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# **Molecular Dynamics Simulation: Principles, Algorithms and Applications**

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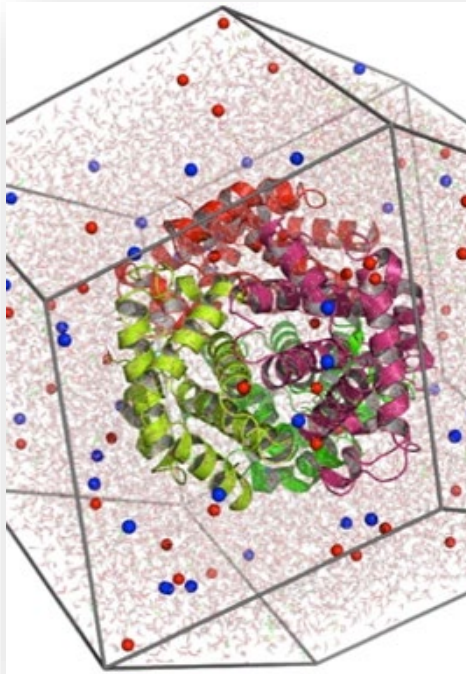
# Outline

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## Background

- Proteins: Structure and Functions
- Why Molecular Dynamics Simulations?
- MD Simulation of Complex Systems



## Principles

- Simulation of Dynamics of Particles
- Molecular Mechanics: Force Field
- Preparation to start a Simulation



## Algorithms

- The Verlet ("leapfrog") Algorithm
- Why Leapfrog Algorithm?
- Frontier: Deep Learning for Molecular Dynamics

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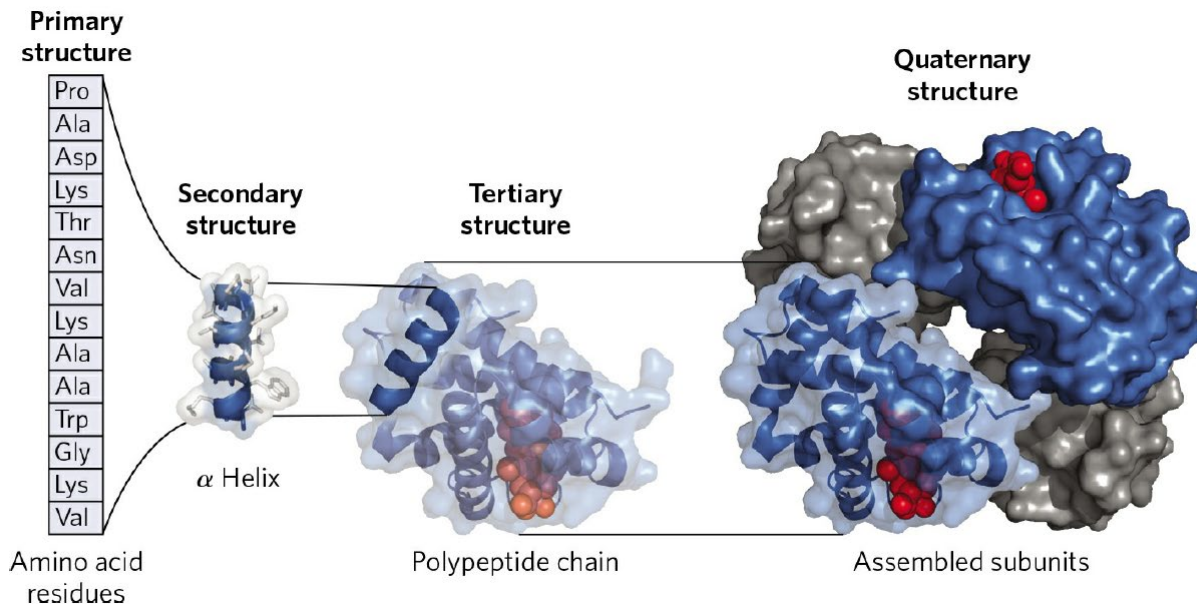


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# Proteins: Structure and Functions

