JOINT INSTITUTE FOR NUCLEAR RESEARCH
Frank Laboratory of Neutron Physics

FINAL REPORT ON THE INTEREST PROGRAMME

INTRODUCTORY COURSE: MD-SIMULATION RESEARCH (FROM ATOMIC FRAGMENTS TO MOLECULAR COMPOUND)

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Abstract

In this report, we utilize the techniques of molecular dynamics in order to make a simulation and study biochemical molecular systems. Molecular dynamics simulation constitutes a bridge between the microscopic scales and macroscopic world, so we are able to use the calculations of classical mechanics. For the purpose of the simulation, we study the Lennard-Jones potential and we make use of the software package DL_POLY. Finally, my future goals in the field are presented.

Project goals

In this project, the main target is to make an introduction to Molecular Dynamics research in order to study:

1) The basic equations, potentials and simulation techniques.
2) The computer code description for simulation of liquid model (Lennard-Jones potential).
3) The use of selected general-purpose code for the simulation of ionic, polymeric and biochemical molecular systems.
4) The theory of the basics of hybrid MD approach (classical quantum-chemistry potentials simulation methods).
5) MD test modeling.

Contents

1. Introduction

Molecular dynamics (MD) is a computer simulation method for analyzing the physical movements of atoms and molecules. It firstly emerged and developed in the early 1950s, right after the Monte Carlo simulations. Nowadays, with the use of supercomputers we have been able to develop better systems of Molecular Dynamics and expand its operation not only for research purpose, but also for applied science. A few decades ago, we could not achieve calculations for many atoms, but now we have reached at a point where the trajectories of 50,000-10,000 atoms are commonly calculated. Our computational power has upgraded up to 500,000 atoms as long as we function with the appropriate processors.

In molecular dynamics simulations we combine microscopic simulations and macroscopic properties through statistical mechanics and the distribution of the system within the ensemble follows a Boltzmann approach.

Another problem scientists faced in the beginning of their approach was whether they should describe their complex system with the aid of quantum mechanics or classical mechanics. Quantum mechanics would be a much better approach, as we have particles, but much more computational power would be necessary. Therefore, scientists use classical mechanics.

2. Theoretical Background

2.1. The basic equations, potentials and simulation techniques

Molecular dynamics is based on Newton's second law, described by the equations:

$m_i \frac{d\boldsymbol{r}_i^2(t)}{dt^2} = \boldsymbol{F}_i(\boldsymbol{r})$, i=1, 2, …, n, where $\boldsymbol{F}_i(\boldsymbol{r}) = -\frac{\partial U(\boldsymbol{r})}{\partial \boldsymbol{r_i}}$.

So, conclusively we can write: $m_i \frac{d\boldsymbol{r}_i^2(t)}{dt^2} = \boldsymbol{F}_i\big(\boldsymbol{r}(t)\big) - \gamma_i m_i \frac{d\boldsymbol{r_i}(t)}{dt} + R_i(t)$.

A simulation of molecular dynamics requires the definition of the potential function, which in total can be described by adding the individual potential energies of any contribution parameter. These contribution parameters are shown in Figure 1 and are the following:

i. Bond stretching (between two atoms)
ii. Angle bending (between three atoms)
iii. Torsion (between four atoms)
iv. Van-der-Waals (or Lennard-Jones) interactions
v. Electrostatics interactions
vi. Hydrogen bonding

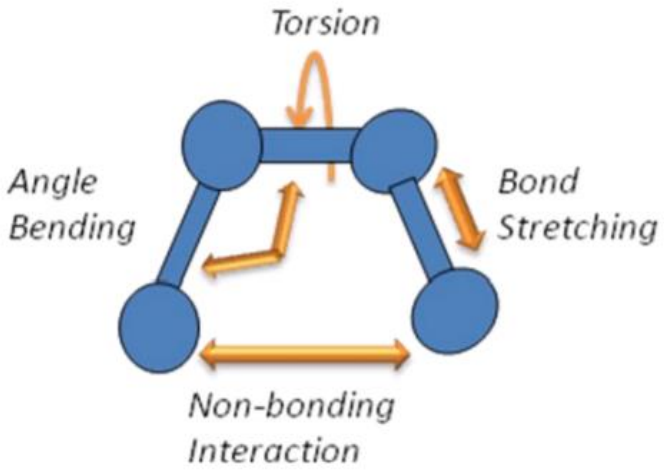

Figure 1: Chemical bonds

The equation of the aforementioned potential is:

