

# Molecular Dynamics Simulation

*theories and principles*

*Senbo Xiao*

# Outline

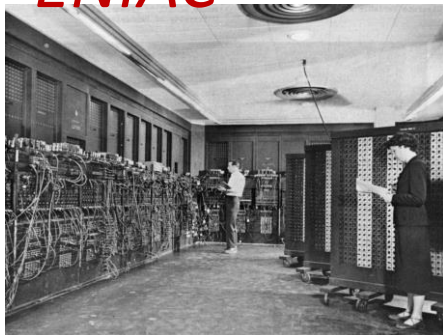
- .Briefs on computer simulations**
- .Introductory Molecular Dynamics (MD) simulations**
- .Practice of MD simulations**

# Computer simulations

Alan Turing



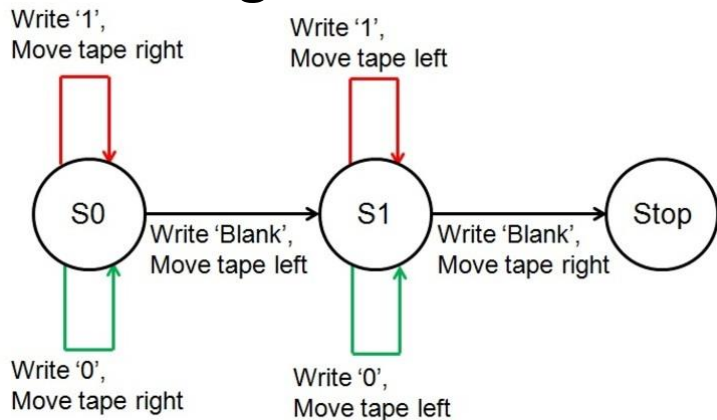
ENIAC



*The Norwegian e-infrastructure*



The Turing machine



Nicholas Metropolis

Martin Karplus



*Chemistry 2013*

# Computer simulations

Computer simulations in research:



- Verification of theories
- Explanation and prediction of experimental results
- Independent exploratory tools

# Computer simulations

## Applications of computer simulations

*Formation of galaxy*

*Weather forecast*

*Flight simulation*

*Massive explosion study*

*High pressure phenomenon*

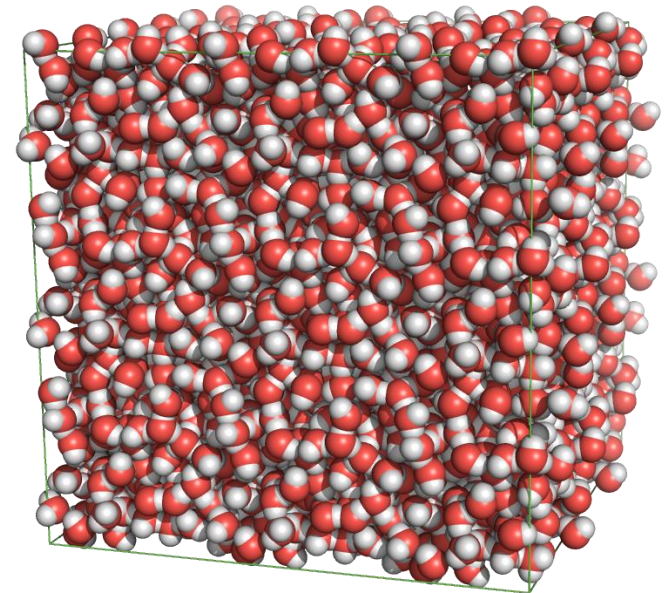
*“The day after tomorrow”*

*Chemical diffusion in the primitive universe*

*Ultrafast dynamics of Super-small system*

# Molecular Dynamics (MD) simulations

- Atomistic resolution
- Classic physics (Newton's laws of motion)
- Small system (nanometers)
- Small time scale (nanoseconds)



A water box

# Molecular Dynamics (MD) simulations

- Simulate interactions of particles (*atoms, molecules, granules, ...*)
- Predict time evolution of N-body systems
- Require parameters of initial **atom coordinates, velocities, interaction potentials, ...**
- Use **finite time step** to integrate Newton's laws

of motion:

$$m_i \vec{a}_i = \vec{F}_i$$



$$m_i \frac{d\vec{v}_i}{dt} = \vec{F}_i$$

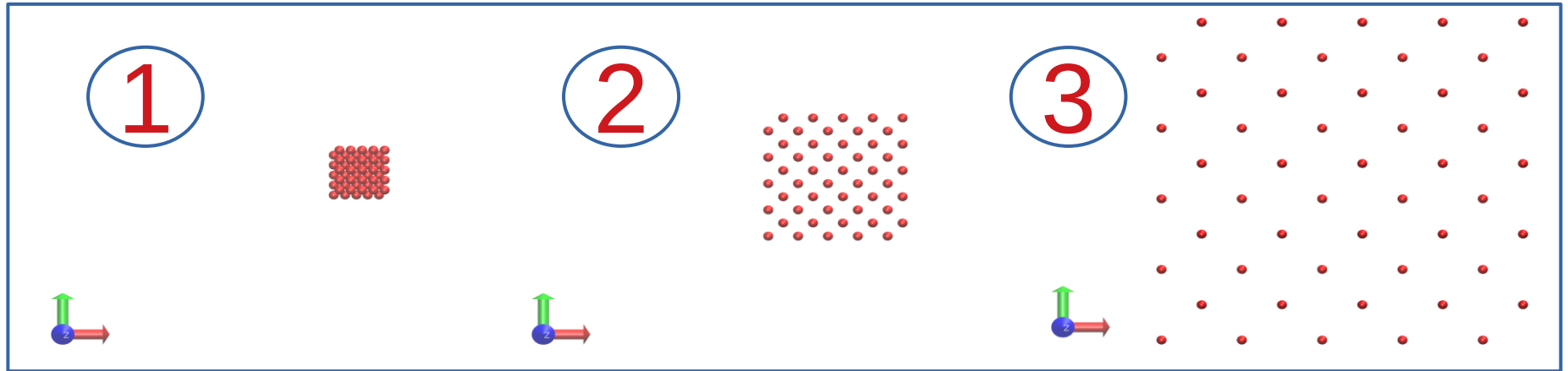


$$m_i \frac{d^2\vec{r}_i}{dt^2} = \vec{F}_i$$

# Molecular Dynamics (MD) simulations

Examples:

1. Calculation cohesive energy: **Not** MD





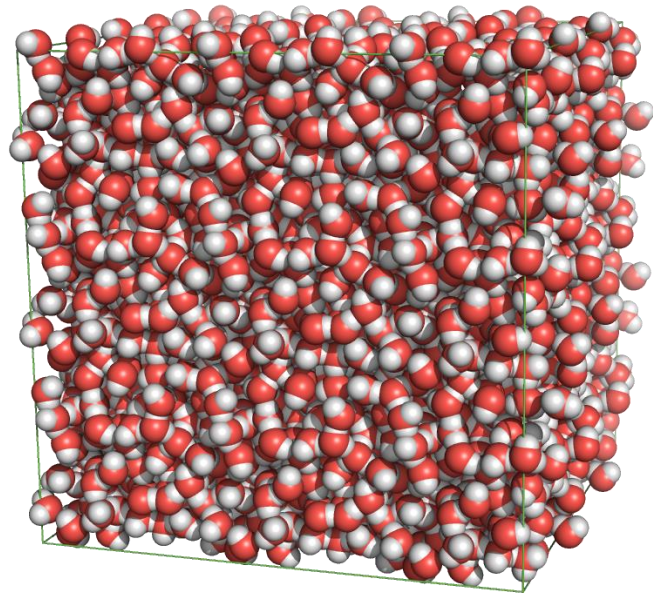
# Molecular Dynamics (MD) simulations

Examples:

## 2. Equilibrating water molecules: MD

Water molecules diffusion at  
a temperature of 300K

A water box

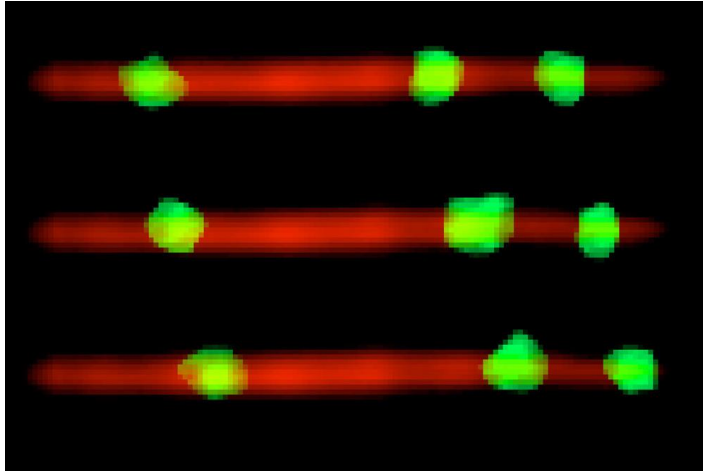


# MD simulation as a powerful tool

Comparison of tools for studying a single protein:

1) Single molecule microscopy

2) X-ray crystallography



3) MD simulation

# MD simulation as a powerful tool

Comparison of tools for studying a single protein:

1) Single molecule microscopy

2) X-ray crystallography

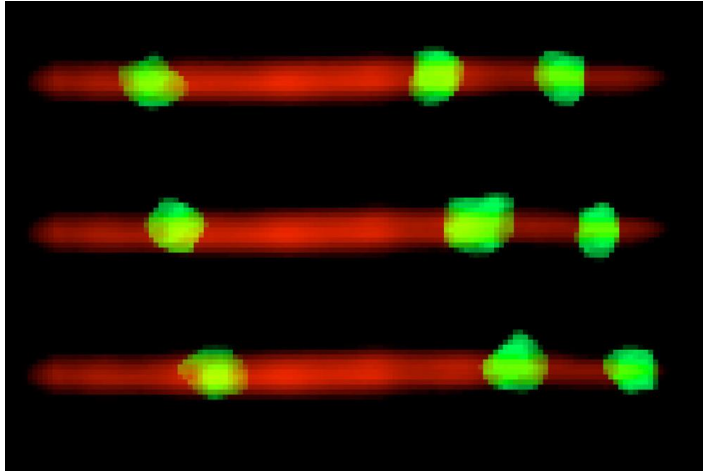


3) MD simulation

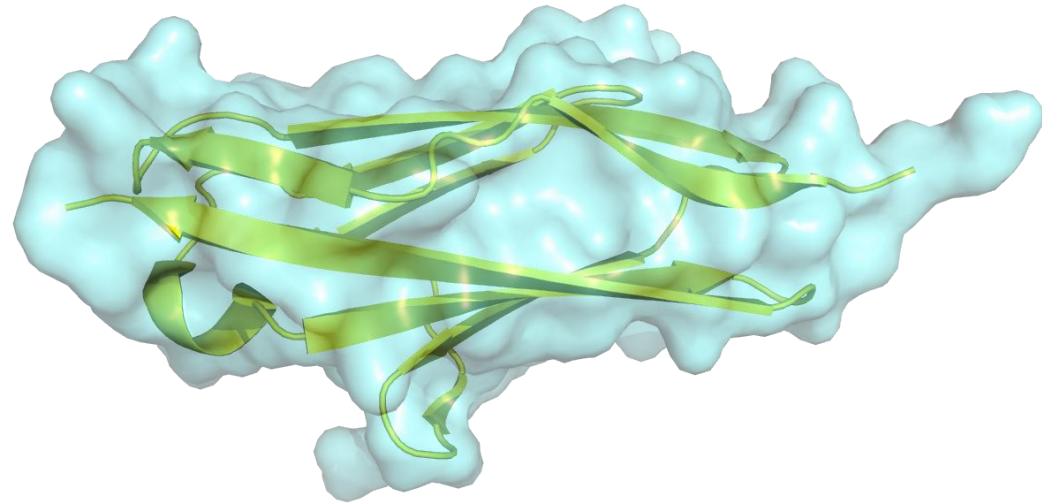
# MD simulation as a powerful tool

A comparison of tools for studying a single protein:

1) Single molecule microscopy



2) X-ray crystallography

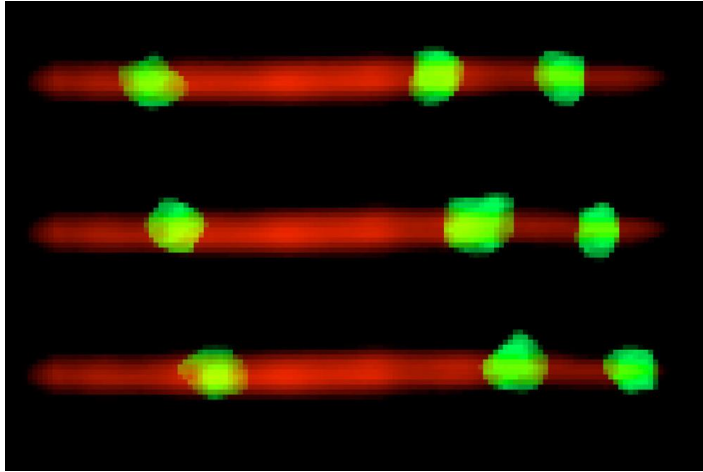


3) MD simulation

# MD simulation as a powerful tool

A comparison of tools for studying a single protein:

1) Single molecule microscopy



2) X-ray crystallography



3) MD simulation

# MD simulation as a powerful tool

A comparison of tools for studying a single protein:

3) MD simulation



# Practice of MD simulations

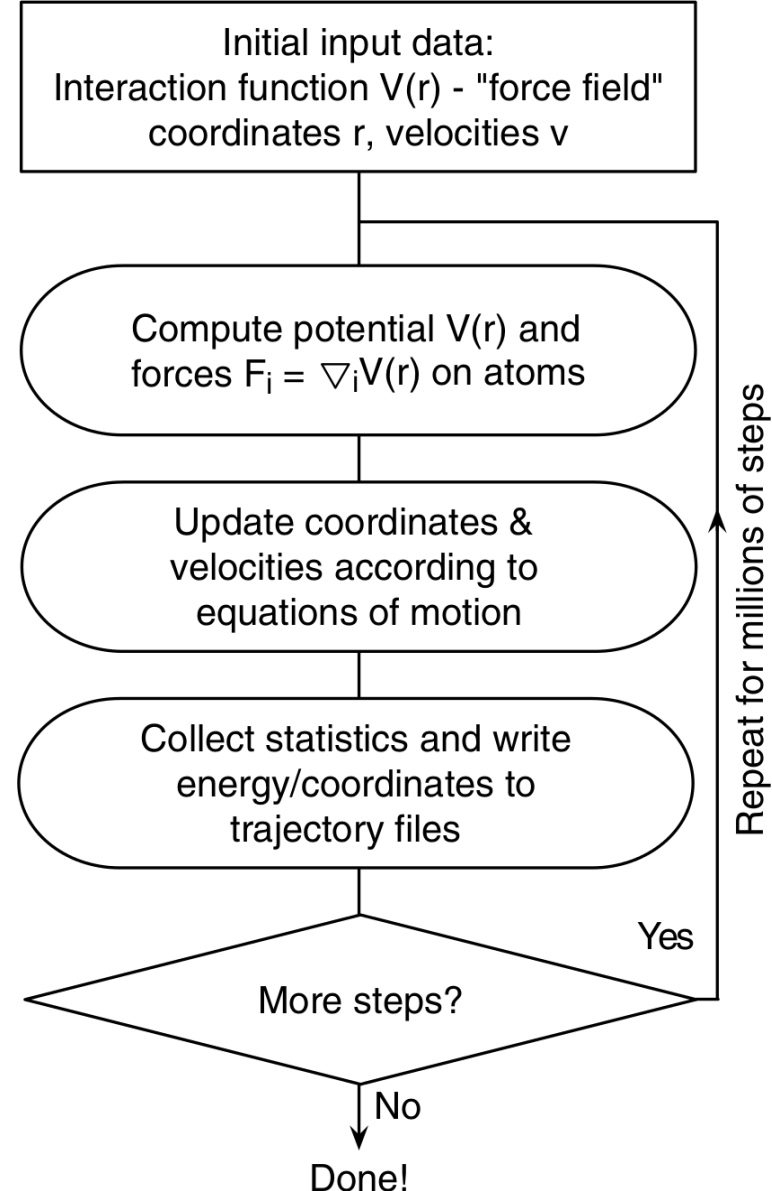
## Common procedure of MD simulations (Analysis not included)

