

Instructions for Major exam

- Major exam: 12th April 2022, 2:15 pm-4:15 pm, LH108 and LH521.
- One hour exam on MOODLE in OFFLINE mode.
- Syllabus: Lectures taught after the MINOR exam.
- Please make sure that your laptop battery is working fine and can hold charge upto 1.5 hrs atleast.
- Please ensure that your laptop is able to connect to the IITD network without any hardware issues.
- No excuse of laptop getting discharged or any technical faults will be considered. In such a case, no request for Viva or re-major will be considered. It is your responsibility to ensure that your exam can go smoothly.
- All of you must attempt the exam. No re-major /viva requests will be entertained at any cost.

Lecture 35

Molecular dynamics simulations

Textbooks:

- Computational Materials Science: J. Gunn Lee
- Molecular Modelling Principles and Applications: Andrew Leach (Chapter 4)
- **Understanding Molecular Simulations: D. Frenkel and B. Smit (Chapter 4)**

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Recap...

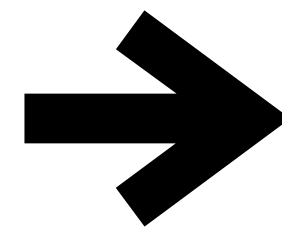
- Computational materials science: Introduction
- Modeling in simulations: potential energy surface and multi-scale modeling
- Developing a model

Computational experiment: *Recipe*

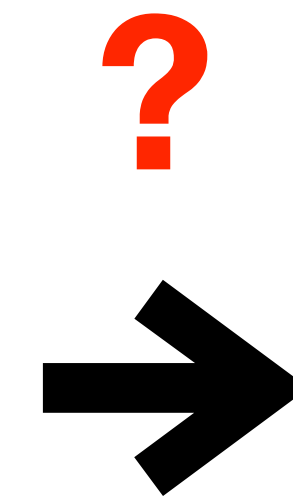
Turning complex ideas into solvable equations



Define a problem

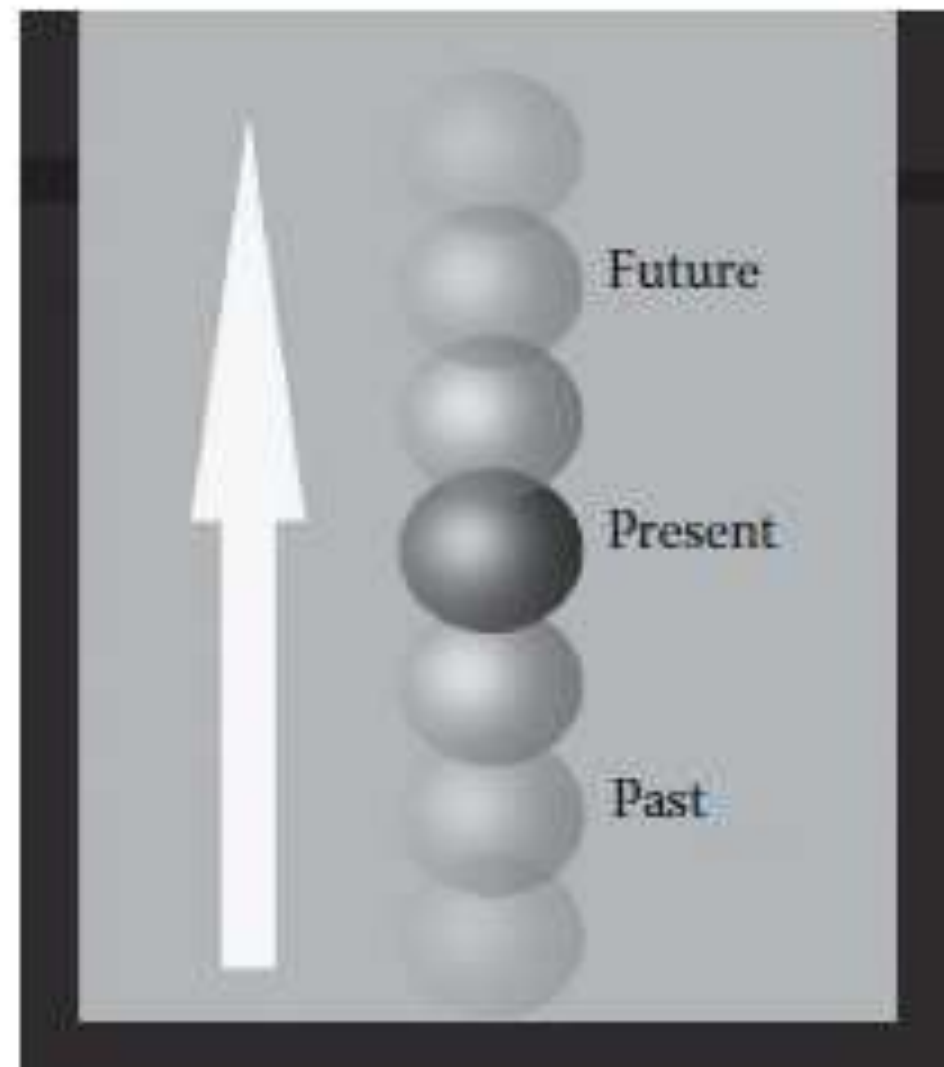


Build a model



- Theory: set of rules to follow
- Simulation: algorithm to solve the problem
- Computer: ???

Classical Systems



Thermal de Broglie wavelength

$$\Lambda = \frac{h}{2\pi m k_B T}$$

h = Planck's constant
T = temperature
m = mass of particle
k_B = Boltzmann's constant

For a system to be classical, the wavelength should be much lesser than the inter-particle spacing

$$\Lambda \ll d$$

Hamiltonian for electronic systems

$$\hat{H} = \sum_{i=1}^N \left(\frac{-\hbar^2}{2m_i} \nabla_i^2 + \hat{V}_i \right)$$

Kinetic energy operator Potential energy operator

Hamiltonian for classical systems

$$H = \sum_i^N \frac{p_i^2}{2m_i} + U(r_1, \dots, r_N)$$

Kinetic energy Potential energy

6N-dimensional hypersurface (phase space)

Opening lines of "States of Matter", D.L. Goodstein

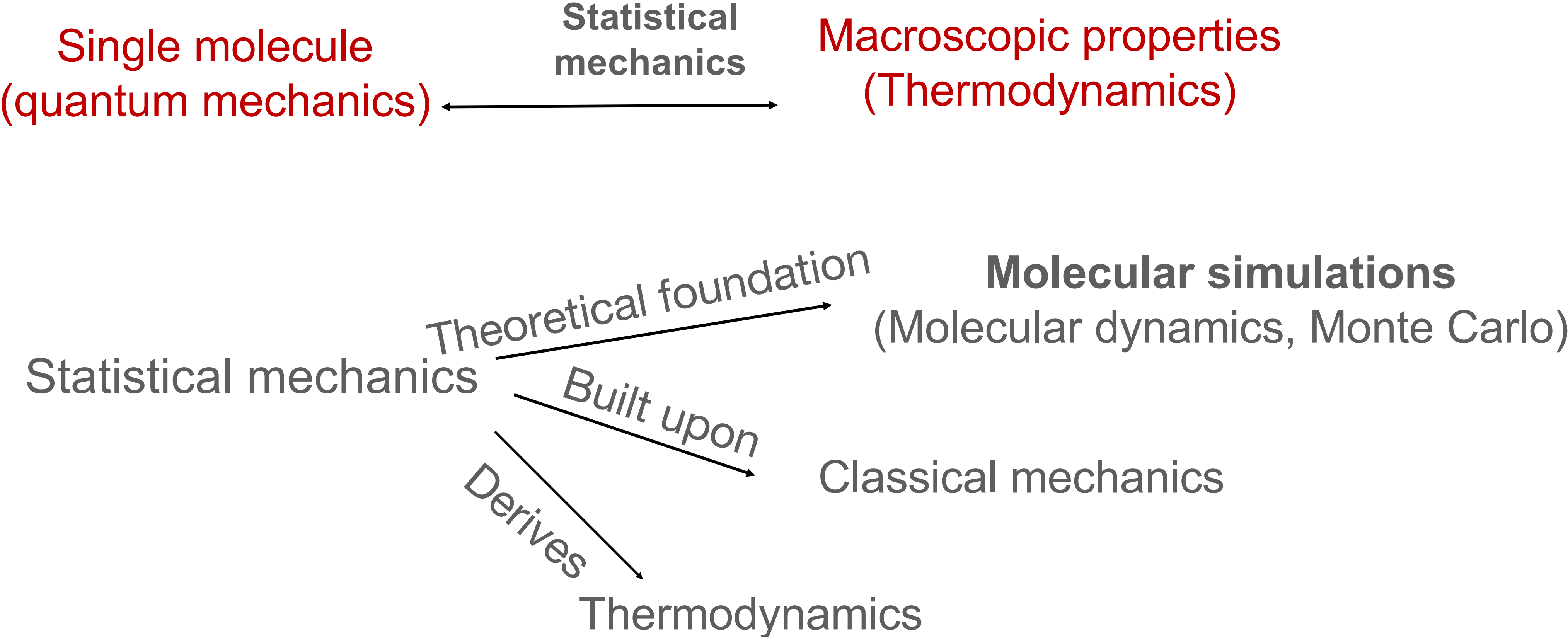
STATISTICAL MECHANICS

1.1 INTRODUCTION: THERMODYNAMICS AND STATISTICAL MECHANICS OF THE PERFECT GAS

Ludwig Boltzmann, who spent much of his life studying statistical mechanics, died in 1906, by his own hand. Paul Ehrenfest, carrying on the work, died similarly in 1933. Now it is our turn to study statistical mechanics.

Perhaps it will be wise to approach the subject cautiously. We will begin by considering the simplest meaningful example, the perfect gas, in order to get the central concepts sorted out. In Chap. 2 we will return to complete

Statistical Mechanics (The Theory)



Some definitions

- **Microstate:** A state or configuration of the system in which the constituent elements i.e. $3N$ position and $3N$ momentum coordinates are specified.

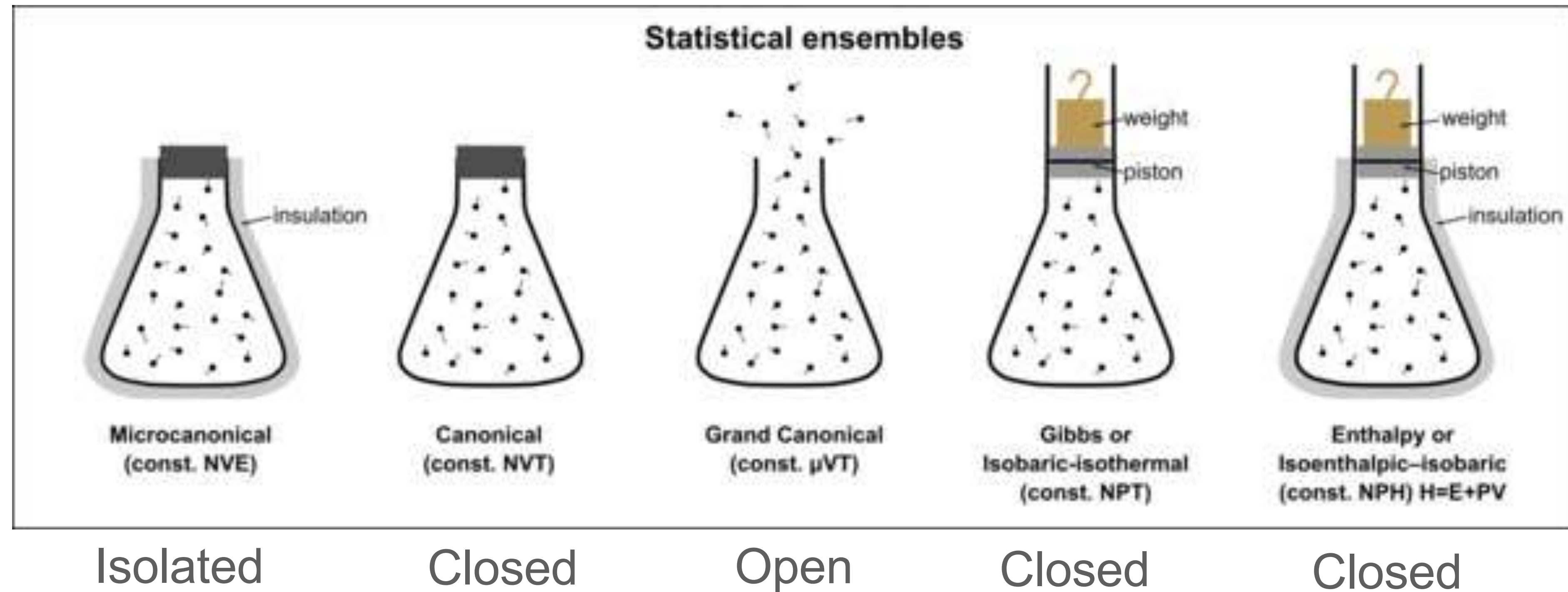
$$\{ \vec{r}_1, \vec{r}_2, \dots, \vec{r}_N; \vec{p}_1, \vec{p}_2, \dots, \vec{p}_N \}$$

- **Ensemble:** A collection of microstates satisfying some common set of macroscopic constraints.
- **Partition function:** Sum over all possible microstates weighted by probability of occurrence of microstates in the ensemble.

