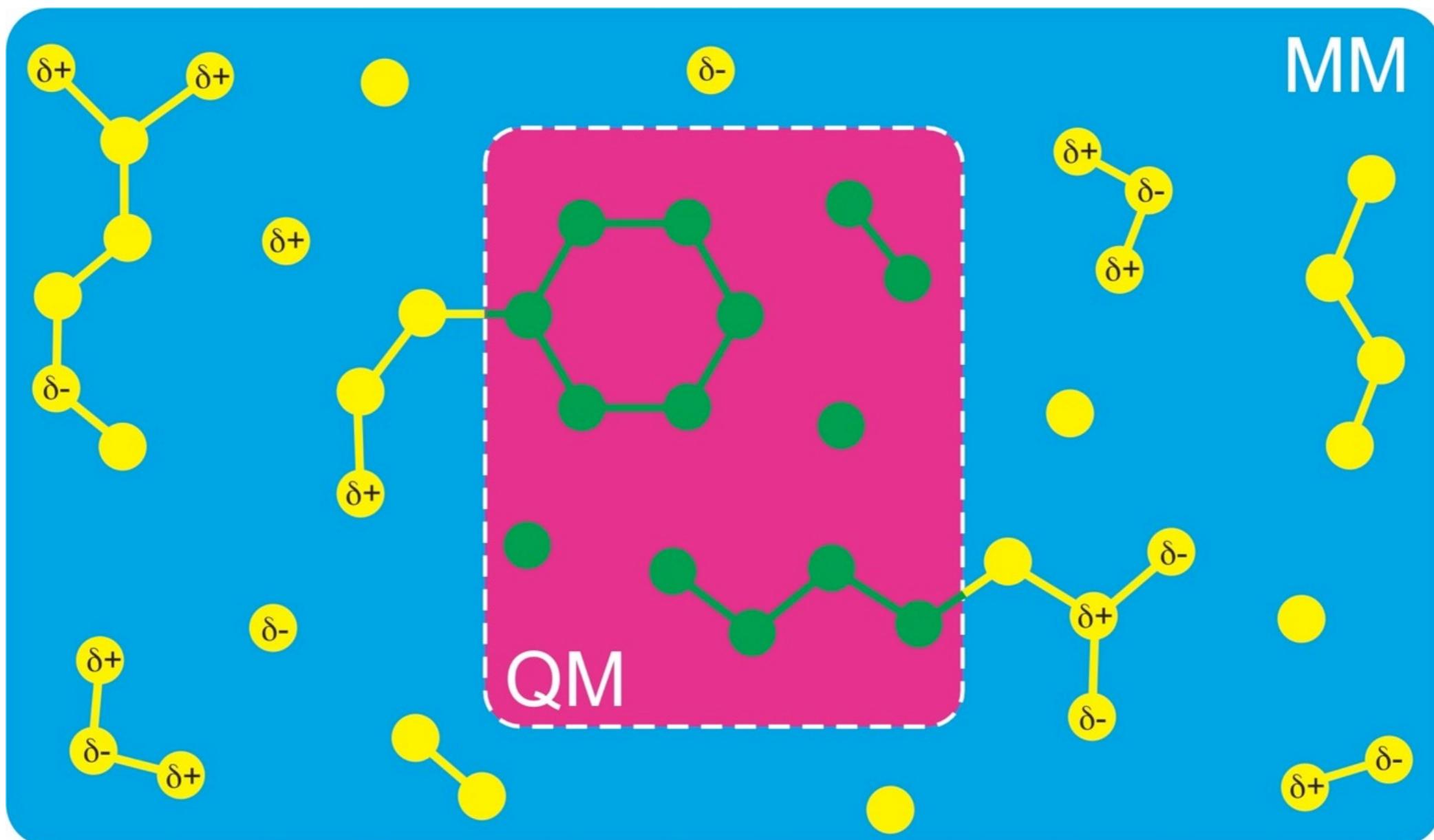
active site: quantum mechanics for electrons

rest: molecular mechanics force field



Michael  
Levitt

Arieh  
Warshel



# Chemistry without test-tubes

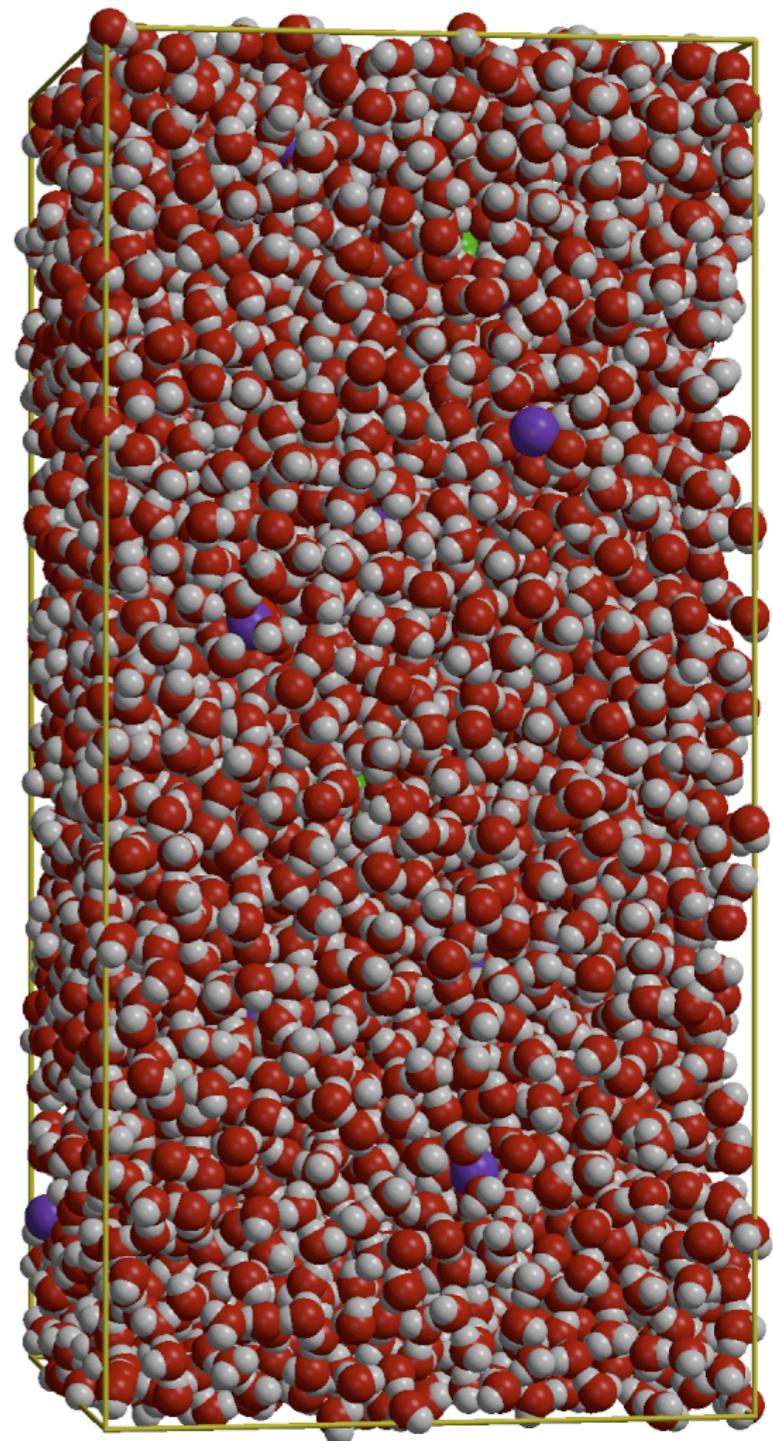
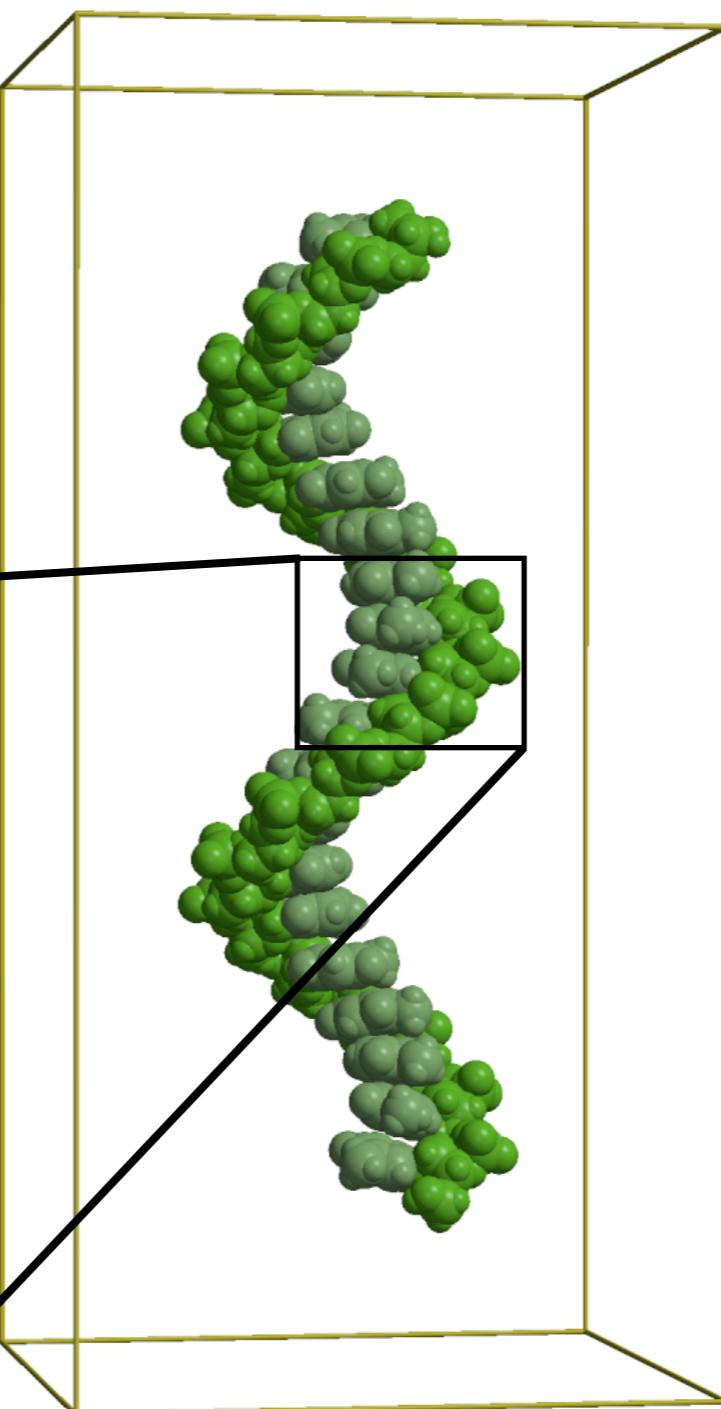
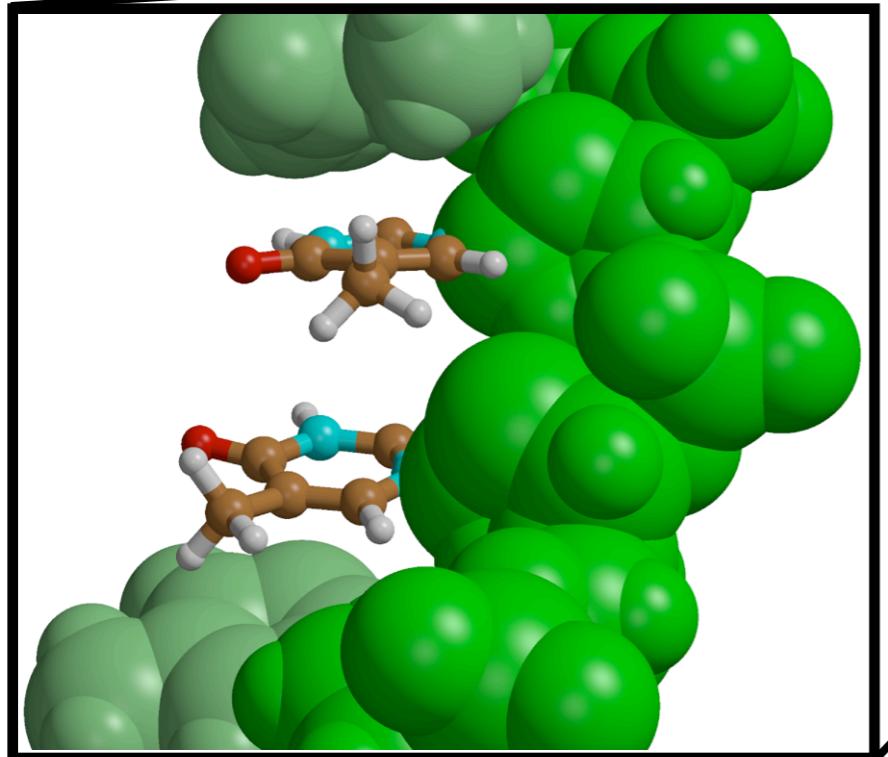
example: radiation damage in DNA