*Implementation of classical mechanics*  
*Newton's equation of motion:*

$$m_i \vec{a}_i = \vec{F}_i$$

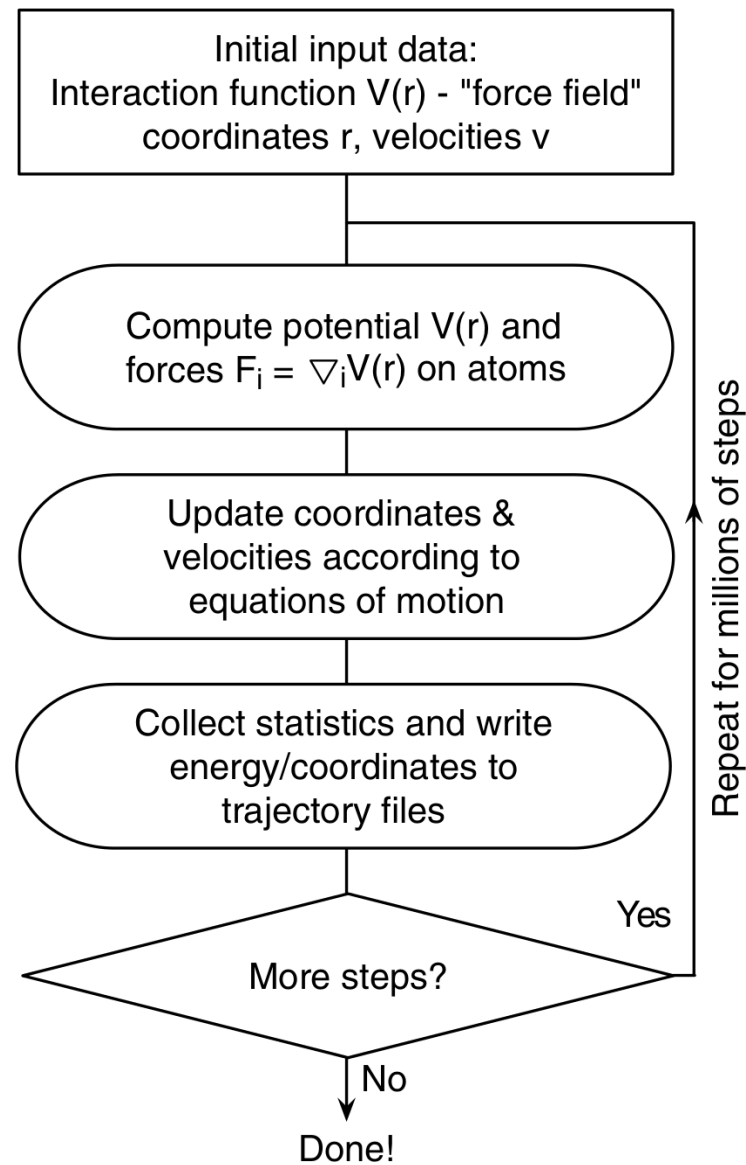
$$m_i \frac{d\vec{v}_i}{dt} = \vec{F}_i$$

$$m_i \frac{d^2\vec{r}_i}{dt^2} = \vec{F}_i$$



*This part is the atomistic modeling section, and deviates depends on individual project.*

*This part is the real MD running section. Generally, one simple command.*





# Practice of MD simulations

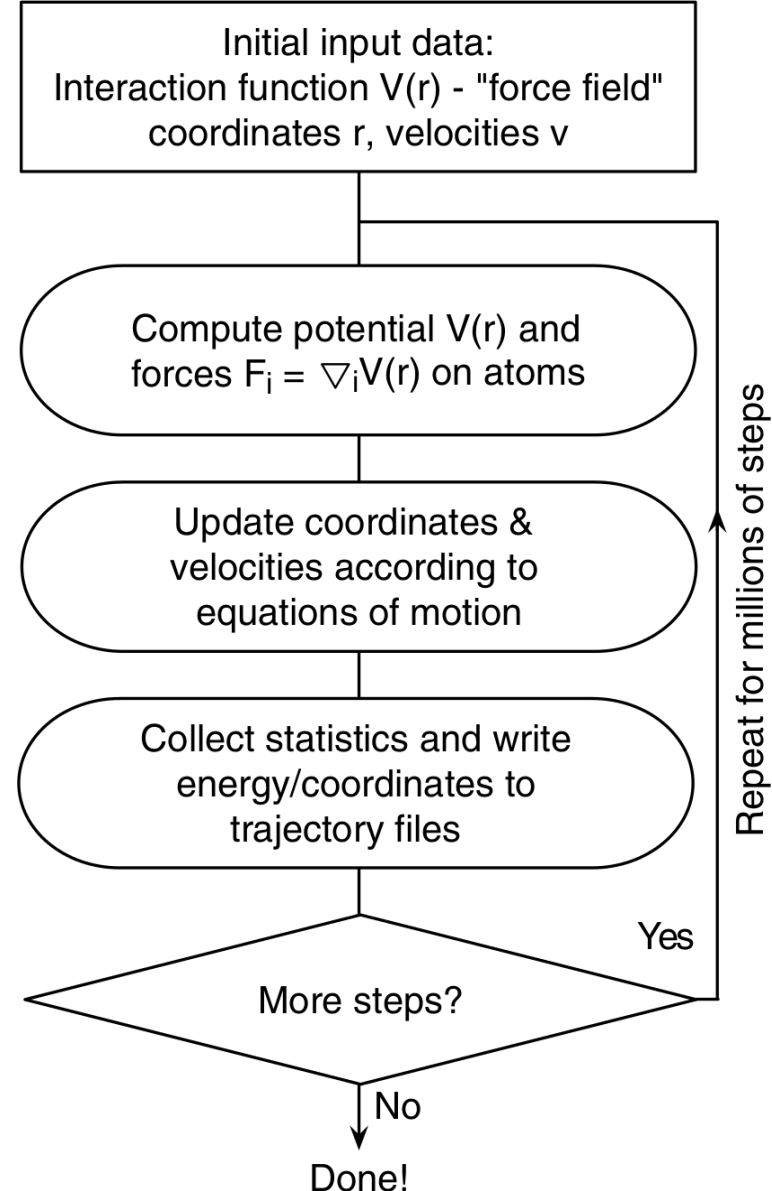
## Common procedure of MD simulations (Analysis not included)

*There are multiple ways to calculate  
force in simulations:*

*ab initio MD*

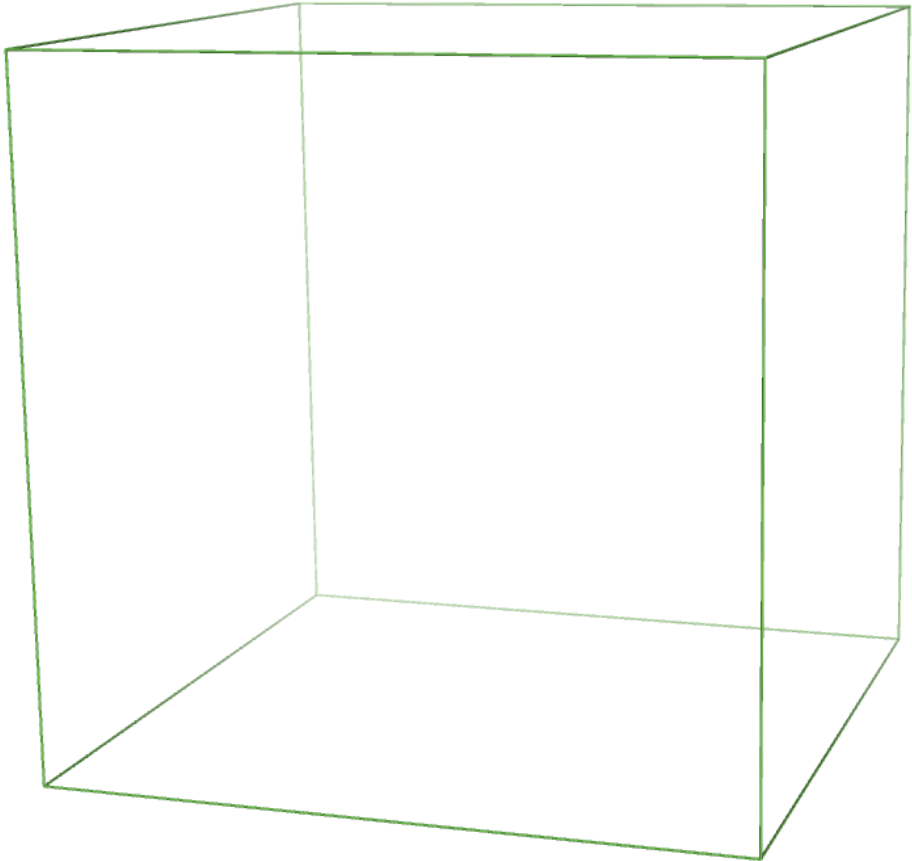
*first-principles MD*

...