Ensembles



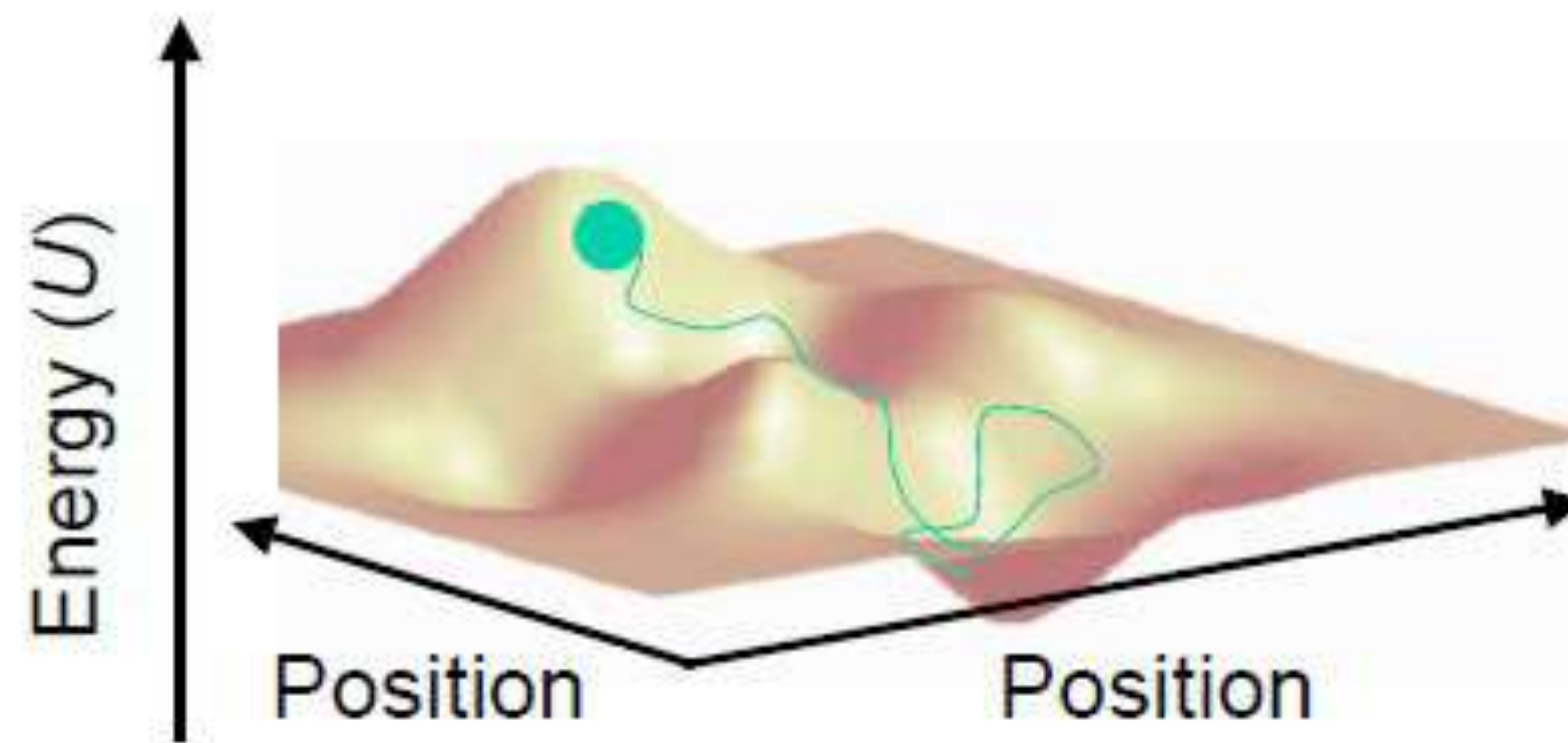
Ensembles



N= no. of particles
V= volume of the system
E= total energy of the system
T= temperature
P= pressure

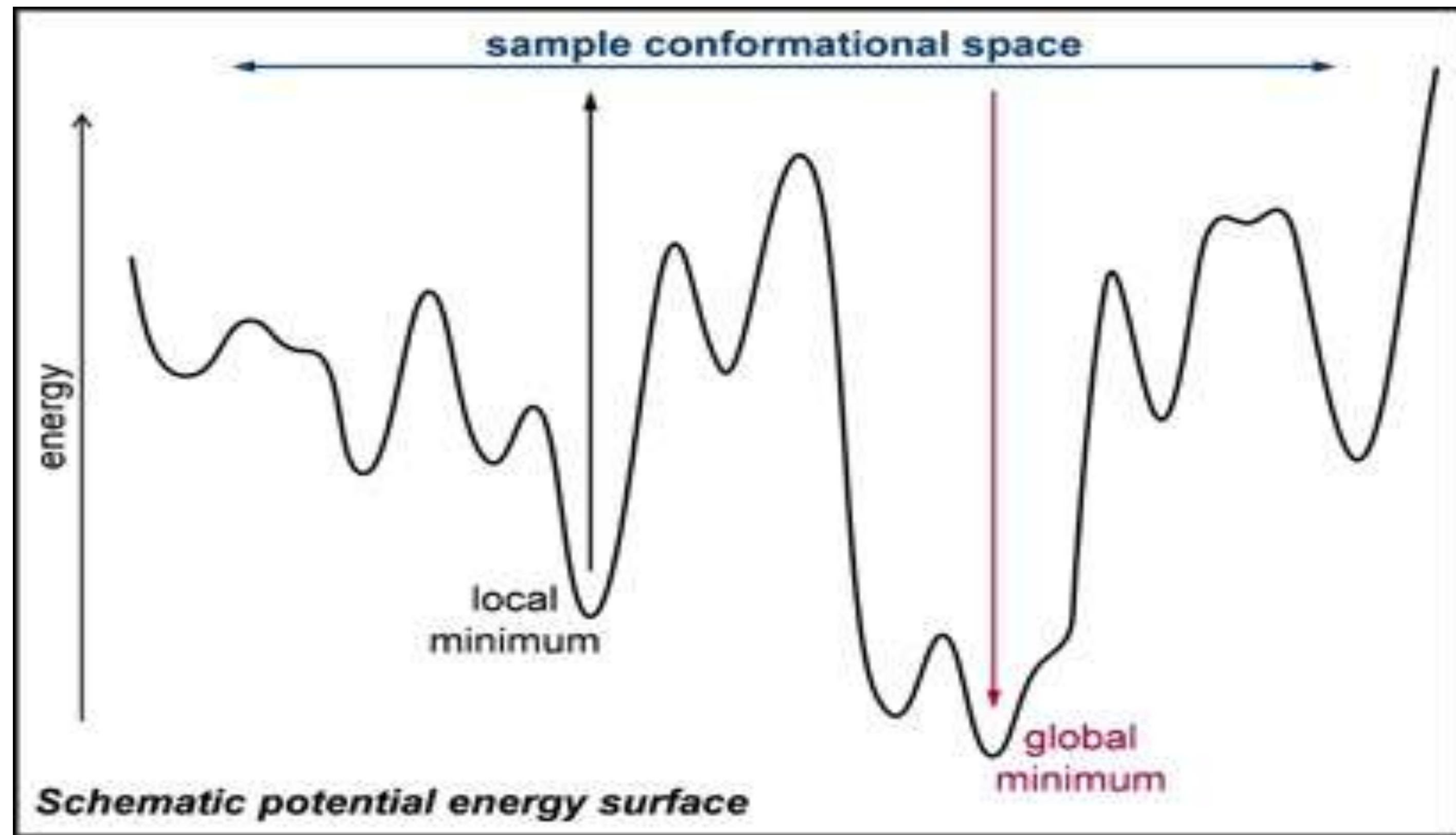
Basic Idea of molecular dynamics simulation

- Mimic the behaviour of atoms in real systems.
- The potential energy function allows to calculate the force experienced by each atom due to the others.
- Newton's law governs the motion of atoms.
- The average behaviour of the system can be observed by sampling all possible points on this landscape.



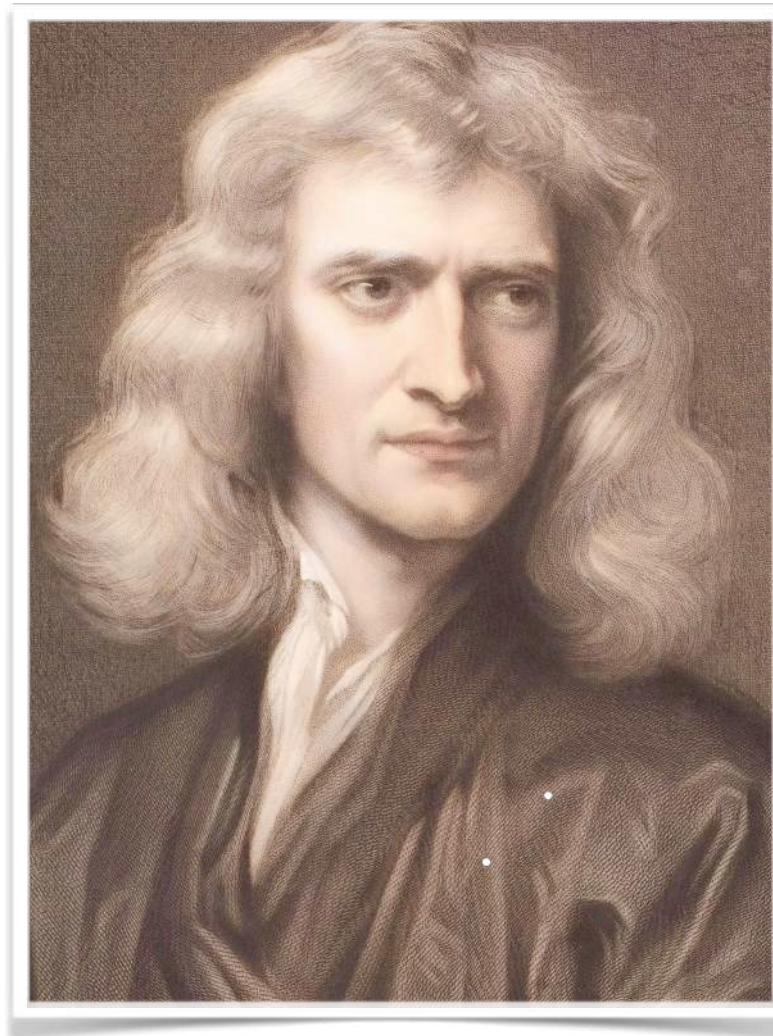
Potential Energy Surface or Potential Energy Landscape

- Each point in the energy landscape corresponds to a “microstate” or configuration of the system
- Target is to sample as many microstates or configurations as possible to obtain an average behaviour or property of the system.



Molecular *dynamics* simulations

Newton's second law of motion



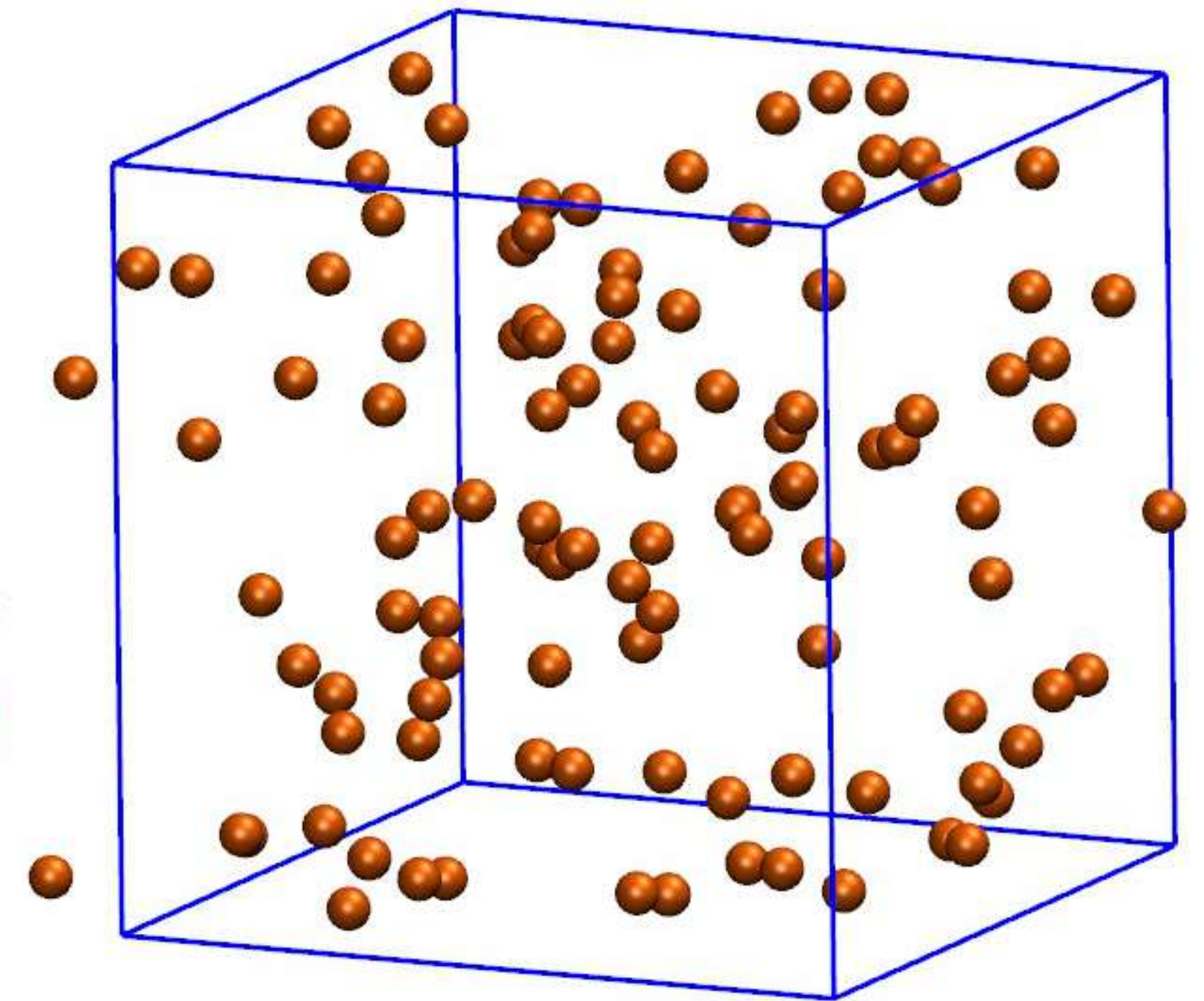
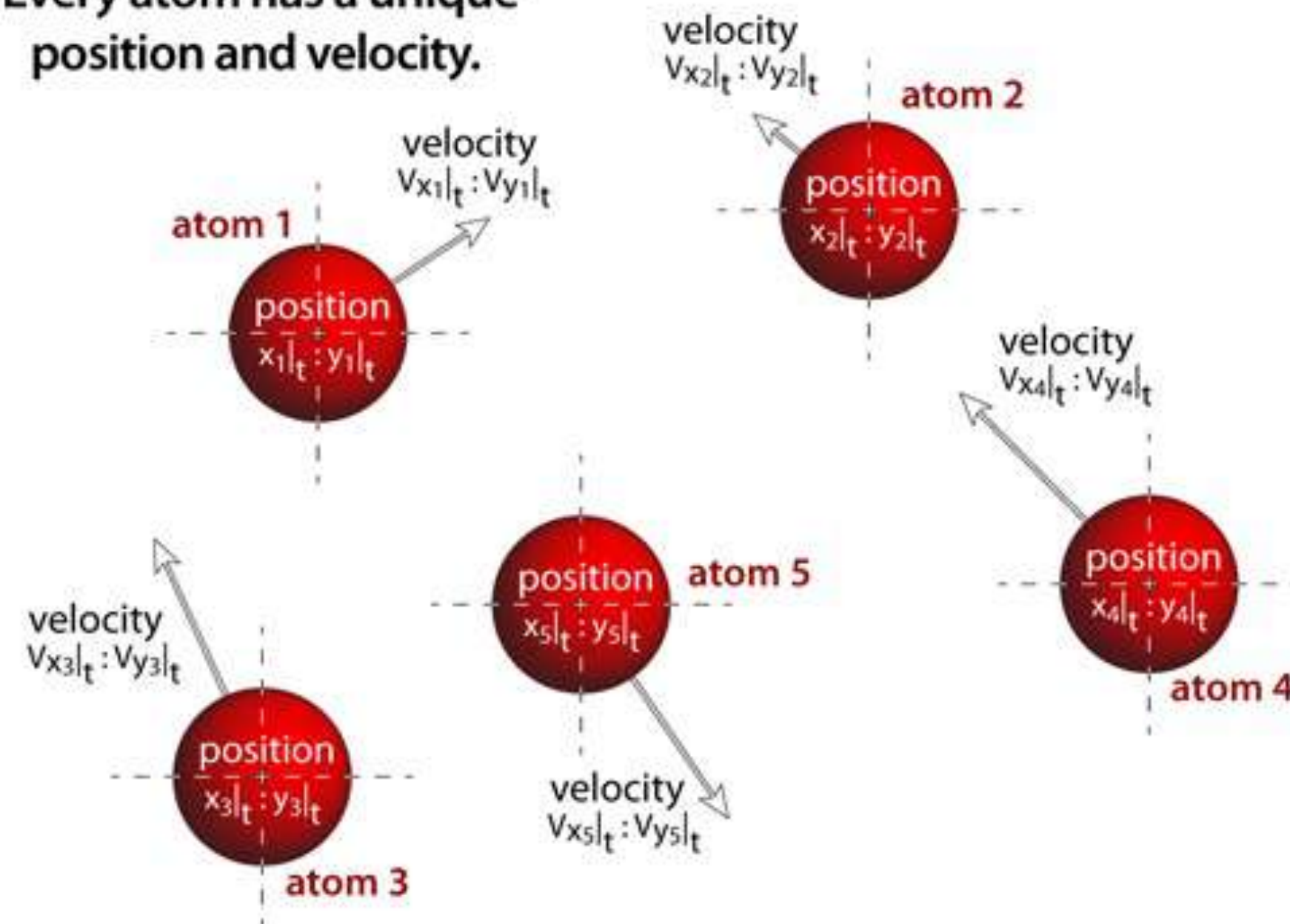
$$\vec{F} = m\vec{a}$$

$$\vec{F}_i = m_i \frac{d^2 \vec{r}_{ij}}{dt^2} = -\nabla U(\vec{r}_{ij})$$

6N-coupled second order
differential equations

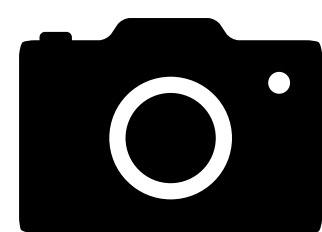
$$U(\mathbf{r}) = \frac{1}{2} \sum_i \sum_{j \neq i} u_{pair}(r_{ij})$$

Every atom has a unique
position and velocity.