thymine dimerization

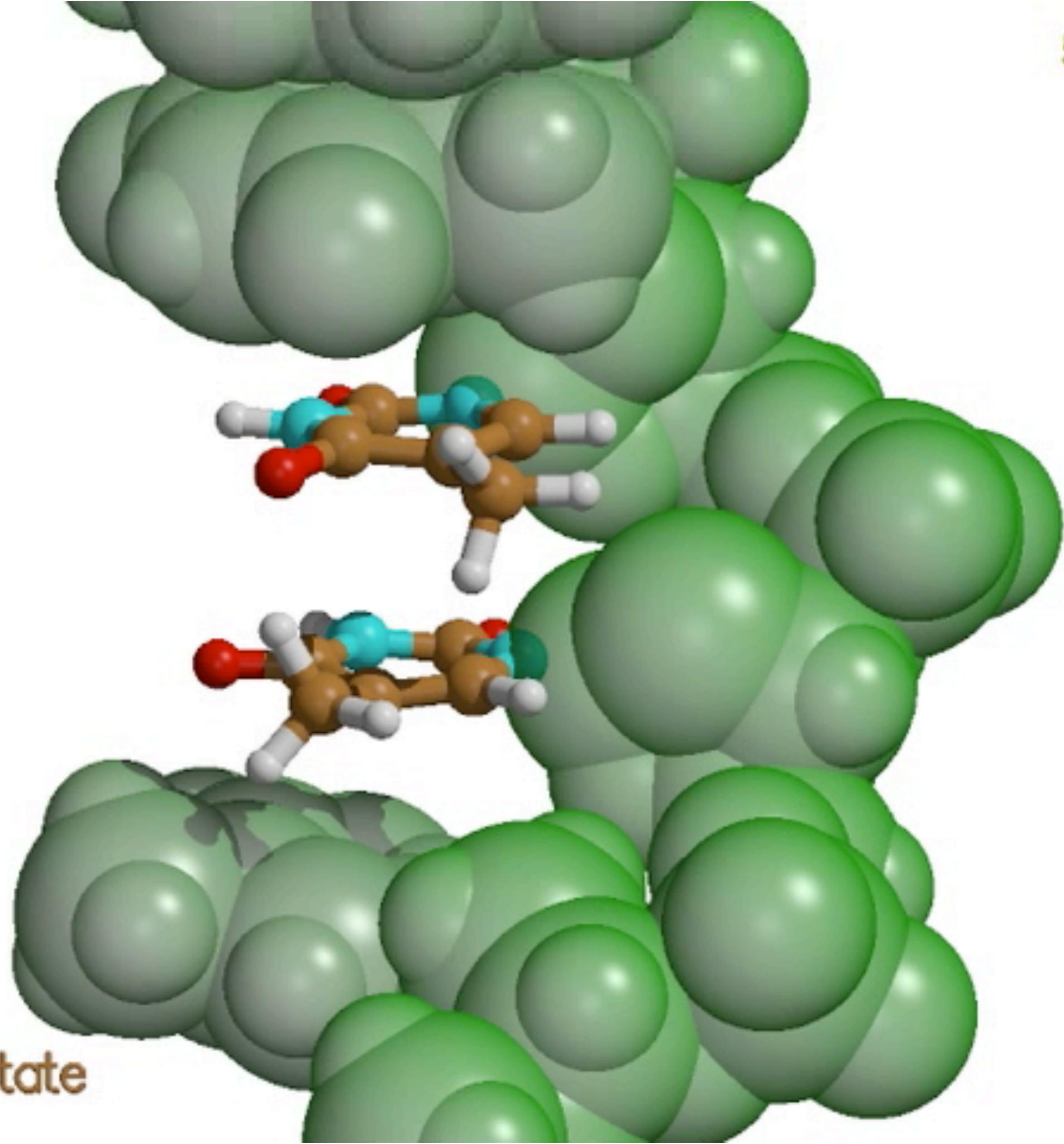
base stack (TT)

CASSCF(8,8)/6-31G

diabatic surface hop



50 fs

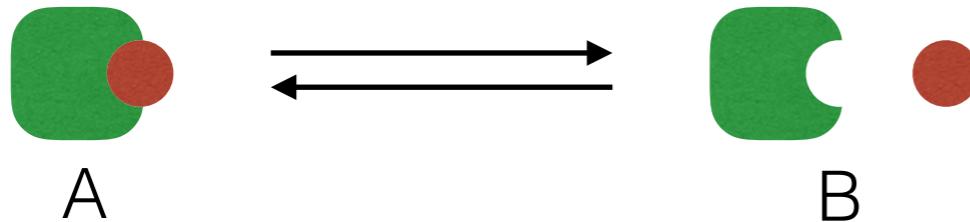


ground-state

# Chemistry without test-tubes

calculating free energies in MD simulations

e.g. binding



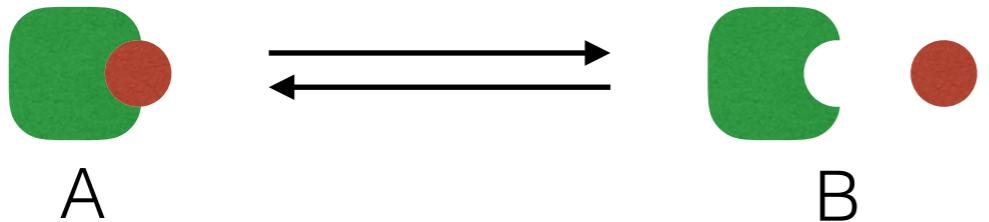
$$G_A = -kT \ln Z_A \quad G_B = -kT \ln Z_B$$

$$\Delta G = G_B - G_A = -kT \ln Z_B/Z_A$$

# Chemistry without test-tubes

calculating free energies in MD simulations

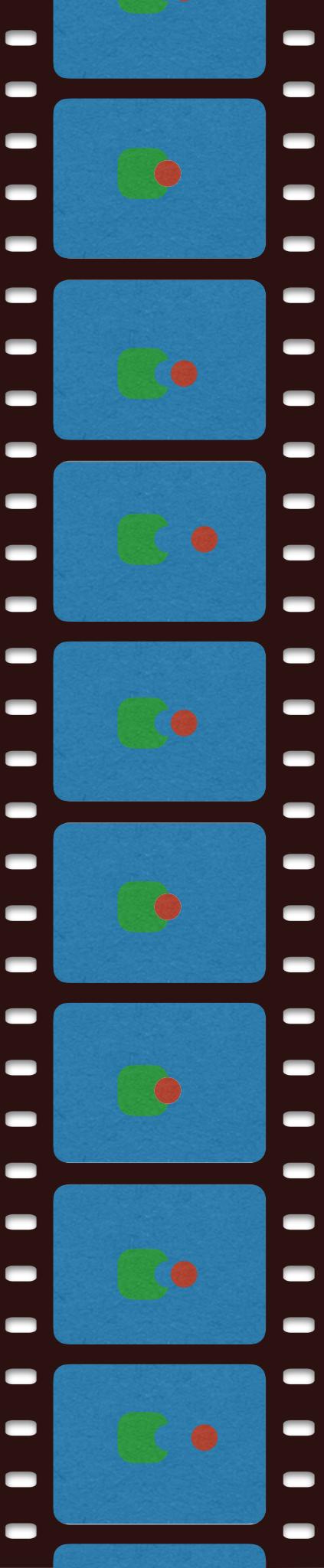
e.g. binding



$$G_A = -kT \ln Z_A$$

$$G_B = -kT \ln Z_B$$

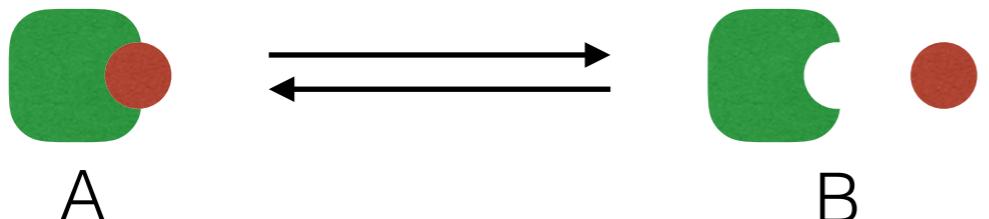
$$\Delta G = G_B - G_A = -kT \ln Z_B/Z_A$$



# Chemistry without test-tubes

calculating free energies in MD simulations

e.g. binding



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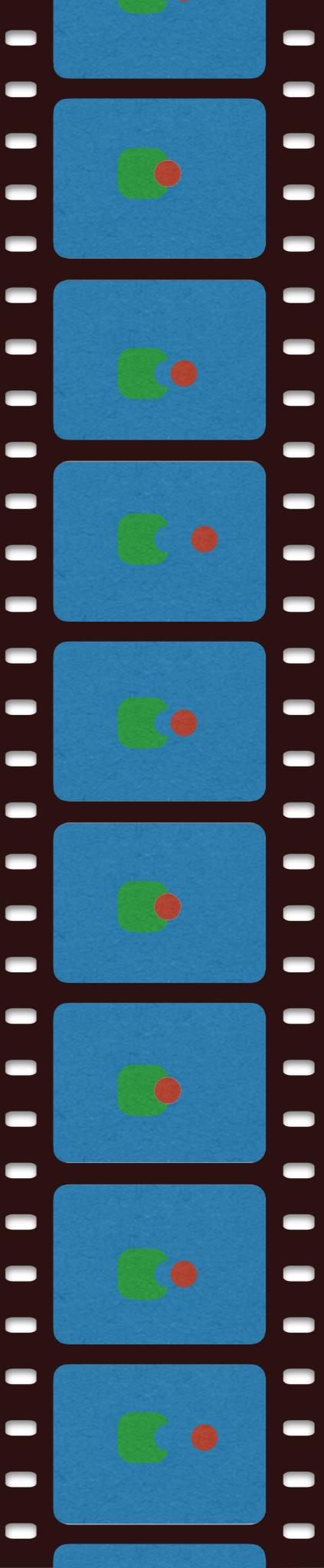
$$G_B = -kT \ln Z_B$$

