

# TITLE OF THE MASTER THESIS

by

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THESIS

for the degree of

MASTER OF SCIENCE



Faculty of Mathematics and Natural Sciences  
University of Oslo

May 2017



# Abstract

This is an abstract text.



To someone

This is a dedication to my cat.



# Acknowledgements

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Anders Hafreager





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# Chapter 1

## Introduction

Why is the subject of this thesis of any interest?

What is our take on the problem?

What do we hope to accomplish?

How will this be of any contribution to anything?

How is the thesis laid out?



# Chapter 2

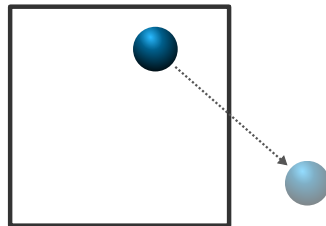
## Molecular dynamics

... Molecular dynamics simulations are computationally expensive. And often scientists must balance statistical precision and CPU time. Technological improvements have provided the ability to simulate larger systems and/or at longer time frames.

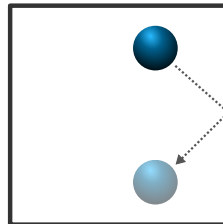
### 2.1 Boundary conditions

Boundary conditions is a crucial detail to decide upon when setting up a molecular dynamic experiment. The way we treat atoms at the boundary can have an immense effect on their behavior and how physically reasonable the results will be. There are several types of boundary conditions one may desire, and one may define custom conditions. A few examples are listed below.

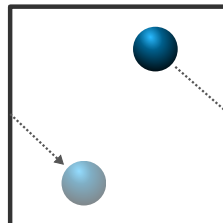
*No boundary conditions.* Particles are not subject to any special rules at any boundary. The system size may be regarded as infinite. This might be a reasonable choice when studying explosions for instance, or in experiments that is on a really short time scale.



*Reflecting boundary conditions,* which acts as hard walls. In stead of passing through the boundary, the velocity component in the direction normal to the face of the boundary changes sign, thus causing the atoms to be confined within the simulation box.



*Periodic boundary conditions,* which allow atoms on separate sides of a boundary to interact through the boundary as if they were neighbors, and atoms crossing the boundary reappears on the other side of the simulation box. This is useful when studying bulk areas of a material or materials that has a periodic structure.



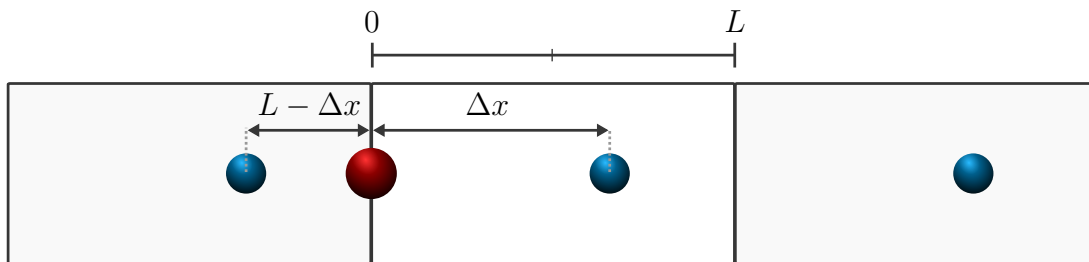
The boundary conditions may include more details than only how to handle the trajectory of atoms intersecting the boundaries. For instance with periodic boundaries, atoms that are far apart are effectively close. These atoms should therefore interact, since their motion would seem artificial otherwise. Thus, the interpretation of atoms positions must in some cases be included in the boundary conditions. In order to interpret atoms positions in the case of periodic boundaries, one has to remember that an atom should not interact with multiple images of another atom. Which image, if not the original, must therefore be decided. Also, an atom should not interact with an image of itself. That could potentially cause strange correlations. The standard way of determining atoms positions is by using the *minimum image convention*.