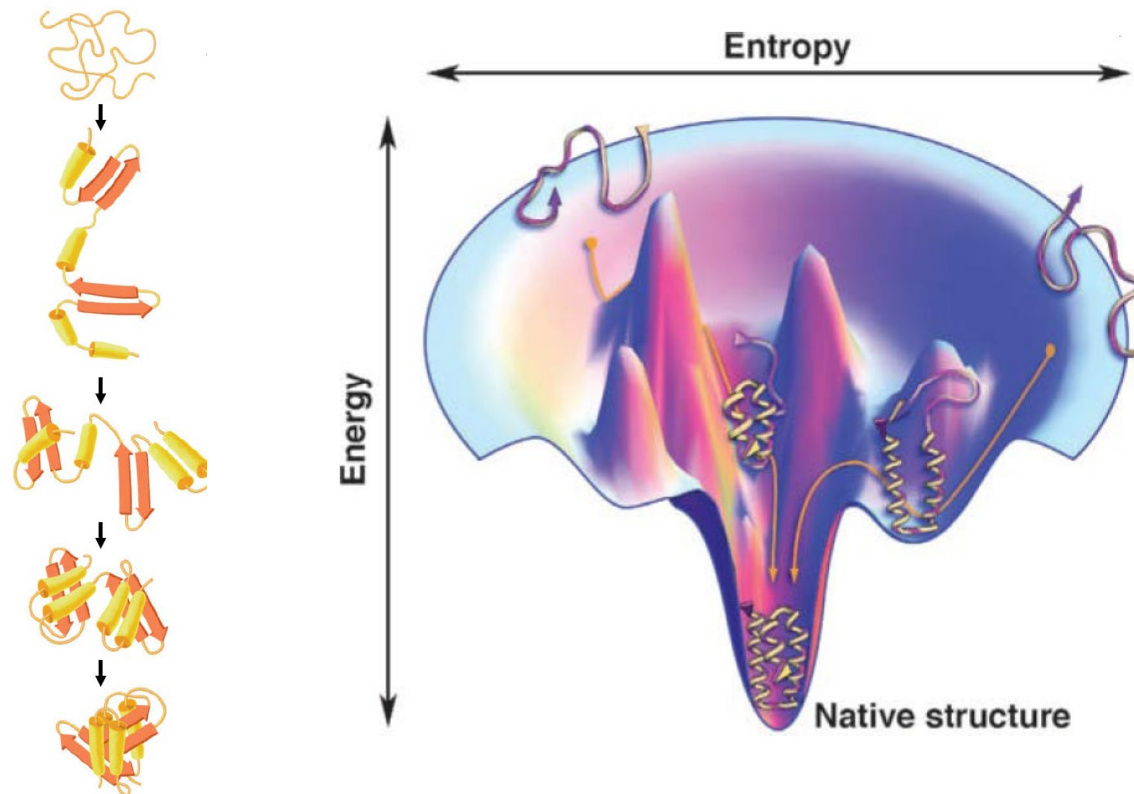
- Protein Structure
  - **3-Dimensional** arrangement of atoms in a protein
  - **4 Levels** of Structure in Proteins



- Protein Functions
  - Antibodies, Enzymes, Messengers ...
  - Determined by **Protein Structure**, which is generally difficult to obtain, especially *in vivo*

# Why Molecular Dynamics Simulations?

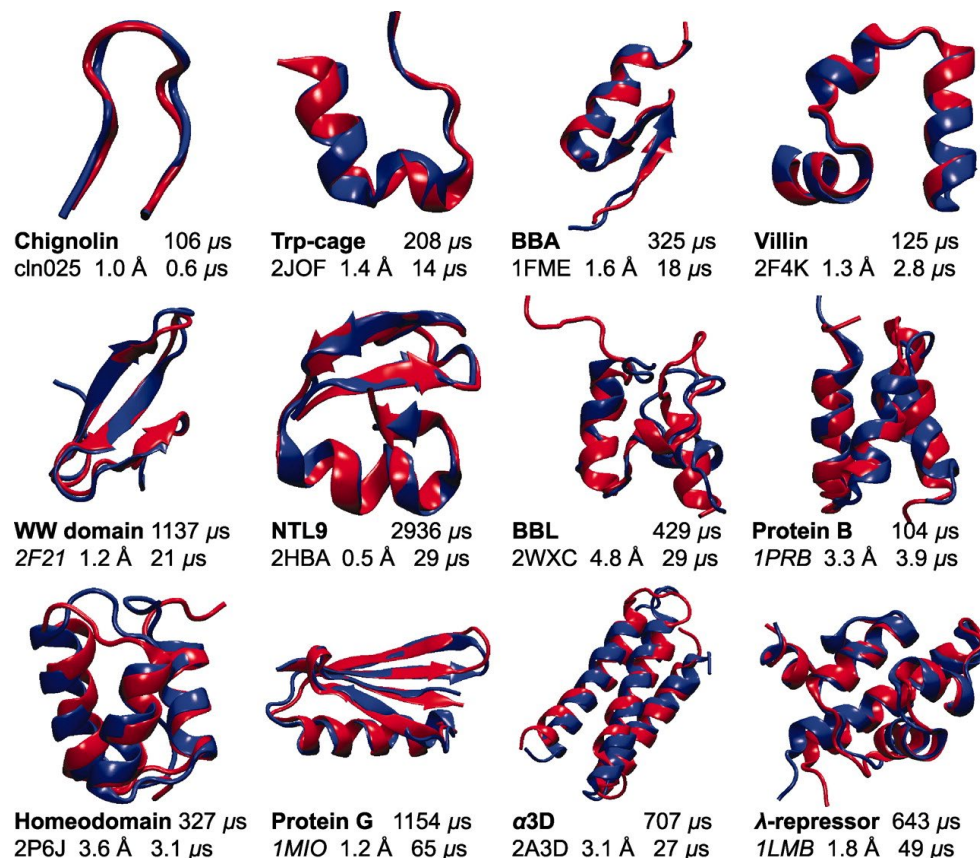
- Protein Structure Prediction: Dive into Protein Folding
  - Thermodynamics: **free-energy funnel**
  - Low energy conformation is **spontaneously** formed, consistent with the protein structure *in vivo*





# Why Molecular Dynamics Simulations?

- Protein Structure Formation: Dive into Protein Folding
- Protein Structure Prediction: **Protein Folding Simulations**