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most naive approach: counting

ergodicity: time average same as ensemble average

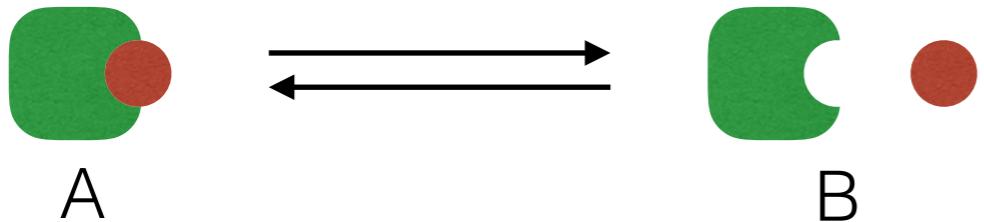
sort frames of a trajectory and compute probabilities



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calculating free energies in MD simulations

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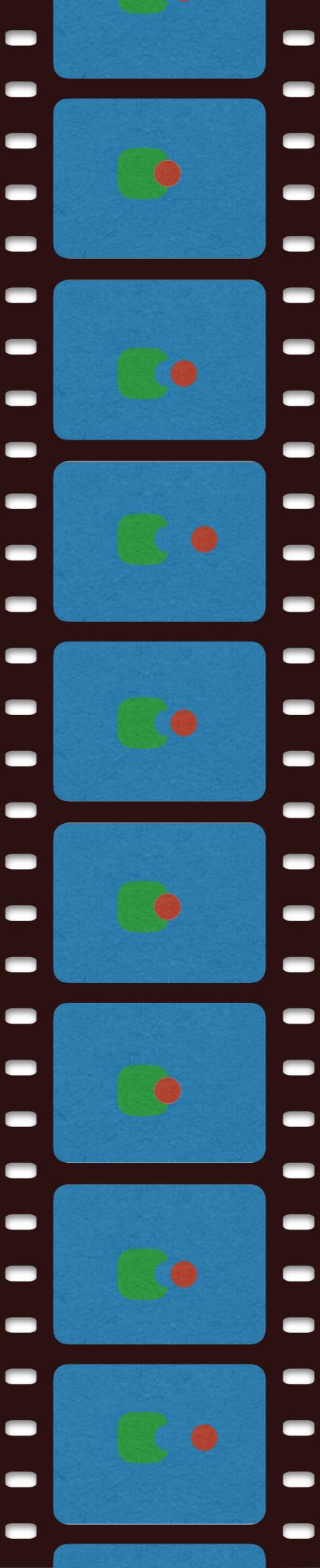
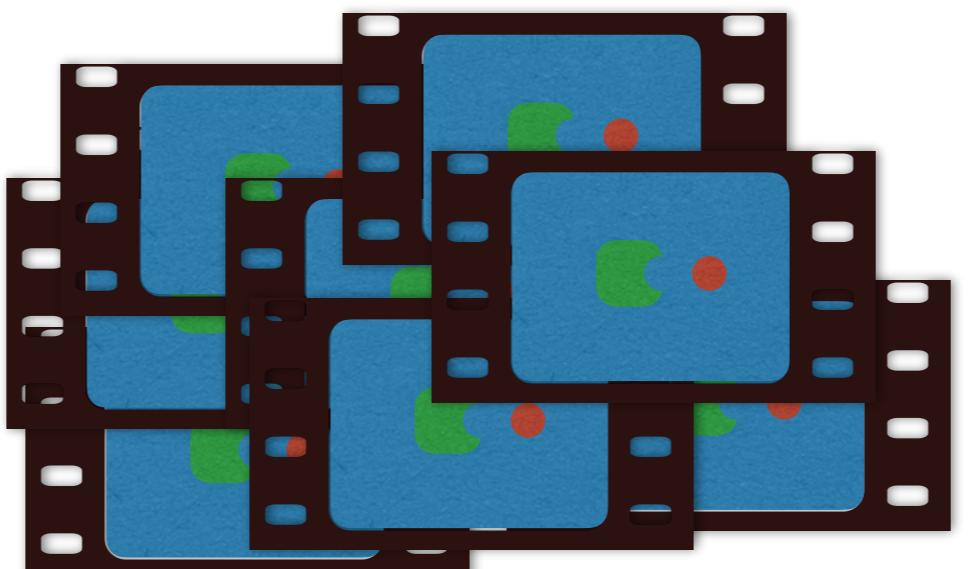
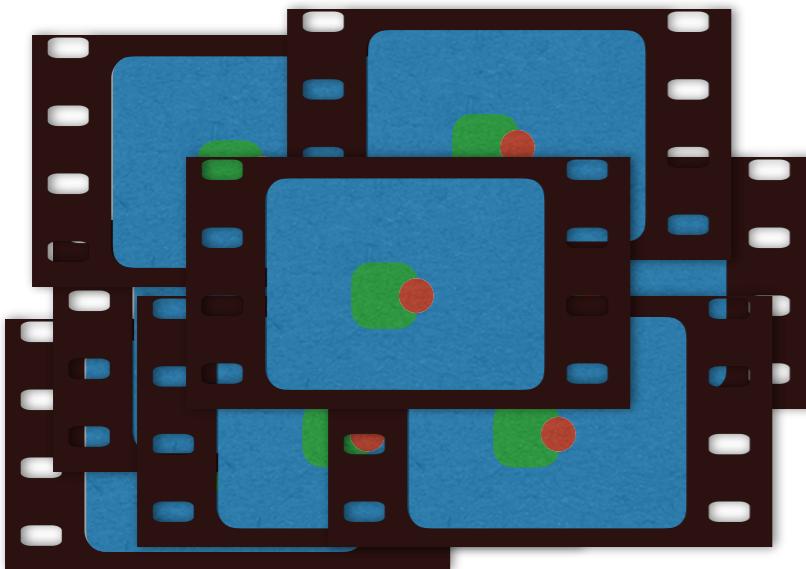
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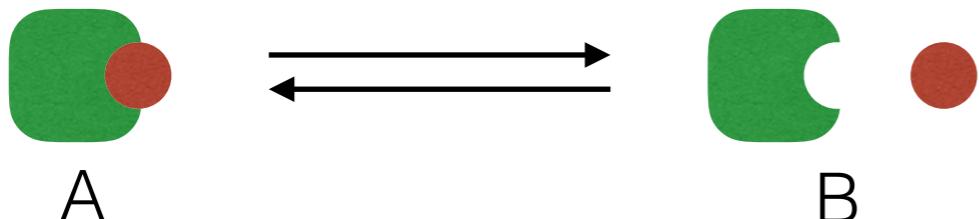
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calculating free energies in MD simulations

e.g. binding



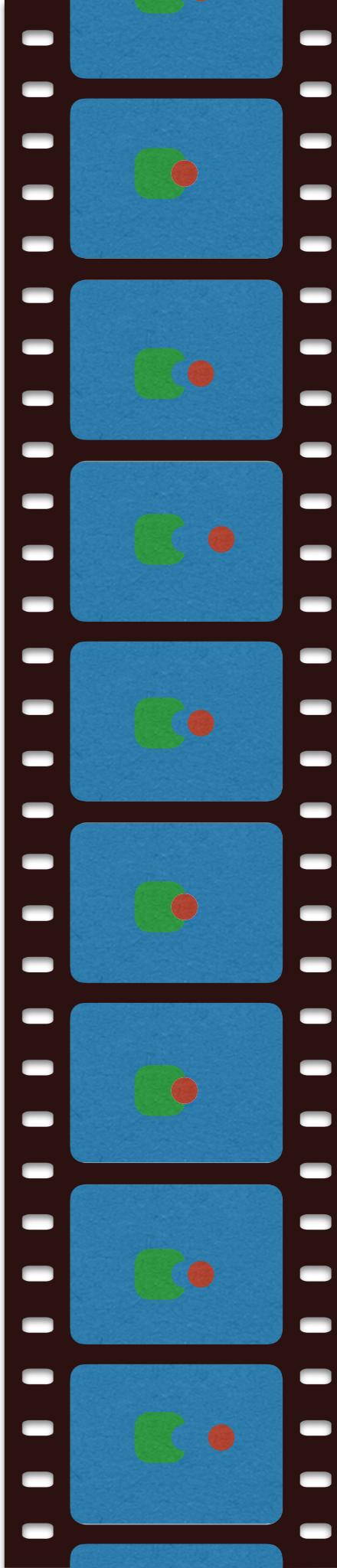
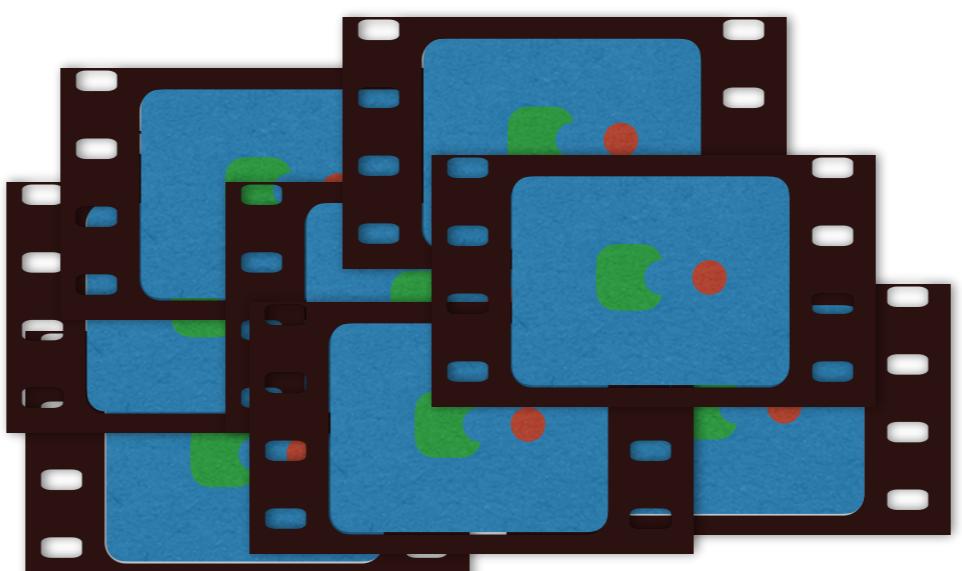
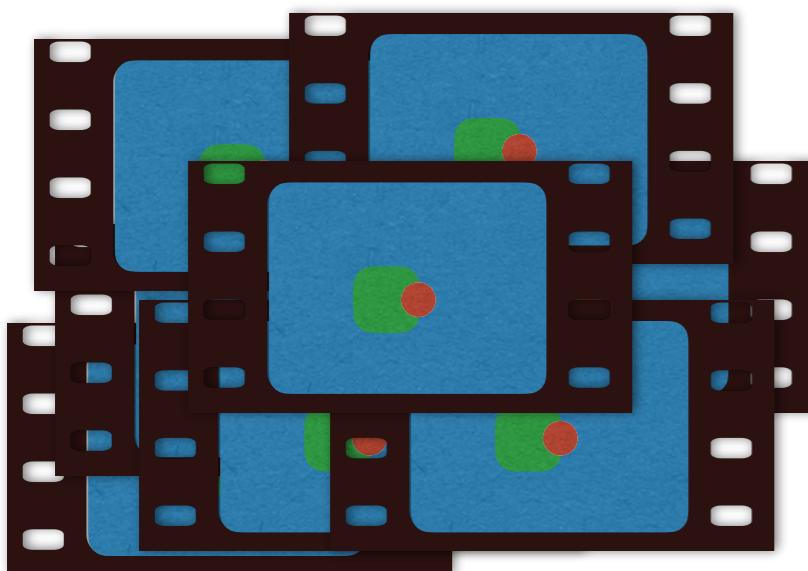
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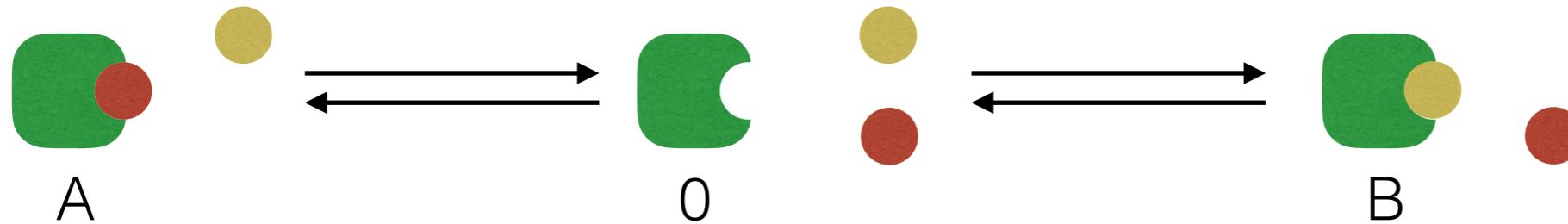


$$\frac{Z_B}{Z_A} = \frac{\sum_{i \in B} e^{-\beta E_i}}{\sum_{i \in A} e^{-\beta E_i}} = \frac{\sum_{i \in B} p_i}{\sum_{i \in A} p_i} = \frac{N_B^{\text{snapshot}}}{N_A^{\text{snapshot}}}$$