# Practice of MD simulations

## Building a MD simulation system from scratch

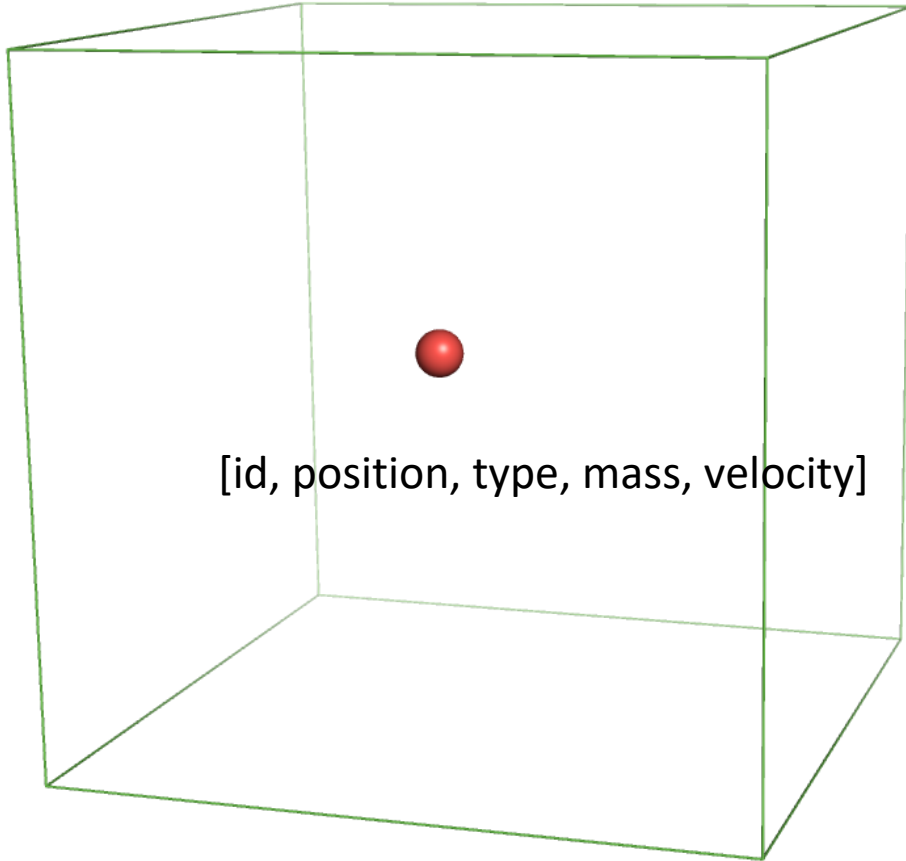


Setting simulation box

Setting up boundary

# Practice of MD simulations

## Building a MD simulation system from scratch

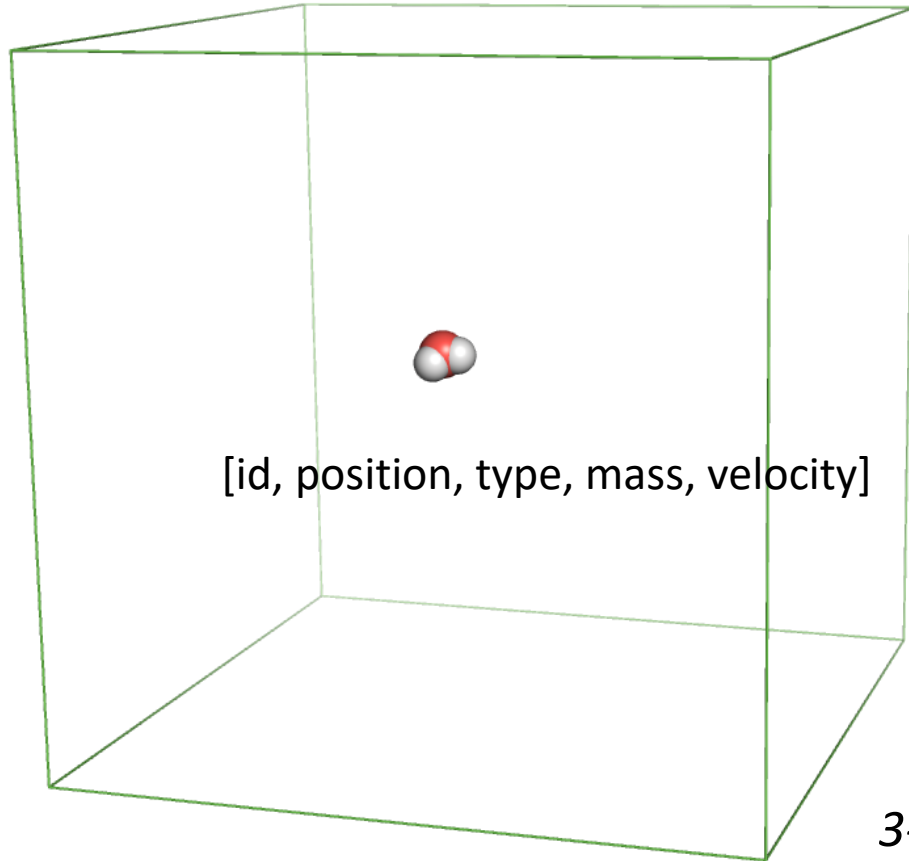


Putting points in the box

Defining properties

# Practice of MD simulations

## Building a MD simulation system from scratch



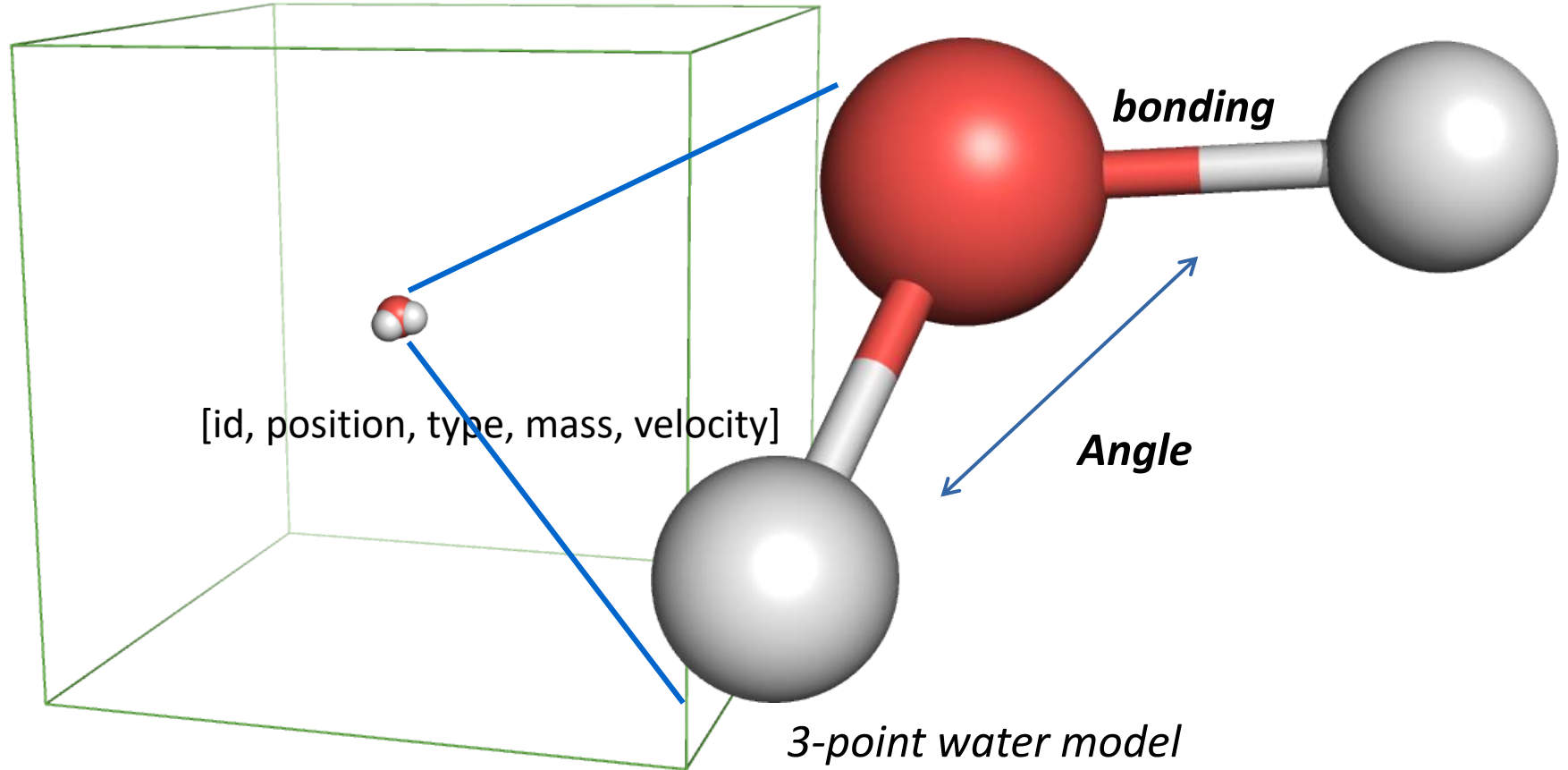
Putting more points

Defining more properties

*3-point water model*

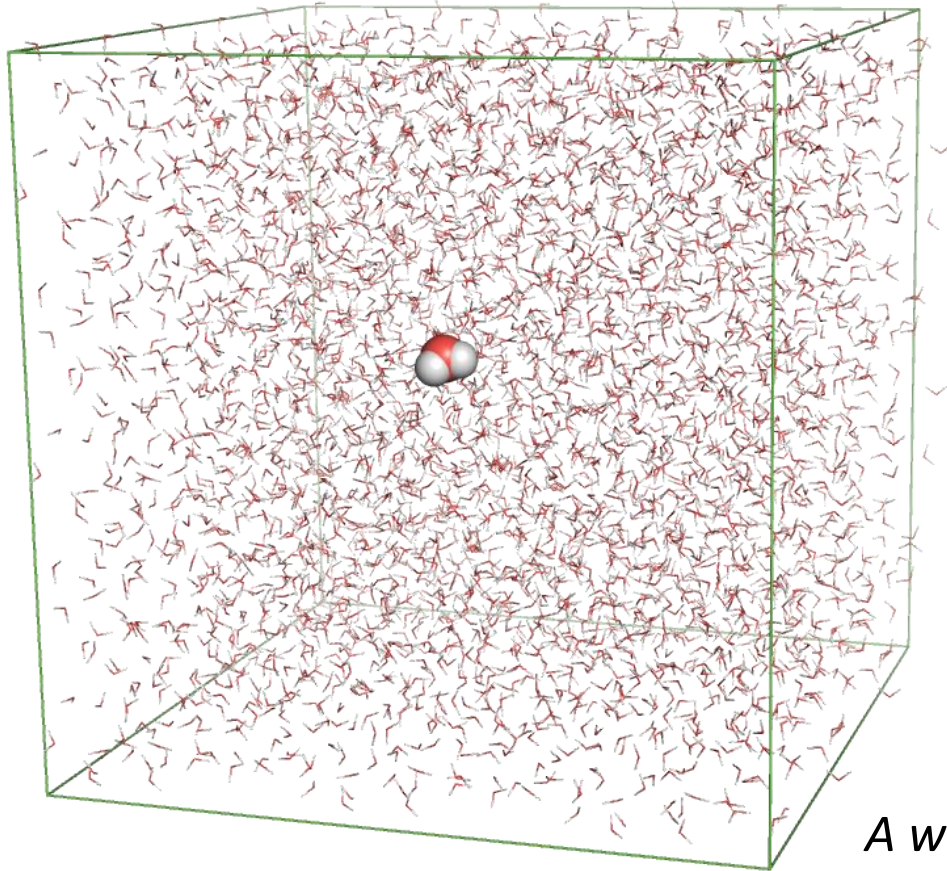