### 2.1.1 Minimum image convention

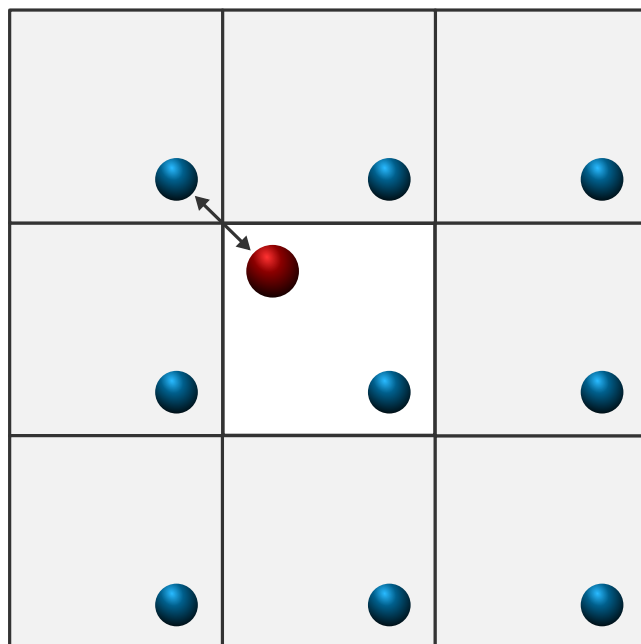
The minimum image convention simply states that the image closest to the reference atom, is the one to consider as the position of the atom. Example cases from 1D and 2D systems are shown in figure 2.1 and figure 2.2 respectfully. In the examples we look at systems consisting of two atoms and we try to determine the minimum image of the smaller, blue atom with respect to the larger, red ref-

erence atom. The original system is distinguishable from the periodic copies by the background color; the periodic copies have slightly darker background. Also, we only bother showing the periodic copies of the atom of consideration, the blue one.

Also, show programmatic test.



**Figure 2.1:** Minimum image convention in 1 dimension. If an atom is separated from the reference atom (red) by more than half the system length,  $L/2$ , the minimum image convention states that the distance between the two is the distance to the periodic copy, which is  $L - \Delta x$ . The white area indicates the system, while the gray areas are periodic replications of the system. Atoms in the gray areas are periodic images of the atom of consideration in the white area.



**Figure 2.2:** Minimum image convention in 2 dimensions. The position of an atom, with respect to the reference atom (red), is the position of the original or any of the replicated images of the other atom that has the shortest distance to the reference atom. The shortest distance in this case is marked with a two-sided arrow. Thus, when computing positional dependent quantities it's the position of the north-west replica that will be considered as the position of the blue atom in this case.



# Chapter 3

## LAMMPS

LAMMPS stands for *Large-scale Atomic/Molecular Massively Parallel Simulator*. It is a classical molecular dynamics simulation code designed to run efficiently on parallel computers. Its development began in the mid 1990s at Sandia National Laboratories, with funding from the U.S. Department of Energy. It was a cooperative project between two DOE labs and three private companies. The development is still ongoing and contributions are revised thoroughly.

Today LAMMPS is an open-source code with extensive and user friendly documentation. This is one of the main reasons why we have chosen to use LAMMPS as opposed to other molecular dynamics software.

### 3.1 Installation

Installing LAMMPS is a fairly simple procedure if only the basic settings are needed.

#### 3.1.1 Linux

Users with a Unix based OS may download the lammps distribution as a tarball from LAMMPS' download page<sup>1</sup> and then unpack it from the command line.

```
1 gunzip filename.tar.gz
2 tar xvf filename.tar
```

The user may then change directory into `/path/to/lammps/src/`, and execute the following commands in order to list available packages.

```
1 make package-status
```

Installing specific packages is accomplished as shown below.