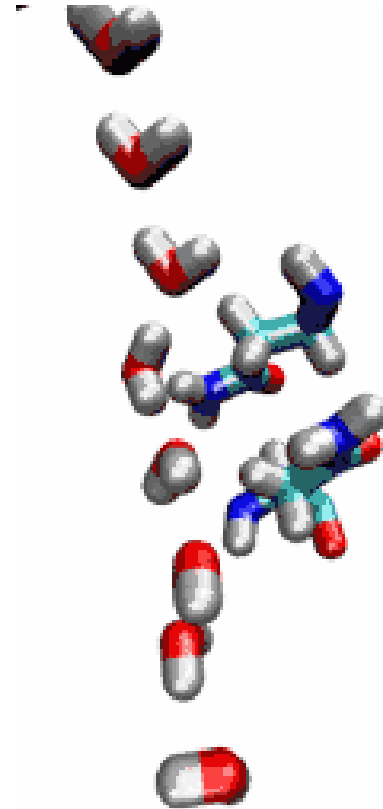
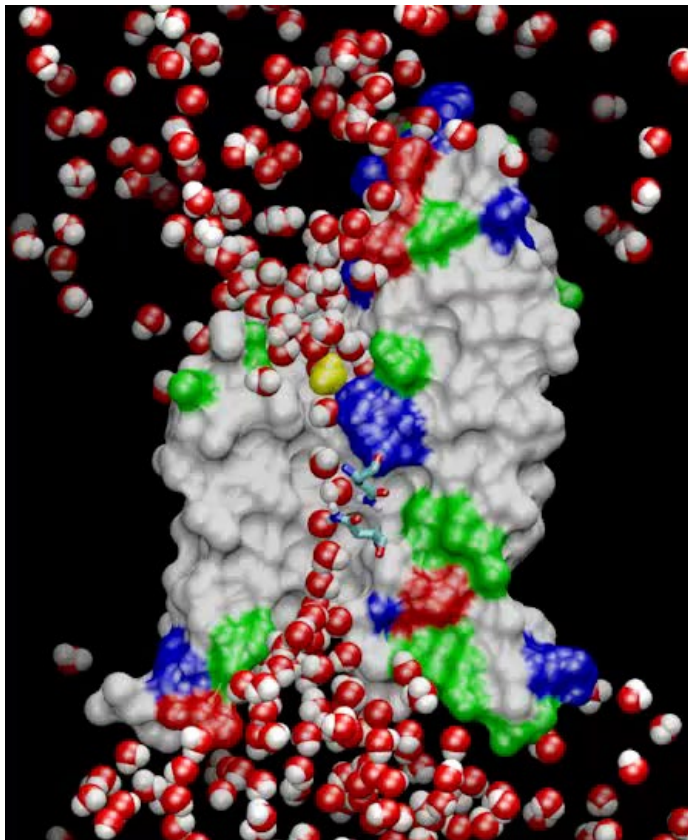




# MD Simulation of Complex Systems

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- MD Simulation: A glimpse of life processes inside our cells
  - A Fancy Example: the Selectivity of the **Aquaporin Water Channel** (*Science* 2002)



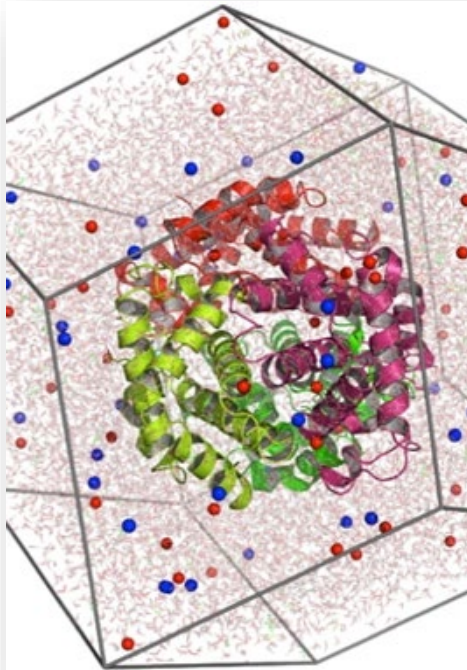
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# Simulation of Dynamics of Particles

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- Newton's Law of Motion: **Second-order ODE**