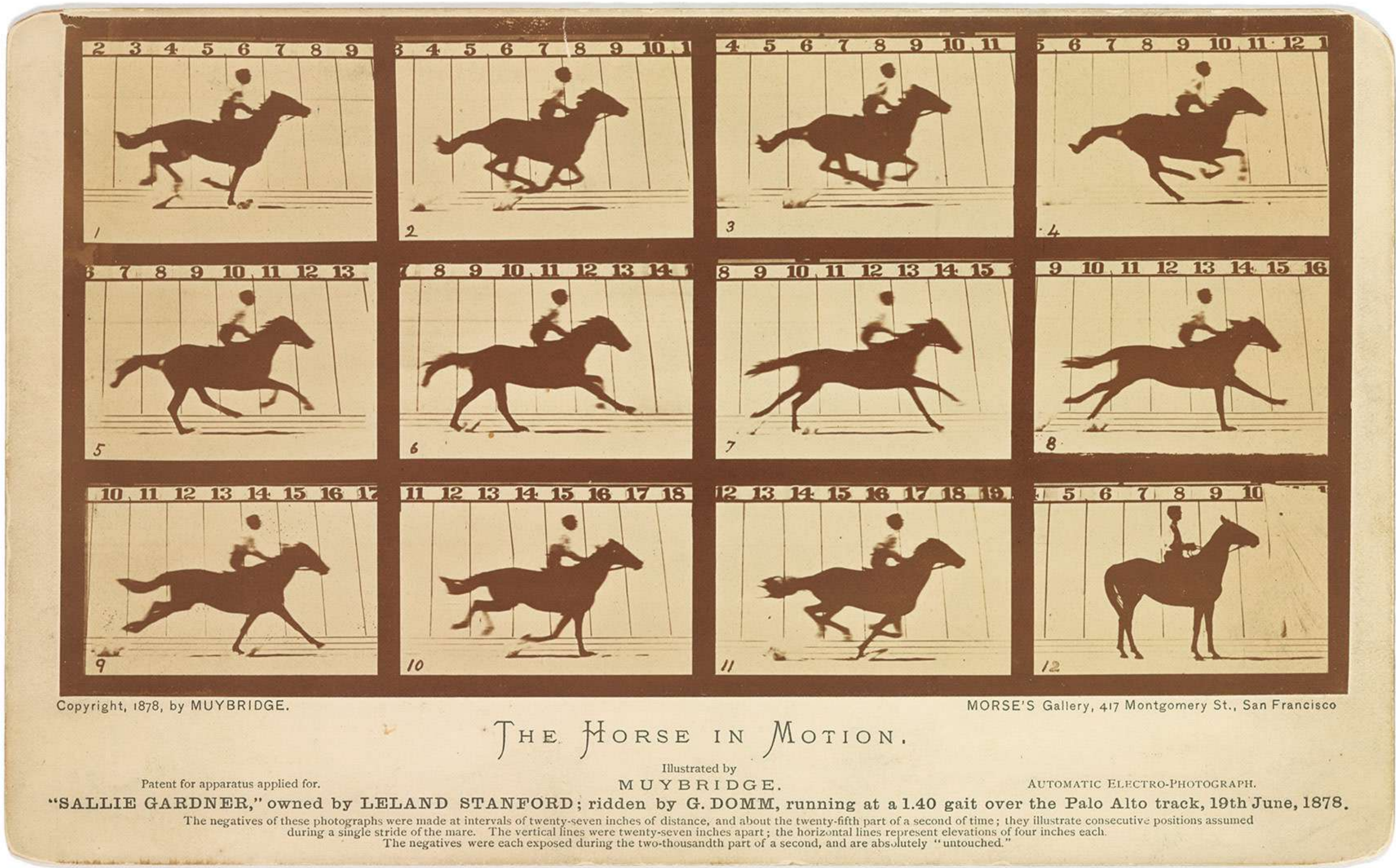


Molecular *dynamics* simulations

In MD, the natural time evolution of a system is computed and the quantity of interest is averaged over a sufficiently long time.



t=0



t=10 mins

Structure of MD algorithm

$\mathbf{r}_i(t_0), \mathbf{v}_i(t_0)$

Initial positions and velocities

$\mathbf{r}_i(t'), \mathbf{v}_i(t')$

Calculate forces at
current time from
positions using $U(\mathbf{r})$

$$U(\mathbf{r}) = \frac{1}{2} \sum_i \sum_{j \neq i} u(r_{ij})$$

$$\mathbf{F}_{ij} = -\nabla U(r_{ij})$$

Integrate equations of motion

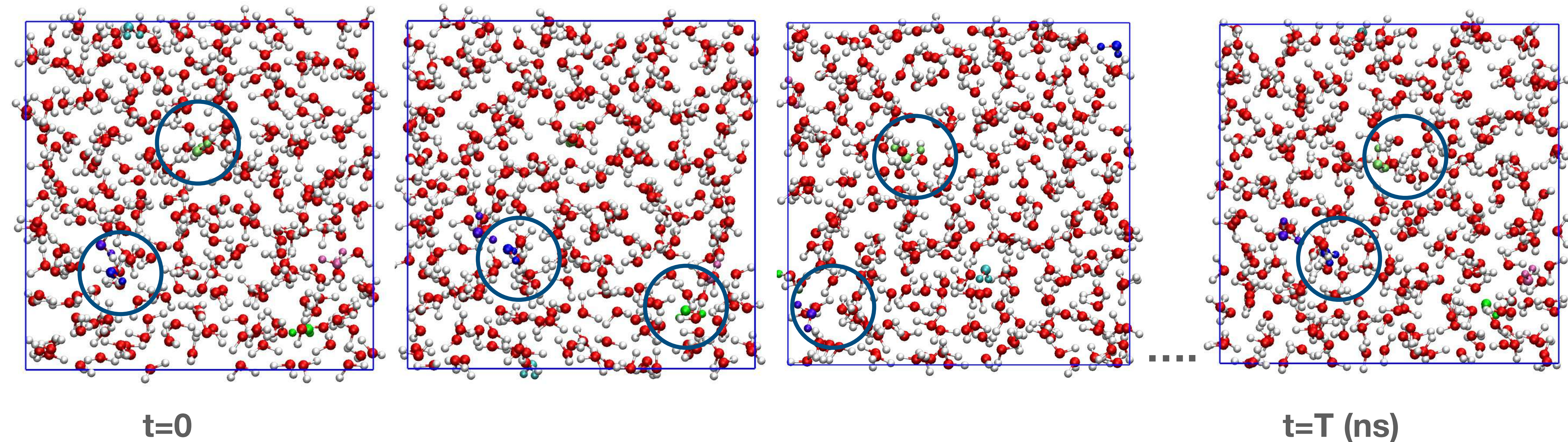
$$\mathbf{a}_i = \frac{\mathbf{F}_{ij}}{m_i}$$

Save Trajectory: \mathbf{r} and \mathbf{v}
(sufficient sampling)

Update

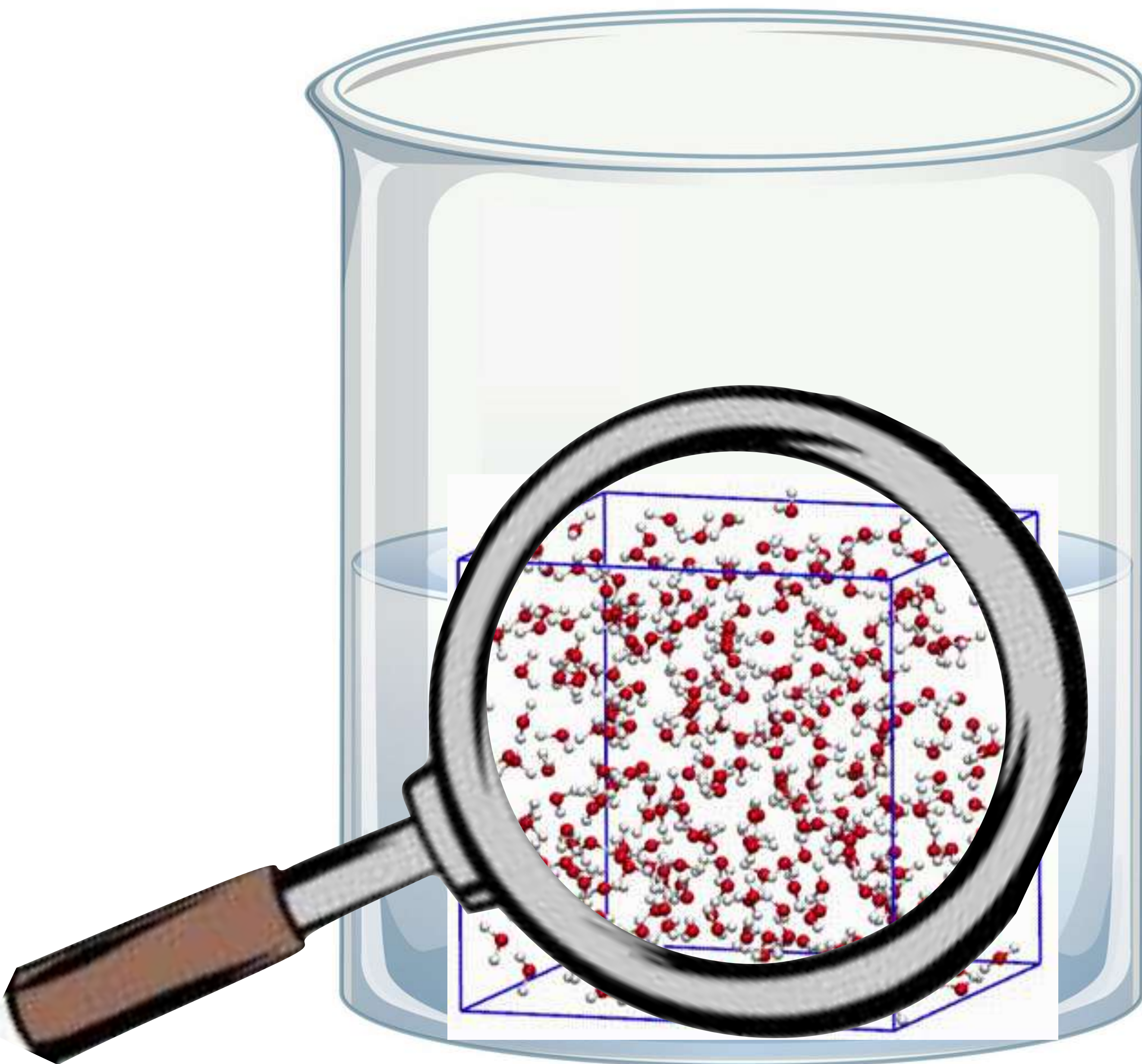
$$t' = t_0 + dt$$

Observing the behaviour of water over time

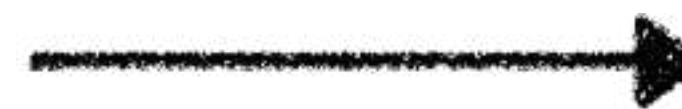


- Average density under certain temperature and pressure conditions
- Hydrogen bonding network
- Diffusion
- Viscosityand many more properties....

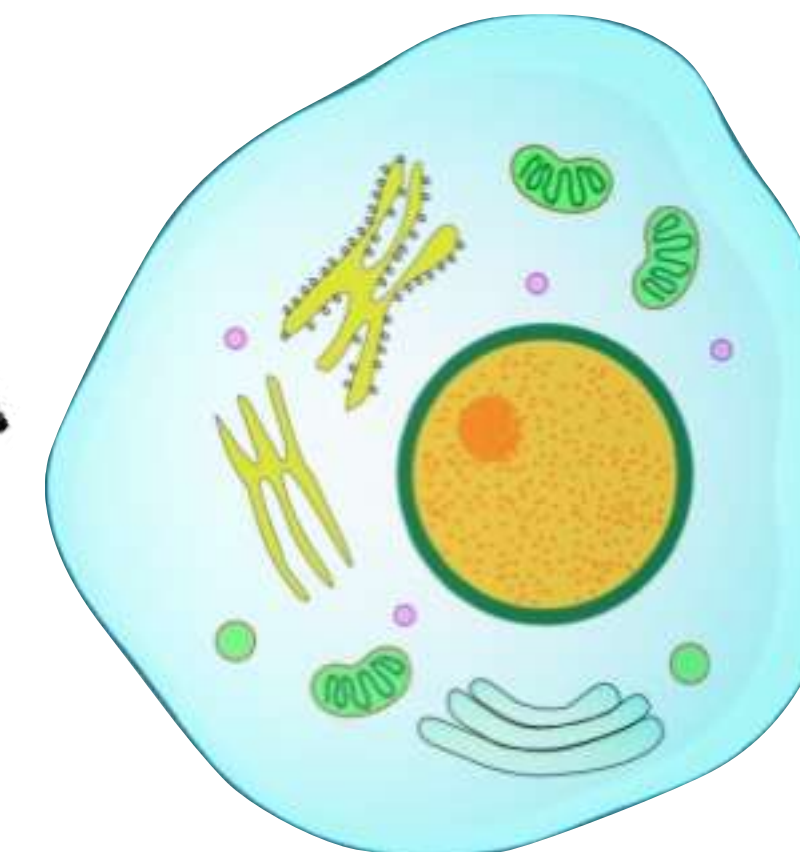
Study water over certain time (nanosceconds)



Solution of
salt/sugar
(Solvent)