# Chemistry without test-tubes

calculating free energy differences in MD simulations

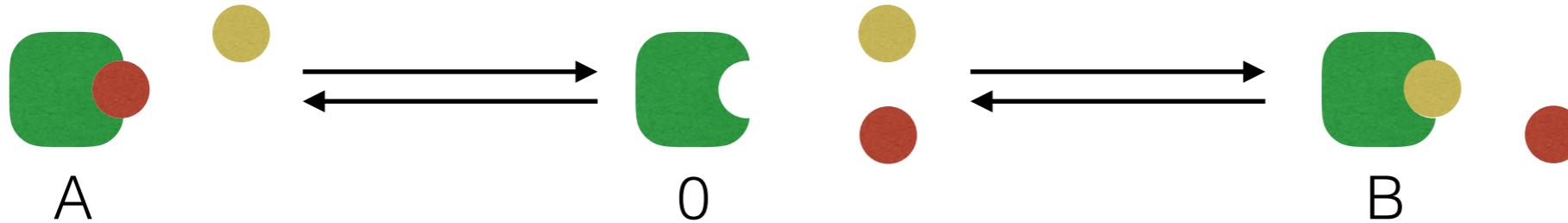
e.g. competitive binding



# Chemistry without test-tubes

calculating free energy differences in MD simulations

e.g. competitive binding



$$G_A = -kT \ln Z_A$$

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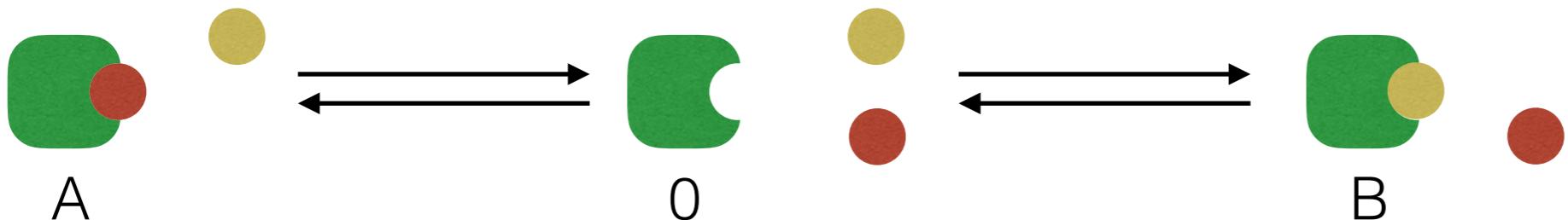
$$G_B = -kT \ln Z_B$$

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# Chemistry without test-tubes

calculating free energy differences in MD simulations

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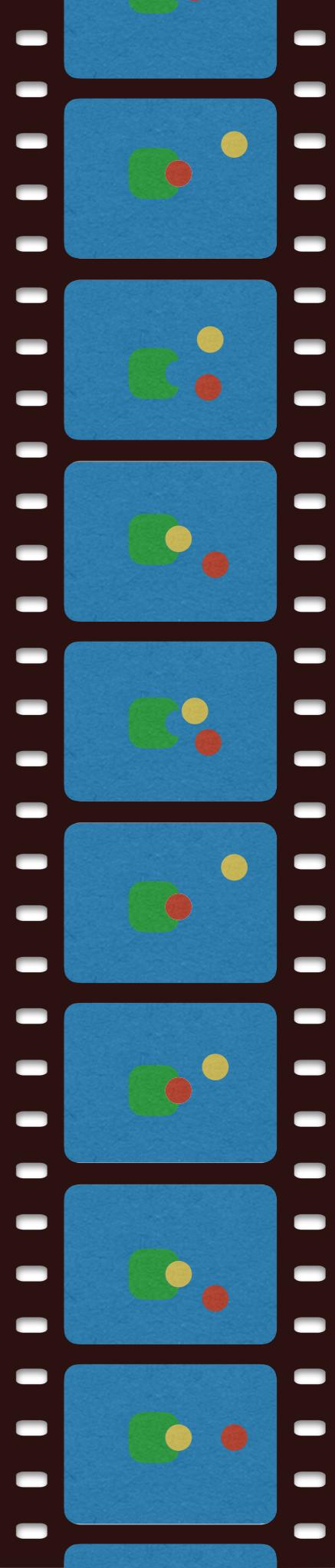
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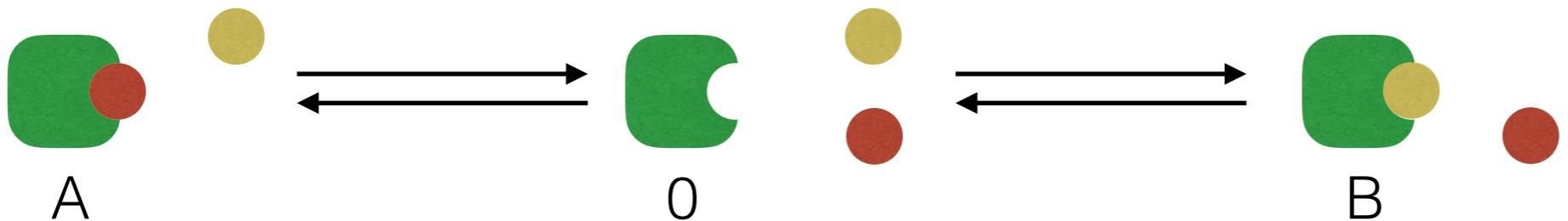
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calculating free energy differences in MD simulations

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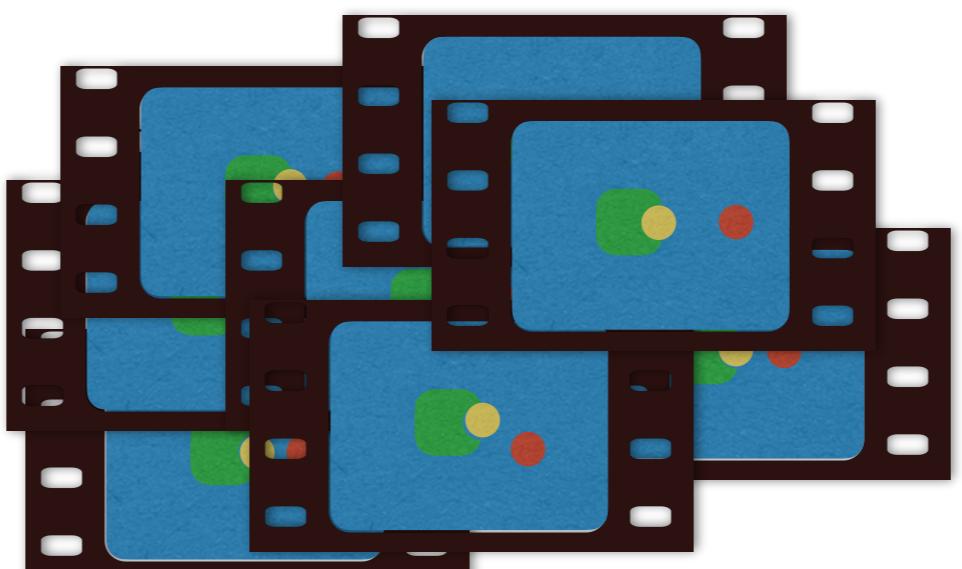
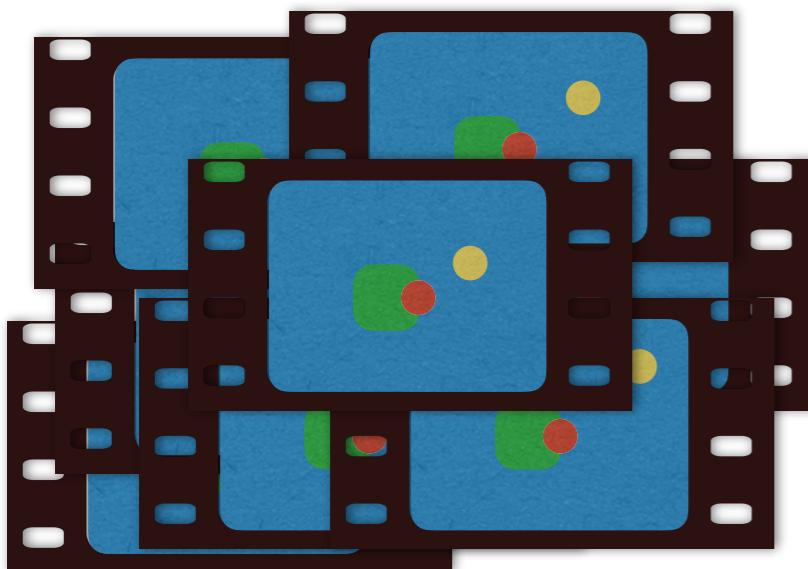
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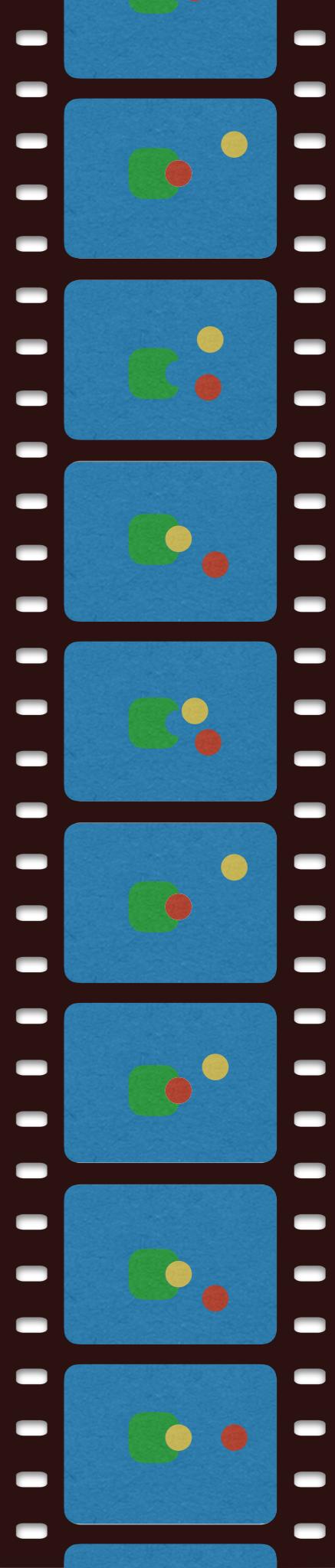
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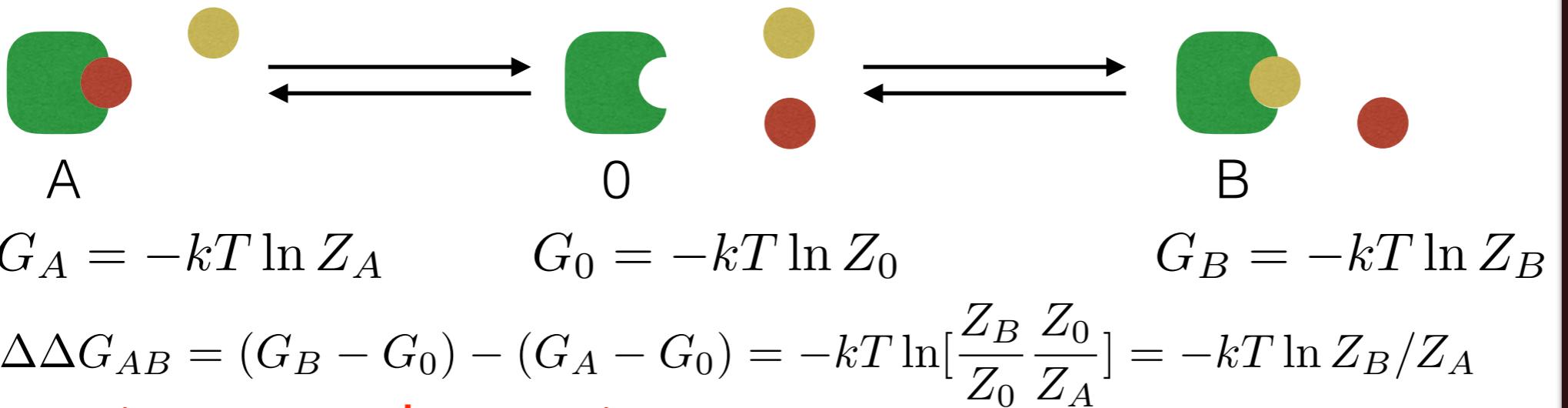
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# Chemistry without test-tubes

