

Molecular Dynamics

Statistical mechanics

- Need ensemble averages for thermodynamic properties
- Ergodic hypothesis: time average = ensemble average
- Classical simulation of atomic motion over time

Propagation

- Integrate Newton's equations of motion
- Small time steps (femtoseconds)
- Repeated force evaluations from potential energy surface

Classical mechanics governs molecular motion:

$$\underbrace{\mathbf{F}_i}_{\text{Force on atom } i} = m_i \underbrace{\mathbf{a}_i}_{\text{Acceleration of atom } i} = m_i \frac{d^2 \underbrace{\mathbf{r}_i}_{\text{Position of atom } i}}{dt^2} = - \underbrace{\nabla_i V}_{\text{Gradient of potential energy}}(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N) \quad (38)$$

Requirements for MD integrator

- Stability over long time scales
- Time reversibility (energy conservation)
- Computationally efficient
- Access to positions and velocities

Simple and robust integration scheme based on Taylor expansions:

$$\underbrace{\mathbf{r}(t + \Delta t)}_{\text{Position}} = \underbrace{\mathbf{r}(t)}_{\text{Position}} + \underbrace{\mathbf{v}(t)}_{\text{Velocity}} \underbrace{\Delta t}_{\text{Timestep}} + \frac{1}{2} \underbrace{\mathbf{a}(t)}_{\text{Acceleration}} \Delta t^2 + \underbrace{\mathcal{O}(\Delta t^4)}_{\text{Big-O notation}} \quad (39)$$

$$\mathbf{r}(t - \Delta t) = \mathbf{r}(t) - \mathbf{v}(t) \Delta t + \frac{1}{2} \mathbf{a}(t) \Delta t^2 + \mathcal{O}(\Delta t^4) \quad (40)$$

Adding both equations:

$$\mathbf{r}(t + \Delta t) = 2\mathbf{r}(t) - \mathbf{r}(t - \Delta t) + \mathbf{a}(t) \Delta t^2 \quad (41)$$

More practical variant that gives direct access to velocities:

$$\mathbf{r}(t + \Delta t) = \mathbf{r}(t) + \mathbf{v}(t) \Delta t + \frac{1}{2} \mathbf{a}(t) \Delta t^2 \quad (42)$$

$$\mathbf{v}(t + \Delta t) = \mathbf{v}(t) + \frac{1}{2} [\mathbf{a}(t) + \mathbf{a}(t + \Delta t)] \Delta t \quad (43)$$

⚙️ Temperature control

- Canonical ensemble (NVT): constant temperature
- Microcanonical ensemble (NVE): constant energy

$$\underbrace{E_{\text{kin}}(t)}_{\text{Kinetic energy}} = \frac{1}{2} \sum_i \underbrace{m_i}_{\text{Mass of atom } i} \underbrace{\mathbf{v}_i^2}_{\text{Velocity}} = \langle E_{\text{kin}} \rangle = \frac{1}{2} \underbrace{n}_{\text{number of degrees of freedom}} \underbrace{k_B}_{\text{Boltzmann constant}} \underbrace{T}_{\text{Temperature}} \quad (44)$$

Challenges:

- Continuous trajectory
- Conserve Autocorrelation / dynamic properties
- Instantaneous temperature

Idea

- Weak coupling to external heat bath
- Rescales velocities to target temperature
- Simple but not rigorous

$$\mathbf{v}_i' = \mathbf{v}_i \sqrt{\frac{\langle E_{\text{kin}} \rangle}{E_{\text{kin}}(t)}} \quad (45)$$

Problems

- Flying ice cube
- Jumps

Idea

- virtual random collisions
- sample target momentum of particles from Boltzmann distribution
- effectively: adding random forces

$$P(t) = \nu \exp(-\nu t) \quad (46)$$

Andersen parameter

Particle collision frequency



Idea

- Scale not exactly, but with noise
- Coupling timescale τ

Properties

- Samples canonical ensemble
- Has conserved quantity, close to true energy

Idea

- random kicks per atom
- added friction term in equations of motion

$$\mathbf{v}_i = \mathbf{p}_i / m_i \quad \dot{\mathbf{p}}_i = \mathbf{F}_i - \underset{\substack{\uparrow \\ \text{Friction coefficient}}}{\gamma} \mathbf{p}_i + \underset{\substack{\uparrow \\ \text{Random kicks}}}{\mathbf{f}_i} \quad (47)$$

$$|\mathbf{f}_i| \in \mathcal{N}(0, 2 m_i \gamma k_B T / \Delta t) \quad (48)$$

Idea

- Scale velocities by dynamic virtual coordinate s
- Propagate s
- Control through mass

$$\mathcal{L}_s = \frac{1}{2} \underbrace{Q}_{\text{Fictitious mass}} \dot{s}^2 - \underbrace{n}_{\text{Degrees of freedom}} k_B T \ln s \quad (49)$$

Time step selection

- Typically 0.5-2 fs for organic molecules
- Must resolve fastest motions (C-H stretching)
- Stability criterion: $\Delta t < 2\sqrt{m/k_{\max}}$

Boundary conditions

- Periodic boundary conditions for bulk systems
- Minimum image convention for interactions

Equilibration

- Initial relaxation period before data collection
- Monitor energy, temperature, and structural properties

Molecular Dynamics

- Classical simulation of atomic motion using Newton's equations
- Time evolution through numerical integration (Verlet algorithms)
- Access to dynamic properties and ensemble averages

Control

- Thermostats maintain constant temperature
- Time step selection critical for stability
- Equilibration required before data collection