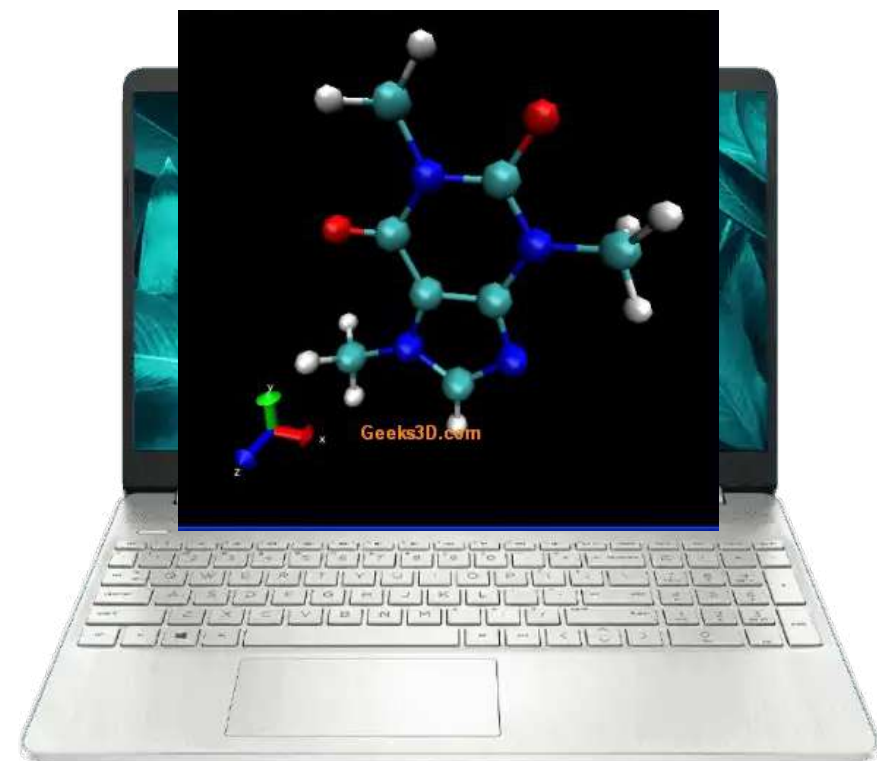


Melting of ice
(Phase diagram)



Solvent for
biomolecules
(Protein folding,
ion transport)

The power of computing and technology



Laptop

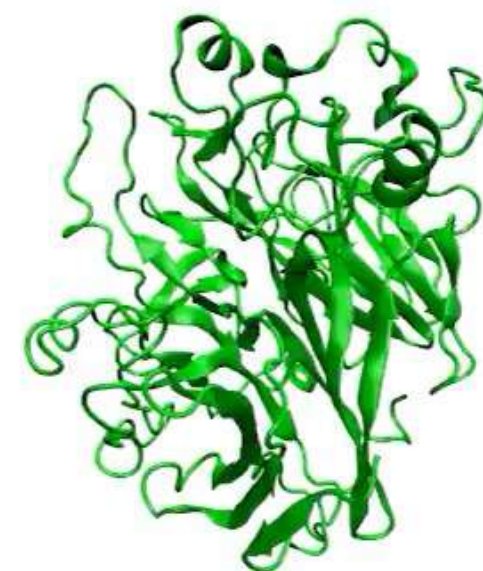
4-8 CPU cores

10-100 atoms



Workstation (GPU)

16-150 CPU cores



Approx. 0.1 million atoms



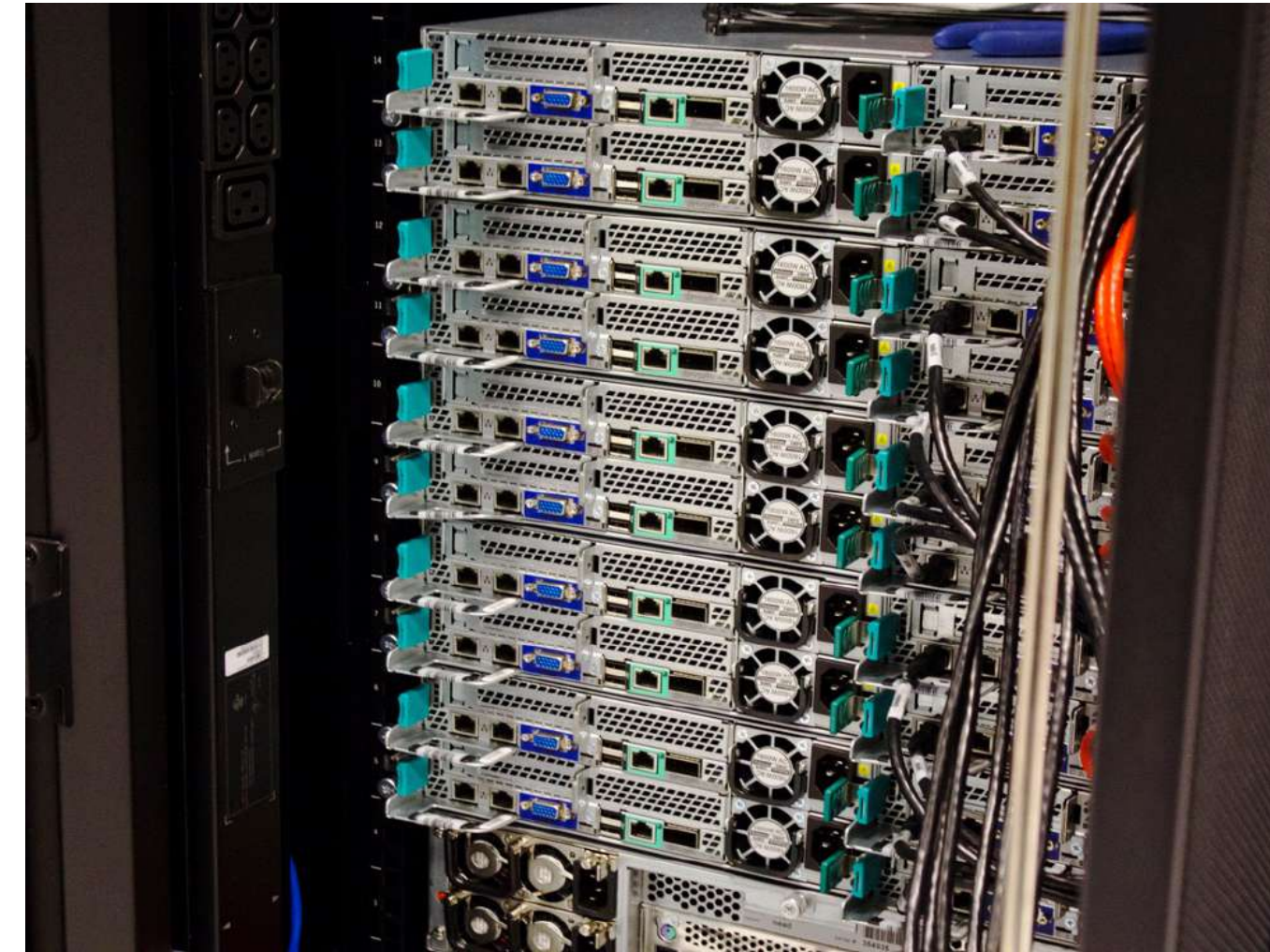
Supercomputer

10000-100000 CPU cores



Approx. 10 million atoms

Supercomputer



Many efficient computers stacked in a rack and connected by high speed network



World's fastest supercomputer: *Fugaku*, Japan
442 PetaFLOPs: can do 442×10^{15} operations per second



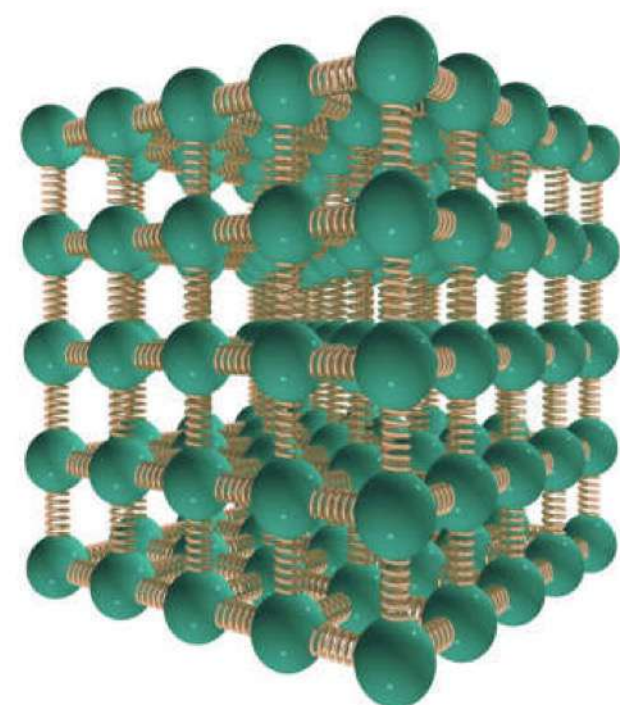
A cluster of computers in 2002...



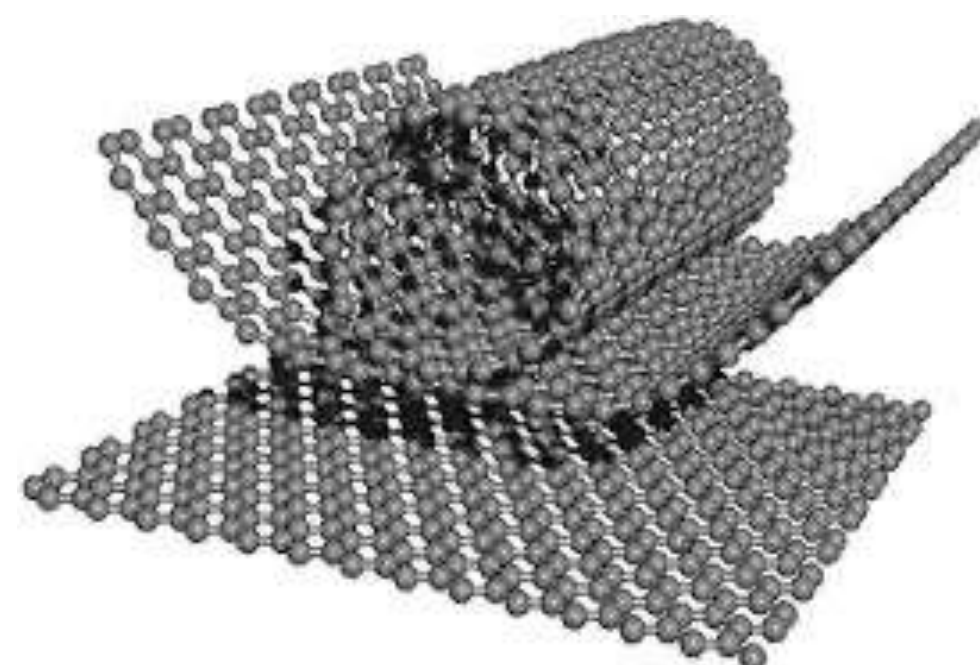
What does computational experiments on Supercomputer enable?

Desipher, Design, Discover, Develop...