---

<sup>1</sup><http://lammps.sandia.gov/download.html>

```
1 make yes-molecule yes-manybody yes-python yes-rigid
```

The above example installs the packages *molecule*, *manybody*, *python* and *rigid*. Next, the user can build LAMMPS using either of the lines below. Assuming the user has MPI installed, line 2 makes the resulting executable compatible with parallelization in MPI.

```
1 make serial
2 make mpi
```

At this point there should be an executable in the `/path/to/lammps/src/` directory named `lmp_serial` or `lmp_mpi`, depending on the previous choice. These are now ready to run. To use it one has to point to this file from the command line at every run. It may be practical to set up a symlink as follows shown below.

```
1 sudo ln -s /path/to/lammps/src/lmp_mpi
   /usr/local/bin/lmp_mpi
```

The executable is now available as `lmp_serial` or `lmp_mpi` from anywhere.

### 3.1.2 Mac OS X with Homebrew

Mac users can follow the procedure described above, however they may also install even easier using *Homebrew*<sup>2</sup>.

```
1 brew tap homebrew/science
2 brew install lammps           # serial version
3 brew install lammps --with-mpi # mpi support
```

Where the user obviously should choose either line 2 or line 3, depending on if the user wants MPI comparability. This will install an executable named "lammps", a python module named "lammps", and resources with standard packages. This is basically it. LAMMPS is now ready to run, however, not all packages are installed.

The location of the resources and available packages can be found using the following command.

```
1 brew info lammps
```

Specific packages are available as options, and may be installed with the following command.

```
1 brew install lammps --enable-manybody
```

In the example shown we installed the package *manybody*.

---

<sup>2</sup><http://brew.sh/>

### 3.1.3 Windows

## 3.2 Running LAMMPS

## 3.3 Efficiency improvements

The major part of the CPU time is spent in the force loop. At every time step we must recompute the force acting on each individual atom. When doing so, we should in theory include the contribution from all other atoms. Having a system consisting of  $N$  atoms would result in  $N(N - 1)/2 \propto N^2$  computations, if we apply Newton's third law. In this section we will look at the most fundamental efficiency improvements applied in molecular dynamics simulations.

### 3.3.1 Cut-off

Depending on the potential in use, the forces become negligible at certain distances. For instance if one uses the Lennard-Jones potential

$$V(r) = 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \quad (3.1)$$

the contributions are practically zero for atoms positioned at a distance  $r \geq 3\sigma$ . Therefore, during a simulation we choose to only account for the contributions from atoms closer than this *cut-off* length. The number of contributions will then only depend on the density, which is an intensive<sup>3</sup> property. Thus, the number of computations is reduced to  $\propto N$ , which is an immense relief in computational expense!

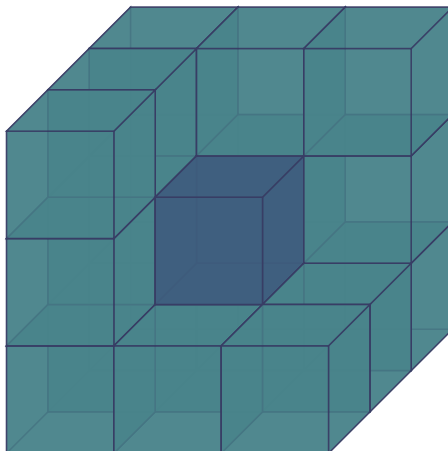
In order to actually do this we must keep track of which atoms are within the cut-off length of each atom. This is achieved using cell lists and neighbor lists.

### 3.3.2 Cell lists and neighbor lists

The main purpose of the cell list is to make the building of neighbor lists more efficient. We need to check which atoms are neighboring atoms, but obviously we do not need to check the entire domain, since the cut-off length is relatively small. Therefore, we partition the system into several cubes of size equal to the cut-off length. We store the atoms contained by a specific cell in a *cell list*. Finally, when we build the neighbor lists we check only the atoms within the neighboring cells and those in the same cell, 27 cells in total. **By neighboring cells we mean...** This is illustrated in figure 3.1.

---

<sup>3</sup>Physical property of a system that does not depend on the system size.



**Figure 3.1:** Illustrative figure of cells of concern when building the neighbor lists. The lighter cubes are neighboring cells; the darker cube is the cell containing the reference atom. The 7 cells in front of the dark cell are removed from the figure, but are also included.

