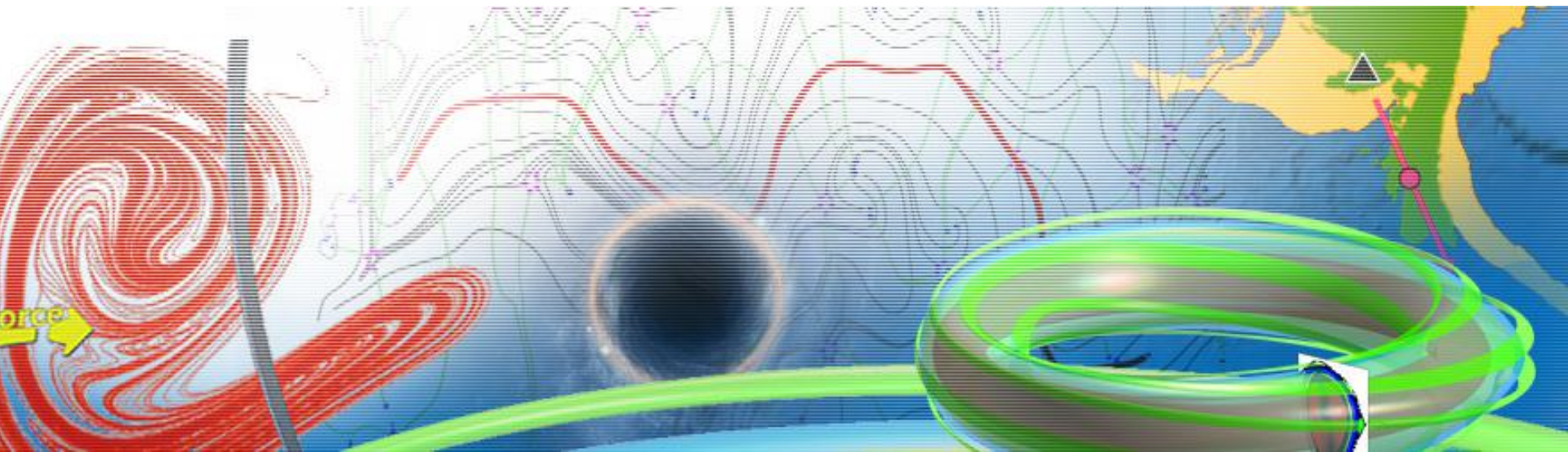


生物动力系统模拟

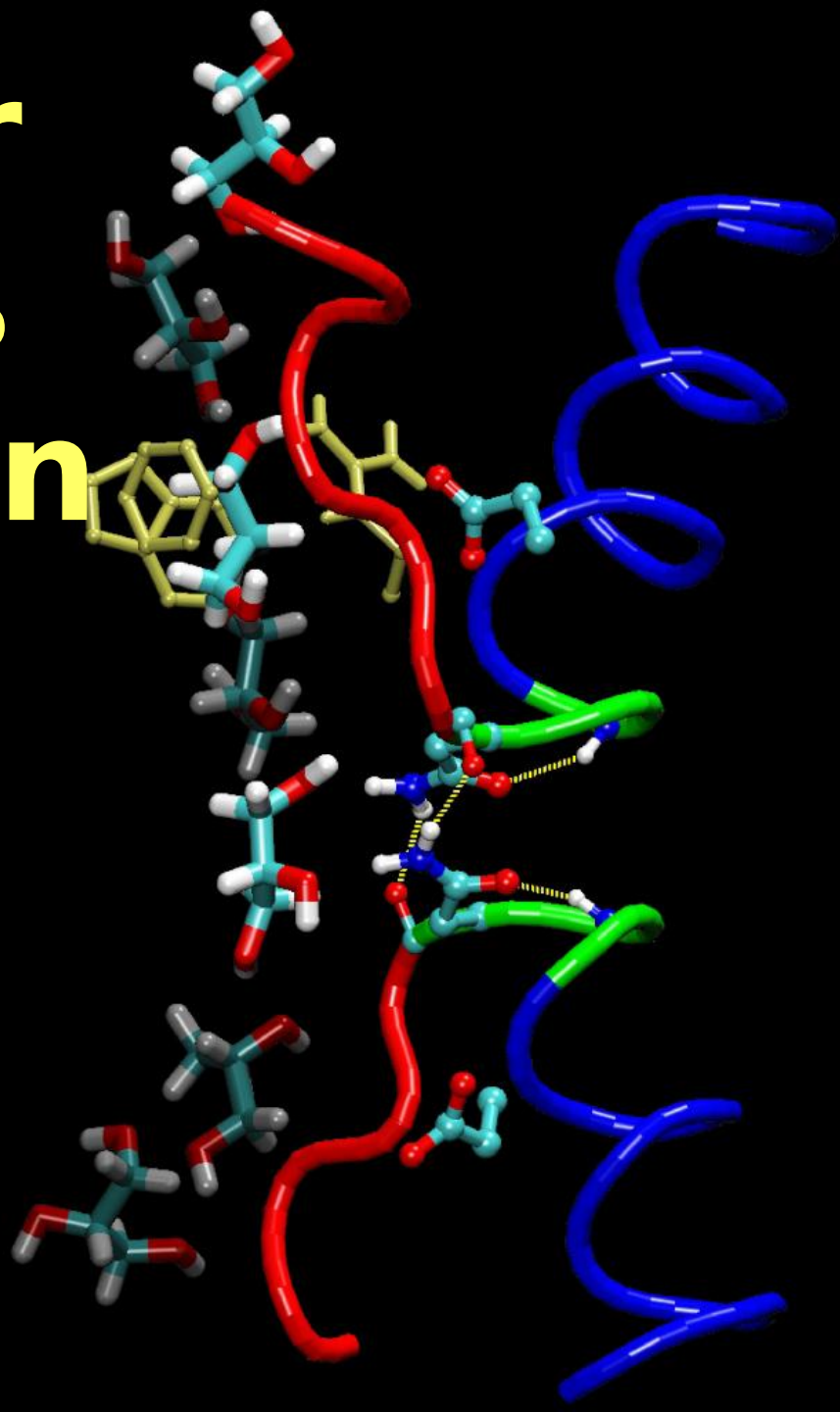


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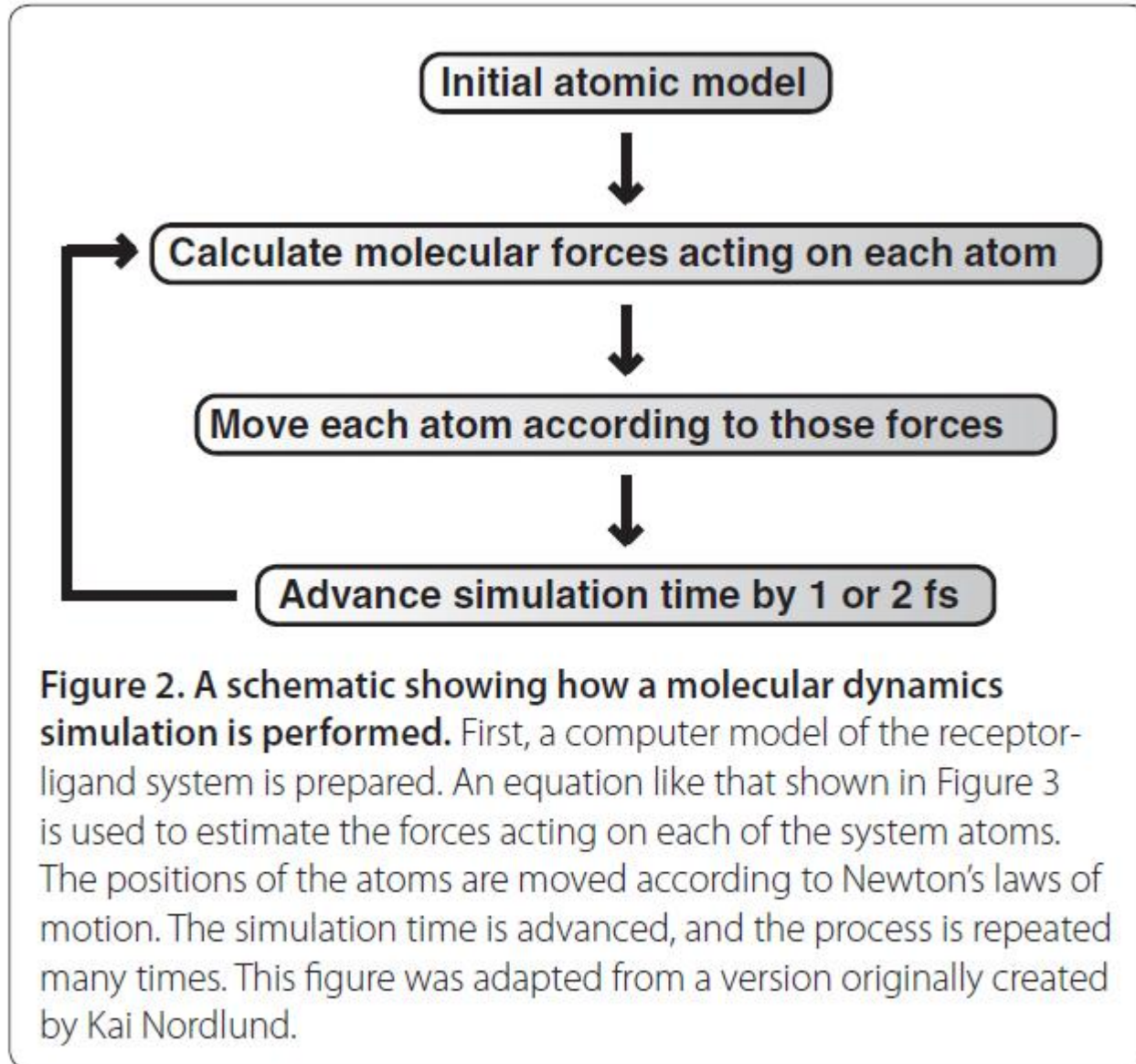


Molecular Dynamics Simulation

(a brief introduction)



Steps



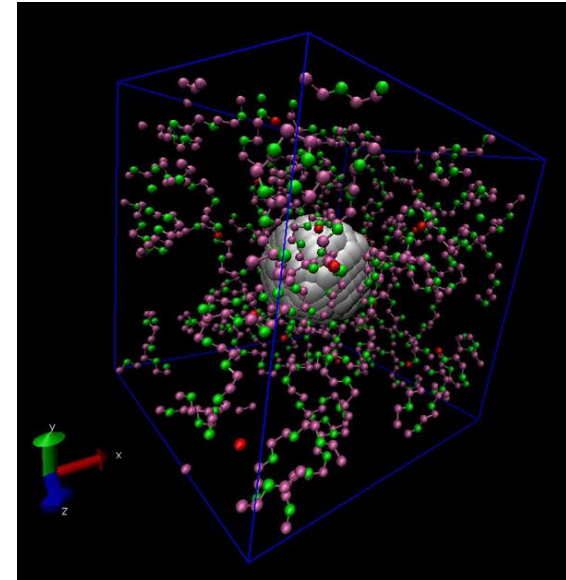
Give atoms initial positions $\mathbf{r}^{(t=0)}$, choose short Δt

Get forces $\mathbf{F} = -\nabla V(\mathbf{r}^{(i)})$ and $\mathbf{a} = \mathbf{F}/m$

Move atoms: $\mathbf{r}^{(i+1)} = \mathbf{r}^{(i)} + \mathbf{v}^{(i)} \Delta t + \frac{1}{2} \mathbf{a} \Delta t^2 + \dots$

Move time forward: $t = t + \Delta t$

Repeat as long as you need



Basic Computation

The classical MD simulations boil down to numerically integrating Newton's equations of motion for the particles (atoms, in the simplest case) which build up the investigated system:

$$m \frac{d^2 \mathbf{r}_i}{dt^2} = \mathbf{F}_i(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N), \quad i = 1, 2, \dots, N.$$

Here \mathbf{r}_i are the position vectors and \mathbf{F}_i are the forces acting upon the N particles in the system.

Quite often forces derive from *potential functions*, $U(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N)$, representing the potential energy of the system for the specific geometric arrangement of the particles:

$$\mathbf{F}_i(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N) = -\nabla_{\mathbf{r}_i} U(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N).$$

This form implies the conservation of the total energy $E = E_{\text{kin}} + U$, where E_{kin} is the instantaneous kinetic energy.

In some context, we use \mathbf{F}_i instead of \mathbf{f}_i .

The fundamental reason is that the system is a Hamiltonian system

In Hamiltonian mechanics, a classical physical system is described by a set of canonical coordinates $\mathbf{r} = (\mathbf{q}, \mathbf{p})$, where each component of the coordinate q_i, p_i is indexed to the frame of reference of the system.