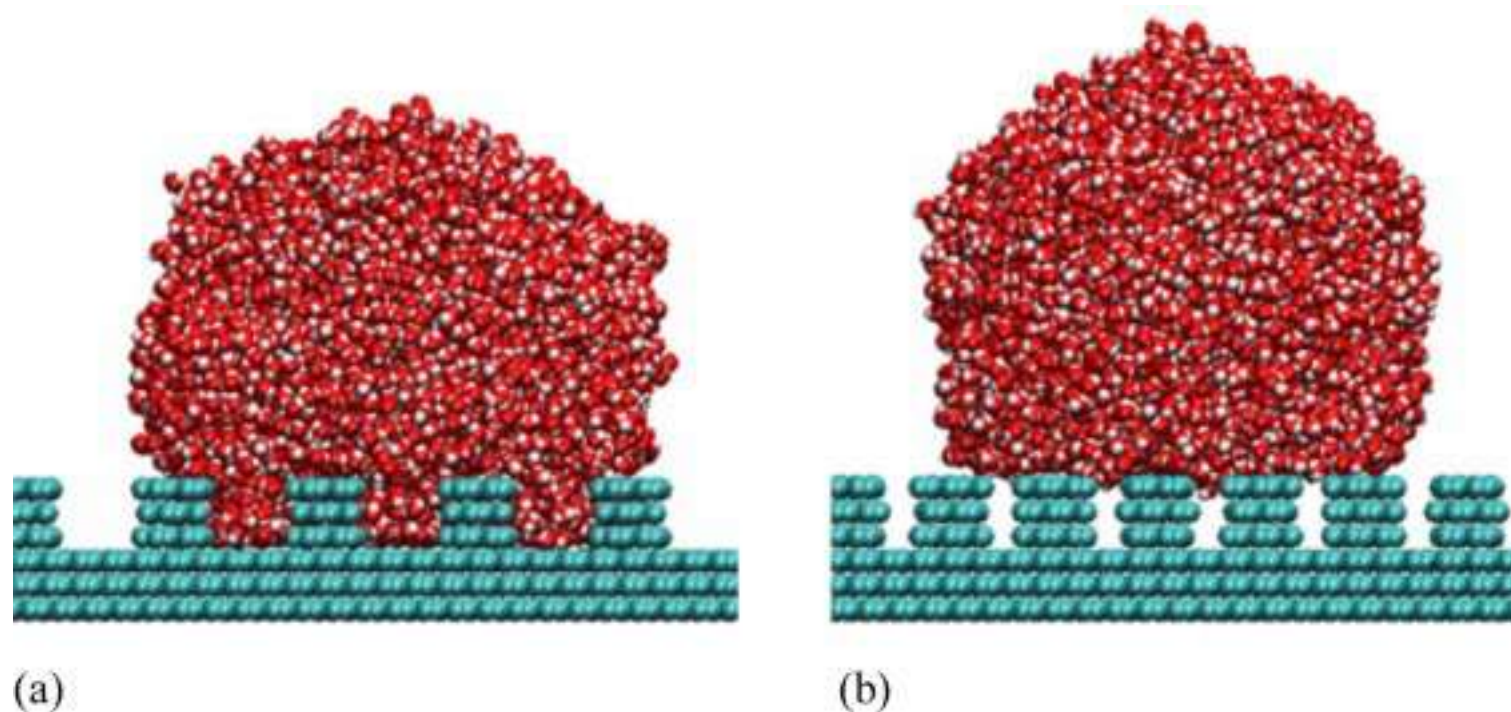
Designing new (nano)materials



Models of crystals

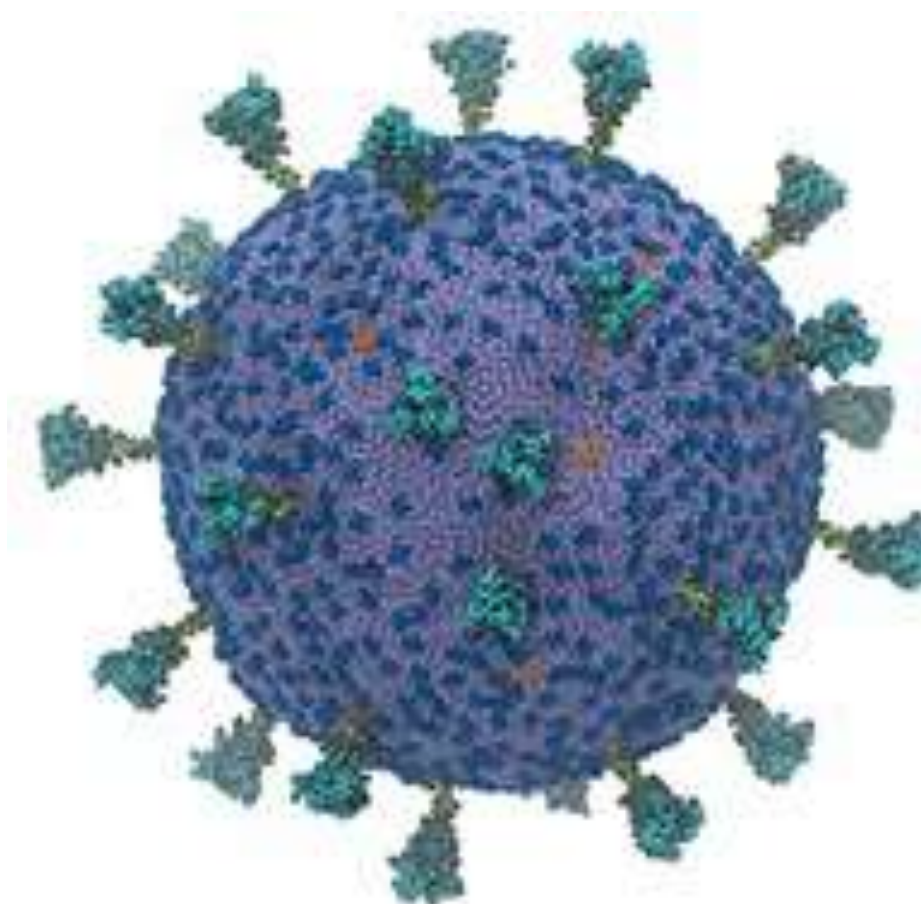


Carbon nanotubes, nanorods, nanosheets

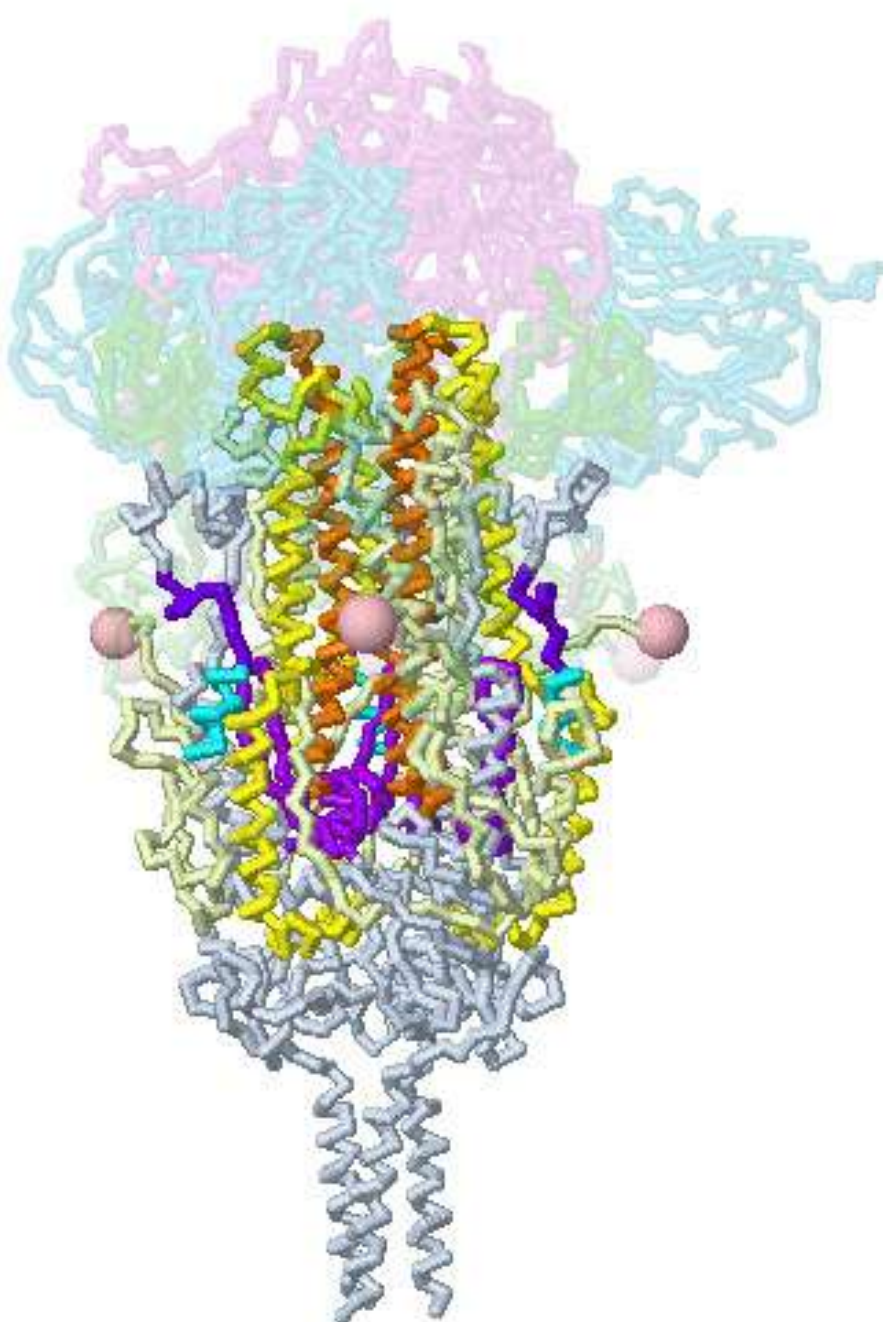


Developing hydrophobic surfaces

Drug design



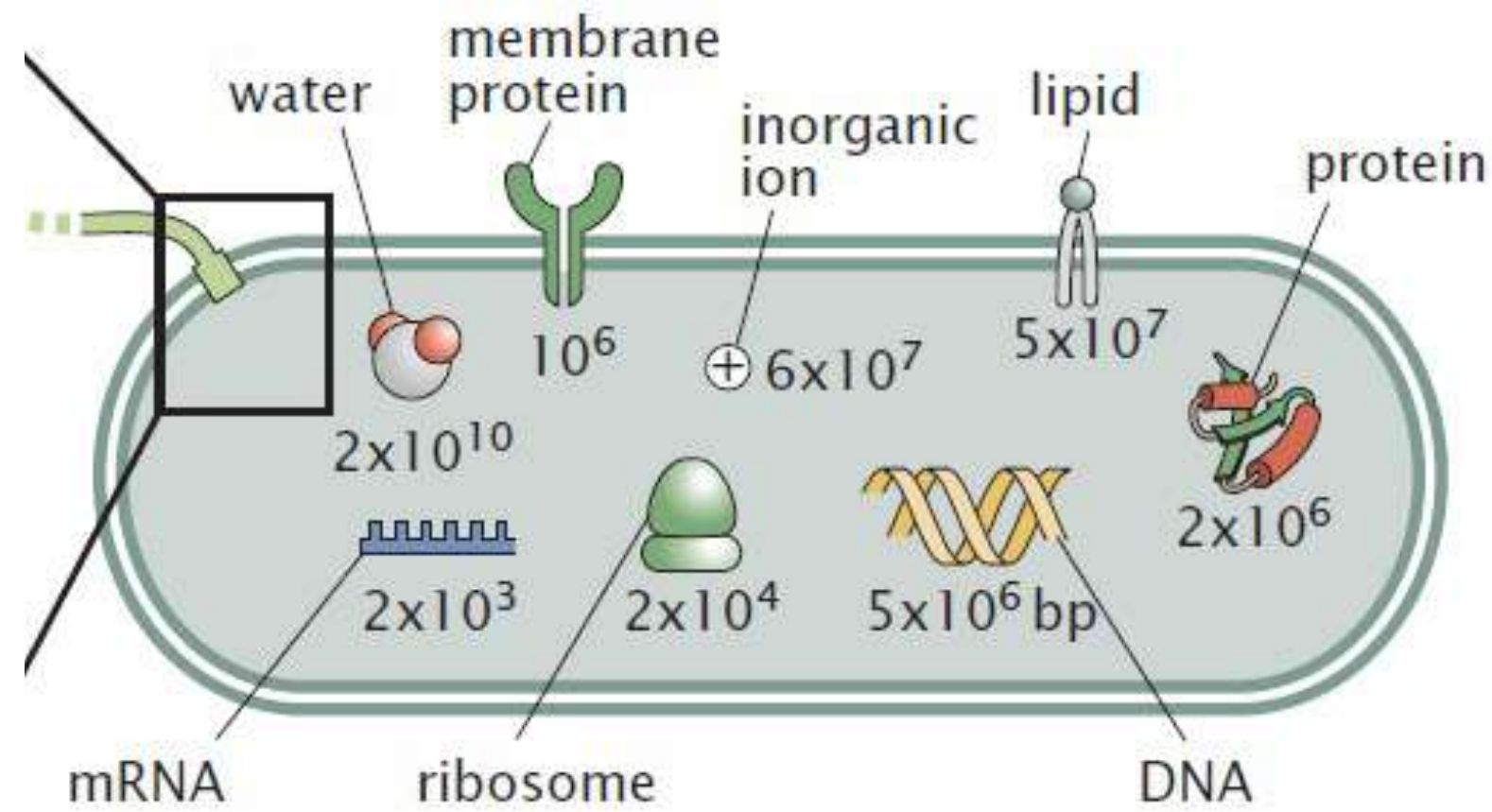
Corona Virus COVID-19
(Complete virus simulation)



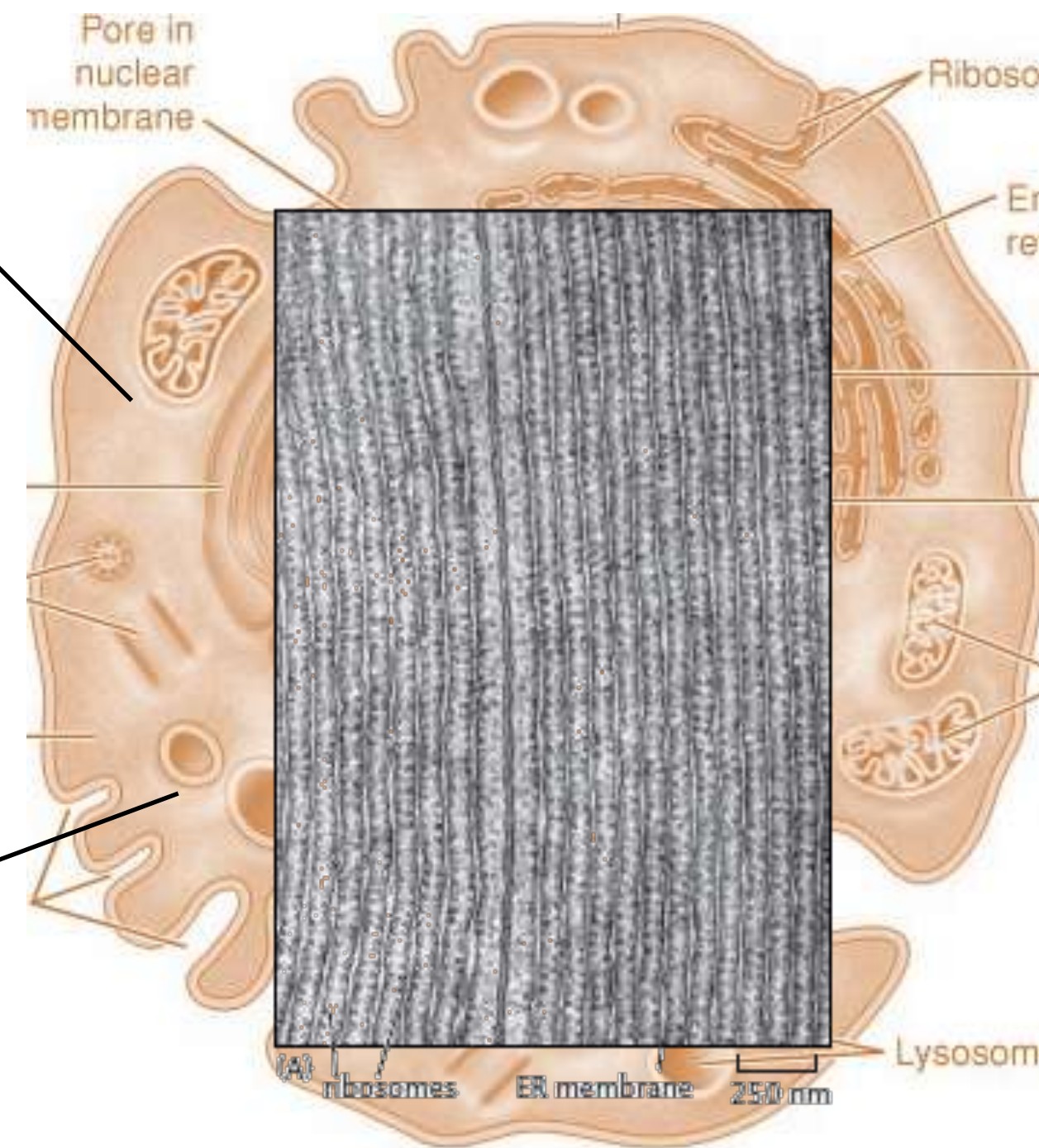
Ultimate challenge:
Simulating the whole living
cell
(Trillion atoms!)

Self assembly: living cell to materials

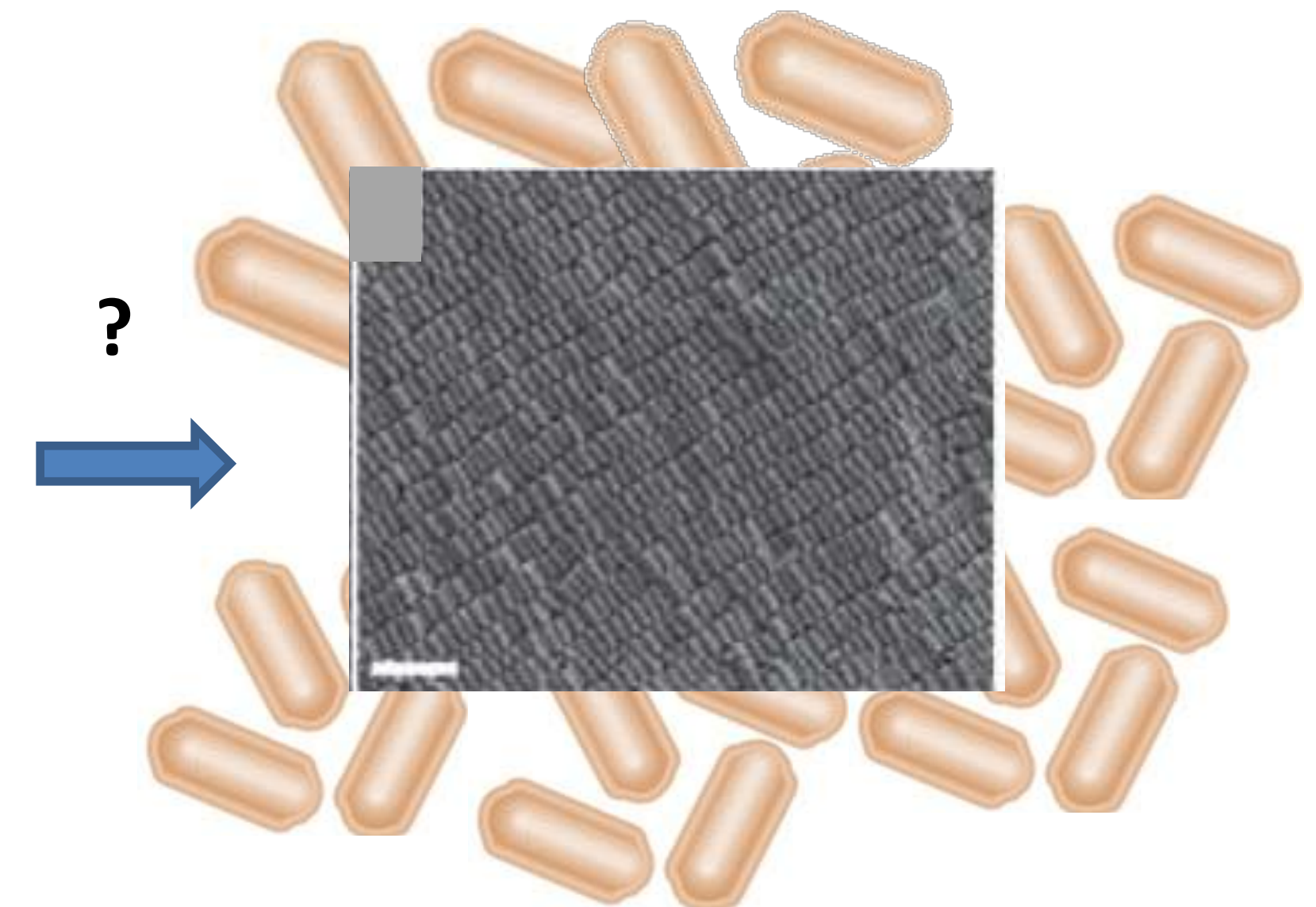
Research glimpse: Applications of MD simulations in our group



Crowded swimming pool



Physical Biology of Cell, Rob Phillips et al.



