Short Course on Molecular Dynamics Simulation

> Lecture 1: Basic Concepts

Professor A. Martini Purdue University

- Awareness of the opportunities and limitations of MD simulation for scientific and engineering research
- Understanding of the compromise between model complexity/realism and computational expense
- Background that enables interpretation of MD studies reported in the literature
- Physical understanding of the theoretic basis of MD modeling

# High Level Course Outline

### 1. MD Basics

- 2. Potential Energy Functions
- 3. Integration Algorithms
- 4. Temperature Control
- 5. Boundary Conditions
- 6. Neighbor Lists
- 7. Initialization and Equilibrium
- 8. Extracting Static Properties
- 9. Extracting Dynamic Properties
- 10. Non-Equilibrium MD

- Molecular dynamics (MD) simulation = computational tool used to describe how positions, velocities, and orientations of molecules change over time.
- The simulation is based on a set of models that describe molecular-scale interactions.
- These models relate energy/force to configuration which are be used to calculate acceleration via Newton's law.
- Numerical integration yields particle velocities, and then each particle is moved through a distance equal to its calculated velocity multiplied by the simulation time step.
- So, MD is used as a computational "experiment" where a system is defined, allowed to evolve, and then observations made based on its evolution.

## **MD** Basics



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• Force  $\rightarrow$  Acceleration  $\rightarrow$  Velocity  $\rightarrow$  Position



#### MD conserves the total energy (Hamiltonian)

$$H(\vec{p}_i, \vec{r}_i) = \sum_{i=1}^{N} \frac{\vec{p}_i^2}{2m_i} + U(\vec{r}_i) \qquad \frac{dH}{dt} = 0$$

$$\bigvee_{\text{KE}} \text{PE}$$

 A given atom is represented by its time-dependent position and momentum vectors

$$\vec{r_i} \quad \vec{p_i} = m\vec{v_i}$$

 At a given instant, consider a plot of the positions and momenta of all N atoms in the system

6 N-dimensional plotting domain  $\rightarrow$  Phase-Space



- Ensembles characterized by fixed values of thermodynamic variables:
  - Energy
  - Temperature
  - Pressure
  - Volume
  - Number of particles
  - Chemical potential
- Basic MD NVE
  - Micro-canonical ensemble
- $\hfill\square$  Other common ensembles NVT, NPT,  $\mu VT$ 
  - Canonical, isothermal-isobaric, grand-canonical

### References

- The following text books were used throughout the development of this course and should be used as references for in depth study
  - Allen, M.P and Tildesley, D.J., Computer Simulation of Liquids, Oxford University Press.
  - Frenkel, D. and Smit, B., Understanding Molecular Simulation: From Algorithms to Applications, Elsevier.
  - Haile, J.M., Molecular Dynamics Simulation: Elementary Methods, Wiley & Sons.
  - Leach, A., Molecular Modeling: Principles and Applications, Prentice Hall.