The time evolution of the system is uniquely defined by Hamilton's equations:

$$\begin{aligned}\frac{d\mathbf{p}}{dt} &= -\frac{\partial \mathcal{H}}{\partial \mathbf{q}} \\ \frac{d\mathbf{q}}{dt} &= +\frac{\partial \mathcal{H}}{\partial \mathbf{p}}\end{aligned}$$

where $\mathcal{H} = \mathcal{H}(\mathbf{q}, \mathbf{p}, t)$ is the Hamiltonian, which often corresponds to the total energy of the system. For a closed system, it is the sum of the kinetic and potential energy in the system.

$$\frac{dp}{dt} = -\frac{\partial V}{\partial q}$$

$$\mathcal{H} = T + V, \quad T = \frac{p^2}{2m}, \quad V = V(q).$$

Note that T is a function of p alone, while V is a function of q alone

$$\frac{d\mathbf{p}}{dt} = -\frac{\partial V}{\partial \mathbf{q}}$$

$$\mathbf{p} = m\mathbf{v} = m\frac{d\mathbf{q}}{dt}$$

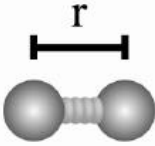
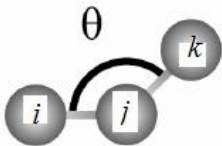
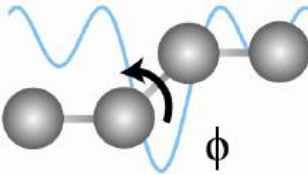
$$m\frac{d^2\mathbf{q}}{dt^2} = -\frac{\partial V}{\partial \mathbf{q}}$$

$$\mathbf{F} = -\frac{\partial V}{\partial \mathbf{q}}$$

$$\mathbf{F}_i = -\frac{\partial V}{\partial \mathbf{q}_i}$$

Bonded

$$\mathbf{V} = \sum_{\text{bonds}} K_r (\mathbf{r} - \mathbf{r}_{eq})^2 + \sum_{\text{angles}} K_\theta (\theta - \theta_{eq})^2 + \sum_{\text{dihedrals}} \frac{V_n}{2} [1 + \cos(n\phi - \gamma)]$$

Non-bonded

$$+ \sum_{i < j} \left[\frac{A_{ij}}{R_{ij}^{12}} - \frac{B_{ij}}{R_{ij}^6} + \frac{q_i q_j}{\epsilon R_{ij}} \right]$$

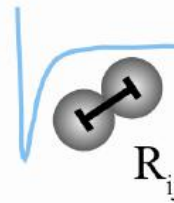
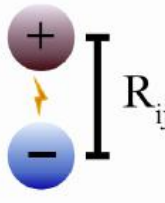
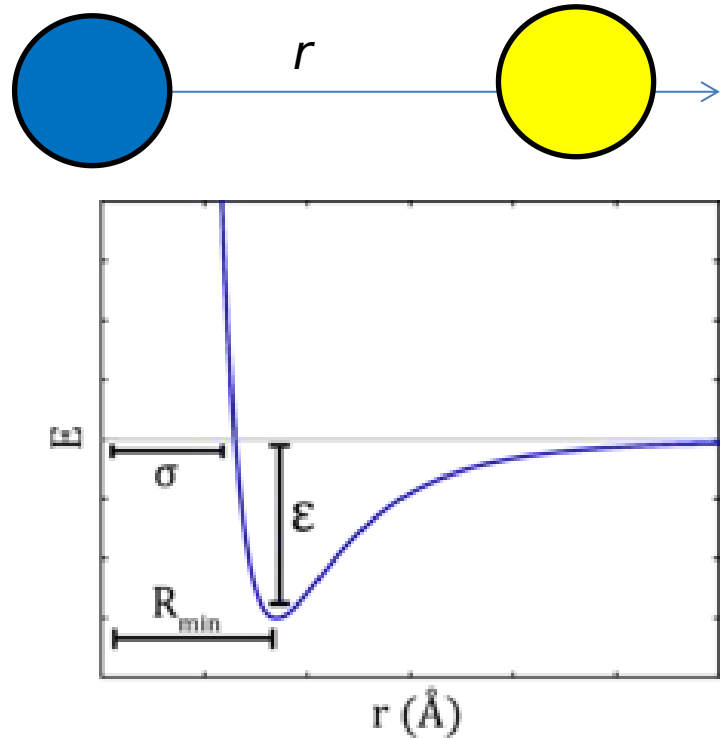



Figure 3. An example of an equation used to approximate the atomic forces that govern molecular movement. The atomic forces that govern molecular movement can be divided into those caused by interactions between atoms that are chemically bonded to one another and those caused by interactions between atoms that are not bonded. Chemical bonds and atomic angles are modeled using simple springs, and dihedral angles (that is, rotations about a bond) are modeled using a sinusoidal function that approximates the energy differences between eclipsed and staggered conformations. Non-bonded forces arise due to van der Waals interactions, modeled using the Lennard-Jones potential, and charged (electrostatic) interactions, modeled using Coulomb's law.

$$\theta = \cos^{-1} \frac{(\mathbf{r}_k - \mathbf{r}_j) \cdot (\mathbf{r}_i - \mathbf{r}_j)}{|\mathbf{r}_k - \mathbf{r}_j| |\mathbf{r}_i - \mathbf{r}_j|}$$

Example



Given that the potential between the two neutral atoms are:

$$V = 4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$

Quiz

What is V when $r = \text{infinity}$?

What is V when $r = \sigma$?

What is V when $r = 0$?

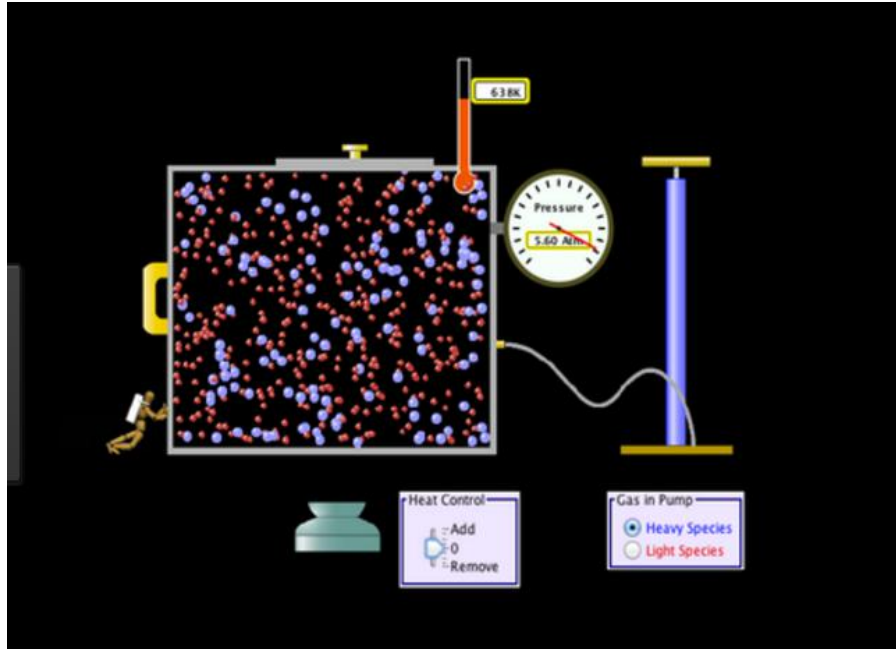
What is the force acting on the yellow

Answer 0

0

$$F = -\frac{\partial V}{\partial r} = \frac{48\epsilon}{r} \left[\left(\frac{\sigma}{r} \right)^{12} - \frac{1}{2} \left(\frac{\sigma}{r} \right)^6 \right]$$

Thermodynamic properties



In usual scientific researches,
thermodynamic properties
(such as temperature and pressure)
are given as conditions.

In MD simulations,

It is the set of atoms that is given as the starting condition.

Thermodynamic properties usually need to be calculated from the simulation.