J. Mater. Chem. A, 2013, **1**, 2370

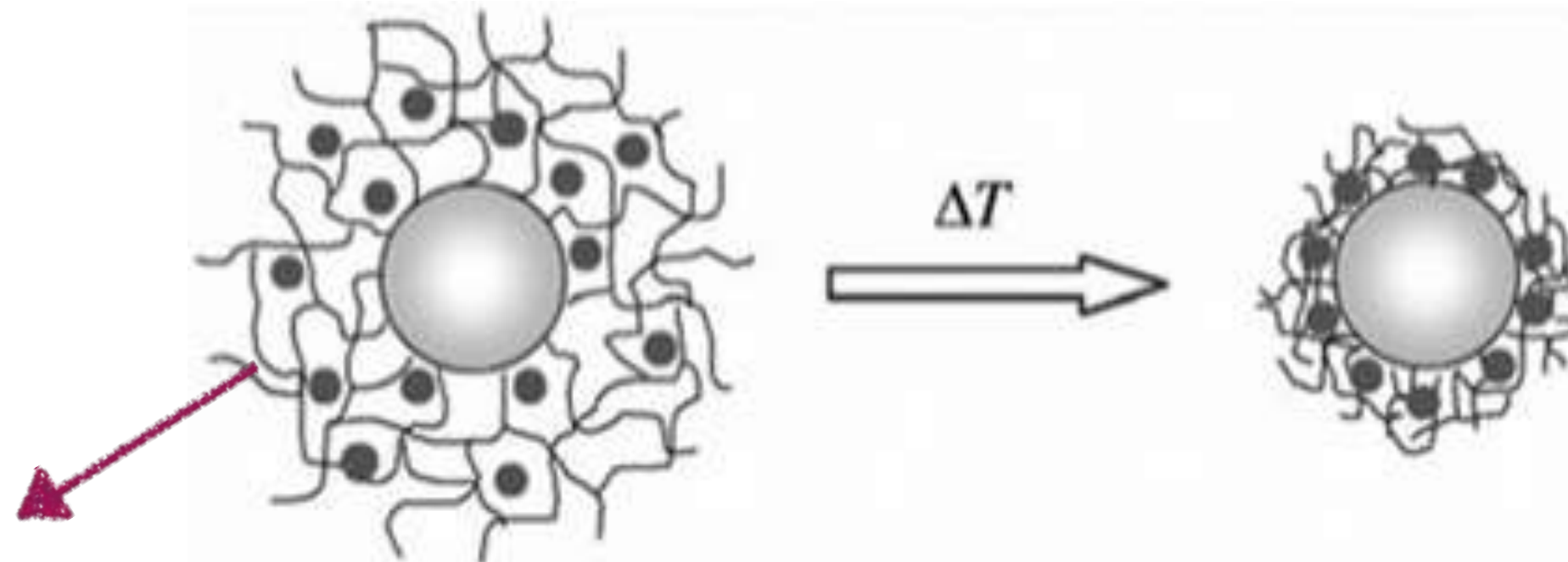
Using Nature's design of biological self-assemblies in designing nanomaterials self-assembly!

Smart polymers

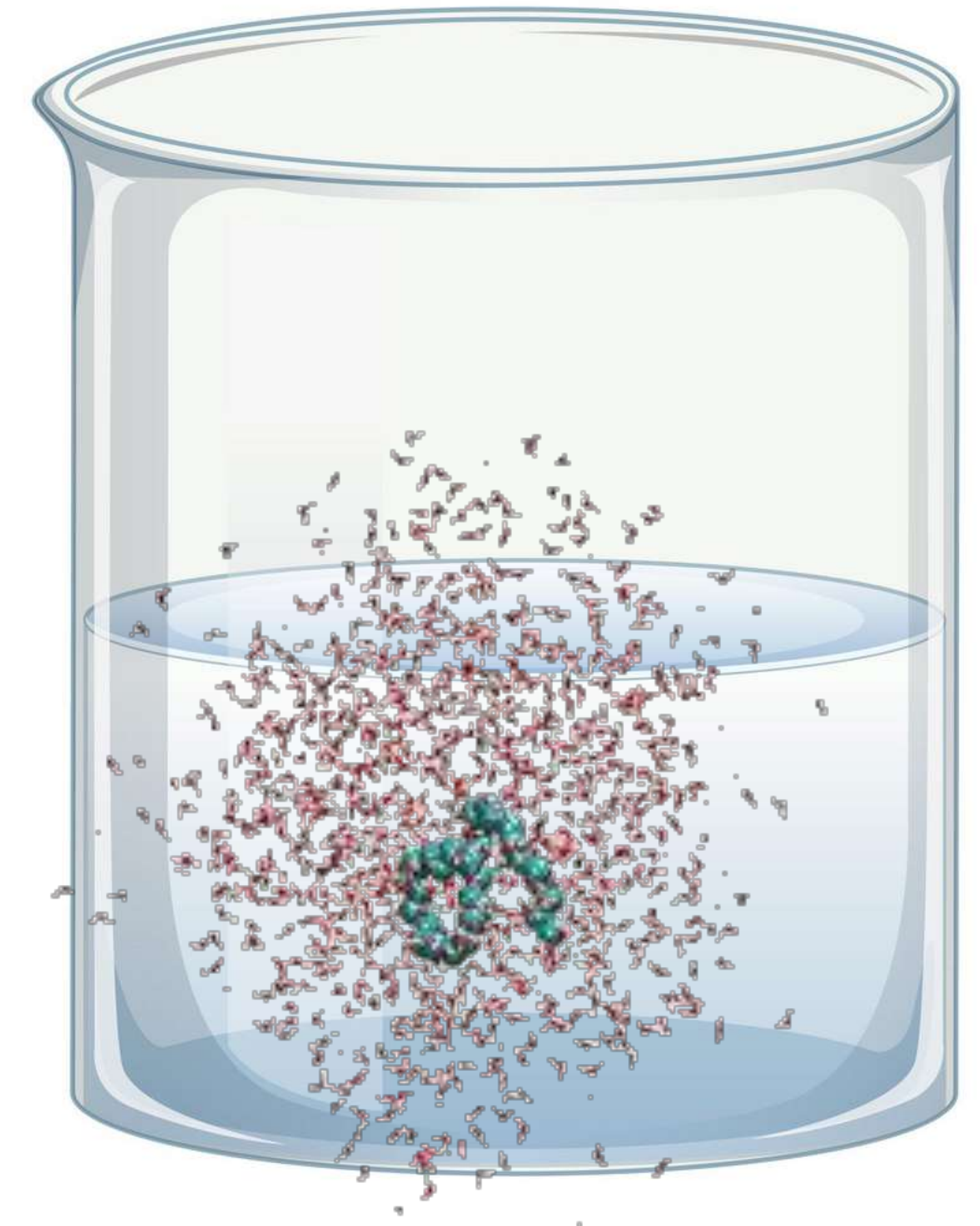
Why they are smart and how can we design new smart materials?



Heating
→
←
Cooling
Or chemicals
called osmolytes



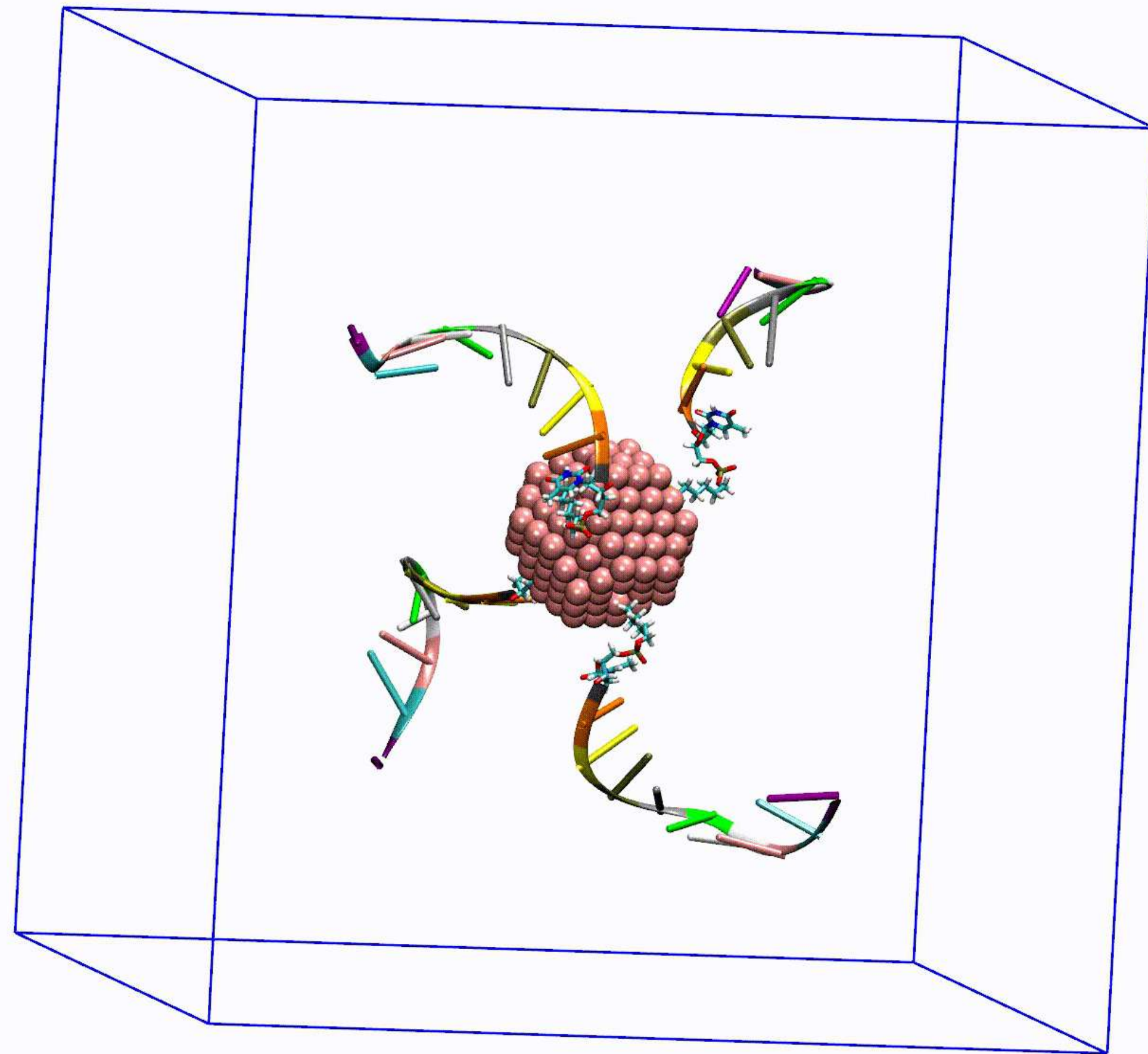
Smart Polymers
(Change their shape and size
in response to external
stimuli)



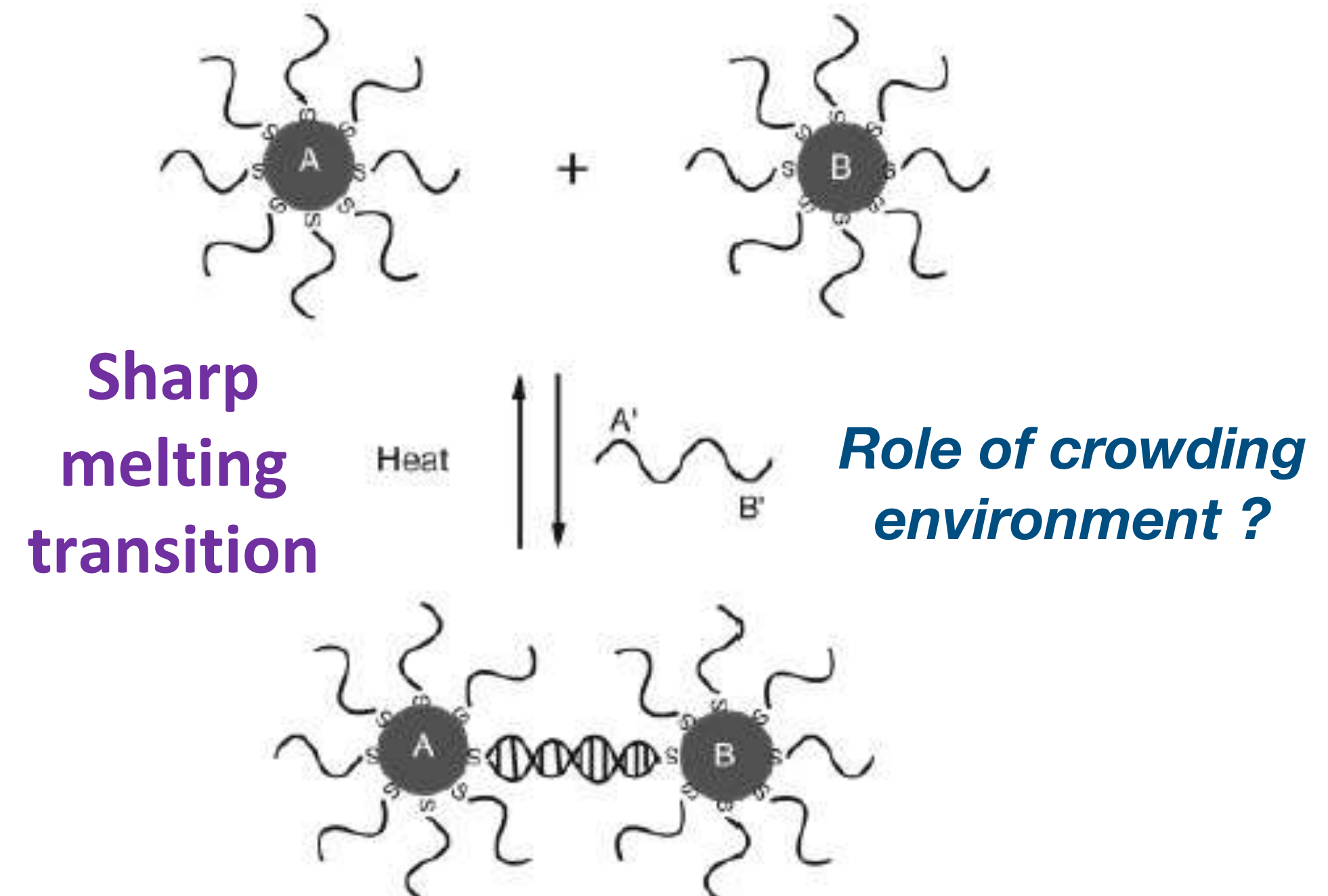
Satyendra Rajput (DN-lab)

D Nayar, NFA van der Vegt, J. Phys. Chem. B 2018, 122, 3587-3595
NFA van der Vegt, D Nayar J. Phys. Chem. B 2017, 121, 9986-9998
D Nayar, Phys. Chem. Chem. Phys. 2020, 22, 18091-18101