# calculating free energy differences

e.g. competitive binding



# most naive approach: counting

ergodicity: time average same as ensemble average

**sort frames of a trajectory and compute probabilities**

# converged MD ensemble?

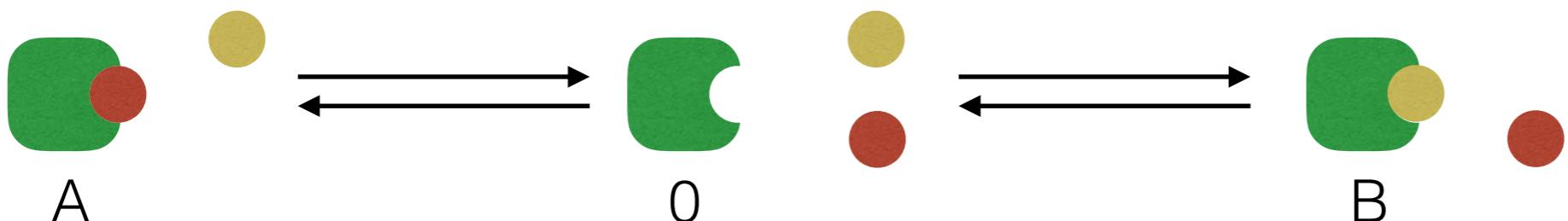
# sufficiently long trajectory

**very difficult in practice**

# Chemistry without test-tubes

calculating free energy differences

e.g. competitive binding



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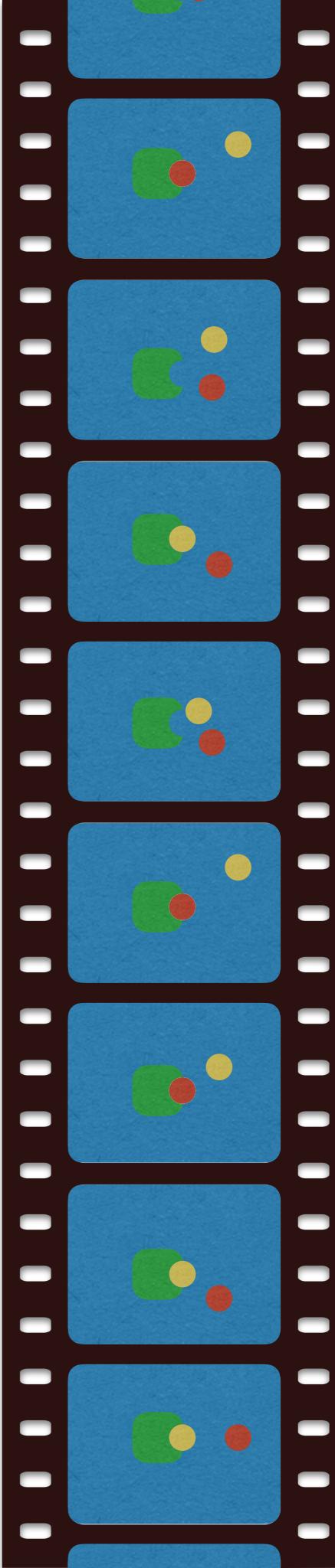
converged MD ensemble?

sufficiently long trajectory

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alternative approaches

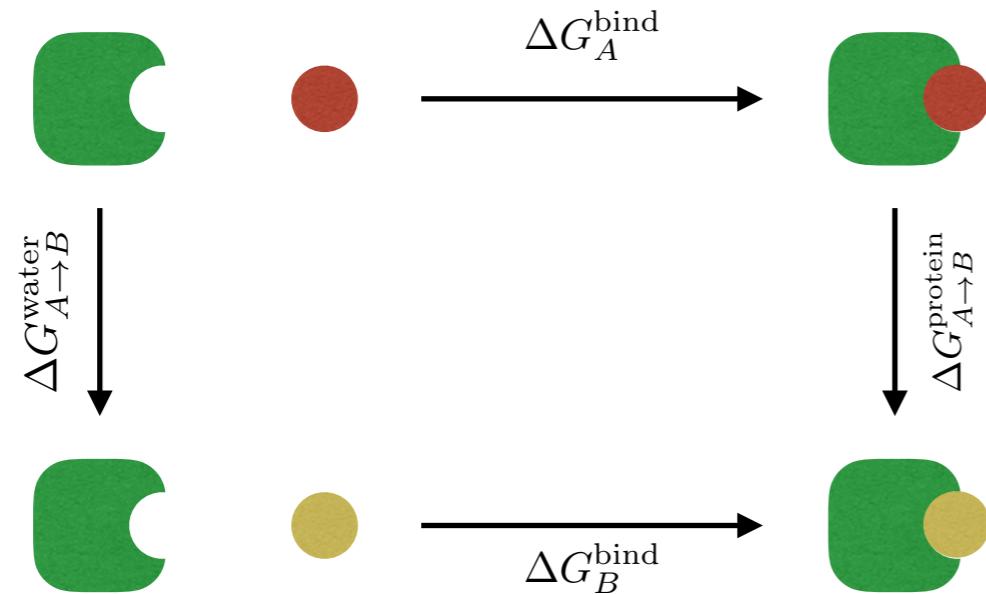
thermodynamic integration



# Thermodynamic integration

calculating free energy differences

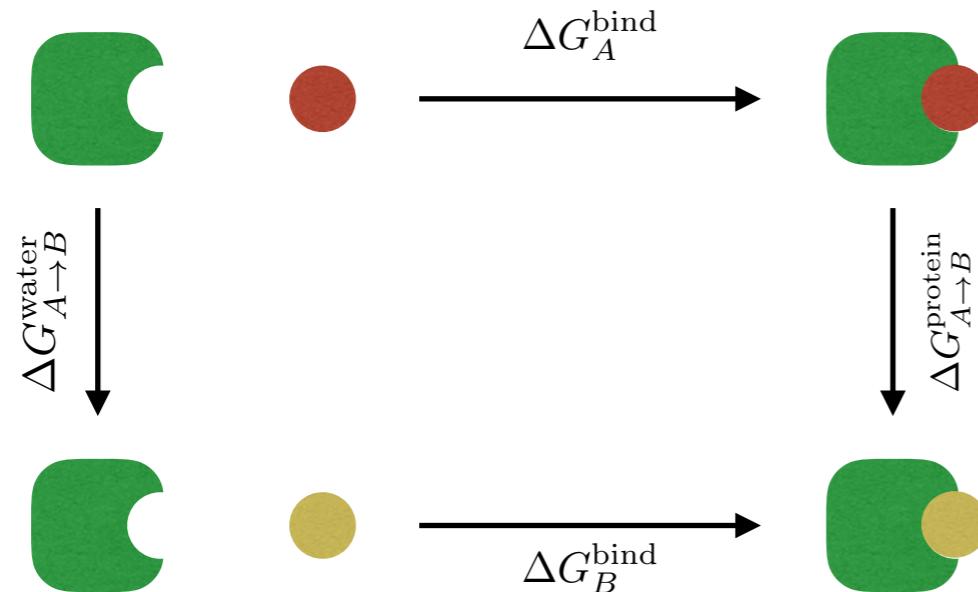
thermodynamic cycle



# Thermodynamic integration

calculating free energy differences

thermodynamic cycle



$$\begin{aligned}\Delta\Delta G_{AB}^{\text{bind}} &= \Delta G_B^{\text{bind}} - \Delta G_A^{\text{bind}} \\ &= \Delta G_{A \rightarrow B}^{\text{protein}} - \Delta G_{A \rightarrow B}^{\text{water}}\end{aligned}$$

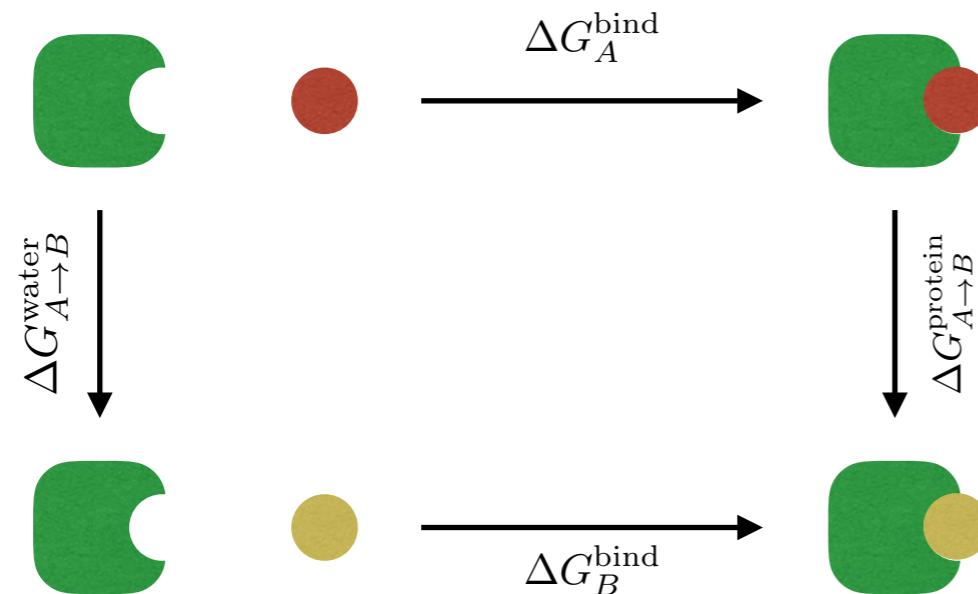
free energy is a state function: independent of path

$$\Delta G_A^{\text{bind}} + \Delta G_{A \rightarrow B}^{\text{protein}} = \Delta G_{A \rightarrow B}^{\text{water}} + \Delta G_B^{\text{bind}}$$