Thermodynamic properties

Temperature

It measures kinetic energies of individual atoms.

It is actually averaged kinetic energy.

1. First we calculate the total kinetic energy

$$E_{\text{kin}} = \frac{1}{2} \sum_{i=1}^N m_i v_i^2$$

2. Then we divide N to get the average kinetic energy

$$E_{\text{kin}}/N$$

3. It is **almost** the temperature T

$$\frac{3}{2} k_B T = \frac{E_{\text{kin}}}{N}$$

$$T = \frac{2E_{\text{kin}}}{3k_B N}$$

Thermodynamic properties

Pressure

$$PV = Nk_{\text{B}}T + \frac{1}{3} \left\langle \sum_{i=1}^N \mathbf{r}_i \cdot \mathbf{F}_i \right\rangle$$

Where $\langle \rangle$ represents “the expectation”

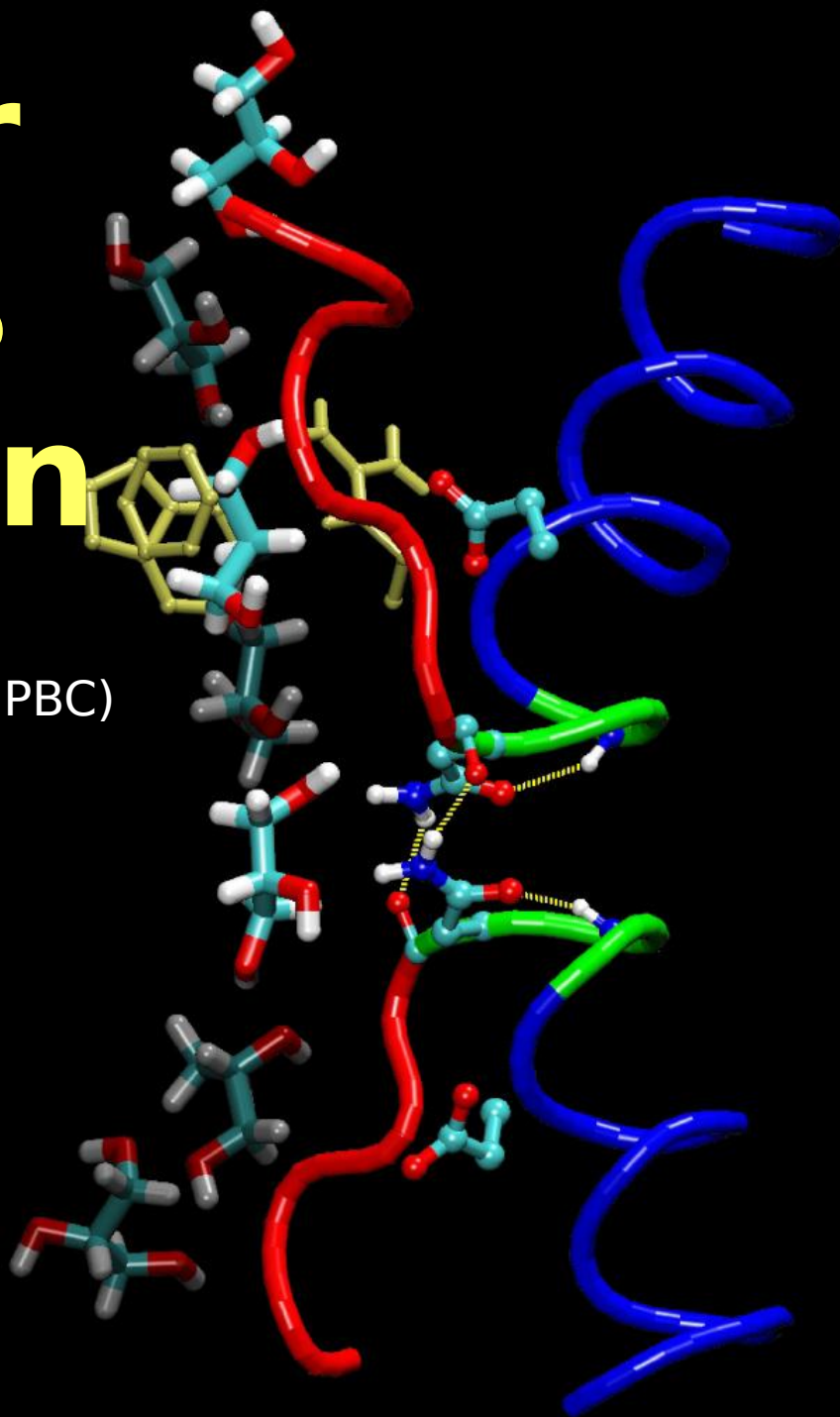
For example, $\langle T \rangle$ means the average temperature.

$$\left\langle \sum_{i=1}^N \mathbf{r}_i \cdot \mathbf{F}_i \right\rangle \neq \frac{\sum_{i=1}^N \mathbf{r}_i \cdot \mathbf{F}_i}{N}$$
$$\left\langle \sum_{i=1}^N \mathbf{r}_i \cdot \mathbf{F}_i \right\rangle = \frac{\sum_{i=1}^N \mathbf{r}_i \cdot \mathbf{F}_i + \dots}{M}$$

