Métodos numéricos para escoamentos

em nano e microescalas

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MOLECULAR DYNAMICS

Statistical Physics

- Molecular simulations generate information at microscopic level.
- How to conect this microscopic information (atomic positions and velocities) into macroscopic observable (temperature, pressure, heat capacity ...) ?!



- <u>Goal</u>: explore the macroscopic properties of a system through microscopic simulations
- <u>Path:</u> through Statistical mechanics

rigorous mathematical approach that relates macroscopic properties with the distribution and motion of atoms and molecules of the N-body system.

Explore both thermodynamic and or kinetic phenomena

Thermodynamics, Kinetic and Dynamics

Thermodynamics describes the driving force for chemical processes



Microscopic state and ensemble



Microscopic state: defined by the atomic positions (r) and momenta (p).

Phase space: r and *p* coordinates in a multidimensional space.



Please, could you be more clear ?!

SURE !

Let me take the most simple case possible:

The 1-D HARMONIC OSCILATOR

Harmonic oscilator - phase space



Harmonic oscilator - phase space



Now, for us :

we have more than 10²³ particles,

we would have a phase space of

6x10²³ dimensions !!!

Ensembles



<u>Ensemble:</u> is a collection of all possible systems which have different microscopic states BUT have AN IDENTICAL macroscopic or thermodynamic state.

- ♦ Each microscopic state has some probability.
- ♦ Distribution function describes everything.

Ensembles

Name	All states of:	Probability distribution	Schematic
Microcanonical (EVN)	given EVN	$\pi_i = \frac{1}{\Omega}$	
Canonical (TVN)	all energies	$\pi(E_i) = \frac{1}{Q} e^{-\beta E_i}$	8889
Isothermal-isobaric (TPN)	all energies and volumes	$\pi(E_i, V_i) = \frac{1}{\Delta} e^{-\beta(E_i + PV_i)}$	88 88 98
Grand-canonical (TVµ)	all energies and molecule numbers	$\pi(E_i, N_i) = \frac{1}{\Xi} e^{-\beta(E_i + \mu N_i)}$	

SO WHAT ?!

Phase space, Ensemble, Microcanonical, Canonical, bla bla ...

Where is the relation with bridges, buildings, cars, real life?

Experiment Molecular Simulation





Macroscopic



Next:

The most important slides of this course !

Average in an ensemble

PROBABILITY (define the conditions of the systems)

$\langle D \rangle = \int P(\mathbf{p}^N, \mathbf{r}^N) D(\mathbf{p}^N, \mathbf{r}^N) d\mathbf{p}^N d\mathbf{r}^N$

OBSERVABLE: physical property that we are interested in ...



$$\overline{D} = \lim_{t \to \infty} \frac{1}{t} \int_{0}^{t} D(t') dt'.$$
OBSERVABLE: physical property that we are interested in ...

The most important slide of this course

Ensemble average = Time average



Remember !!!

Ensemble average = Time average



Molecular simulations

Molecular simulation provides the way to:

1) Calculate time averages of an observable

2) Visit the most important points in the phase space.



Knowing the phase space and time averages, one knows the macroscopic properties.

Figure 5.1: Motion of a point in a two-dimensional phase space. The diagram only maps the temporal evolution of two coordinates, $\mathbf{r}_{x_1}(t)$ and $\mathbf{p}_{x_1}(t)$, out of the 6 N coordinates, $\mathbf{r}_{x_1}(t)$, $\mathbf{r}_{x_2}(t)$, ..., $\mathbf{r}_{x_N}(t)$, $\mathbf{p}_{x_1}(t)$, $\mathbf{p}_{x_2}(t)$, ..., $\mathbf{p}_{x_N}(t)$. The arrows indicate the continuous increase of time.