$$m \frac{d^2 r(t)}{dt^2} = F = -\nabla U(r)$$

- Equivalent **First-order ODEs**

$$\frac{dr(t)}{dt} = v(t)$$

$$m \frac{dv(t)}{dt} = F(t)$$

- Finite Difference Approximation comes to an **(Explicit) Euler Method**

$$v_{n+1} = v_n + \frac{F_n}{m} dt$$

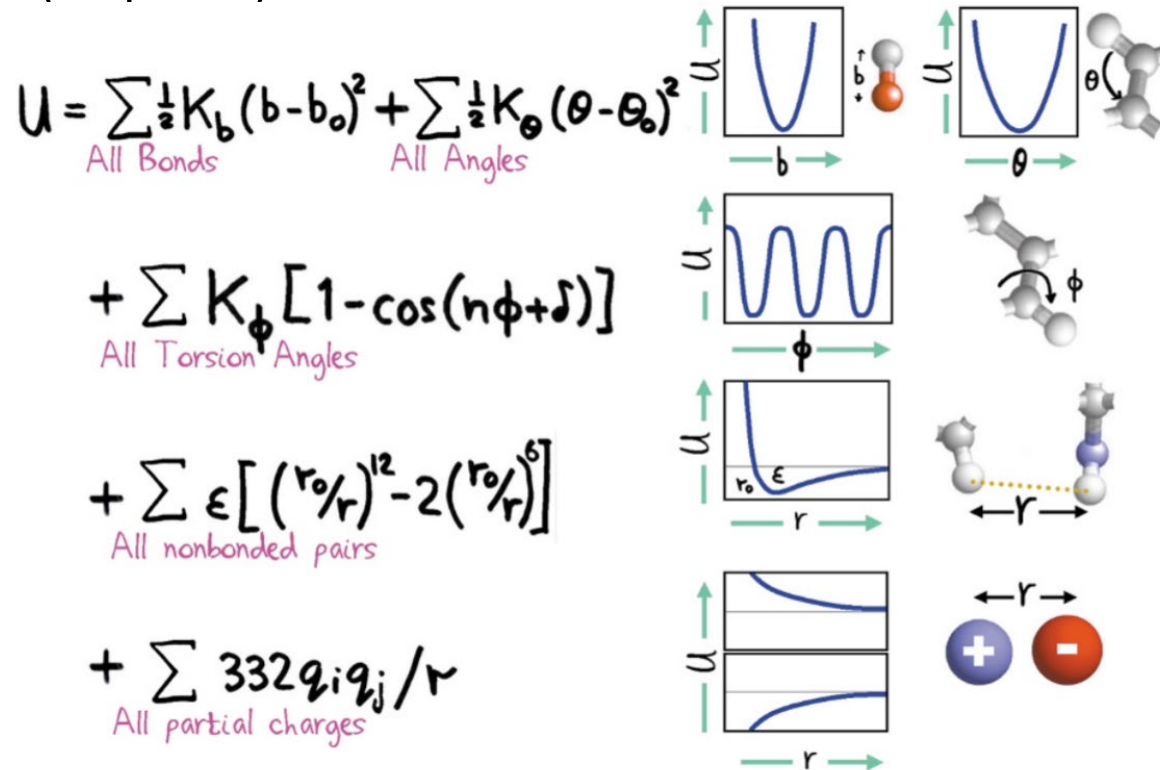
$$r_{n+1} = r_n + v_n dt$$

- **N-body Problem**: for each particle  $i$ , we have

$$m_i \frac{d^2 r_i(t)}{dt^2} = \sum_j F_{ij}(t) = - \sum_j \nabla_i U(|r_{ij}(t)|)$$

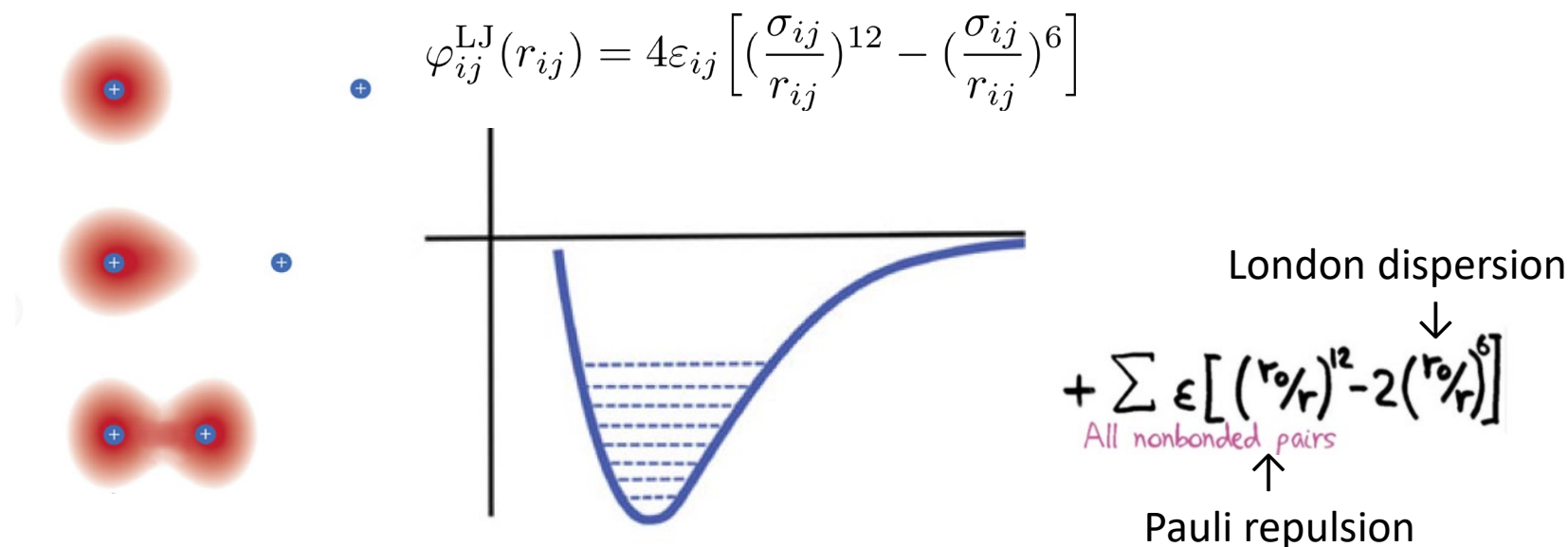
# Molecular Mechanics: Force Field

- Potential Energy Function  $U = U_{bonded} + U_{non-bonded}$
- **Force Field**: the **function form** of the potential and a **set of parameters** for different types of atoms, bonds and interactions etc.
- A general (empirical) force field