# Practice of MD simulations

## Building a MD simulation system from scratch



# Practice of MD simulations

## Building a MD simulation system from scratch



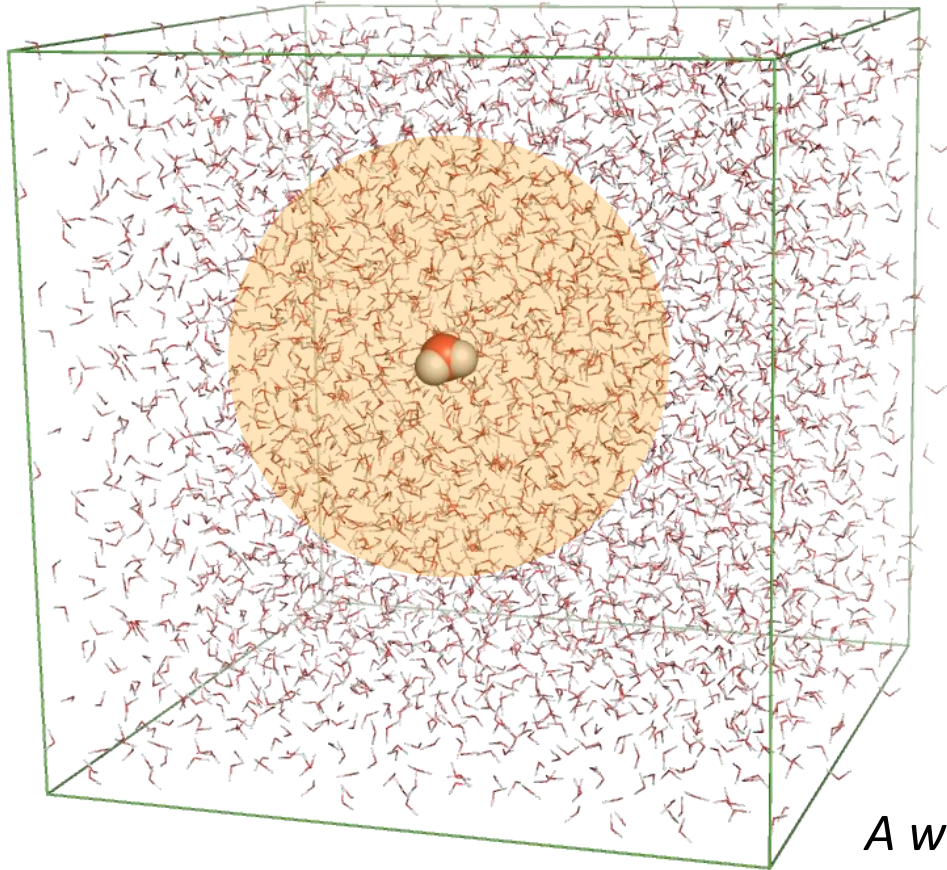
Making many

Copy & paste

*A water box*

# Practice of MD simulations

## Building a MD simulation system from scratch



*A water box*

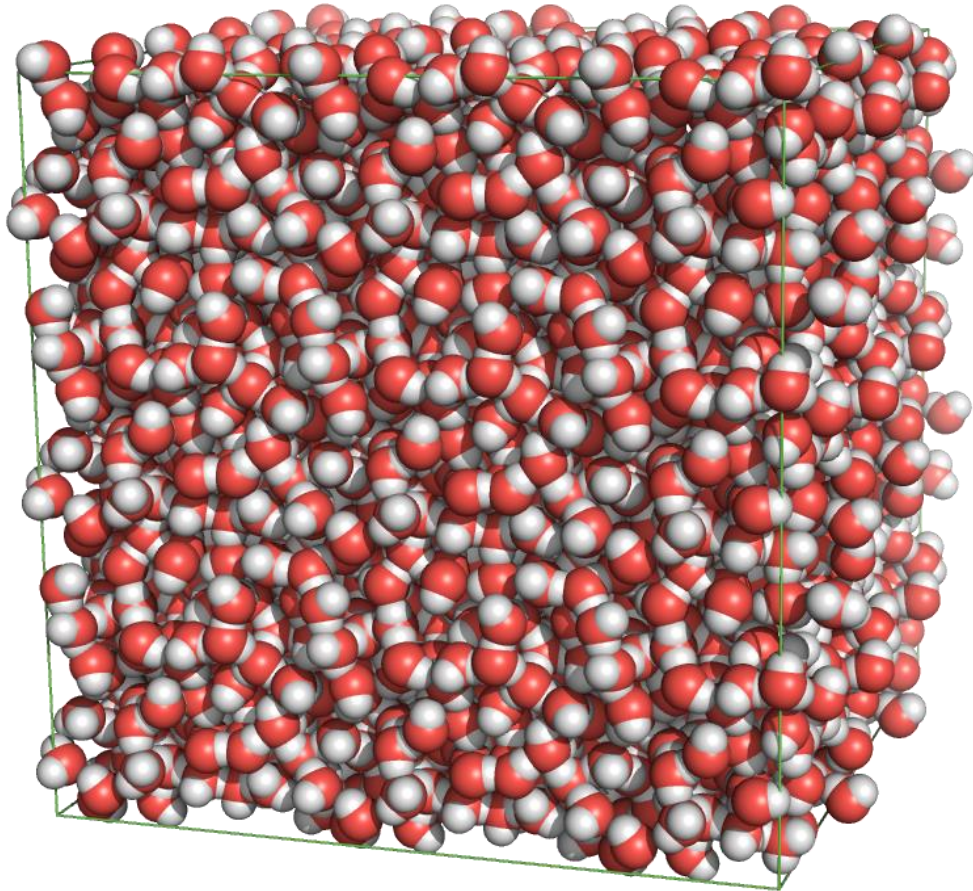
Computational efficiency

Defining cut-off



# Practice of MD simulations

## Building a MD simulation system from scratch



Done structural modeling



