

# Molecular Dynamics Simulations

Simulations of the motion of atoms and molecules. Trajectories of molecules (position versus time) are calculated by numerically solving equations of motion originating from the Newton laws:

**Force=mass\* acceleration,  $F=m*a$**

Forces between interacting particles and potential energy are defined by molecular mechanics force fields.

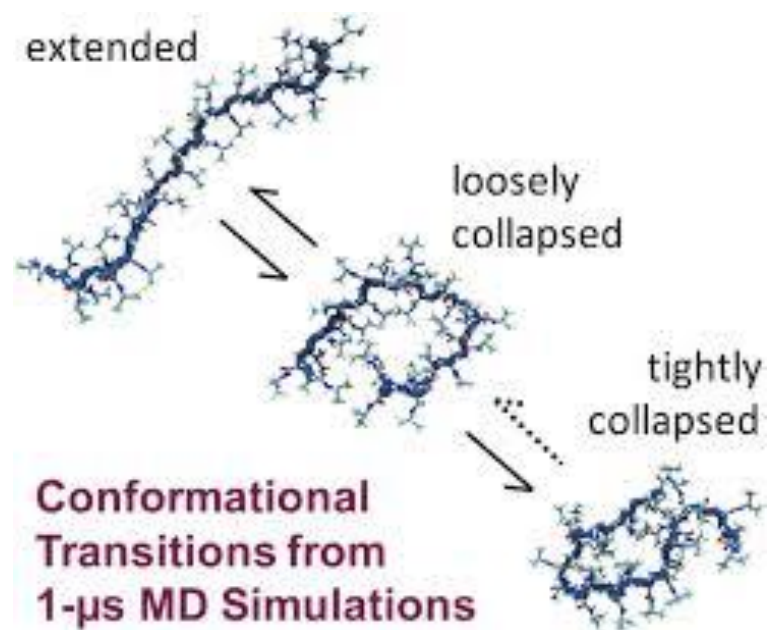
**Main area of applications: materials science and modeling of biomolecules.**

**Examples of potential: gravitation field, electrostatic field**

Potential energy – characterises forces that depend only on the position of the particle in space. Consequently, the potential energy also depends only on the position