# Molecular Mechanics: Force Field

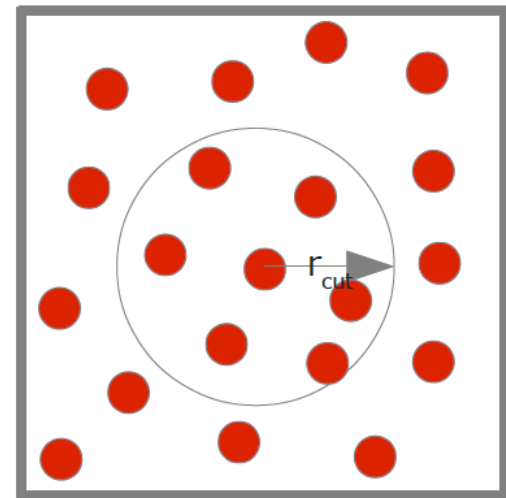
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- Van der Waals Interaction: **Lennard-Jones Potential**





# Molecular Mechanics: Force Field

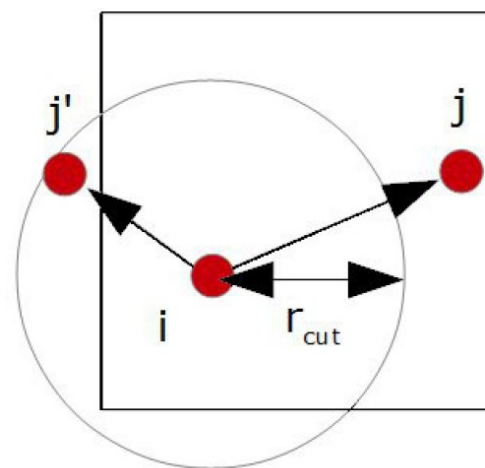
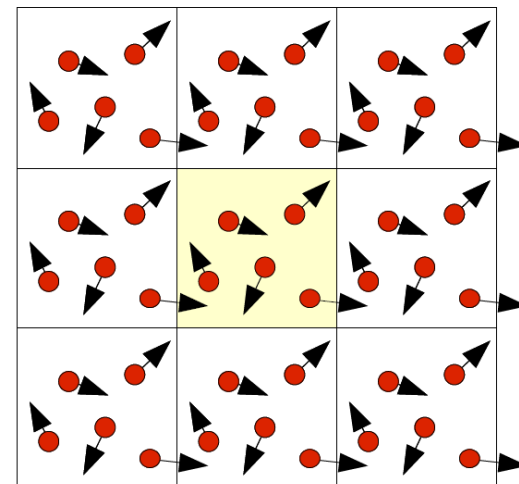
- Potential Energy Function  $U = U_{bonded} + U_{non-bonded}$
- **Force Field**: the **function form** of the potential and a **set of parameters** for different types of atoms, bonds and interactions etc.
- A general (empirical) force field
- Van der Waals Interaction: **Lennard-Jones Potential**
- The Potential **Cut-off**
  - In principle pair potentials have **infinite** range
  - For potentials like Lennard-Jones potential the value quickly becomes negligible when atoms gradually separate
  - Apply an (empirical) **cut-off condition**  $r_{cut}$





# Preparation to start a Simulation

- The **Periodic Boundary Condition (PBC)**
  - The system is in fact **infinite** in extent
  - Idea: the **periodic cell** is assumed to be **replicate** in the same way as a unit cell in crystallography
  - Purpose: create a system **without surfaces**
- The **Minimum Image Convention**
  - The cut-off setting: Net interaction experienced by each atom includes contribution from only **one image** of the other atom in the system
  - Purpose: **only the closest images** of any two atoms contribute to the calculated energy / force
- The **Initial Conditions**
  - Initial **atom positions**: usually obtained by x-ray crystallography or cryo-em (NOT *in vivo*!)
  - Initial **velocities**: usually generated from a series of random seeds, then scaled to match the required system temperature



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# The Verlet (“leapfrog”) Algorithm

- **Algorithm**

$$\mathbf{v}_{n+\frac{1}{2}} = \mathbf{v}_n + \frac{h}{2} \mathbf{M}^{-1} \mathbf{F}_n$$

$$\mathbf{r}_{n+1} = \mathbf{r}_n + h \mathbf{v}_{n+\frac{1}{2}}$$

$$\mathbf{v}_{n+1} = \mathbf{v}_{n+\frac{1}{2}} + \frac{h}{2} \mathbf{M}^{-1} \mathbf{F}_{n+1}$$



where  $h := \Delta t$  denotes the (fixed) time interval, and the force

$$\mathbf{F}_n = \mathbf{F}(\mathbf{r}_n) = -\nabla U(\mathbf{r}_n)$$

computed at the **end** of a given step is reused at the **start** of the following step, lead to a similar cost to Euler Method

- “Leapfrog”

- Update positions and velocities at **interleaved** time points, staggered in such a way that they “leapfrog” over each other.

