

# ATOMIC MODELING OF ARGON

PROJECT 5 — FYS3150

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November 27, 2015

## Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Building a working MD-program</b>	<b>2</b>
2.1	Periodic boundary conditions . . . . .	2
2.2	Zero out momentum . . . . .	3
2.3	Face-centered cubic lattice . . . . .	4
2.4	Lennard-Jones potential . . . . .	4
2.5	Velocity Verlet, a symplectic integrator . . . . .	6
2.6	Sampling quantities . . . . .	6
<b>3</b>	<b>Simulations</b>	<b>7</b>
3.1	Energy conservation of integration method . . . . .	7
3.2	Melting temperature of system . . . . .	7

## 1 Introduction

Molecular dynamics (referred to as MD), deals with the time evolution of a system of particles, typically atoms or molecules. Being first explored in the late 1950's, it has had a wide range of applications, in fields as materials science, biochemistry and biophysics. It is based on the simple idea of considering a finite number of molecules and letting them interact for a fixed amount of time, which gives us an idea of how the system evolves.

In this project we examine what goes into creating a working MD-program that can compute various physical quantities and then proceed by considering some specific systems where we look at, amongst other, the kinetic energy, the initial temperature required in order to reach a desired final temperature, and finding the diffusion constant for the system in order to compute the melting temperature.

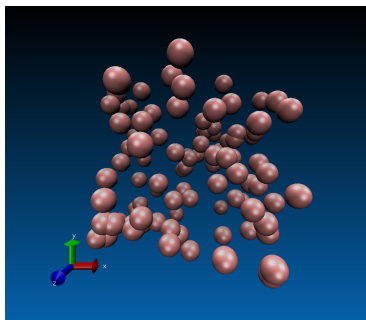


Figure 1: First iteration of the program — no boundary conditions and no force acting on the atoms. The atoms move with a constant speed in the direction of their initial velocity and the initial positions are uniformly distributed.

## 2 Building a working MD-program

Initially, we are presented with the skeleton of a MD-program, and we are tasked with filling in the blanks. In this section, we walk through each of the steps that went into the implementation of the program, from skeleton to working program. The process can be summarized as

- 1) Introduce periodic boundary conditions.
- 2) Implement a function for setting the net-momentum for the system to zero.
- 3) Make the atoms conform to a face-centered cubic lattice configuration.
- 4) Introduce the force model to the system, given by the Lennard-Jones potential.
- 5) Implement the Velocity-Verlet algorithm in order to get a better conservation of energy.
- 6) Write functions for sampling and storing physical quantities

Running the program in its initial state yields a random configuration of the atoms. Since there is no force acting on the molecules they move in straight lines determined by their initial velocity vector. Their motion is unbounded, due to the periodic boundary condition not being implemented yet. This can be seen in figure 1.

### 2.1 Periodic boundary conditions

We want our system to conform to periodic boundary conditions. The reasons for doing this is that to a certain extent the system of finite size more closely resembles that of an infinite size. It is important that the bounding box which

determines the boundary of the system is of sufficient size, so we do not get artifacts that arise from the fact that an atom can interact with itself.

There are two approaches to the implementation of periodic boundary condition. The most basic, and the one we will employ here is to have an atom exit through one face of the bounding box, and reappear through the opposite face.

Another approach is to not restrict the coordinates of the atom using the bounding box, and instead use the *periodic image* of the atom when calculating interactions with "nearby" particles.

We implement the function `applyPeriodicBoundaryConditions` in the `System`-class. Our method is simply iterating over each atom, and in the cases where we find an atom outside the bounding box, we add/subtract the size of the box. If we let the vector  $\mathbf{r}_i$ , with components  $r_q$  for  $q = x, y, z$ , denote the position of atom  $i$  at any given time, we simply let the position be governed by the following relation:

$$r_q = \begin{cases} r_q + L_q, & r_q < 0; \\ r_q - L_q, & r_q > L_q; \\ r_q, & \text{else.} \end{cases}$$

Here  $L_q$  is assumed to be the dimensions of the system in direction  $q = x, y, z$ .