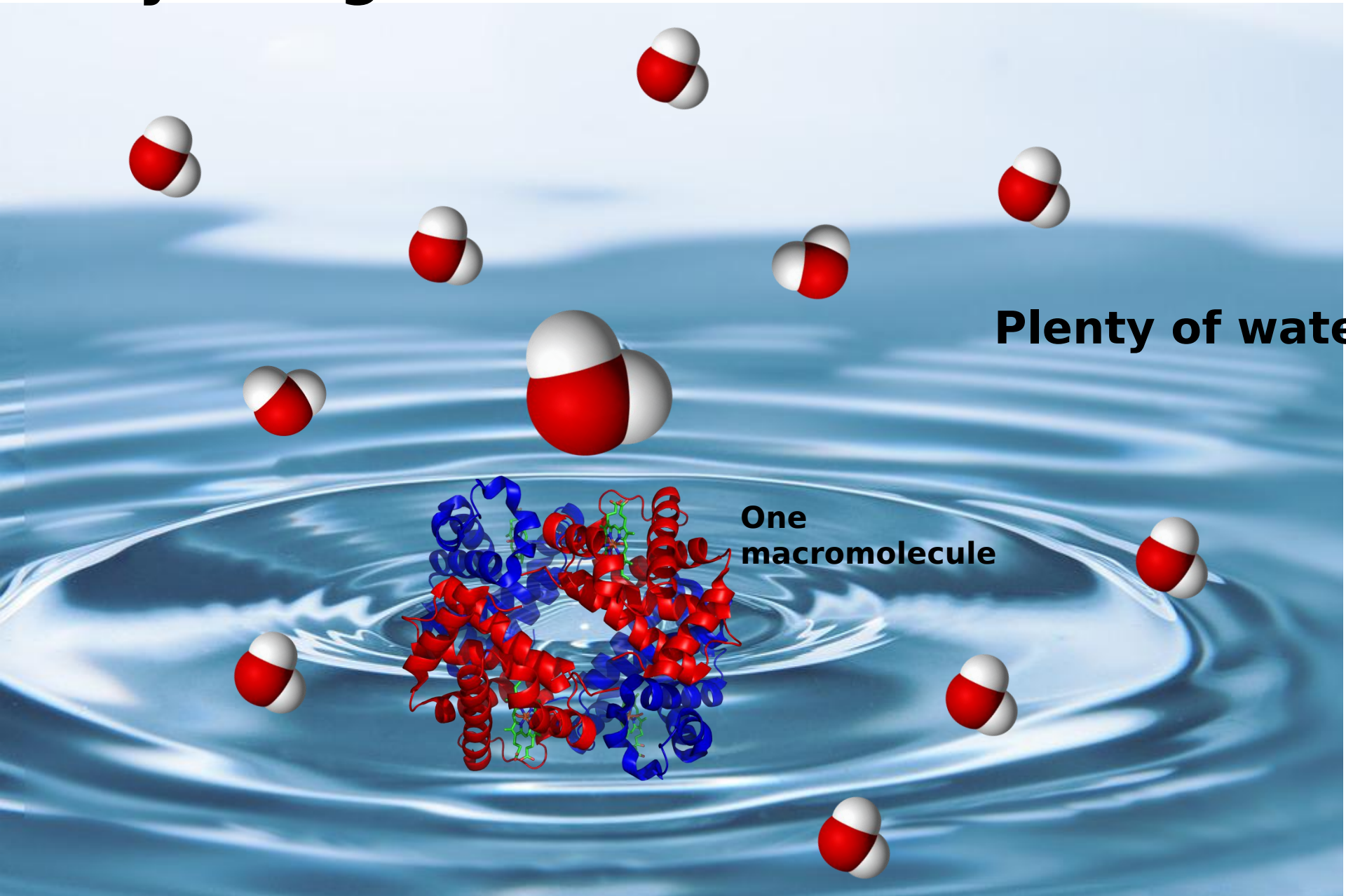
For ideal gas $\left\langle \sum_{i=1}^N \mathbf{r}_i \cdot \mathbf{F}_i \right\rangle = 0$, $PV = Nk_{\text{B}}T$

Molecular Dynamics Simulation

Periodic Boundary Condition (PBC)

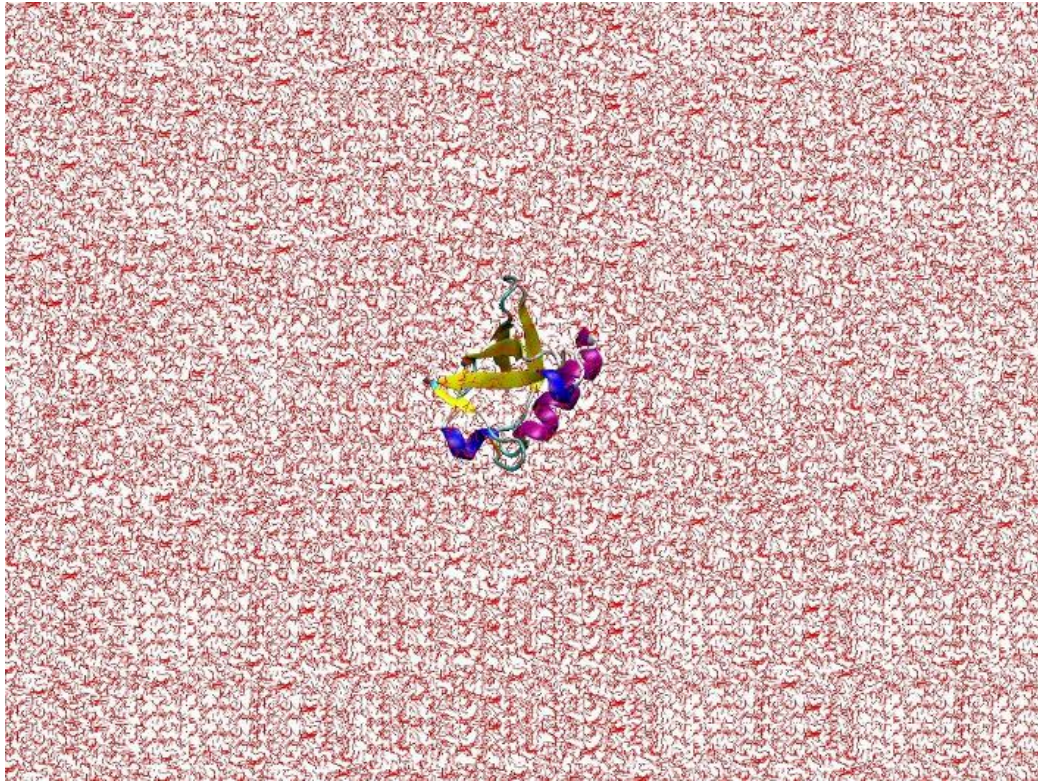


Why using PBC?



Because there is always a boundary.

And dynamics at the boundary is dramatically different from the inner



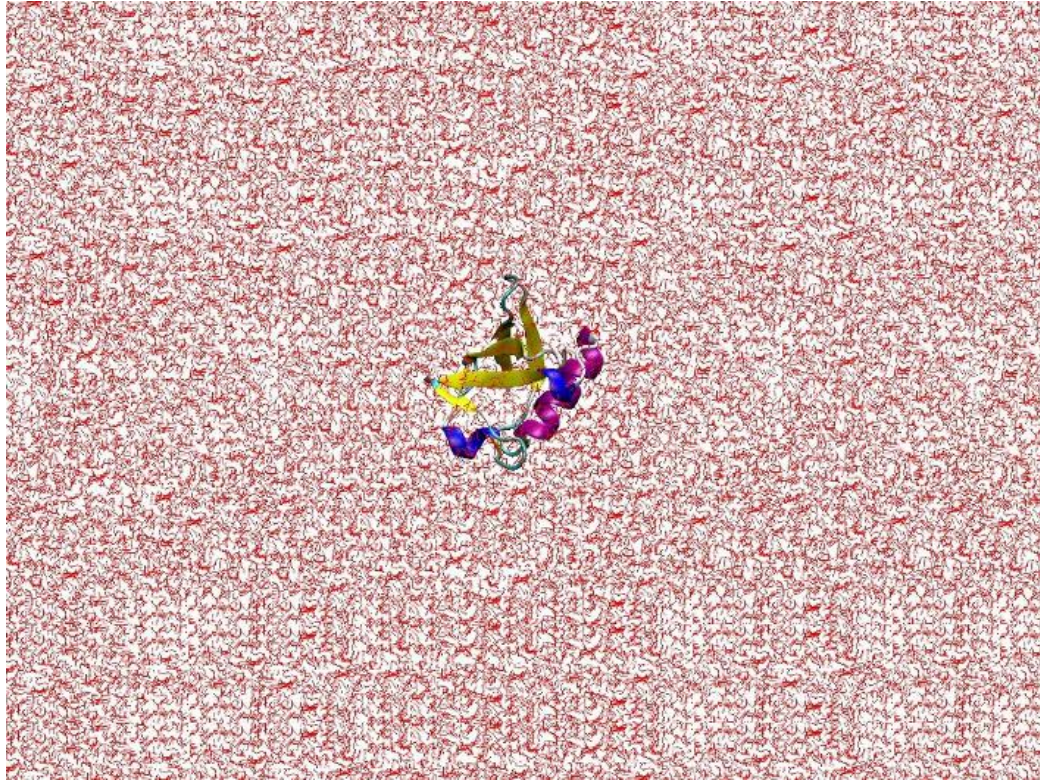
L

If L is large, then boundary effect is **relatively** small and can thus be ignored

$$\frac{L^2}{L^3} = \frac{1}{L}$$

Macroscopically observable water should be sufficient.