- **Störmer’s Rule**

- Eliminate velocities to obtain

$$\mathbf{M}(\mathbf{r}_{n+1} - 2\mathbf{r}_n + \mathbf{r}_{n-1}) = -h^2 \nabla U(\mathbf{r}_n)$$



# The Verlet (“leapfrog”) Algorithm

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- **Brief Derivation** of leapfrog algorithm

Consider the Taylor Expansion in terms of the time interval  $h$  as

$$\mathbf{r}(t+h) = \mathbf{r}(t) + \dot{\mathbf{r}}(t)h + \ddot{\mathbf{r}}(t)\frac{h^2}{2!} + \dddot{\mathbf{r}}(t)\frac{h^3}{3!} + \mathbf{r}^{(4)}(t)\frac{h^4}{4!} + O(h^5) \quad (1)$$

take  $t = nh$  where  $n$  is some integer, we obtain

$$\mathbf{r}_{n+1} = \mathbf{r}_n + \dot{\mathbf{r}}_n h + \ddot{\mathbf{r}}_n \frac{h^2}{2!} + \dddot{\mathbf{r}}(t) \frac{h^3}{3!} + \mathbf{r}^{(4)}(t) \frac{h^4}{4!} + O(h^5) \quad (2)$$

Similarly, we have

$$\mathbf{r}_{n-1} = \mathbf{r}_n - \dot{\mathbf{r}}_n h + \ddot{\mathbf{r}}_n \frac{h^2}{2!} - \dddot{\mathbf{r}}(t) \frac{h^3}{3!} + \mathbf{r}^{(4)}(t) \frac{h^4}{4!} + O(h^5) \quad (3)$$

(2) – (3) to obtain

$$\mathbf{r}_{n+1} - \mathbf{r}_{n-1} = 2\dot{\mathbf{r}}_n h + \ddot{\mathbf{r}}_n \frac{2h^3}{3!} + O(h^5) \quad (4)$$





# The Verlet (“leapfrog”) Algorithm

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- **Brief Derivation** of leapfrog algorithm

Devide  $2h$  through (4), by definition we have

$$\mathbf{v}_n = \frac{1}{2h}(\mathbf{r}_{n+1} - \mathbf{r}_{n-1}) = \dot{\mathbf{r}}_n + \ddot{\mathbf{r}}_n \frac{h^2}{3!} + O(h^4) \quad (5)$$

rearrange (2) to give

$$\mathbf{r}_{n+1} - \mathbf{r}_n = \left( \dot{\mathbf{r}}_n + \ddot{\mathbf{r}}_n \frac{h^2}{3!} \right) h + \ddot{\mathbf{r}}_n \frac{h^2}{2!} + O(h^4) \quad (6)$$

substitute (5) to (6) and divide throughout by  $h$ , we have

$$\frac{1}{h}(\mathbf{r}_{n+1} - \mathbf{r}_n) = \mathbf{v}_n + \ddot{\mathbf{r}}_n \frac{h}{2!} + O(h^3) \quad (7)$$

hence by Newton’s Law of Motion, we obtain

$$\mathbf{v}_{n+\frac{1}{2}} = \mathbf{v}_n + \frac{h}{2} \mathbf{M}^{-1} \mathbf{F}_n + O(h^3) \quad (8)$$



# The Verlet (“leapfrog”) Algorithm

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- **Brief Derivation** of leapfrog algorithm

where we define

$$\mathbf{v}_{n+\frac{1}{2}} = \frac{\mathbf{r}_{n+1} - \mathbf{r}_n}{h} \quad (9)$$

$$\mathbf{v}_{n-\frac{1}{2}} = \frac{\mathbf{r}_n - \mathbf{r}_{n-1}}{h} \quad (10)$$

to represent the half time step velocities.

In conclusion of (8)(9)(10), we have the algorithm

$$\mathbf{v}_{n+\frac{1}{2}} = \mathbf{v}_n + \frac{h}{2} \mathbf{M}^{-1} \mathbf{F}_n \quad (11)$$

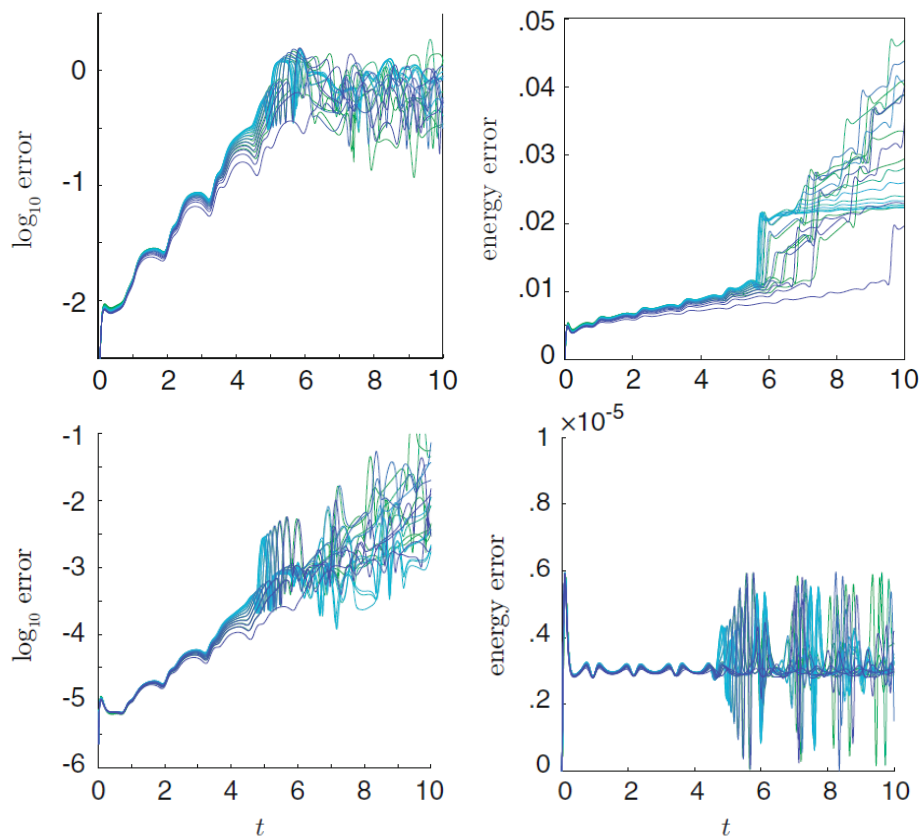
$$\mathbf{r}_{n+1} = \mathbf{r}_n + h \mathbf{v}_{n+\frac{1}{2}} \quad (12)$$