# Practice of MD simulations

## Building a MD simulation system from scratch

*Modeling process*

*1. simulation box*

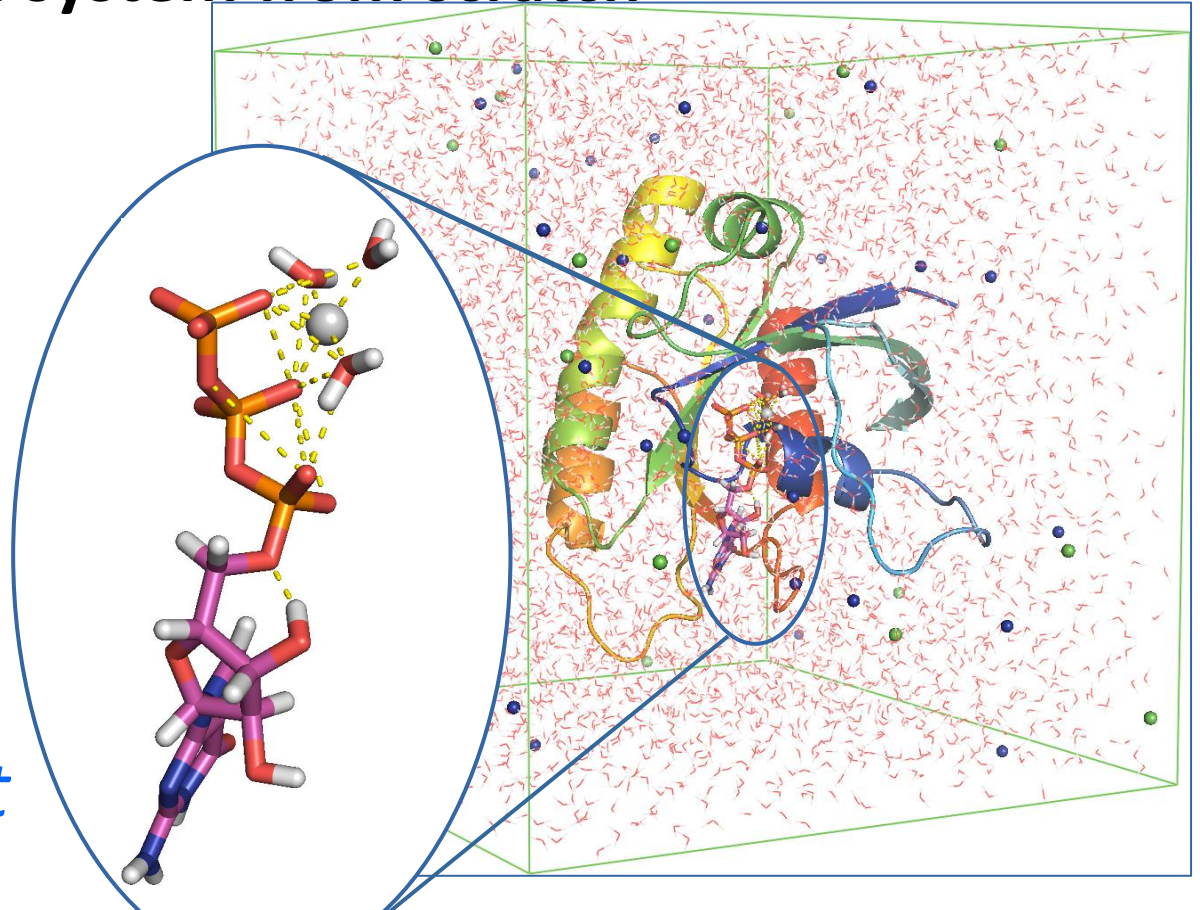
*2. boundary*

*3. biomolecules*

*4. ligands*

*5. solvation*

*6. cytosol environment*

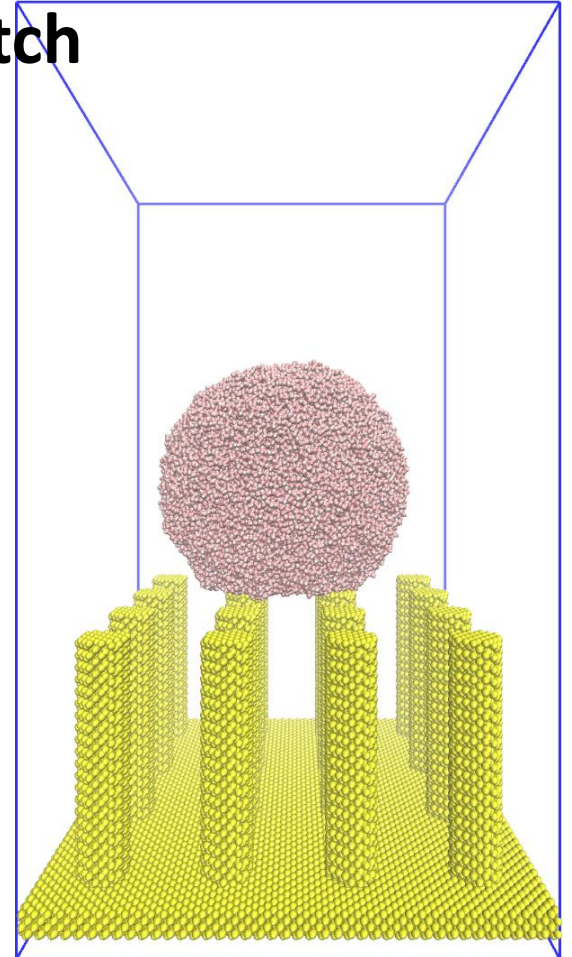
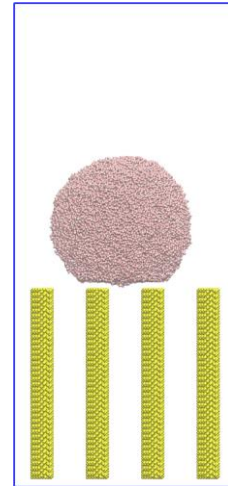


# Practice of MD simulations

## Building a MD simulation system from scratch

Modeling process

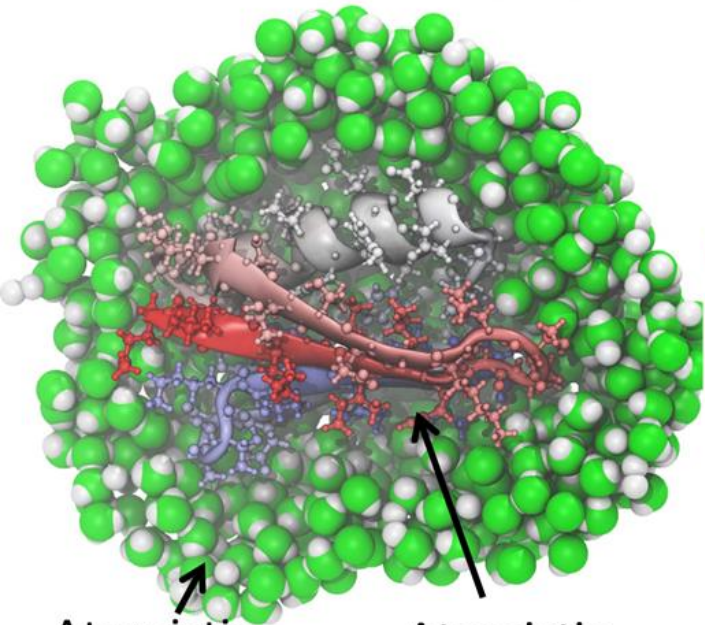
- 1. simulation box*
- 2. boundary*
- 3. periodicity?*
- 4. water droplet size?*
- 5. pillar height?*