For example, 18 grams of water + 1 protein



$$\mathbf{p} = m\mathbf{v} = m \frac{d\mathbf{q}}{dt}$$

About how many water molecules in the boundary? $\frac{10^{16}}{10^{24}} = 10^{-8}$

What is the percentage? $\frac{10^{16}}{10^{24}} = \frac{1}{10^8} = 0.00000001$

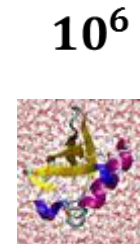
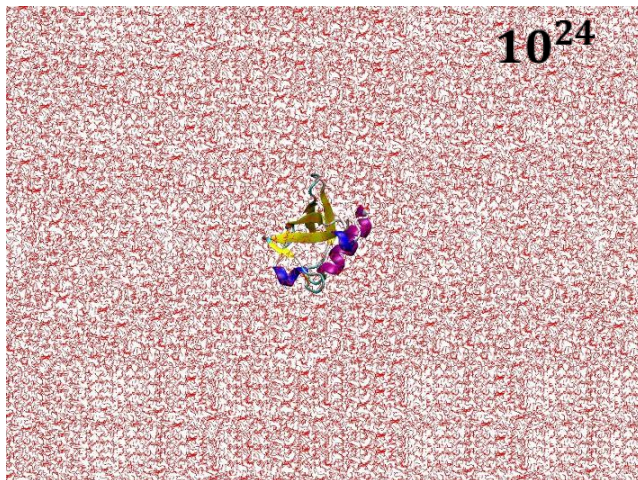
Conclusion: The boundary effect can be ignored

But, can we simulate a system with 10^{24} water molecules?



No Way!

The typical number of particles which can be handled in MD simulation nowadays is of the order 10^6



But, is the boundary effect ignorable for a system with only 10^6 water



Water molecules in the boundary: $\frac{\partial V}{\partial y} = \frac{48\epsilon}{r} \left[\left(\frac{\sigma}{r} \right)^{12} - \frac{1}{2} \left(\frac{\sigma}{r} \right)^6 \right]$

Water molecules in total: 10^6

Percentage: $\frac{10^4}{10^6} = \frac{1}{10^2} = 0.01$

Conclusion: The boundary effect cannot be ignored

Solution:

Periodic Boundary Condition

**1. It is an infinite system
(no boundary effect)**

**2. Although infinite,
Computation is finite**

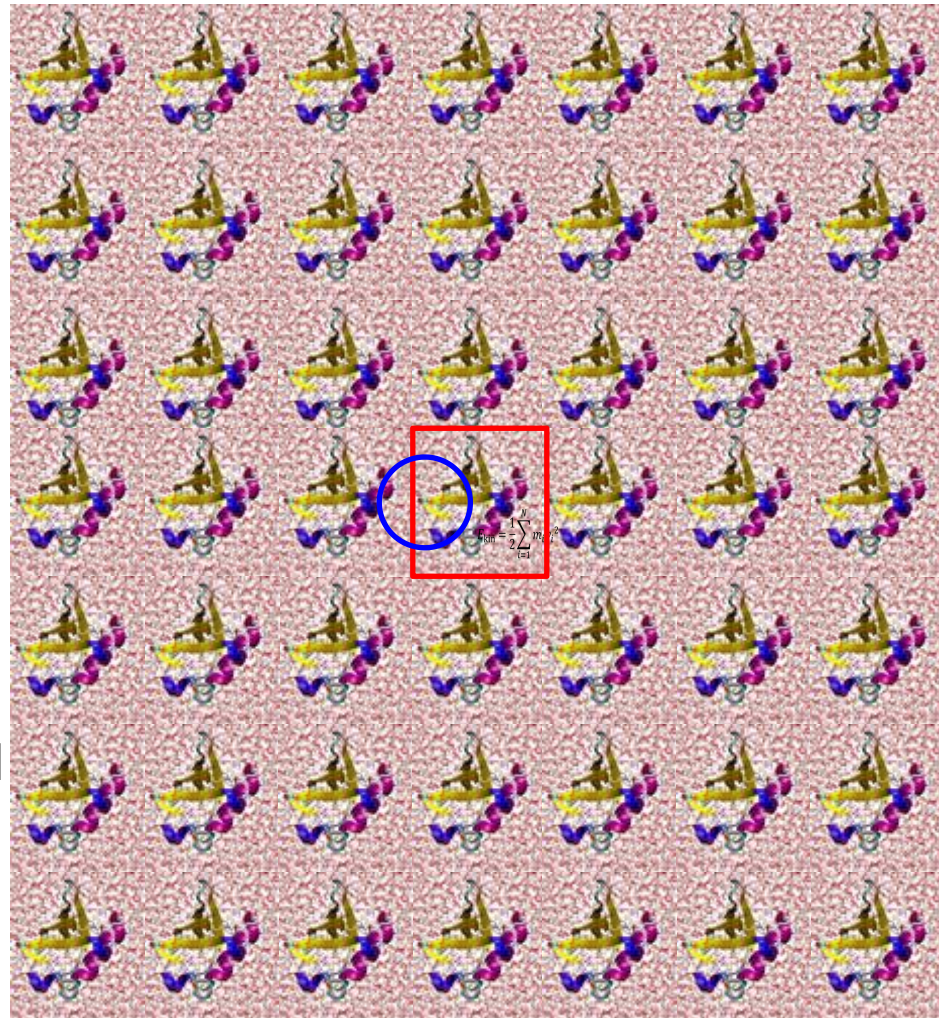
Just consider atoms
in the original box.