$$\mathbf{v}_{n+1} = \mathbf{v}_{n+\frac{1}{2}} + \frac{h}{2} \mathbf{M}^{-1} \mathbf{F}_{n+1} \quad (13)$$

which is consistent with the algorithm stated in the beginning.

# Why Leapfrog Algorithm?

- Leapfrog Algorithm: **Second-Order Method** (Proof is omitted)
  - Why not apply higher-order Runge-Kutta Method (e.g. RK4)?
- **Error Growth** in Numerical Integration of ODEs

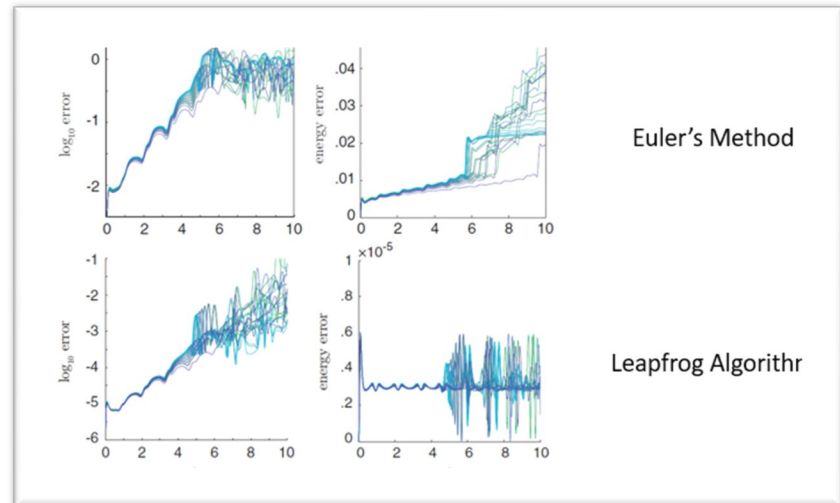


Euler's Method

Leapfrog Algorithm

# Why Leapfrog Algorithm?

- Leapfrog Algorithm: **Second-Order Method** (Proof is omitted)
  - Why not apply higher-order Runge-Kutta Method (e.g. RK4)?
- **Error Growth** in Numerical Integration of ODEs
  - Molecular dynamics trajectories need to be very long compared to the time step, thus **how the error grows in long simulations** is essential
  - **Chaotic nature** of molecular dynamics, sensitivity to perturbations, the **global error** is expected to grow rapidly (exponentially) in time unavoidably
  - However, leapfrog algorithm has significant **stability of energy** that the energy error DO NOT accumulate in time
- This is actually an extremely **non-trivial** property! Many common numerical algorithms of ODE is not suitable for MD Simulation for this reason.







# Why Leapfrog Algorithm?

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- A glimpse of the essence: **Geometric Integrators** for Hamiltonian Systems
  - Methods that conserve a **certain geometric property** *i.e.* **Symplecticness** of the phase flow
  - Mathematically, symplecticness is the property that  $d\mathbf{p} \times d\mathbf{r}$  is a **conserved quantity**
  - Symplectic methods (e.g. leapfrog algorithm) preserve a **perturbed energy-like invariant** *i.e.* these algorithms possess **in-built long term stability** (proof is omitted)

# Why Leapfrog Algorithm?

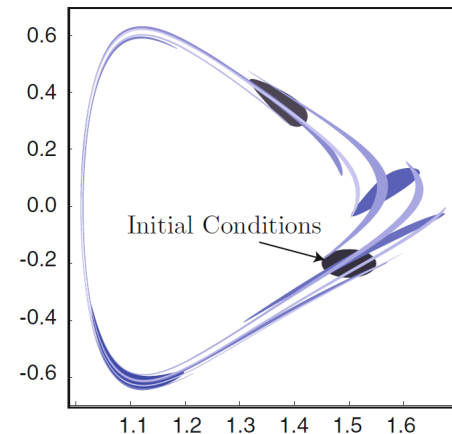
- A glimpse of the essence: **Geometric Integrators** for Hamiltonian Systems
- The Dynamics of a **Hamiltonian system**