# Thermodynamic integration

calculating free energy differences

thermodynamic cycle



$$\begin{aligned}\Delta\Delta G_{AB}^{\text{bind}} &= \Delta G_B^{\text{bind}} - \Delta G_A^{\text{bind}} \\ &= \Delta G_{A \rightarrow B}^{\text{protein}} - \Delta G_{A \rightarrow B}^{\text{water}}\end{aligned}$$

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difficult to evaluate with MD simulations

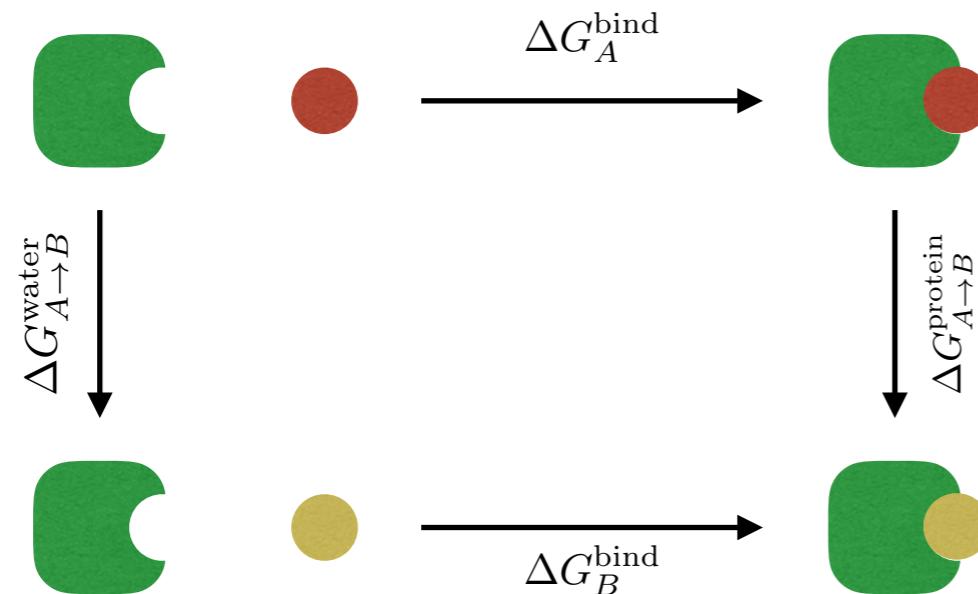
$$\Delta G_A^{\text{bind}}$$

$$\Delta G_B^{\text{bind}}$$

# Thermodynamic integration

calculating free energy differences

thermodynamic cycle



$$\begin{aligned}\Delta\Delta G_{AB}^{\text{bind}} &= \Delta G_B^{\text{bind}} - \Delta G_A^{\text{bind}} \\ &= \Delta G_{A \rightarrow B}^{\text{protein}} - \Delta G_{A \rightarrow B}^{\text{water}}\end{aligned}$$

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difficult to evaluate with MD simulations

$$\Delta G_A^{\text{bind}}$$

$$\Delta G_B^{\text{bind}}$$

'easy' (sometimes) to evaluate with MD simulations

$$\Delta G_{A \rightarrow B}^{\text{water}}$$

$$\Delta G_{A \rightarrow B}^{\text{protein}}$$

# Thermodynamic integration

why ‘easy’?

interpolate the energy function

*in silico* everything is possible



# Thermodynamic integration

why ‘easy’?

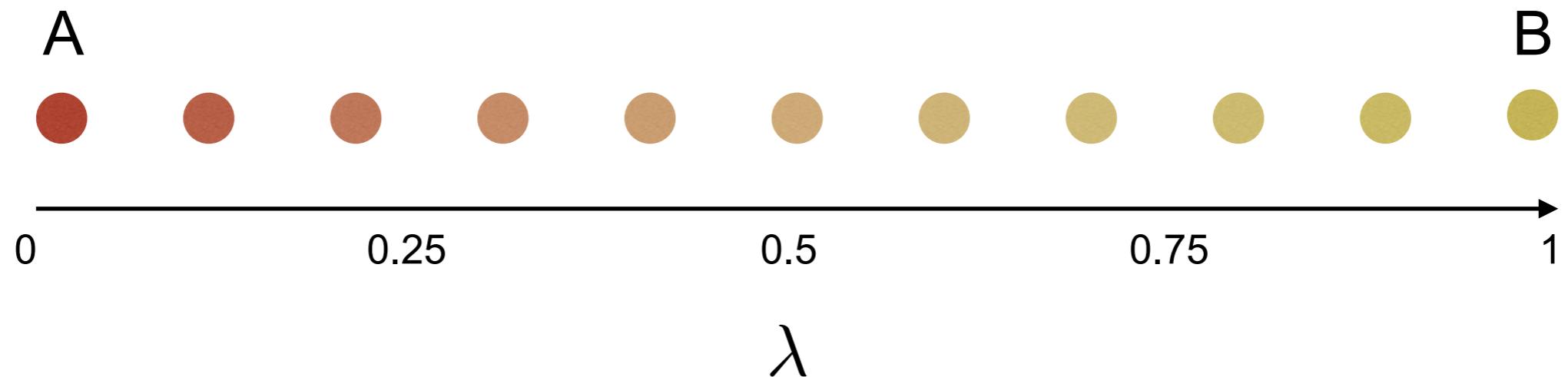
interpolate the energy function

*in silico* everything is possible

$$E^A(\mathbf{p}_1, \mathbf{p}_2, \dots, \mathbf{r}_1, \mathbf{r}_2)$$

$$E^B(\mathbf{p}_1, \mathbf{p}_2, \dots, \mathbf{r}_1, \mathbf{r}_2)$$

$$E(\lambda, \mathbf{p}_1, \mathbf{p}_2, \dots, \mathbf{r}_1, \mathbf{r}_2) = (1 - \lambda)E^A(\mathbf{p}_1, \mathbf{p}_2, \dots, \mathbf{r}_1, \mathbf{r}_2) + \lambda E^B(\mathbf{p}_1, \mathbf{p}_2, \dots, \mathbf{r}_1, \mathbf{r}_2)$$



# Thermodynamic integration

why ‘easy’?

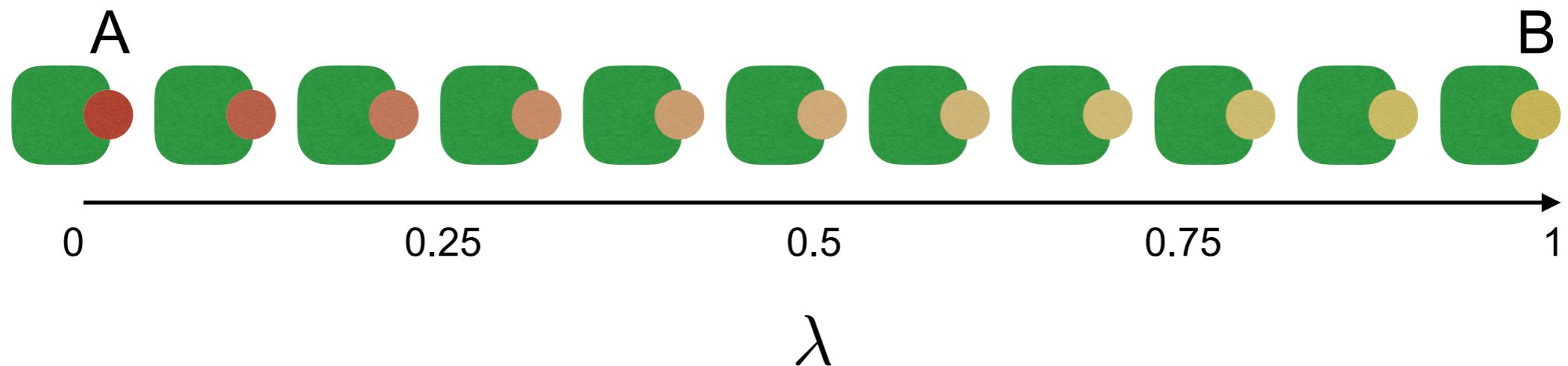
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# Thermodynamic integration

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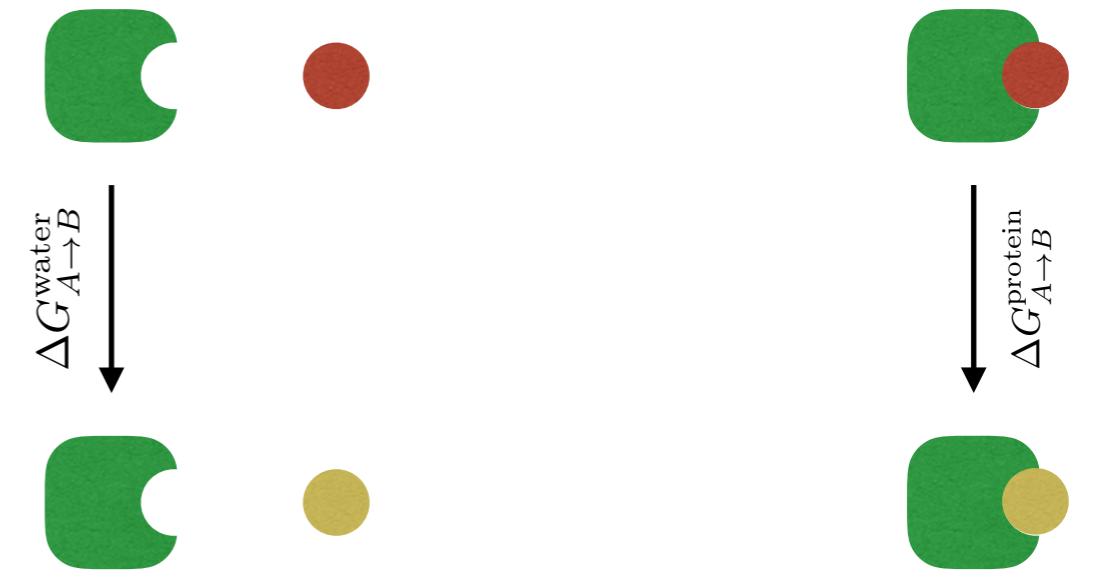
$$E^A(\mathbf{p}_1, \mathbf{p}_2, \dots, \mathbf{r}_1, \mathbf{r}_2)$$

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partition function

$$\begin{aligned} Z(\lambda) &= \sum_i e^{-\beta E(\lambda, \mathbf{P}_i, \mathbf{R}_i)} \\ &= \sum_i e^{-\beta [(1-\lambda)E^A(\mathbf{P}_i, \mathbf{R}_i) + \lambda E^B(\mathbf{P}_i, \mathbf{R}_i)]} \end{aligned}$$



$$\mathbf{P}_i \equiv \begin{pmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \\ \dots \\ \mathbf{p}_N \end{pmatrix}_i \quad \mathbf{R}_i \equiv \begin{pmatrix} \mathbf{r}_1 \\ \mathbf{r}_2 \\ \dots \\ \mathbf{r}_N \end{pmatrix}_i$$

