

# Biomolecular Simulation

## BT2123

### Lecture 3 : Phase space and simple harmonic oscillator

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# Methodology : MD simulations

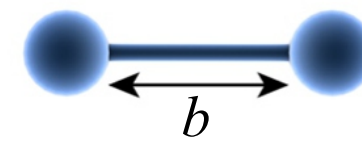
- Pick particles, masses and potential.
- Initialize positions and momentum.

$$-\frac{dU}{dr_i} = m_i \frac{d^2 r_i}{dt^2}$$

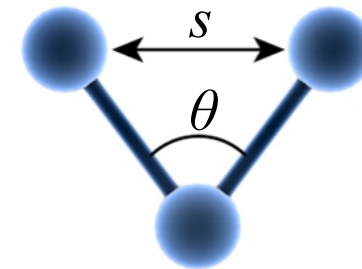
- Solve  $F = m a$  to determine  $r(t)$ ,  $v(t)$ .
- Compute properties along the trajectory
- Try to use the simulation to answer physical questions.

## Canonical ensemble

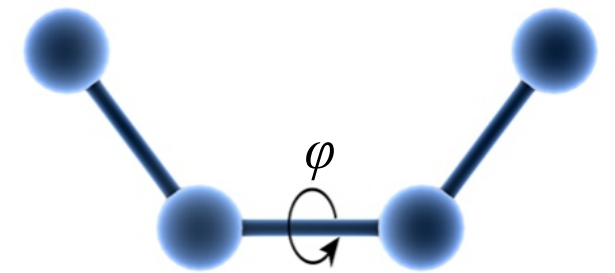
N = 10, 000 to 1, 000,000  
P = 1 atm  
T = 300 K



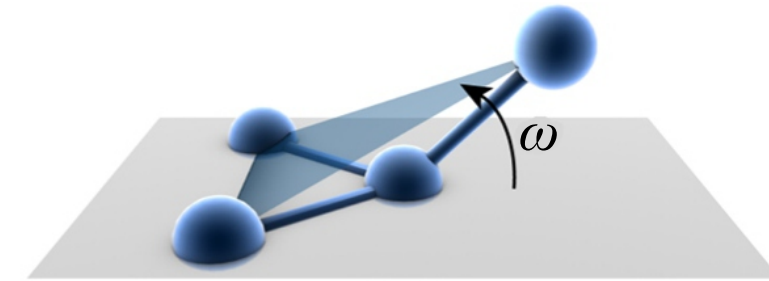
Bond Stretching



Angle bending



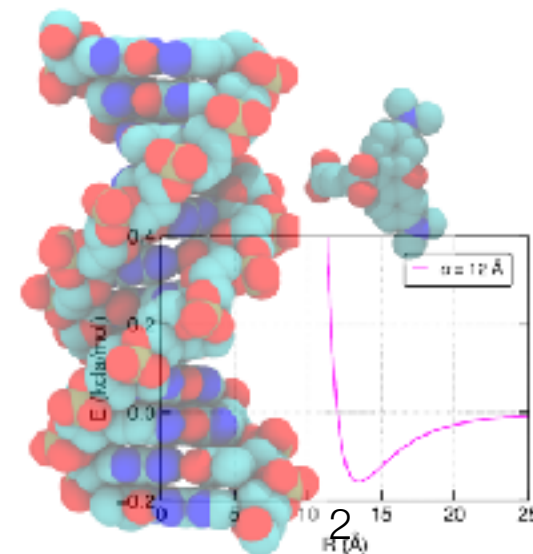
Proper dihedral torsion



Improper dihedral torsion

Source: Behzad Mehrafrooz

$$U = \sum_{\text{bonded}} \left\{ \begin{aligned} &k(r_{ij} - r_0)^2 \\ &+ k_\theta(\theta - \theta_0)^2 \\ &+ k(1 + \cos(n\psi + \phi)) \end{aligned} \right\} \\ + \sum_{i>j} \left\{ \begin{aligned} &-U_{\min} \left[ \left( \frac{R_{\min}}{r_{ij}} \right)^{12} - 2 \left( \frac{R_{\min}}{r_{ij}} \right)^6 \right] \\ &+ \frac{Cq_i q_j}{\epsilon_0 r_{ij}} \end{aligned} \right\}$$



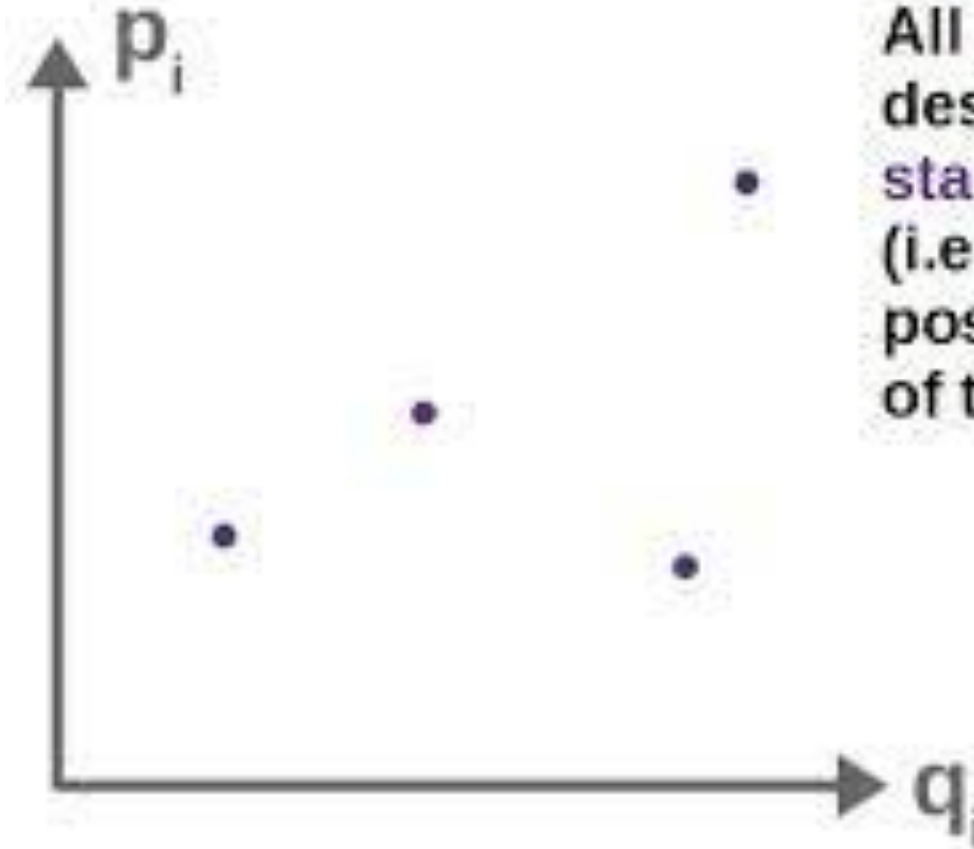
Hamiltonian mechanics

Newtonian mechanics

Lagrangian mechanics



# Phase space



All of these points describe different **states** of the system (i.e. different values of position and momenta of the system)