$$U(\mathbf{r}) = U_b + U_\theta + U_\phi + U_\omega + U_{LJ} + U_{el} + U_{HB} + \ldots$$

and the corresponding explanation of each term of this equation is as follows:

i. Valence length potential: $U_b = \frac{1}{2}\sum_b K_b(r - b_0)^2$

ii. Valence angle potential: $U_\theta = \frac{1}{2}\sum_\theta K_\theta(\theta - \theta_0)^2$

iii. Torsion dihedral potential: $U_\varphi = \frac{1}{2}\sum_\varphi K_\varphi[\cos(n\varphi - \delta) + 1]$

iv. Van-der-Waals (or Lennard-Jones) interaction potential: $U_{LJ} = \sum_{i,j}[\frac{A}{r_{ij}^{12}} - \frac{B}{r_{ij}^{6}}]$

v. Electrostatics potential: $U_{el} = \sum_{i,j}\frac{q_i q_j}{\varepsilon r_{ij}}$

vi. Hydrogen bonding potential: $U_{HB} = \sum_{i,j}[\frac{A\prime}{r_{ij}^{12}} - \frac{B\prime}{r_{ij}^{10}}]$

The next step of Molecular Dynamics is to generate the velocity of the equations:

$T(t) = \frac{1}{3Nk_B}\sum_{i=1}^{n} m_i {v_i}^2$ and $\boldsymbol{v_i} = \frac{d\boldsymbol{r_i}}{dt}$.

2.2. The Lennard-Jones potential

The Lennard-Jones potential is one of the most archetype models for intermolecular interactions and especially in liquid simulations. It describes the potential energy of the interaction between

two non-binding atoms or molecules based on their distance of separation. The function of this potential is:

$$V(r) = 4\varepsilon[\left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^{6}]$$

where ε and σ are parameters with different values for each element. The respective graph is shown below, in Figure 2.

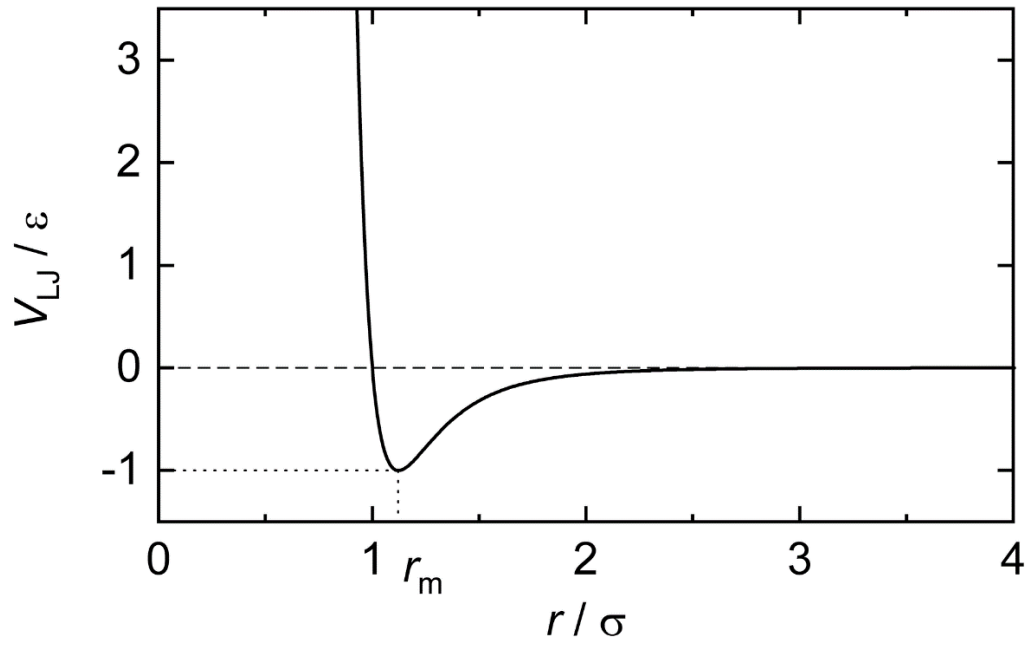

Figure 2: The Lennard-Jones potential energy dependence on the atomic distance

At this point we have to define three functions, the radial distribution function (RDF), the order parameter and Boltzmann distribution.