Designing functionalized gold nanoparticle self-assemblies in crowded environment

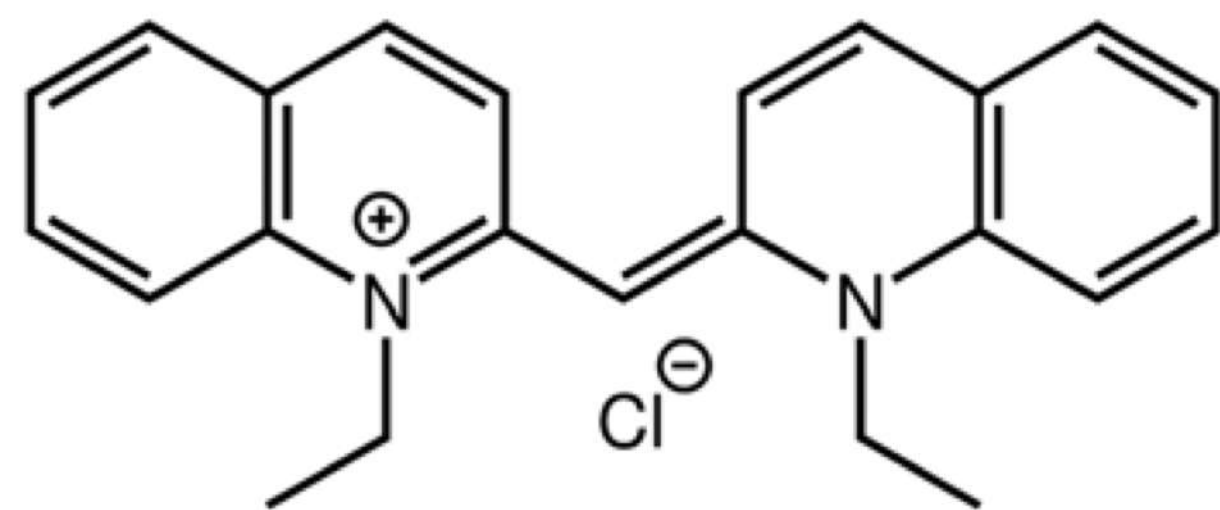


Self-assembled gold nanoparticles find applications in drug delivery and therapeutics

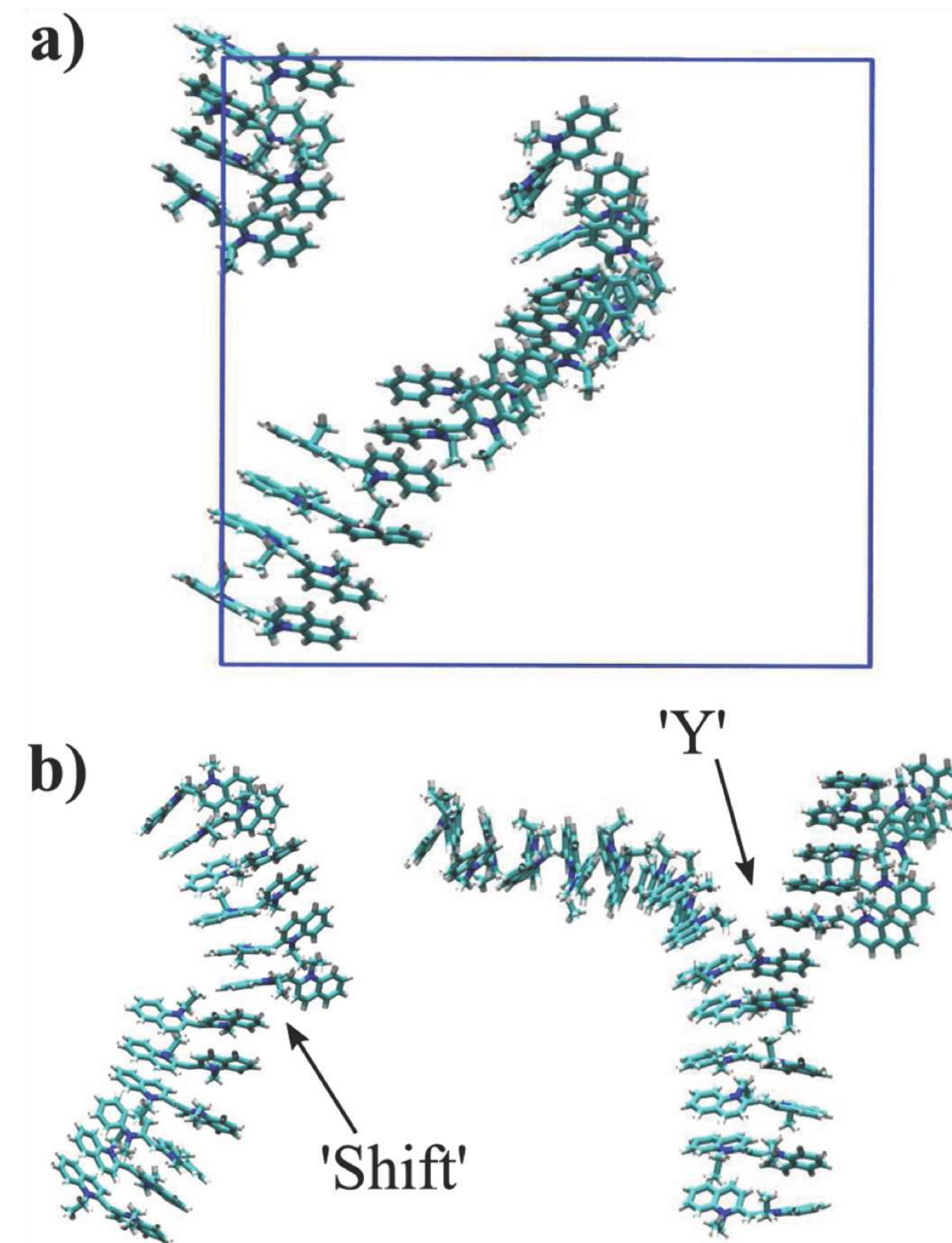
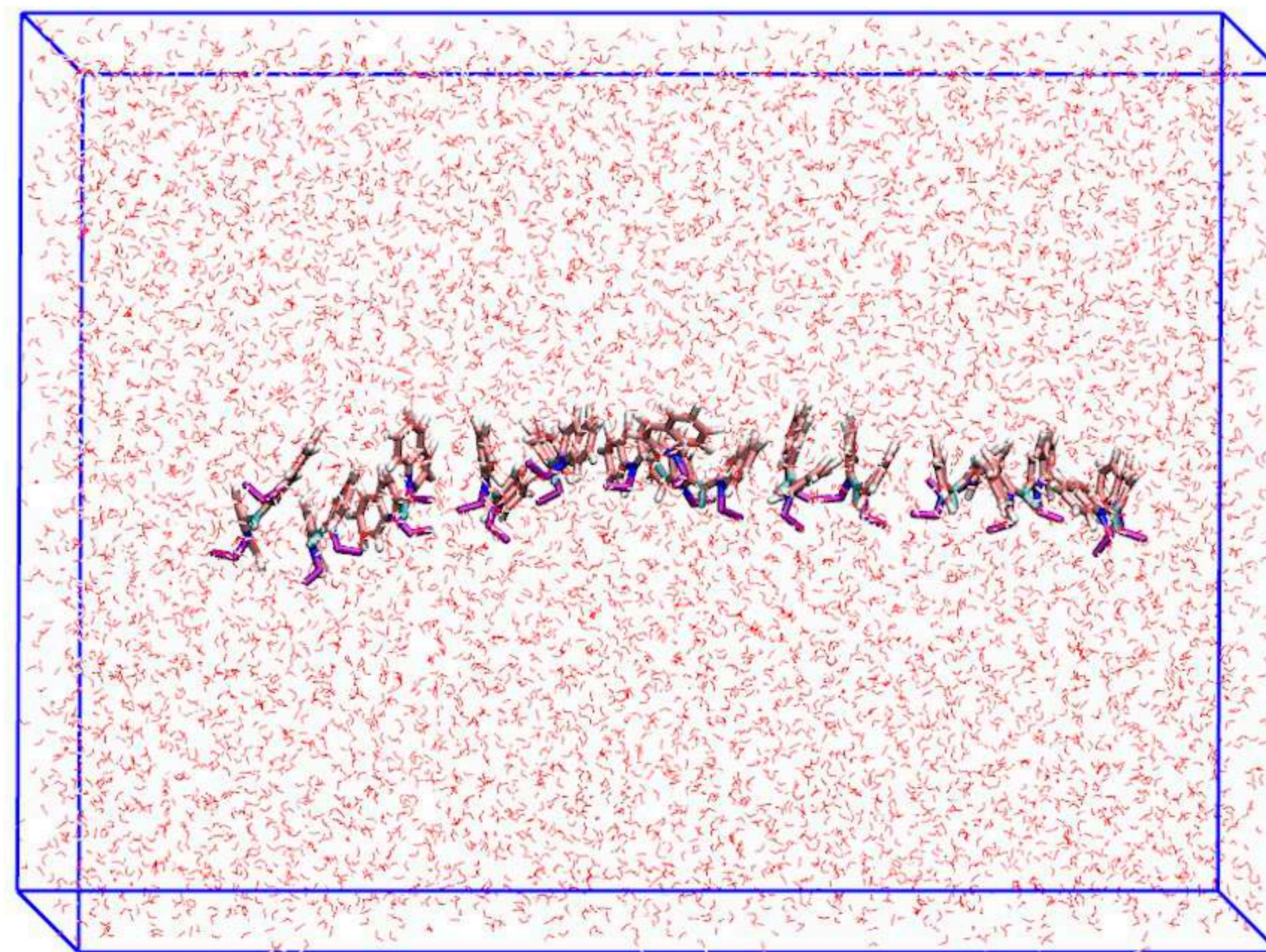