# Practice of MD simulations

## Complexities and resolutions

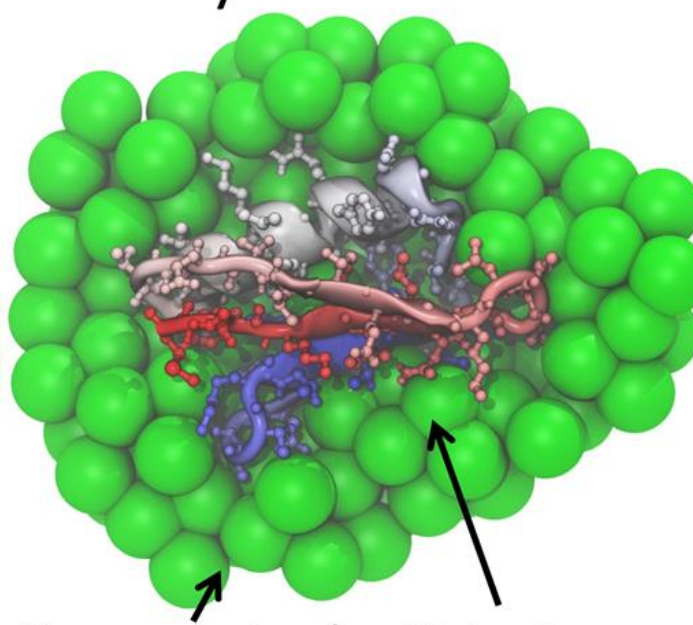
Atomistic Model



Atomistic  
Water

Atomistic  
Protein

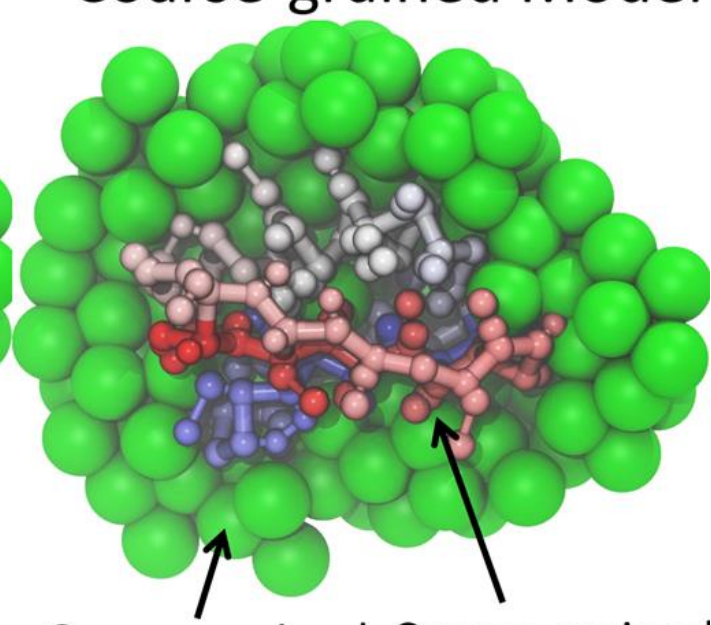
Hybrid Model



Coarse-grained  
Water

United-atom  
Protein

Coarse-grained Model



Coarse-grained  
Water

Coarse-grained  
Protein

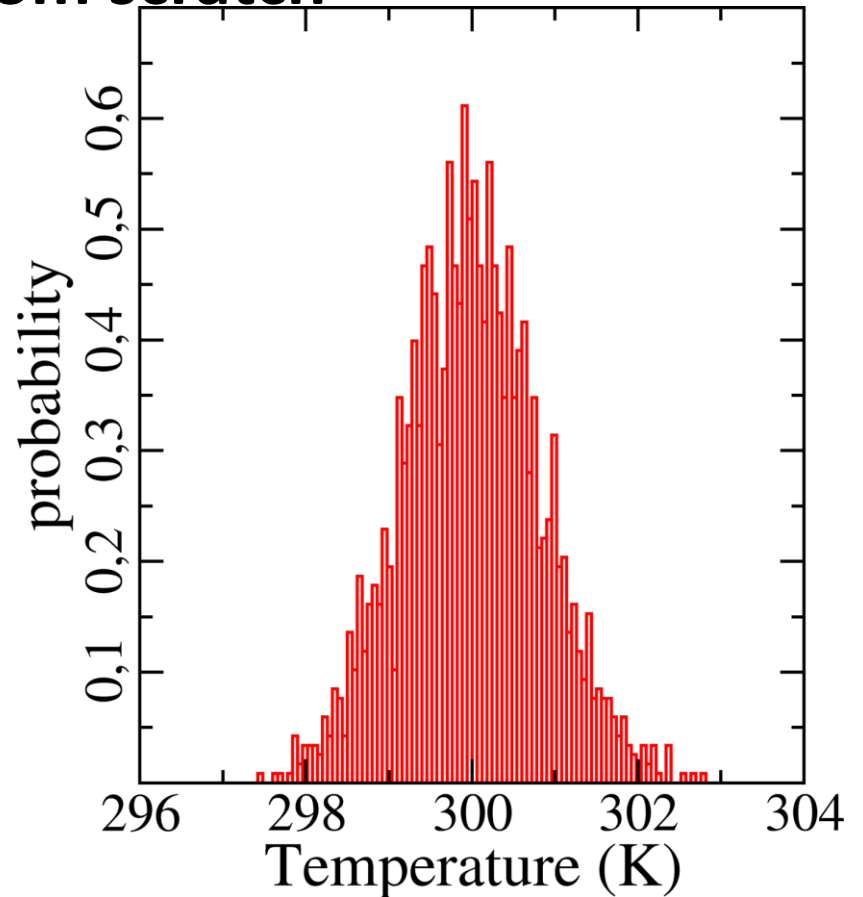
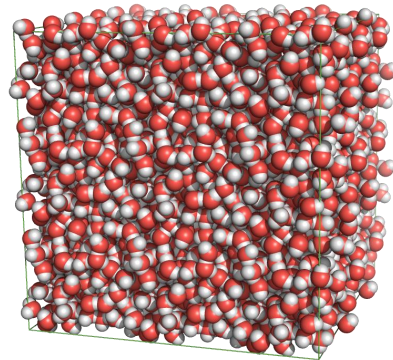


# Practice of MD simulations

## Building a MD simulation system from scratch

Define temperature  
by assign velocities on particles

$$\left\langle \frac{1}{2} m_i v_i^2 \right\rangle = \frac{3}{2} k_b T$$

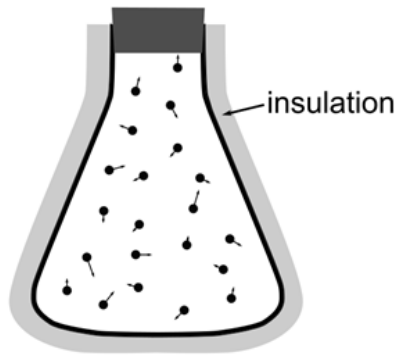


# Practice of MD simulations

## Building a MD simulation system from scratch

Choose ensemble (simulation conditions):

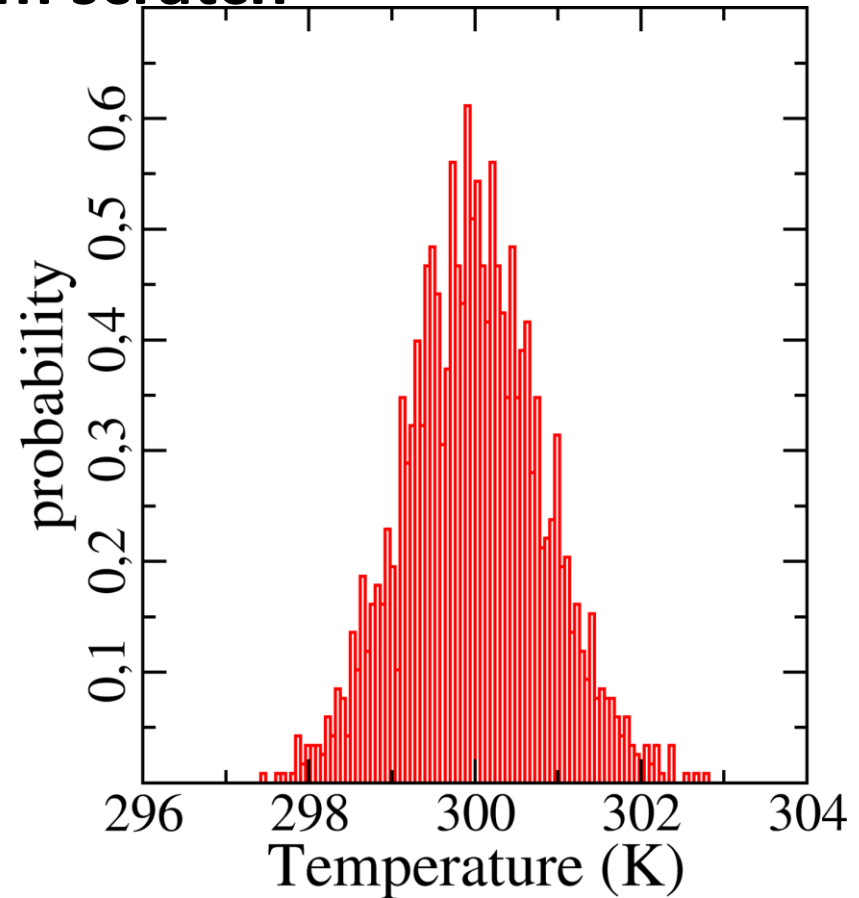
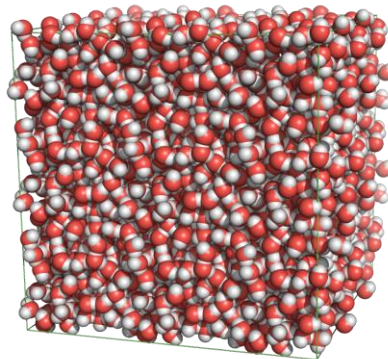
**Npt, NVT, NVE, ...**



Microcanonical



Canonical

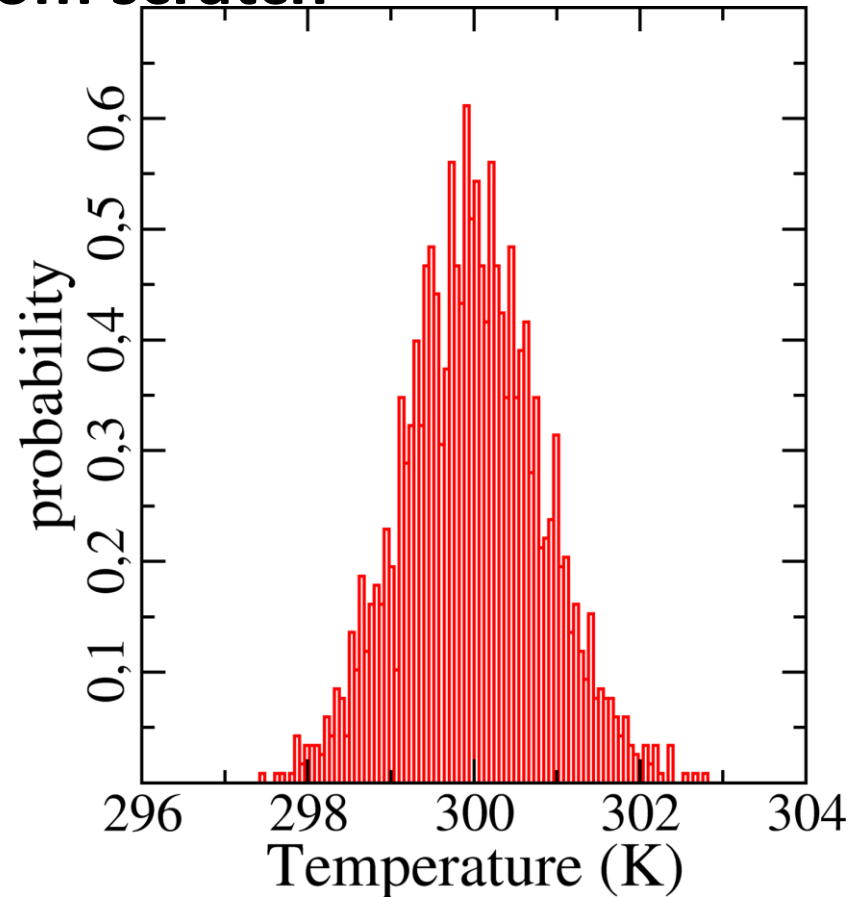
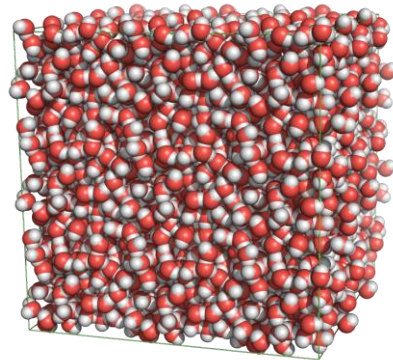
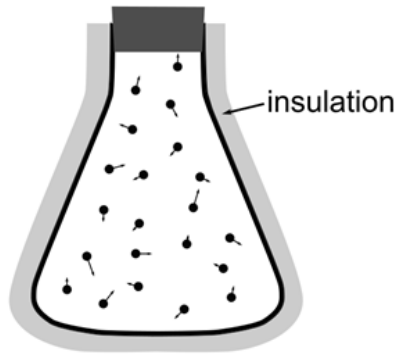