The radial distribution function is the probability to find the center of a particle in a given position at a radial distance r from the center of a reference sphere. It is used in MD simulation in order to monitor the equilibrium of the systems and is described by the following function:

$$\rho g(r) = \frac{1}{N} < \sum_{i}^{N} \sum_{j \neq i}^{N} \delta[r - r_{ij}] >$$

where N is the total number of atoms, ρ=N/V is the atomic density, r_{ij} is the radius-vector between two centers i and j, <…> is the time average and g equals to zero for distance less than one atomic diameter and equals to one for larger distances.

The next function is the order parameter, which accounts for a measure of the degree of order across the boundaries in a phase transition system. Function parameter γ is widely used for distinguishing of the equilibrium states:

$$\gamma_x = \frac{1}{N}\sum \cos(\frac{4\pi x_i}{a})$$

$$\gamma_y = \frac{1}{N}\sum \cos(\frac{4\pi y_i}{a})$$

$$\gamma_z = \frac{1}{N}\sum \cos(\frac{4\pi z_i}{a})$$

$$\gamma = \frac{1}{3}[\gamma_x + \gamma_y + \gamma_z]$$

The last function is Boltzmann distribution (H-function) and is used for the monitoring of the equilibrium.

$$H_x(t) = \int_{-\infty}^{+\infty} f(v_x) ln f(v_x) dv_x$$

Example of an MD simulation for Lennard-Jones system

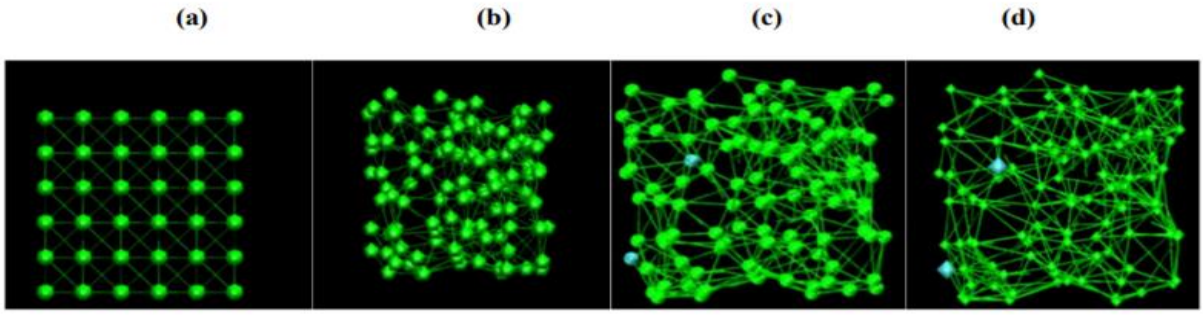

Figure 3: Sequential snapshots of the Lennard-Jones model configurations, where (a) t=0, (b) t=1, (c) t=10, (d) t=100 ps.

2.3. MD simulation package

The simulation package used for the objectives of this course is DL_POLY, which developed at Daresbury Laboratory by I.T. Todorov, W. Smith, A.M. Elena and others. It is a package for modeling the molecular dynamics of complex systems. DL_POLY has three input and three output files.

i. Input files

- CONFIG

- CONTROL
- FIELD

ii. Output files
- OUTPUT
- REVCON
- HISTORY

3. MD Simulation Example

In this section we will present the stereo image (Figures 4 and 5), snapshots from our used software, of a molecule called Ubiquitin. Ubiquitin is a small regulatory protein consisted of 76 amino acids, found in most tissues of eukaryotic organisms and is of significant importance for living systems. The ubiquitination system functions in a wide variety of cellular processes, including:

- Antigen processing
- Apoptosis
- Biogenesis of organelles
- Cell cycle and division
- DNA transcription and repair
- Differentiation and development
- Immune response and inflammation
- Neural and muscular degeneration
- Maintenance of pluripotency
- Morphogenesis of neural networks
- Modulation of cell surface receptors, ion channels and the secretory pathway
- Response to stress and extracellular modulators
- Ribosome biogenesis
- Viral infection