During simulations we need to be a bit cautious about what we define as the *distance between* two atoms  $i$  and  $j$ . Typically, we see this as the distance through the system, but due to our periodic boundary conditions there might be a shorter path through one of the borders of the system. This is formally stated as the *minimum image criterion*[1].

## 2.2 Zero out momentum

The Maxwell-Boltzmann distribution is good for velocities because it fairly accurately represents the way velocities are distributed in an ideal gas. The distribution was defined initially by Maxwell, for the specific purpose of describing particle speeds inside a stationary container with no interaction. The distribution is directly dependent on the temperature of the system as well as the mass of each particle. We want to initialize each atom with a random velocity given by the Maxwell-Boltzmann distribution.

Mathematically, the distribution function reads

$$P(v_i) dv_i = \left( \frac{m_i}{2\pi k_B T} \right)^{1/2} e$$

The problem that arises when using the Maxwell-Boltzmann distribution is that in its initial state the system has a non-zero net momentum. This causes the system to drift. This is why we want to implement the function `removeMomentum` in the `System`-class. Its purpose is to compute the total momentum of the system, and then remove a small portion of momentum from each atom in order to have a net momentum of zero.

We compute the velocity of the center of mass of the system, and then subtract this velocity from each atom. Let  $m_i$  and  $v_i$  denote the mass and

velocity of atom  $i$  respectively and let  $M$  and  $V$  denote the total mass of the system and the velocity of the center of mass. Then

$$V = \sum_{i=1}^n m_i v_i, \quad M = \sum_{i=1}^n m_i$$

where  $n$  is the total number of atoms in the system. We then need to subtract the value  $V_{\text{sub}} = V/M$  from each  $v_i$ .

### 2.3 Face-centered cubic lattice

We now, instead of having random initial positions, want the atoms to form a crystal structure. In a face-centered cubic lattice (FCC), each unit cell has, in addition to the eight corner lattice points, one lattice point for each face.

A *unit cell* is a group of atoms which can be stacked on top and next to each other to form a grid structure. The *lattice constant* defines the size of the unit cell, and is denoted  $b$ . In this project we are assuming cubic grids, so we let  $N$  denote the number of unit cells in each dimension.

We now define a local coordinate system for each unit cell as

$$\begin{aligned} \mathbf{r}_1 &= 0\hat{\mathbf{i}} + 0\hat{\mathbf{j}} + 0\hat{\mathbf{k}}, & \mathbf{r}_2 &= \frac{b}{2}\hat{\mathbf{i}} + \frac{b}{2}\hat{\mathbf{j}} + 0\hat{\mathbf{k}}, \\ \mathbf{r}_3 &= 0\hat{\mathbf{i}} + \frac{b}{2}\hat{\mathbf{j}} + \frac{b}{2}\hat{\mathbf{k}}, & \mathbf{r}_4 &= \frac{b}{2}\hat{\mathbf{i}} + 0\hat{\mathbf{j}} + \frac{b}{2}\hat{\mathbf{k}}. \end{aligned}$$

The origin for an arbitrary unit cell is then given (globally) as

$$\mathbf{R}_{i,j,k} = i\hat{\mathbf{u}}_1 + j\hat{\mathbf{u}}_2 + k\hat{\mathbf{u}}_3$$

We implement the function `createFFCLattice` in the `System`-class which takes  $N$  and  $b$  as arguments. The initial configuration for an example system is displayed in figure 2.