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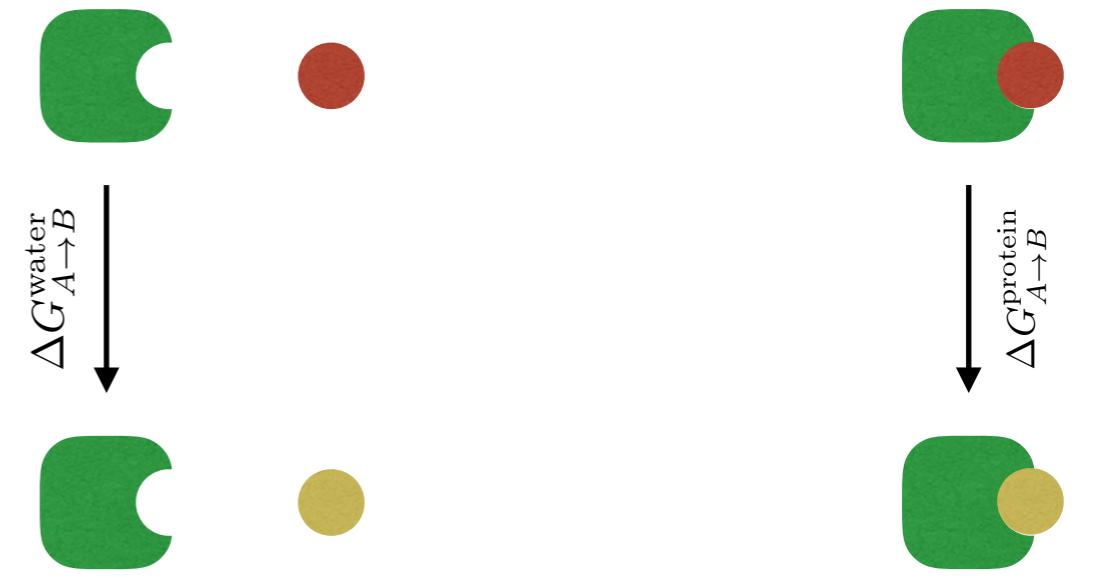
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free energy

$$G(\lambda) = -kT \ln Z(\lambda)$$

how does this help?



$$\mathbf{P}_i \equiv \begin{pmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \\ \dots \\ \mathbf{p}_N \end{pmatrix}_i \quad \mathbf{R}_i \equiv \begin{pmatrix} \mathbf{r}_1 \\ \mathbf{r}_2 \\ \dots \\ \mathbf{r}_N \end{pmatrix}_i$$

# Thermodynamic integration

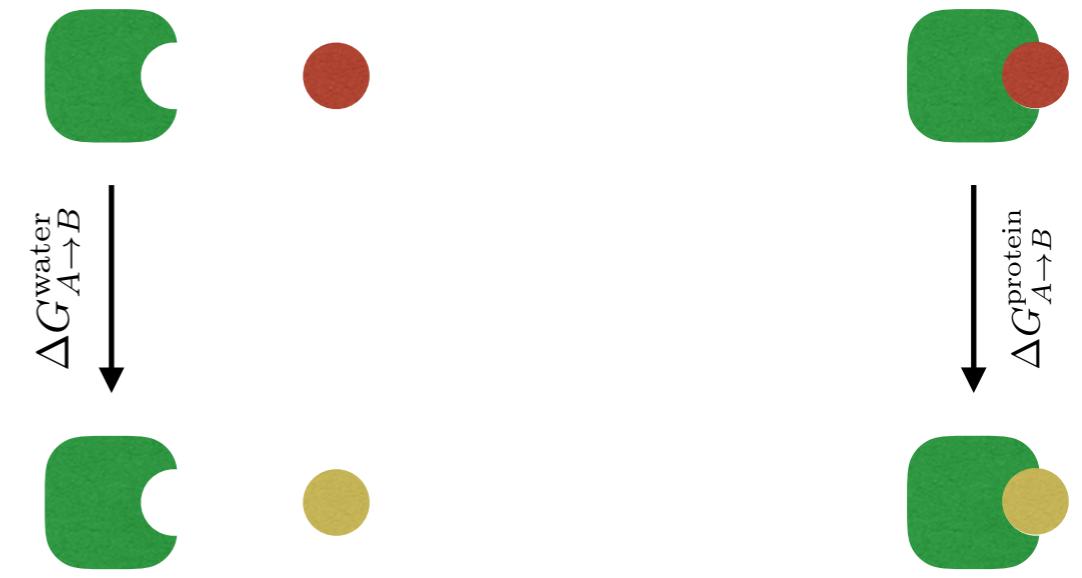
why ‘easy’?

interpolate the energy function

partition function

replace sum by integration (classical)

$$\begin{aligned} Z(\lambda) &= \sum_i e^{-\beta E(\lambda, \mathbf{P}_i, \mathbf{R}_i)} \\ &= \int \int e^{-\beta E(\lambda, \mathbf{P}, \mathbf{R})} d\mathbf{P} d\mathbf{R} \end{aligned}$$



$$\mathbf{P} \equiv \begin{pmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \\ \dots \\ \mathbf{p}_N \end{pmatrix} \quad \mathbf{R} \equiv \begin{pmatrix} \mathbf{r}_1 \\ \mathbf{r}_2 \\ \dots \\ \mathbf{r}_N \end{pmatrix}$$

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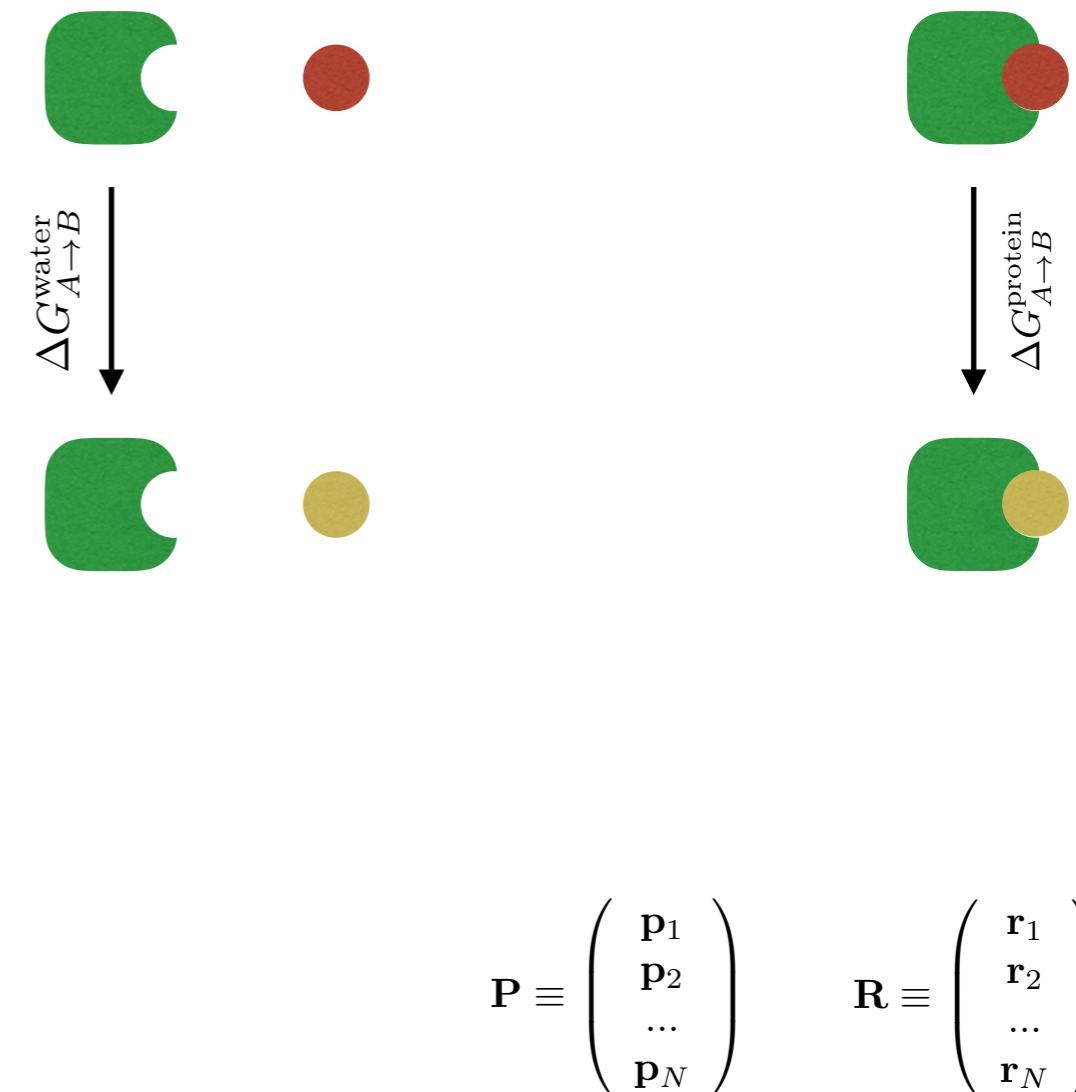
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free energy

$$G(\lambda) = -kT \ln Z(\lambda)$$

derivative of free energy

$$\begin{aligned} \frac{\partial G}{\partial \lambda} &= -\frac{kT}{Z(\lambda)} \frac{\partial Z}{\partial \lambda} \\ &= \int \int \frac{\partial E(\lambda)}{\partial \lambda} \frac{e^{-\beta E(\lambda, \mathbf{P}, \mathbf{R})}}{Z} d\mathbf{P} d\mathbf{R} \\ &= \left\langle \frac{\partial E(\lambda)}{\partial \lambda} \right\rangle_\lambda \end{aligned}$$



# Thermodynamic integration

why ‘easy’?

interpolate the energy function

derivative of free energy

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free energy

$$\Delta G_{A \rightarrow B} = \int_0^1 \left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda} d\lambda$$