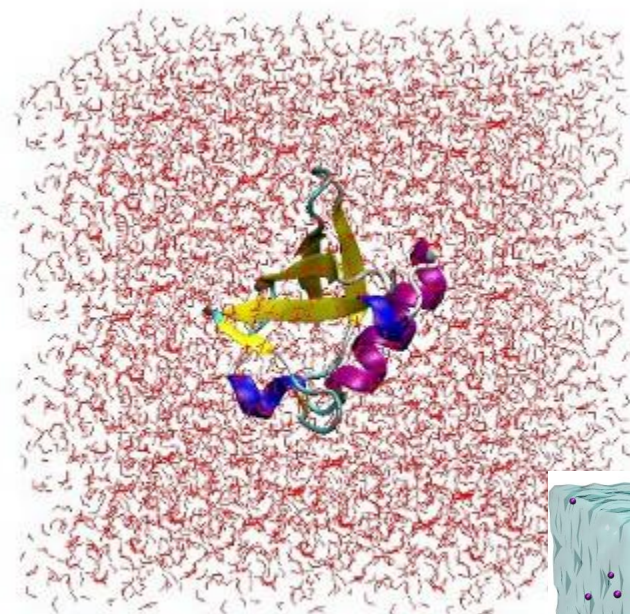
Force field – the set of forces

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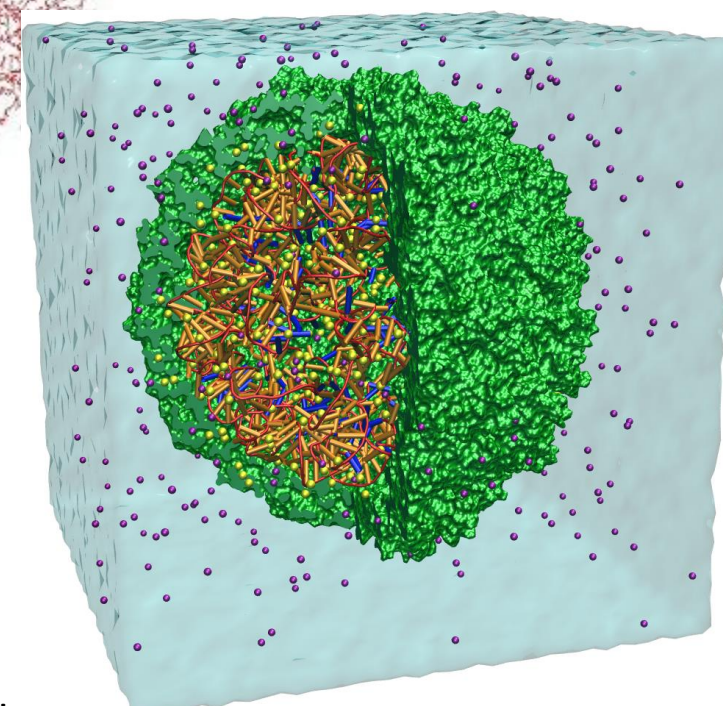


<https://pubs.acs.org/doi/pdf/10.1021/acs.jpcb.6b09165?rand=fu7wimf5>

[https://www.ks.uiuc.edu/Research/STMV/images/virus\\_webpage.full.png](https://www.ks.uiuc.edu/Research/STMV/images/virus_webpage.full.png)



[http://ringo.ams.stonybrook.edu/index.php/MD\\_Simulation:\\_Protein\\_in\\_Water](http://ringo.ams.stonybrook.edu/index.php/MD_Simulation:_Protein_in_Water)



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# Molecular Dynamics Simulations

- Each atom is treated as a single particle
- Each particle has a radius and polarizability
- Interactions are treated as “springs” with an equilibrium distance (harmonic oscillators)
- Atoms are treated as hard spheres (balls)
- Collisions are perfectly elastic (the total kinetic energy and momentum is conserved, no changes in the particle shape)
- Atomic charges remain unchanged during the motion
- Bonds cannot be created (or destroyed)

## Limitations

**bigger systems for longer timescales – longer computation time**

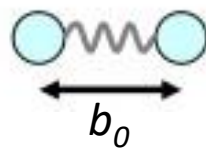
- protein aggregation on atomistic level, adsorption and diffusion mechanisms
- enzymes activity and insight into detailed catalytic activity mechanisms

# Molecular Dynamics Simulations

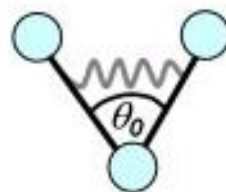
- Build the molecule – find the  $(x,y,z)$  position of all atoms
- Create (or apply existing) the force field
- Find the optimal structure (energy minimization)
- Solve the Newton's equations of motions of all atoms in the force field for each time point

# Molecular Dynamics Simulations

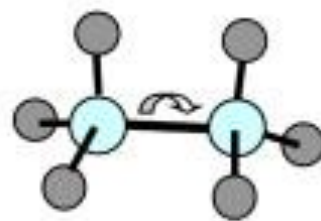
$$U(\vec{R}) = \frac{1}{2} \sum_{bonds} K_b (b - b_0)^2 +$$