### 2.4 Lennard-Jones potential

The Lennard-Jones potential approximates the interaction between a pair of atoms. In its most common form it reads

$$U(r_{ij}) = 4\varepsilon \left[ \left( \frac{\sigma}{r_{ij}} \right)^{12} - \left( \frac{\sigma}{r_{ij}} \right)^6 \right],$$

where  $r_{ij}$  is the distance between atom  $i$  and atom  $j$  and  $\varepsilon$  is the depth of the potential well. The quantity  $\sigma$  is the distance for which the potential is zero. With an expression for the potential we can sum over all distinct pairs of atoms and acquire an expression for the total potential energy  $V$ :

$$V = \sum_{i>j} U(r_{ij}).$$

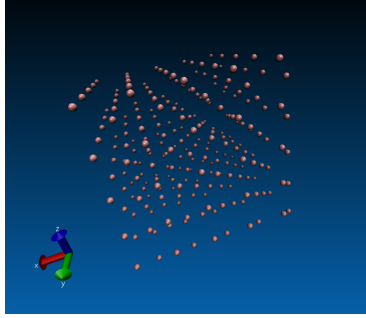


Figure 2: Initial configuration of a FFC-based lattice. We have here used a lattice constant  $b = 5.26\text{\AA}$  and the number of unit cells in each dimension is  $N = 5$ . This specific system has a density of  $\rho = M/V = 4N^3m/b^3N^3$  where  $m$  is the mass of each atom,  $b$  and  $N$  given as above. This evaluates to approximately  $0.1445\text{ a.m.u./\AA}^3$ .

The force exerted on atom  $i$  by atom  $j$  is then given as the negative gradient of the potential between the two:

$$\mathbf{F}(r_{ij}) = -\nabla U(r_{ij}).$$

The three force-components are given by:

$$F_q(r_{ij}) = -\frac{\partial U}{\partial r_{ij}} \frac{\partial r_{ij}}{\partial q_{ij}} \quad (q = x, y, z)$$

Analytically, this evaluates to

$$F_q(r_{i,j}) = 24\varepsilon \left[ \left( \frac{2\sigma^{12}}{r_{ij}^{13}} \right) - \left( \frac{\sigma^6}{r_{ij}^7} \right) \right] \quad (q = x, y, z).$$

The brute force way of computing this is summing over each distinct pair of atoms, and computing the mutual force between them. This however, constitutes a fairly heavy computational load that quickly scales with the size of the system. For a total of  $n$  atoms in the system, we have a time complexity of  $\mathcal{O}(n^2)$ . Luckily more efficient methods are available, most notably is the Verlet list method.

We need to chose the parameters  $\sigma$  and  $\varepsilon$  so that they are suited for simulation of argon. It turns out that  $\sigma = 3.405\text{\AA}$  and  $\varepsilon = 119.8k_B K$  with  $k_B = 1$  in MD-units.

Argon has a melting point of  $\approx 84K$  and a boiling point of  $\approx 87K$ . If we run the simulations, once for a temperature of  $40K$ , once for  $85K$  and finally once for  $120K$  we should see indications of three different phases. The results shows that the model somewhat accurately manages to capture these phase transitions. Snapshots taken at the same point in time for all three cases are presented in figure 3.

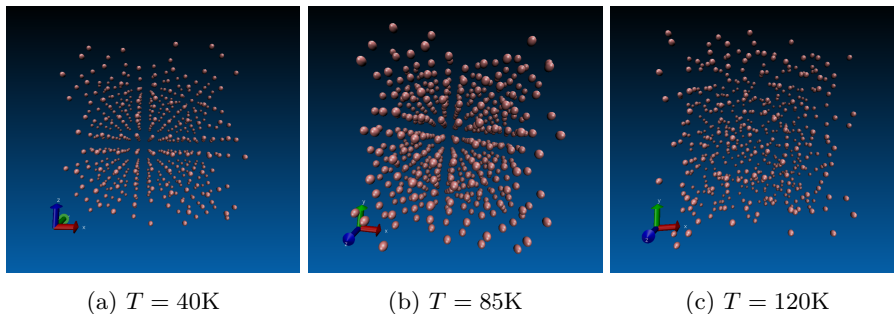


Figure 3: Snapshots taken of the system at frame 500/999 for temperatures of 40, 85 and 120 kelvin. It is a bit difficult to conclude from the pictures, one really needs to see the system in motion, but the system do behave more or less like a solid, a liquid and a gas for respective temperatures. It is possible to see a certain change in the entropy of the system across the three images. These made use of the Velocity-Verlet integration method.