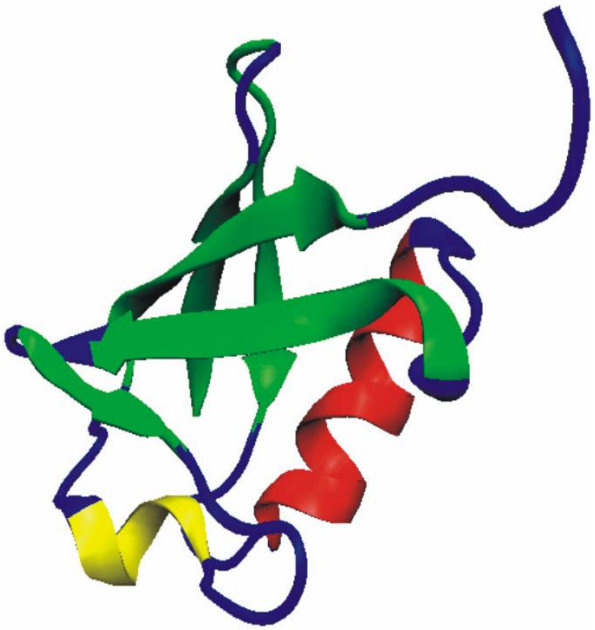

Figure 4: Structure of ubiquitin (red colour: α-helix, yellow colour: one short piece of 310-helix, green colour: a mixed β-sheet with five strands)

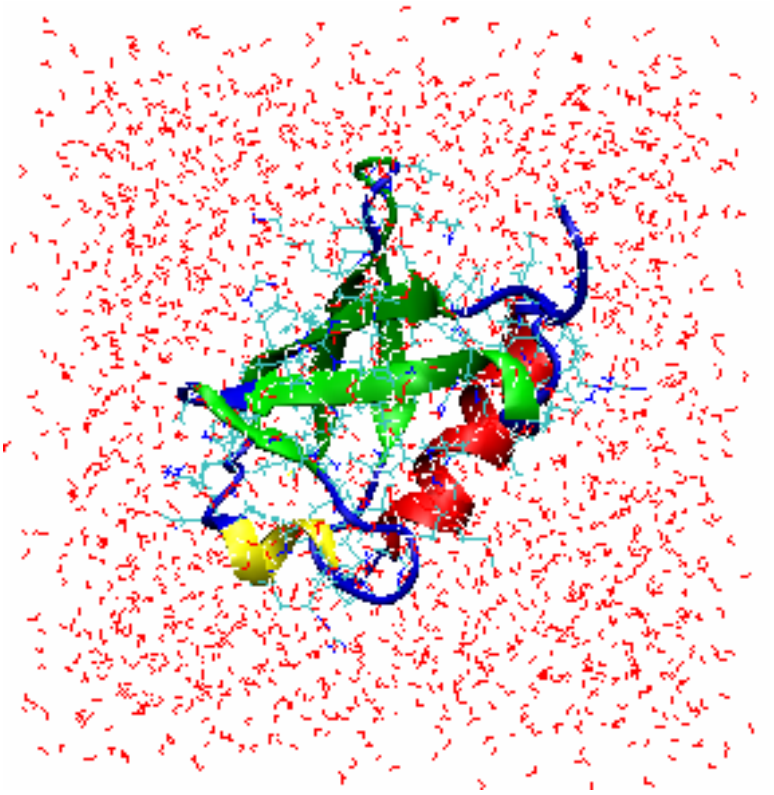

Figure 5: Ubiquitin structure in a water box

4. Future Goals

My future goals contain a Master's degree, possibly in astrobiology. I would like to combine molecular dynamics simulations with the astrobiology path, in order to understand the origin of cellular life.

5. Acknowledgements

I want to thank the INTEREST program for providing us such a great opportunity to extend our knowledge and obtain experience by renowned researchers. I also want to express my deep gratitude to my supervisor Professor Kholmirzo Kholmurodov for giving me the privilege to participate in this project and for his valuable guidance and support. His teaching methods and his kindness made me acquire maximum gains from this project.

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