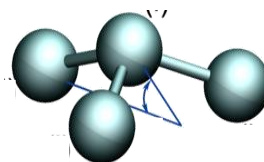
$$\frac{1}{2} \sum_{angles} K_\theta (\theta - \theta_0)^2 +$$



$$\sum_{dihedrals} K_\phi [1 + \cos(n\phi - \delta)] +$$



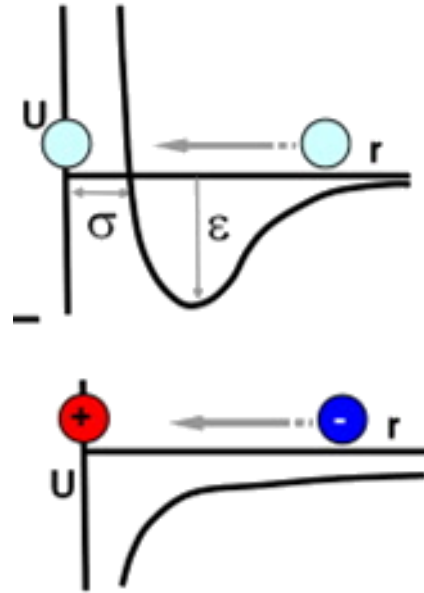
$$\sum_{impropers} K_\omega (\omega - \omega_0)^2 +$$



# Molecular Dynamics Simulations

$$\sum_{i>j} \left( \frac{A_{ij}}{r_{ij}^{12}} - \frac{B_{ij}}{r_{ij}^6} \right) +$$

$$\sum_{i>j} \frac{q_i q_j}{4\pi\epsilon_0 r_{ij}}$$



Energy minimization methods -  
to compute the equilibrium configuration of molecules

# Molecular Dynamics Simulations

## The Verlet algorithm

### Taylor expansion

$$\vec{r}_i(t + \Delta t) = \vec{r}_i(t) + \frac{d\vec{r}_i(t)}{dt} \Delta t + \frac{1}{2} \frac{d^2\vec{r}_i(t)}{dt^2} \Delta t^2 + \frac{1}{6} \frac{d^3\vec{r}_i(t)}{dt^3} \Delta t^3 + O(\Delta t^4)$$

$$\vec{r}_i(t - \Delta t) = \vec{r}_i(t) - \frac{d\vec{r}_i(t)}{dt} \Delta t + \frac{1}{2} \frac{d^2\vec{r}_i(t)}{dt^2} \Delta t^2 - \frac{1}{6} \frac{d^3\vec{r}_i(t)}{dt^3} \Delta t^3 + O(\Delta t^4)$$

$$\vec{r}_i(t + \Delta t) = 2\vec{r}_i(t) - \vec{r}_i(t - \Delta t) + \frac{d^2\vec{r}_i(t)}{dt^2} \Delta t^2 + O(\Delta t^4)$$

# Molecular Dynamics Simulations

## The Verlet algorithm

Velocity:

$$\vec{v}_i(t) = \frac{d\vec{r}_i(t)}{dt} = \frac{\vec{r}_i(t + \Delta t) - \vec{r}_i(t - \Delta t)}{2\Delta t}$$

Kinetic Energy:

$$E(t) = \sum_{i=1}^N \frac{m\vec{v}_i(t)^2}{2}$$



# Molecular Dynamics Simulations

## The Verlet algorithm

The position of the atom is updated with  $\Delta t$  step

$$\vec{r}_i(t + \Delta t) = \vec{r}_i(t) + \vec{v}_i(t)\Delta t + \frac{1}{2}\vec{a}_i(t)\Delta t^2$$

The velocity is updated with  $(\Delta t + \Delta t/2)$  step:

$$\vec{v}_i\left(t + \frac{\Delta t}{2}\right) = \vec{v}_i(t) + \frac{1}{2}\vec{a}_i(t)\Delta t$$

Acceleration at  $(t + \Delta t)$ :

$$\vec{a}_i(t + \Delta t) = -\left(\frac{1}{m_i}\right)\nabla U(\vec{r}_i(t + \Delta t))$$

Velocity at:

$$(t + \Delta t) \quad \vec{v}_i(t + \Delta t) = \vec{v}_i\left(t + \frac{\Delta t}{2}\right) + \frac{1}{2}\vec{a}_i(t + \Delta t)\Delta t$$