## 2.5 Velocity Verlet, a symplectic integrator

In order to improve upon the fairly poor energy conservation of the Euler-Cromer method, we chose to implement the Velocity Verlet integrator. The algorithm is dependent on us having computed the forces for the first step and consists of three steps per time-step:

$$\begin{aligned}\mathbf{v}(t + \Delta t/2) &= \mathbf{v}(t) + \frac{\mathbf{F}(t)}{m} \frac{\Delta t}{2}, \\ \mathbf{r}(t + \Delta t) &= \mathbf{r}(t) + \mathbf{v}(t + \Delta t/2)\Delta t, \\ \mathbf{v}(t + \Delta t) &= \mathbf{v}(t + \Delta t/2) + \frac{\mathbf{F}(t + \Delta t)}{m} \frac{\Delta t}{2}.\end{aligned}$$

We implement this algorithm in the `integrate` method in the `VelocityVerlet`-class. The method takes a system of atoms and a time step  $\Delta t$  as arguments. We also introduce the private auxiliary variable `m_first_step`, which helps us takes care of the initial calculation of the forces.

Of interest now is how our new method of integration compares with the old one. One way of looking at this is by examining the fluctuations in the total energy as functions of the time step  $\Delta t$ . This will be examined in upcoming sections.

## 2.6 Sampling quantities

We now have pretty much a working program, however we still need to sample the physical properties of the system at each time step. For this we turn to the `StatisticsSampler`-class where we will implement the methods for sampling the density, kinetic and potential energy and temperature of the system. The methods are named accordingly.

We first start by considering the kinetic and potential energy of the system. We already have computed the potential energy, in the `LennardJones`-class, so we are now interested in computing the kinetic energy. The kinetic energy of an arbitrary atom  $i$  is defined as  $E_k^i = m_i v_i^2 / 2$ , and so the total kinetic energy  $E_k$  of the system is simply

$$E_k = \sum_{i=1}^n E_k^i = \sum_{i=1}^n \frac{1}{2} m_i v_i^2,$$

where  $m_i$  and  $v_i$  is the mass and velocity atom  $i$  and  $n$  is again the total number of atoms in the system.

We are also interested in the instantaneous temperature of the system, and the equipartition theorem [2] can help us with this. The theorem relates the average energy of a system to its temperature and gives us the relation  $\langle E_k \rangle = (3/2)k_b T$  which can be solved for temperature:

$$T = \frac{2}{3} \frac{E_k}{n k_b}.$$

Notice the removal of the brackets — we are only interested in the *instantaneous* temperature at any point in time. We also recall that since our units are scaled, Boltzmann's constant is equal to one.

## 3 Simulations

In this section we consider various systems and simulate them using the program devised in the previous section.

### 3.1 Energy conservation of integration method

We initially decided to use the Velocity-Verlet integration method as opposed to Euler-Cromer for its good energy conservation. We now simulate a set of similar systems with varying temperature and look at how the fluctuations in total energy scales with the timestep  $\Delta T$ . In order to do this we can consider the standard-deviation of the total energy.

### 3.2 Melting temperature of system

## List of Figures

1	Initial state of the program . . . . .	2
2	Crystalline structure in argon . . . . .	5
3	Argon phases . . . . .	6

## References

- [1] [https://en.wikipedia.org/wiki/Periodic\\_boundary\\_conditions#Practical\\_implementation:\\_continuity\\_and\\_the\\_minimum\\_image\\_convention](https://en.wikipedia.org/wiki/Periodic_boundary_conditions#Practical_implementation:_continuity_and_the_minimum_image_convention)
- [2] [https://en.wikipedia.org/wiki/Equipartition\\_theorem](https://en.wikipedia.org/wiki/Equipartition_theorem)