Equilibrium properties

Nstep	Etotal	Upot	Virial	Temp
	kJ/mol	kJ/mol	kJ/mol	K
20	-4.8215	-6.0300	2.0563	96.90
40	-4.8216	-5.9691	1.1320	92.01
60	-4.8216	-5.9057	0485	86.93
80	-4.8216	-5.9630	.8602	91.52
100	-4.8218	-5.9696	.9501	92.04

Temperature: 92.3979 ± 3.2927 [K] Potential: $-5.9739 \pm .0409$ [kJ/mol] Total Energy: $-4.8215 \pm .0017$ [kJ/mol] Translational Energy: $1.1523 \pm .0411$ [kJ/mol] Virial: $1.0893 \pm .6904$ [kJ/mol] Pressure: 143.1503 ± 71.6967 [bar]

Stochastic x Deterministic



3) Dynamics

How to solve the classical equations of motion for all particles in different conditions (Temperature, Pressure and any other themodynamical parameters) ?.

Solution: Given by Sir Isaac Newton over 300 years ago !!

$$m\frac{d^{2}\vec{r}_{i}}{dt^{2}} = -\nabla_{i}V(\vec{r}_{1},\vec{r}_{2}....\vec{r}_{N})$$

We have to solve the Newton's motion equation in time for each of the ith particle in the system.

Newton's equations of motion

$$m\frac{d^2\vec{r}_i}{dt^2} = -\nabla_i V(\vec{r}_1, \vec{r}_2....\vec{r}_N)$$



The properties can be obtained by sampling the system at a given ensemble (NPT, NVT, NVE, gran-canonical, ...)

$$\left\langle \mathbf{A} \right\rangle_{\text{NVT}} = \int d\Gamma \,\rho_{\text{NVT}} \,\mathbf{A}(\Gamma) \\ \rho_{\text{NVT}}(\Gamma) = \frac{e^{-\beta \mathcal{H}(\Gamma)}}{Z_{\text{NVT}}} \quad \text{where} \begin{cases} \beta = \frac{1}{k_{\text{B}}T} \\ \mathcal{H} = K + V \\ Z_{\text{NVT}} = \int d\Gamma \rho_{\text{NVT}} \end{cases}$$

$$Ergodic \\ Hypothesis \left\langle \mathbf{A} \right\rangle_{\text{NVT}} = \lim_{t_{\text{sim}} \to \infty} \frac{1}{t_{\text{sim}}} \int_{t_0}^{t_0 + t_{\text{sim}}} \mathbf{A}(\tau) d\tau$$

- □ What is molecular dynamics ?
- Computer simulation technique that allows one to predict the time evolution of a system of interaction particles (atoms, molecules, granules, etc.)

□ Steps:

- 1) Set the system of interest:
- a) Initial conditions (initial positions and velocities of all particles)
- b) Interatomic potential (to describe the forces between the particles)

Schematic diagram of a basic MD code



Write to the disc final atomic configuration & finish

Piece of the code

Program MolDyn

! This a very simple Molecular Dynamics code call init

10 call force call integrator time = time + dt call sample if (time.lt.maxtime) goto 10

> stop end

Building your own code

- **Subroutines**
- **<u>Init</u>**: to initialize the system to be simulated
- **<u>Force</u>**: to calculate the forces
- **Integrator:** to solve numerically the equation of motion
- <u>Sample</u>: to analyse and accumulate the trajectory
- Variables
- <u>time</u> = instant of time of the simulation
- <u>dt</u> = time step to solve the equations of motion
- <u>maxtime</u> = maximum time wanted

Limitations of the MD technique (I)

1) Classical description of interatomic interaction

 Electrons are not present explicitly (Potential energy surface)

• PES is approximated by an analytic function that gives the potential energy U as a function of coordinates.

• Forces comes from the gradient of a PES.

Limitations of the MD technique (II)

2) In classical MD the Schrodinger equation for nuclei is replaced with the Newton equation.

How good is this approximation?

Quantum effects are significant when the de Broglie wavelength Λ is larger than the inter-particle distance.

 $\lambda_{dB} = \left(\frac{2\pi\hbar^2}{mk_BT}\right)^{T}$

2. Classical description of atomic motion (continued)

L

For the thermal motion we can use the thermal de Broglie wavelength:

$$\Lambda_{th} = \frac{n}{\sqrt{2\pi m k_B T}}$$
 For T = 300 K we have $\Lambda_{th} = 1$ Å for a H atom
 $\Lambda_{th} = 0.19$ Å for a Si atom
 $\Lambda_{th} = 0.16$ Å for an Ar atom
 $\Lambda_{th} = 0.07$ Å for a Au atom

Typical interatomic spacing in solid-state materials is d ~ 1-3 Å. Therefore:

- The wave nature of electron dominates over the particle behavior, electrons can not be considered within classical approximation.
- All atoms, except for the lightest ones such as H, He, Ne, can be considered as "point" particles at sufficiently high temperature (d >> Λ) and classical mechanics can be used to describe their motion.