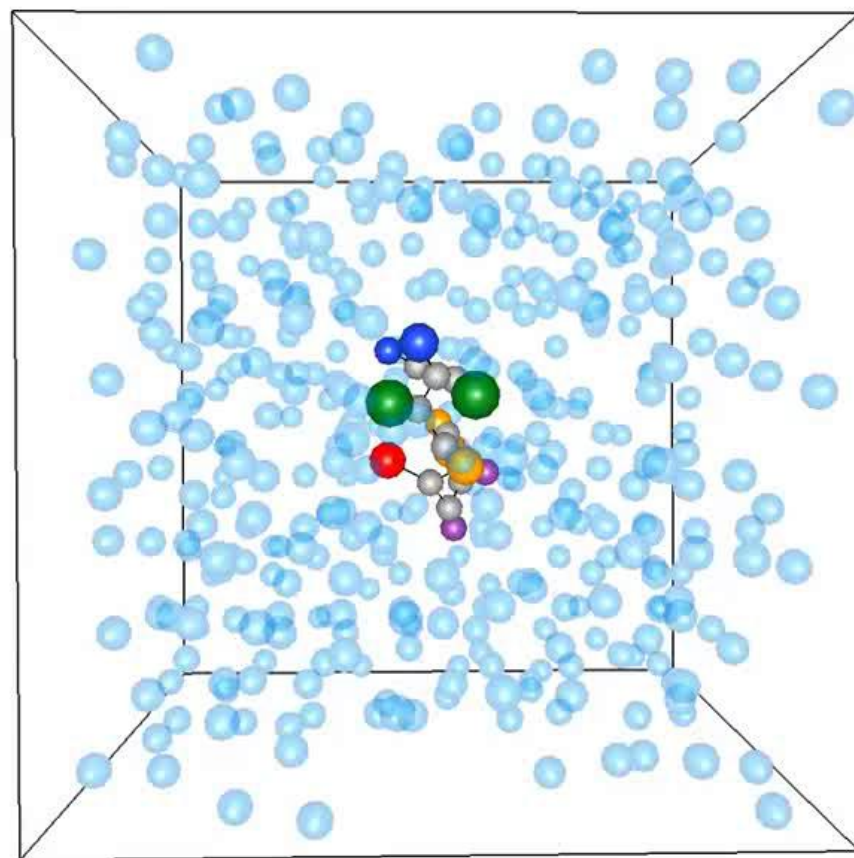
Other atoms just copy

**3. What is the role played
by other atoms?**

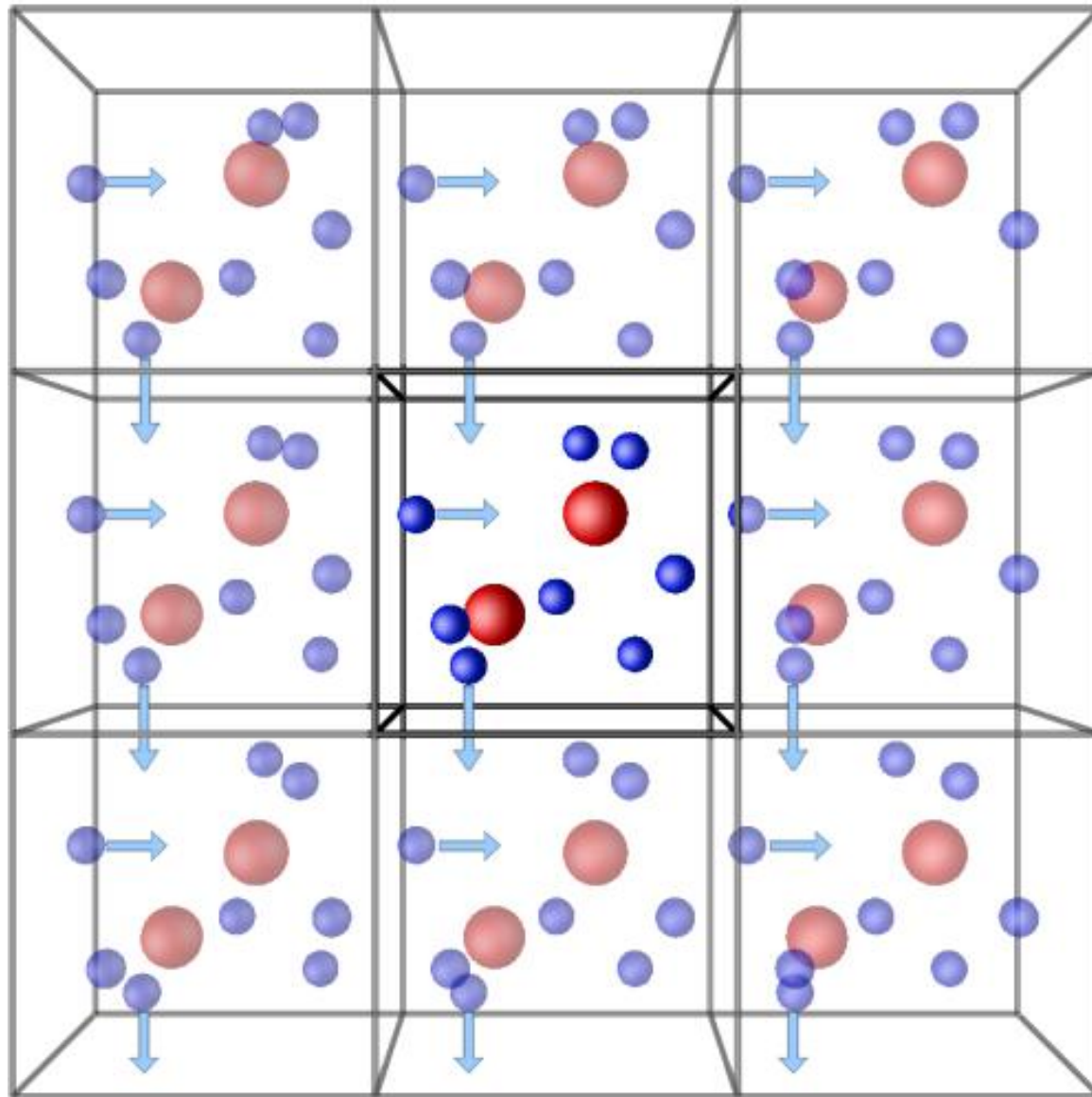
They replace atoms
in the box (此入彼出)