# Practice of MD simulations

## Building a MD simulation system from scratch

Pressure tensor:

$$P = \frac{1}{V} \left\{ \sum_i m v_i^2 - \sum_{i < j} r_{ij} F_{ij} \right\}$$



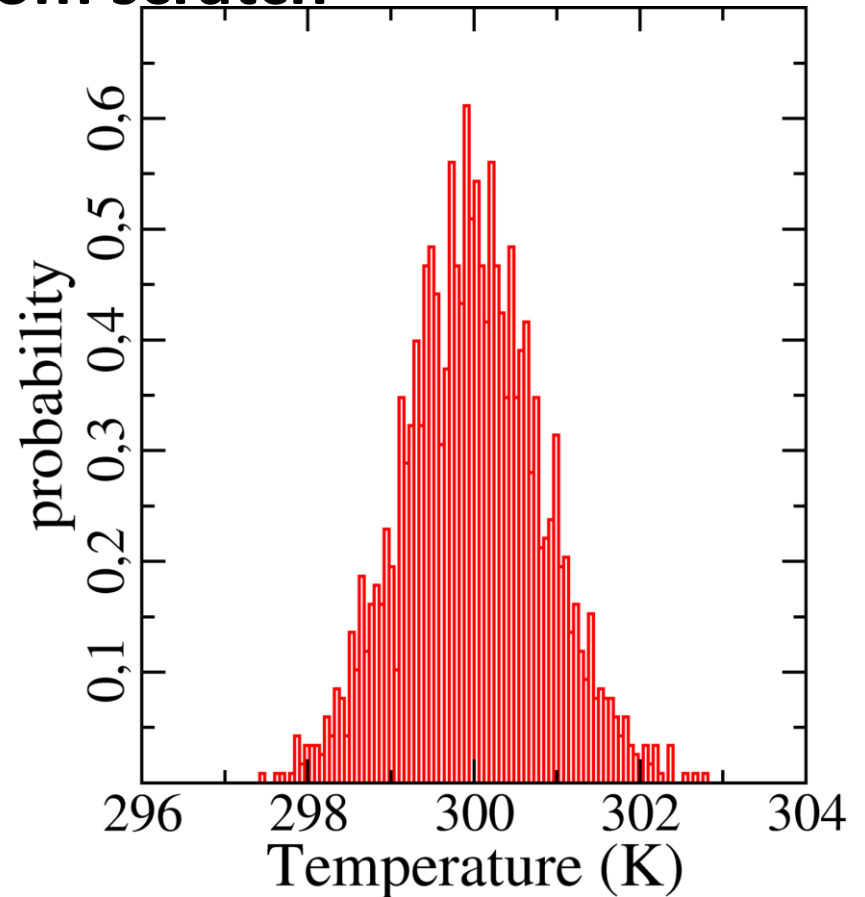
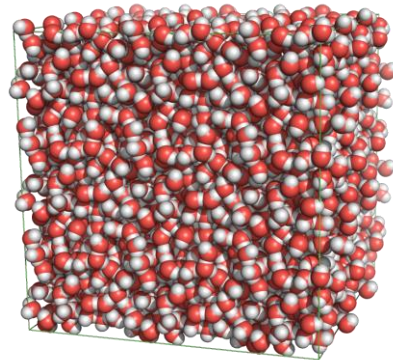
# Practice of MD simulations

## Building a MD simulation system from scratch

Setting constraint, adding extra field,  
applying force, ...

Setting output frequency and  
variables.

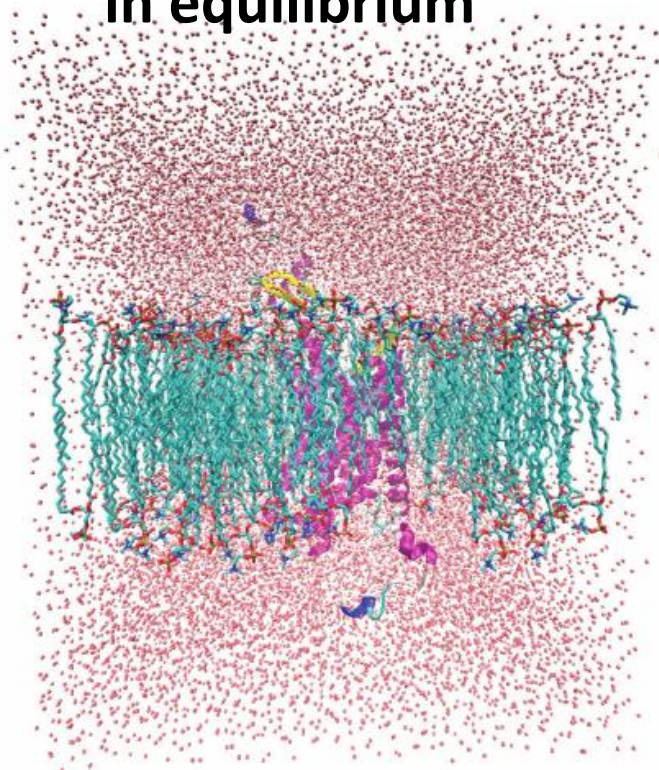
Run and collect data ....



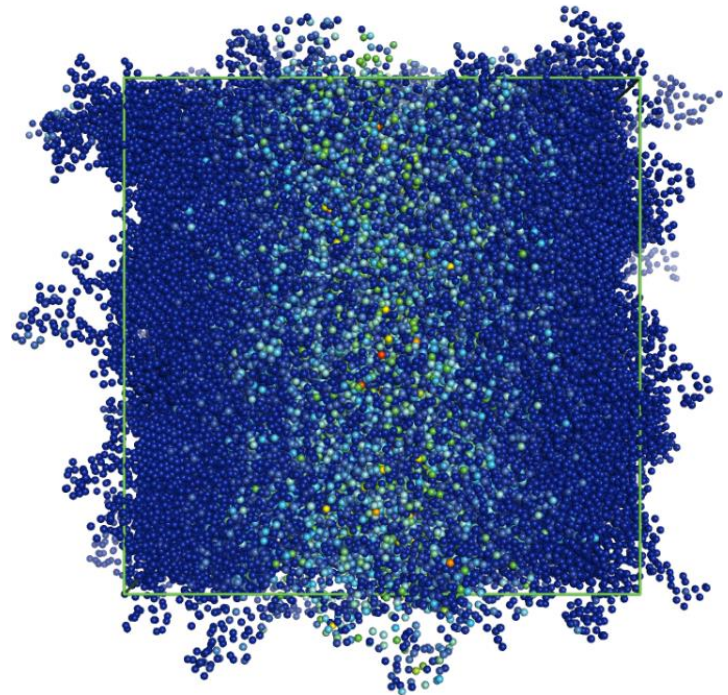
# Practice of MD simulations

## Equilibrium vs. Non-equilibrium

**Membrane protein  
in equilibrium**



**Thermal transport in  
polymer nanocomposites**





# Practice of MD simulations

## General guidelines:

- Think about **the question** before doing anything
- Choose or borrow potential/force-field parameters if possible
- (try not to make new potential/force-field parameter)
- Statistics, repetition and repetition
- Control simulations, significance tests
- ...

# Molecular Dynamics (MD) simulations

## **Chemistry and biology**

*Structural prediction, drug design, energy calculation,  
dynamics of large biomolecules, ...*

## **Computational physics and statistics**

*theory verification, many-body motion,  
ensemble properties, phase transition, ...*

## **Materials science**

*crystal defects, material performance, microscopic  
fracture, interface design, melting, nanostructuring, ...*

# Molecular Dynamics (MD) simulations

## Pros:

1. Only need description of inter-atomic interactions
  2. No assumption is made
  3. Provide atomistic coordinate and velocity trajectories
- ...

## Cons:

1. Classical inter-atomic interactions
  2. Poor description of light elements' motion
  3. Small time and size scales
- ...

# Further reading

1. D. Frenkel, B. Smit

## **Understanding Molecular Simulation**

*-From Algorithms to Applications*

Academic Press

2. D. C. Rapaport

## **The Art of Molecular Dynamics Simulation**

Cambridge University Press