Interatomic interactions



Fig. 2.2 Le Sage's picture of attraction between particles of matter [249].





What does atomistic modeling involve?

- Atomic scale modelling of materials (interaction between atoms)
 ENERGY can be calculated by:
 - quantum mechanical calculation of energy as a function of structure.
 - effective potentials (analytical functions of the energy as a function of geometry which can be "parameterized" using experimental or quantum mechanics data
 Lennard-Jones, Morse, etc. (physicists), embedded-atom method, etc. (materials scientists), force fields (chemists), reactive potentials,...





First principles calculations

Numerically solving Schrodinger's equation:

Density Functional Theory (DFT)

Pseudopotentials

Quantum-Espresso, SIESTA, VASP and Gaussian

Composition

Structures





Kohn - Nobel Prize 99
Properties
Thermodynamics
Lattice Parameters
Elastic constants
Electronic Structure
Kinetics

Tailoring interatomic potentials

Strategy • Assumption: DFT accuracy is OK

- Effective potential fitted to DFT
- Improve functional form for effective potential
- Goal Construct effective potential with "DFT accuracy"
 More accurate and less computationally expensive

EDIP (Environment Dependent Interatomic Potential) (Justo et al. - PRB 97)
Tangney-Scandolo Potential (MgO and SiO₂) (Tangney & Scandolo JCP 03)
Potentials Guest-Frameworks (Miranda & Scandolo)
Potentials for nanostructure systems (Miranda & Ceder)



Lennard-Jones: A simple two-parameter form



Part 2 - Forces

Lennard-Jones potential

- The L-J potential is approximate. The form of the repulsion term has no theoretical justification;
- The repulsion force should depend EXPONENTIALLY on the distance,
- But the repulsion term of the L-J formula is more convenient due to the ease and efficiency of computing r¹² as the square of r⁶.
- The attractive long-range potential, however, is derived from **DISPERSION** interactions (London).

Potentials for complex molecules

Potential Energy

Empirical Force Field (e.g., CHARMM, OPLS, Amber, (MMFF))



Potentials for complex molecules

$$U = \sum_{AII Bonds} \frac{1}{k} \left(b - b_{0} \right)^{2} + \sum_{AII Angles} \frac{1}{k} \left(0 - \theta_{0} \right)^{2} \left(1 - \cos(n\varphi + J) \right)$$

$$+ \sum_{AII Torsion Angles} \frac{1}{k} \left(\frac{1}{k} - \cos(n\varphi + J) \right)$$

$$+ \sum_{AII Torsion Angles} \frac{1}{k} \left(\frac{1}{k} - \frac{1}{k} - \frac{1}{k} - \frac{1}{k} \right)^{2} - 2\left(\frac{n\varphi_{1}}{k}\right)^{2}$$

$$+ \sum_{AII nonbonded pairs} \frac{3329i9j}{k} \left(\frac{1}{k} - \frac{1}{k} - \frac{1}{k} \right)^{2} = \frac{1}{k} \left(\frac{1}{k} - \frac{1}{k} - \frac{1}{k} - \frac{1}{k} \right)^{2} = \frac{1}{k} \left(\frac{1}{k} - \frac{1}{k} - \frac{1}{k} - \frac{1}{k} - \frac{1}{k} \right)^{2} = \frac{1}{k} \left(\frac{1}{k} - \frac{1}{k$$

Michael Levitt, Nature Structural Biology 8, 392 - 393 (2001) The birth of computational structural biology



Lennard-Jones potential

The L-J potential is approximate. The form of the repulsion term has no theoretical justification;

the repulsion force should depend **EXPONENTIALLY** on the distance,

but the repulsion term of the L-J formula is more convenient due to the ease and efficiency of computing r^{12} as the square of r^{6} .

The attractive long-range potential, however, is derived from **DISPERSION** interactions (London).

Potentials for complex molecules

Empirical Potential Energy Function



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