# Thermodynamic integration

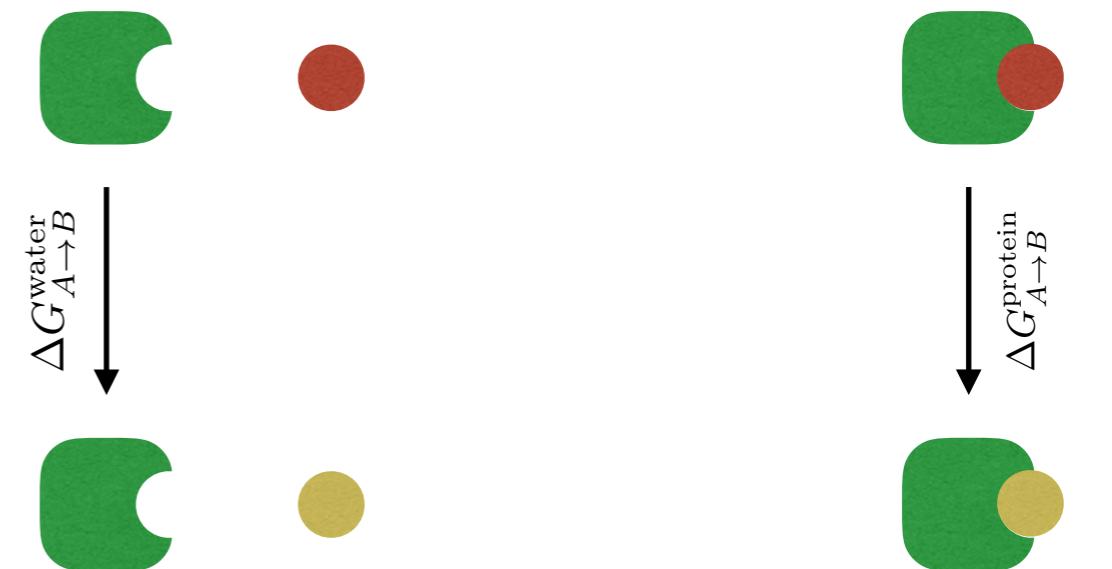
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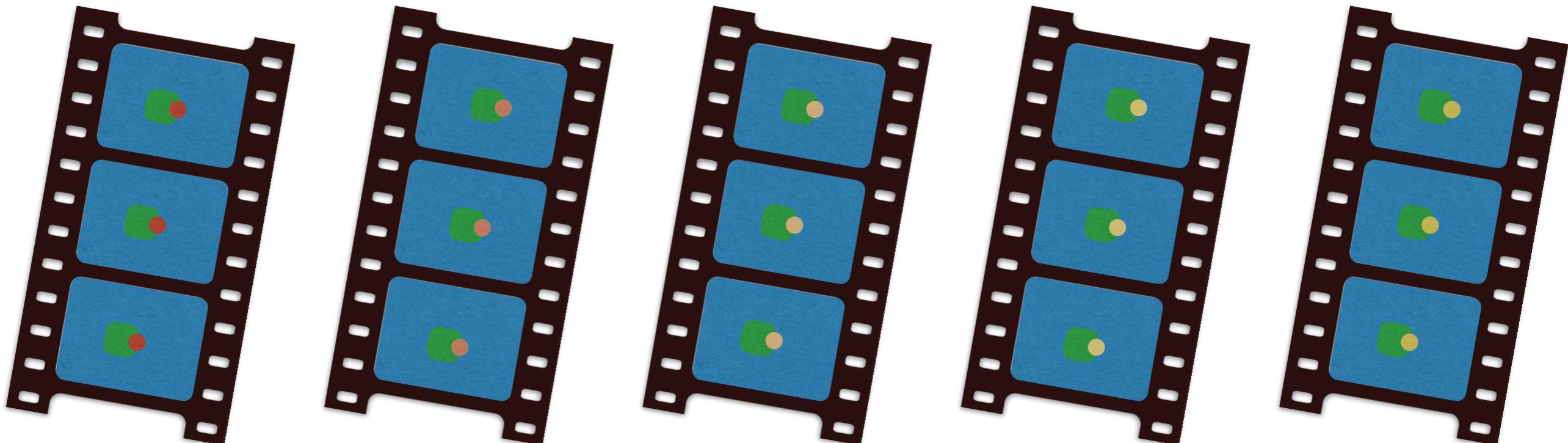
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$$\Delta G_{A \rightarrow B} = \int_0^1 \left\langle \frac{\partial E}{\partial \lambda} \right\rangle_\lambda d\lambda$$

multiple MD trajectories



$$\Delta G_{A \rightarrow B}^{\text{protein}}$$



$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.0}$$

$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.25}$$

$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.50}$$

$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.75}$$

$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=1.0}$$

# Thermodynamic integration

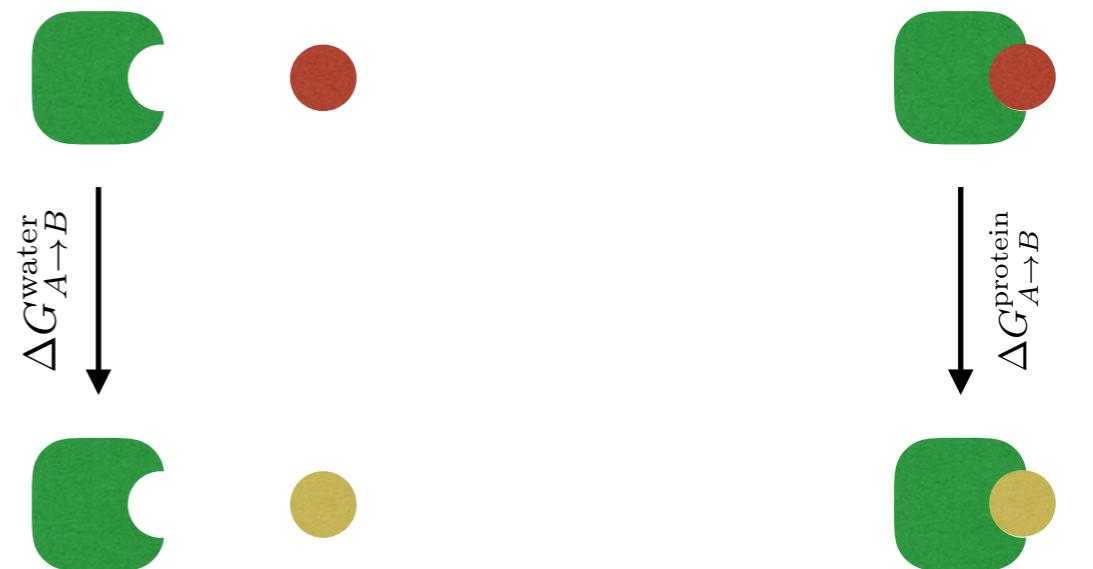
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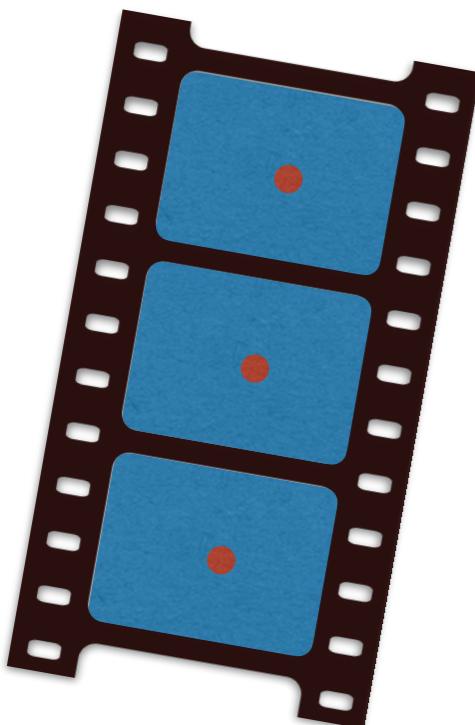
free energy

$$\Delta G_{A \rightarrow B} = \int_0^1 \left\langle \frac{\partial E}{\partial \lambda} \right\rangle_\lambda d\lambda$$

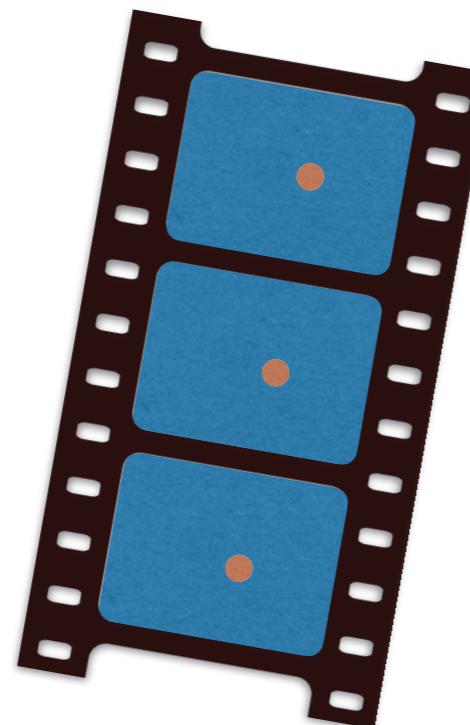
multiple MD trajectories



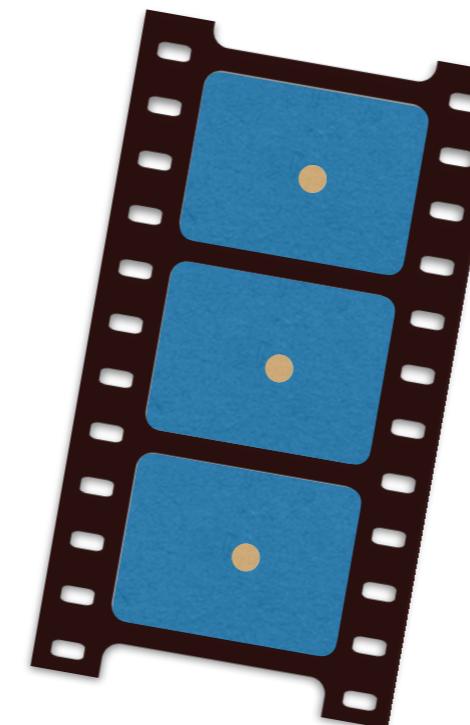
$$\Delta G_{A \rightarrow B}^{\text{water}}$$



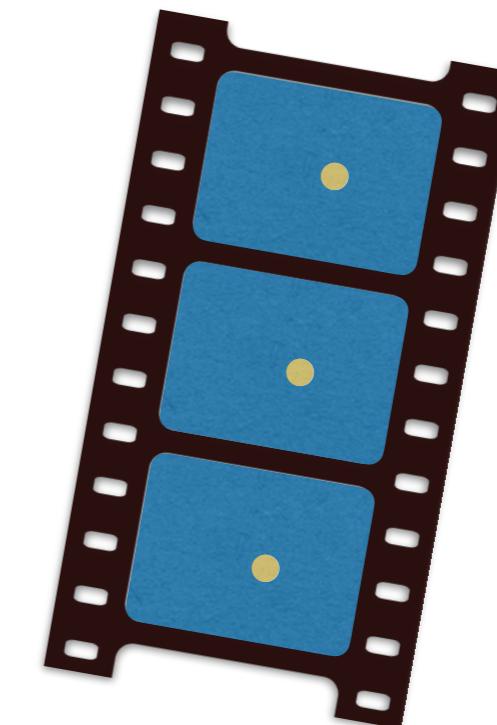
$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.0}$$



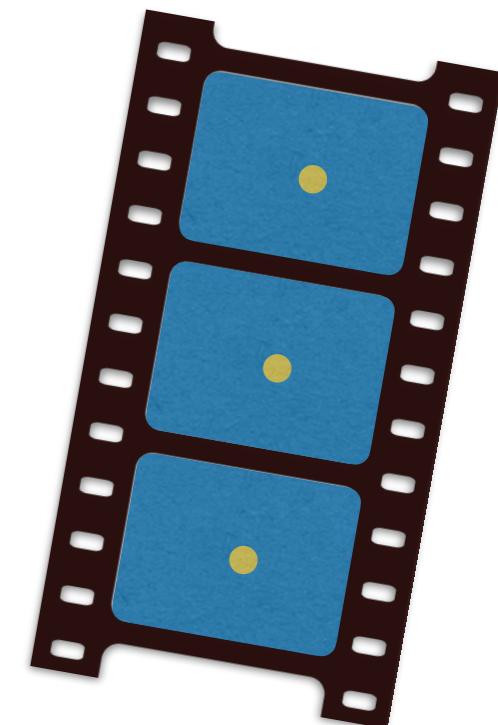
$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.25}$$



$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.50}$$



$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=0.75}$$



$$\left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda=1.0}$$

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## in practice

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derivative of free energy

$$\frac{\partial G}{\partial \lambda} = \left\langle \frac{\partial V(\lambda)}{\partial \lambda} \right\rangle_\lambda$$