Designing molecular sensors for living cells

Self-assembly of fluorescent dyes

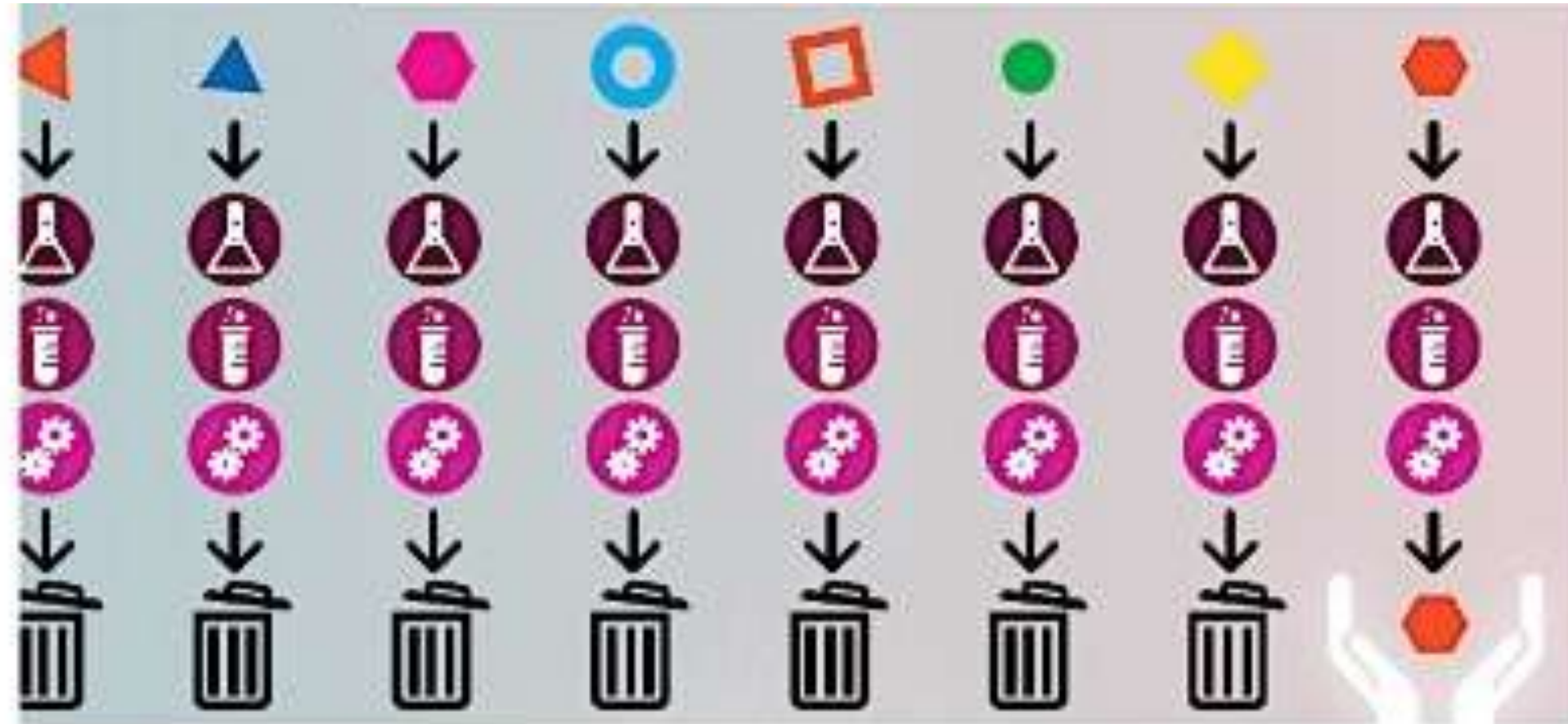


Pseudo isocyanine dye

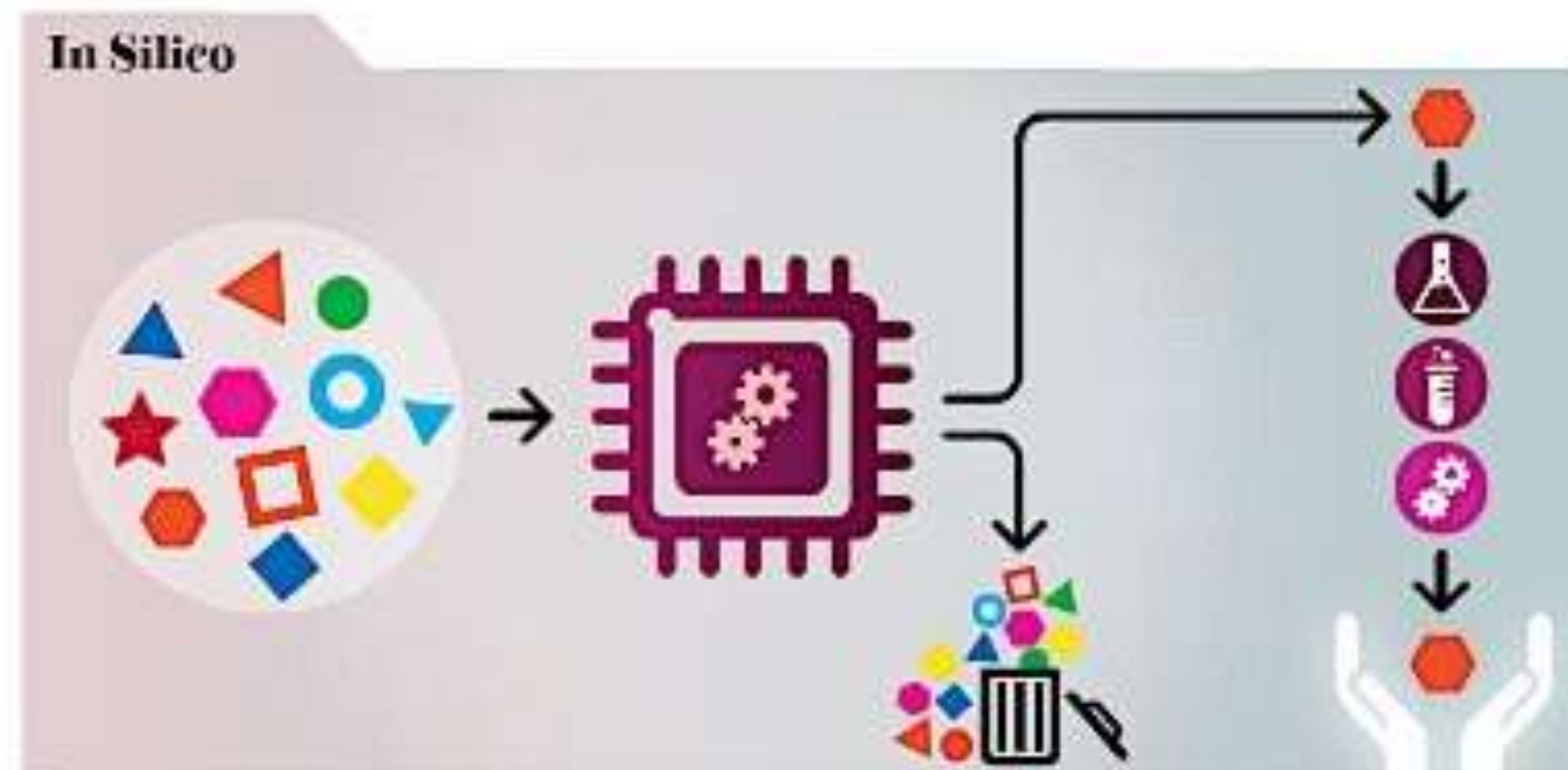


Artificial Intelligence in Materials Science

Experiments

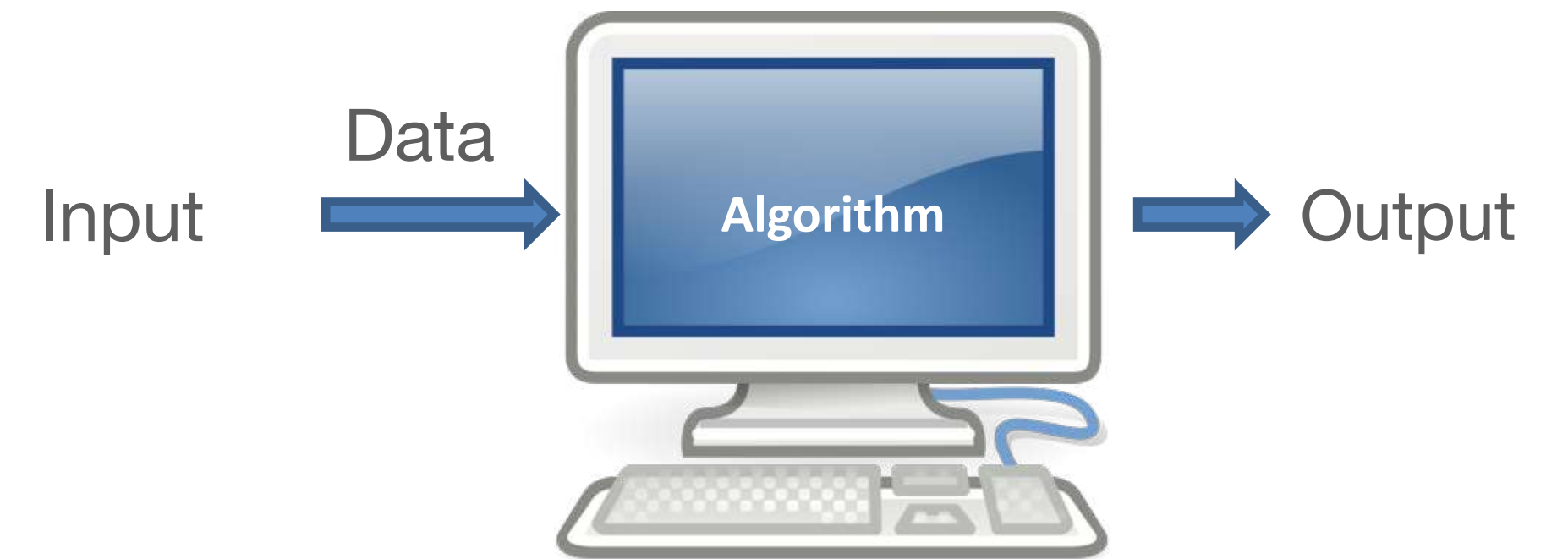


Machine learning

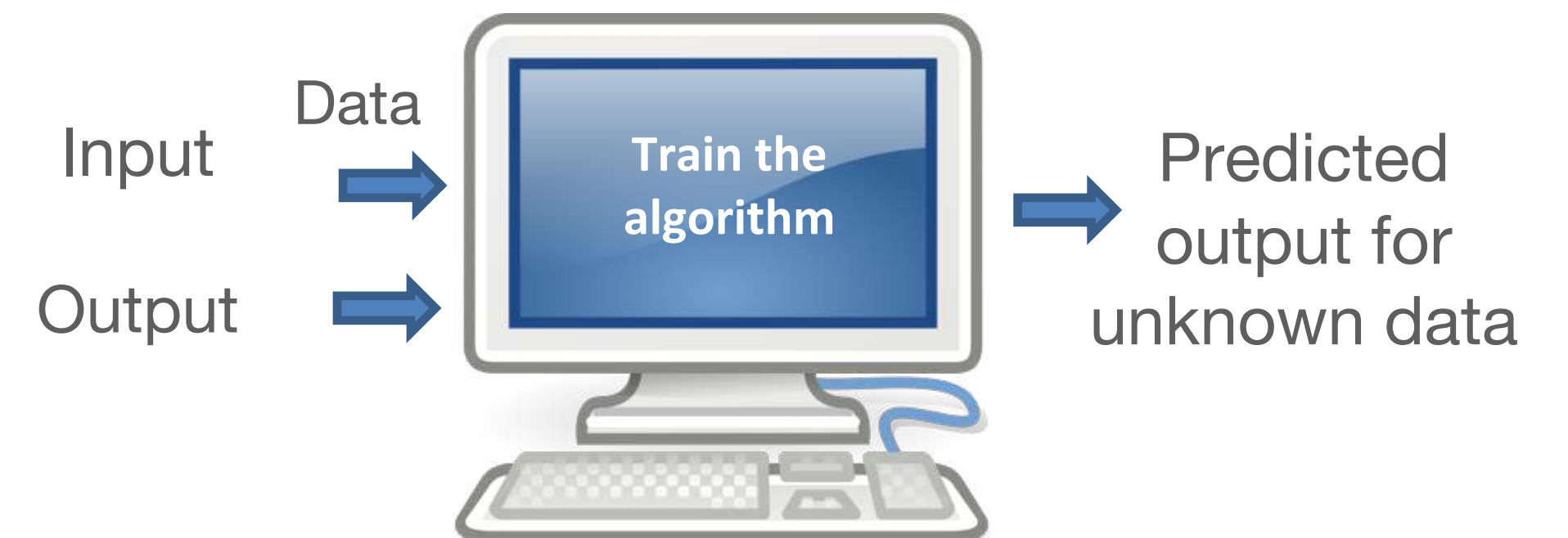


[1] Jain, A., Shin, Y. & Persson, K. A. Computational predictions of energy materials using density functional theory. *Nature Reviews Materials* 1, 15004 (2016).

General Computing



Machine learning

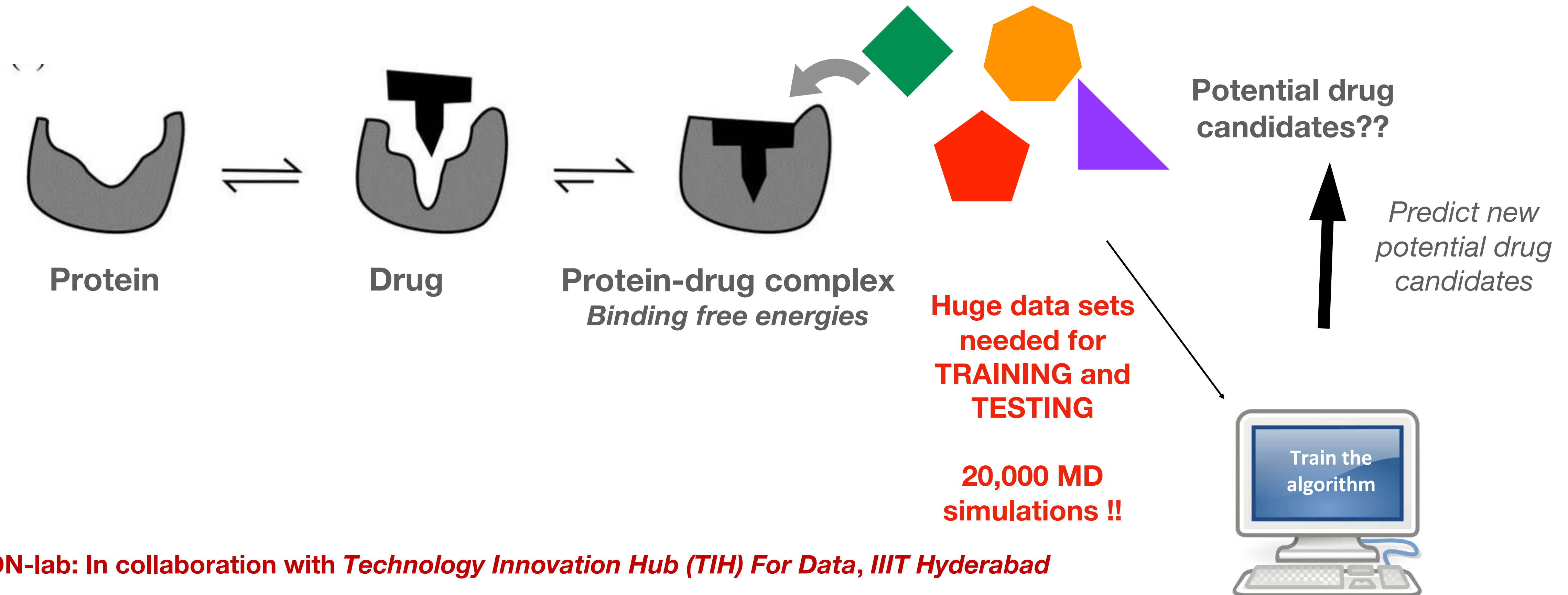


- Materials Discovery
- Materials Design
- Structure-property relationships

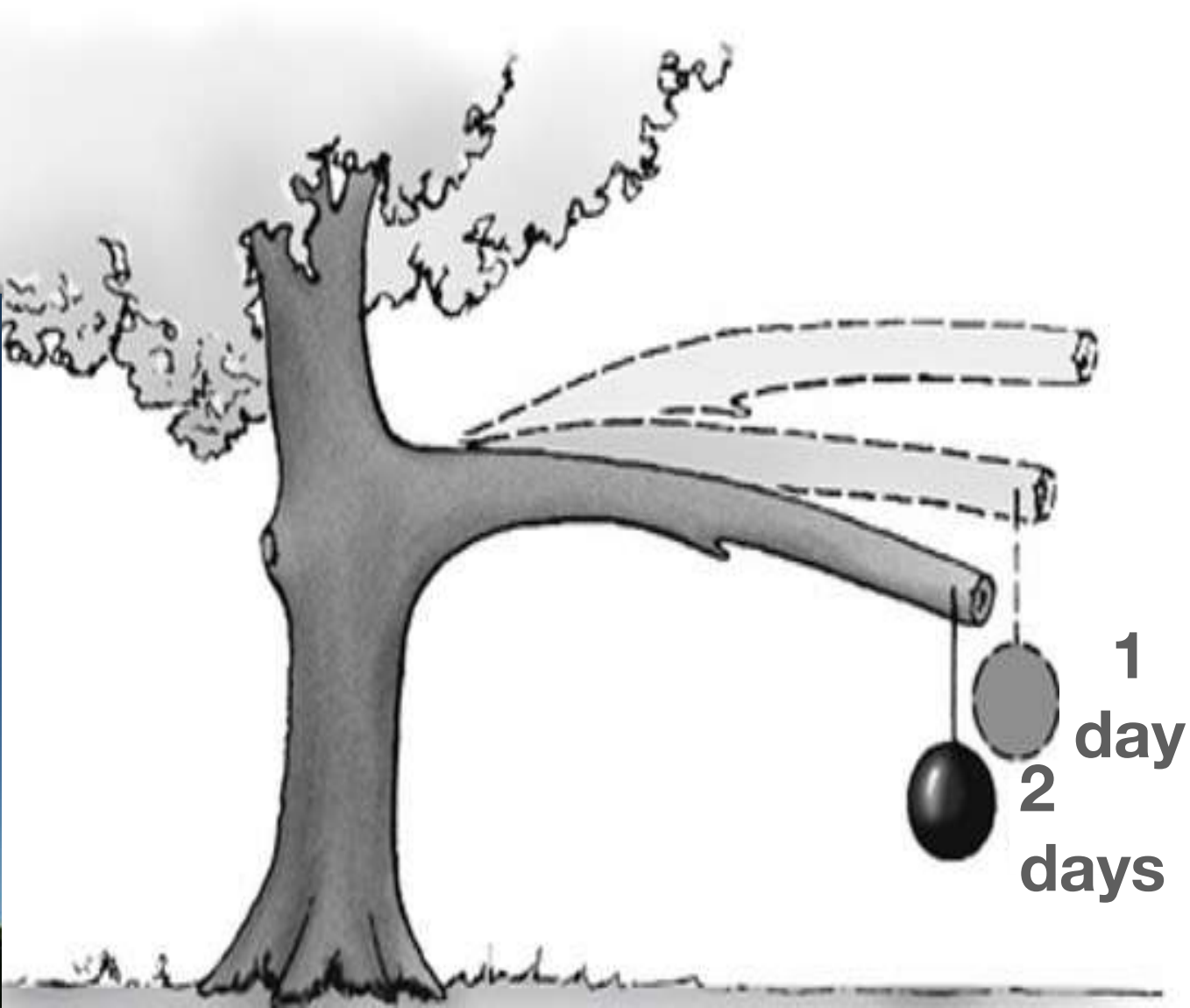
Machine Learning for Drug Design:

Generating Ultra-large Datasets for ML models using MD simulation

Which drug molecule can bind to protein to cure the disease?



Our journey through the last few weeks...



Some good books to read..

Food for curious minds!

- *Brain: The Story of You* (BBC Documentary also available) and *Incognito* by David Eagleman
- *The Double Helix* by James Watson
- *What is Life?* by Erwin Schroedinger
- *Phantoms in the Brain* by V. S. Ramachandran
- *Entropy Demystified* by A. Ben-Naim
- *Surely, You're Joking Mr. Feynman* by Richard P. Feynman
- *The Power of Habit* by Charles Duhigg
- *The New Science of Strong Materials* by J. E. Gordon
- *The Hope Circuit* by Martin Seligman
- *What You can Change and What You Can't* by Martin Seligman

Thank you all for being an awesome and a wonderful class. You have survived the course topics courageously through the online lectures! 😊

Thanks for asking all the interesting questions that helped me in making the lectures more interesting (or were they really interesting!?!..).

It has been an amazing experience teaching and interacting with you all !

Keep up the creative spirit, inquisitive energy and the burning curiosity!

All the very best for your future!

Looking forward to working with some of you in near future!