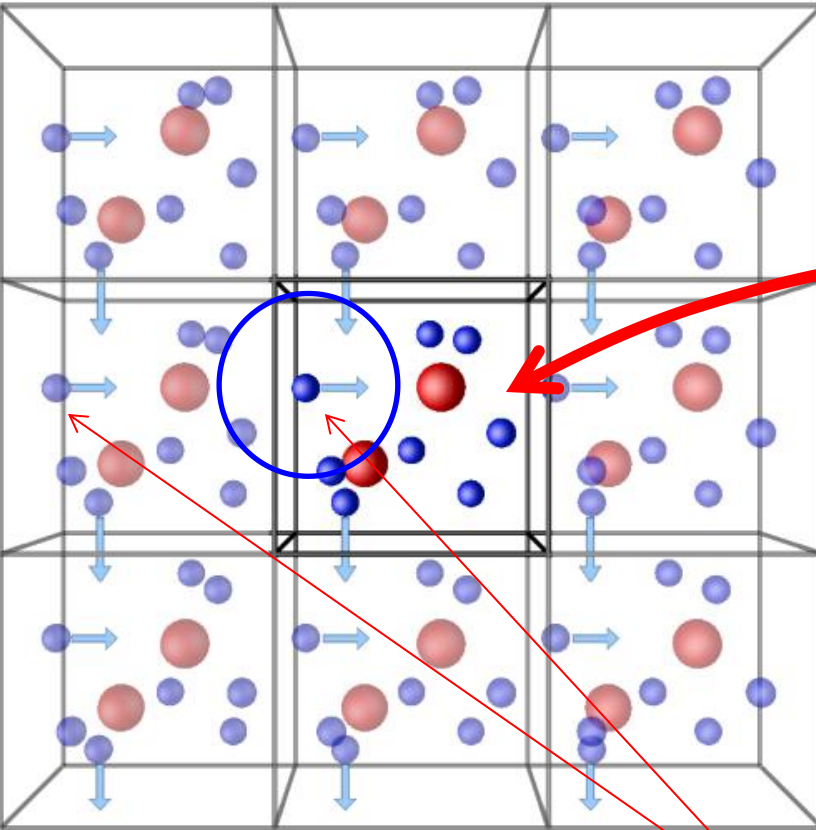
They may exert force to
atoms in the box





Solution: Periodic Boundary Condition





1. Particles in the box are mentally replicated infinitely by rigid translation in all the three Cartesian directions, completely filling the space.

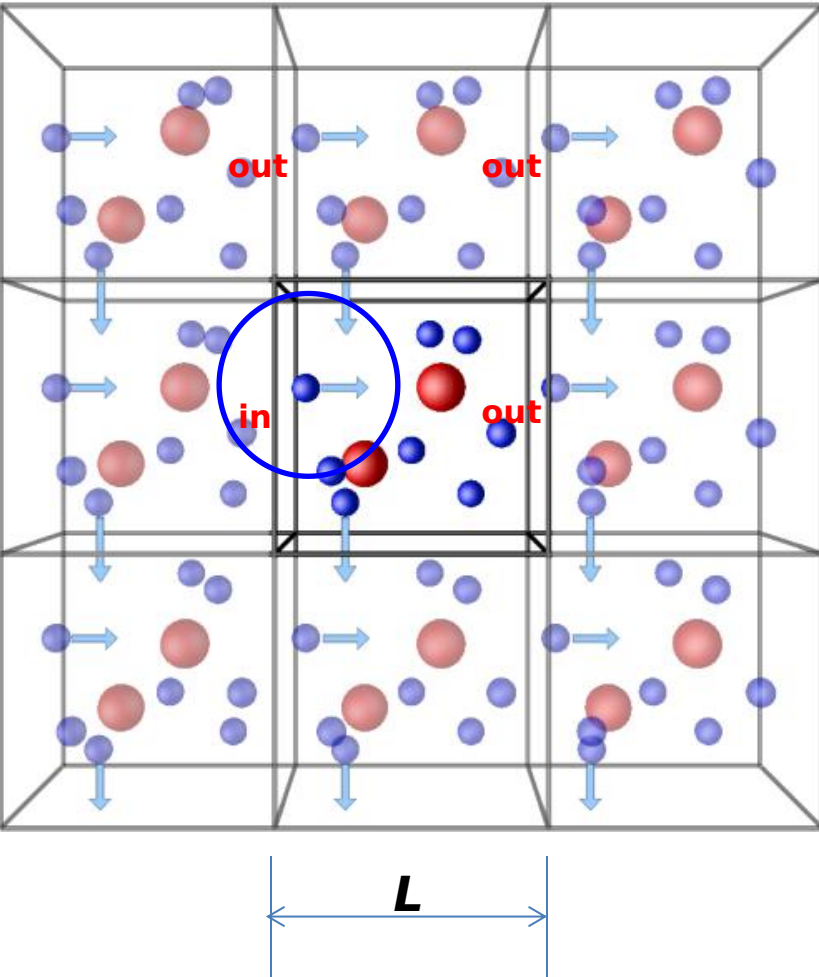
2. All the “image” particles move solidary with the “original” particle from the simulated box. When a particle enters or leaves the simulation region, an image particle leaves or enters the simulation region, such that the number of particles in the simulation region is always conserved.

3. Only particles in the box are simulated. Other particles are just copies.

Question: which particle needs I to calculate force on it?

4. How to calculate the force? There are so many particles acting on it!!!

5. Use a cut-off circle with radius R .



A trick:

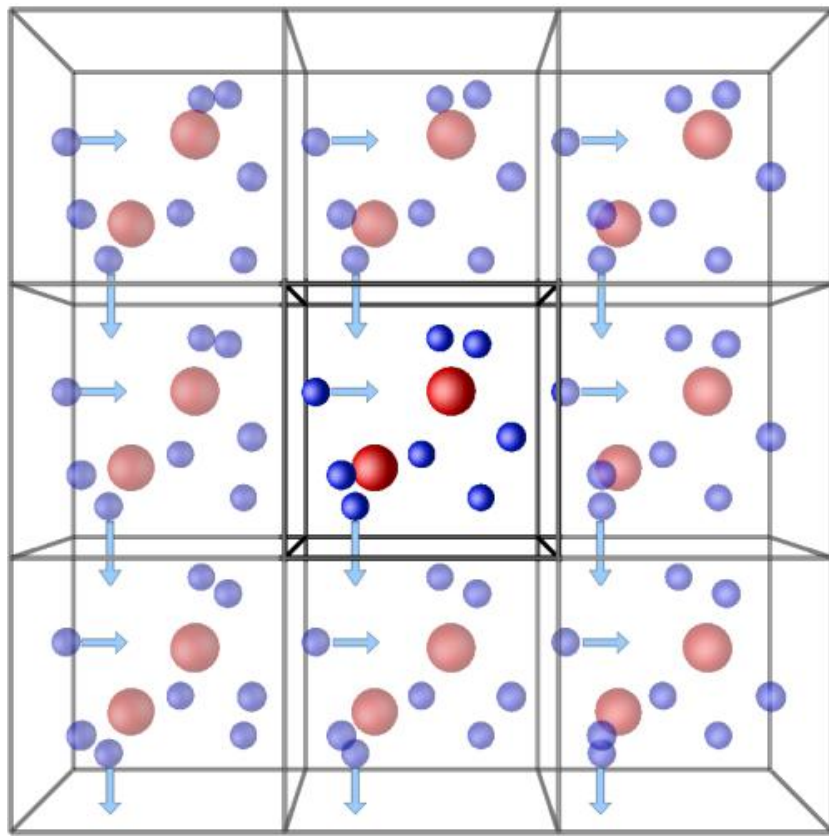
By carefully choosing the radius R , only one image particle locates within the

The particle within the circle is not necessarily the one in the simulation

consider only the closest and neglect

Criterion for choosing R

$$2R < L$$



6. The surface effects are thus virtually eliminated

(because the system is essentially infinite)

7. What really amazing is that:

Although the system is infinite,

one needs only to calculate N particles

Others just copy.