- Hamilton's Equations

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

- **Highly restricted** by conservation laws or volume preservation, violation of which leads to a **gradual corruption** of the solution
- Volume Preserving Flows: **Liouville's Theorem**

$$\frac{\partial}{\partial t} \rho = -\{\rho, \mathcal{H}\}_{\text{PB}} := -\sum_{i=1}^f \left( \frac{\partial \rho}{\partial q_i} \frac{dq_i}{dt} - \frac{\partial \rho}{\partial p_i} \frac{dp_i}{dt} \right)$$





# Why Leapfrog Algorithm?

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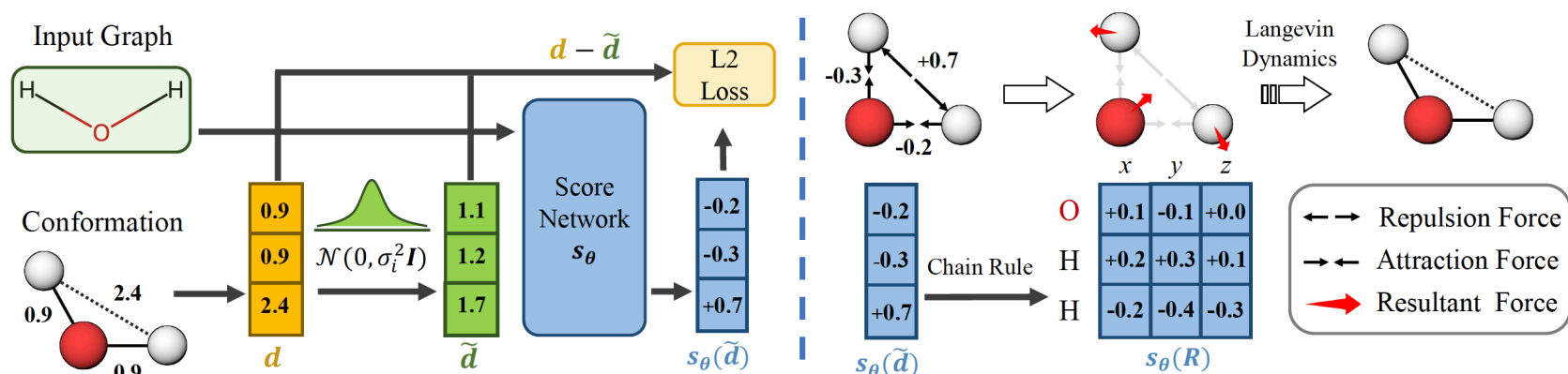
- A glimpse of the essence: **Geometric Integrators** for Hamiltonian Systems
- The Dynamics of a **Hamiltonian system**
- Connection between **MD Simulations** and Hamiltonian System?
  - Quick intro to Statistical Mechanics: **Microcanonical Ensemble (NVE Ensemble)**, energy as a conserved quantity
  - Hamiltonian systems, satisfy Liouville Theorem
  - Hence **symplecticness** of algorithms is required
- The Symplecticness of **Leapfrog Algorithm**
  - The Symplectic nature of the leapfrog algorithm can be shown by deriving the algorithm **directly** from the **Liouville Equation** or **Hamilton's principle of least action**
  - (The latter) finally leads to

$$M(\mathbf{r}_{n+1} - 2\mathbf{r}_n + \mathbf{r}_{n-1}) = -h^2 \nabla U(\mathbf{r}_n)$$

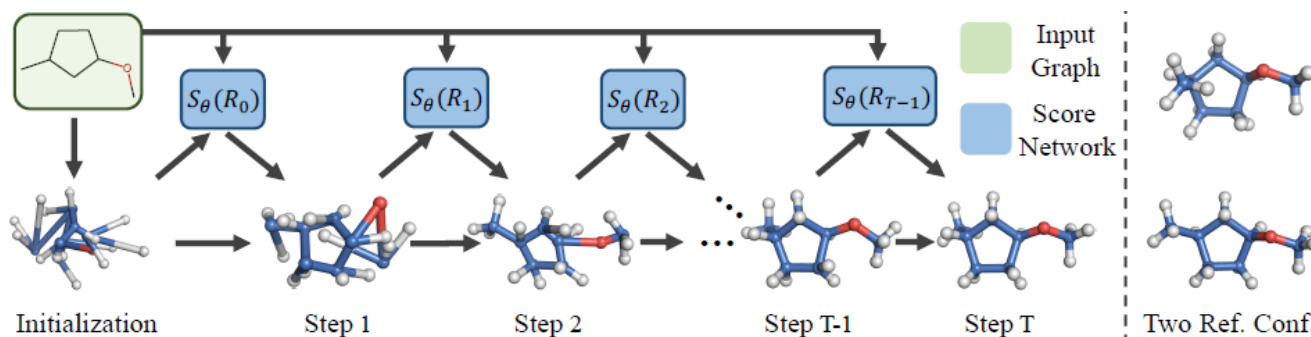
which is **Störmer's Rule!**

# Frontier: Deep Learning for Molecular Dynamics

- ConfGF (ICML'21)
  - Learning a Force Field via **Graph Isomorphism Network (GINs)**



- Perform Dynamics Simulation (Conformation Optimization) via **Langevin Dynamics**





# References

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- [2] Smith, W. (2014). Elements of molecular dynamics. *GitLab*.  
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# Thank you

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