### 3.3.3 Parallelization

It might be misleading to refer to parallelization as an efficiency improvement, when on the contrary it most likely increases the CPU time usage. However, the real time consumed may be greatly decreased. It is intuitive that partitioning the work and processing these simultaneously will decrease the time as compared to processing it serially.

The speedup is defined as

$$S = \frac{T_s}{T_p}, \quad (3.2)$$

where  $T_s$  is the time used when executing the program on a single processor, and  $T_p$  the time used when running on  $p$  processors simultaneously.

The time spent running a parallel implementation of a code using  $p$  processors is seldom trivially  $T_p = T_s/p$ . This is due to the fact that there is a certain amount of time used on *overhead*. This includes interprocess communications, idling and excess computations. In molecular dynamics simulations there is communication between processors when building the cell- and neighbor lists, and when computing thermodynamical properties such as energy, pressure, temperature, etc..

During this project the author has mainly been using the local supercomputer at the department of physics at the University of Oslo. It provides users with the possibility to run up to 256 processes at once. Though, before doing so, it is considered as good practice to check the speedup obtained by using several numbers of cores.

In order to compute the speedup we initialized a system containing  $15 \times 15 \times 15$

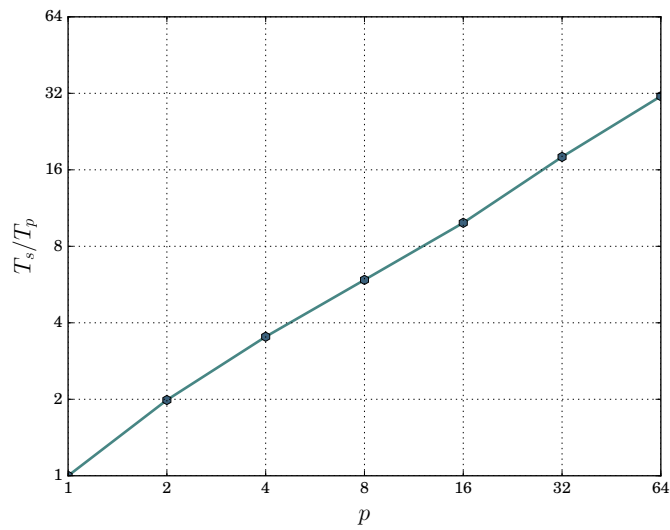
unit cells of beta-cristobalite and saved it as a restart file. We then remotely ran the input script shown in Listings 3.1 from the supercomputer using 1, 2, 4, 8, 16, 32 and 64 processors in the same fashion as shown in Listing 3.2. The resulting speedup of using the respective number of processors is plotted in figure 3.2.

```
1  include "system.in.init"
2  read_restart ${filename}
3  include "system.in.settings"
4
5  variable N equal 1
6  variable T equal 293
7
8  neighbor 0.3 bin
9  neigh_modify delay 10
10
11 timestep 0.002
12
13 dump myDump slabUpperGroup atom 1 dumpFiles/surface_*.dump
14
15 fix nvt all nvt temp ${T} ${T} 1.0
16 run ${N}
```

**Listing 3.1:** LAMMPS input script executed using several numbers of processors, and timed separately.

```
1  mpirun -n 8 lmp_mpi -in speedup.in -var filename
    speedup.restart
```

**Listing 3.2:** Command used to execute the input script speedup.in on 8 parallel processors and set the filename variable to speedup.restart.



**Figure 3.2:** Speedup as a function of number of processors.

The result indicate that the speedup is in fact not simply  $S = p$ . Anyhow, we clearly see the advantage of using 64 processors as opposed to 1. We can finish a job that would have taken an hour in two minutes! Also, we clearly see that the initial claim holds; this is not more efficient when regarding CPU time. In fact this result suggest that using 1 processor is twice as energy efficient as using 64.

# Chapter 4

## Setting up the system

We wish to construct a system consisting of **two** elements made out of silica: a slab and a sphere cap. In order to do this we need to generate the spacial position coordinates (x,y,z) of every single atom. Considering that we are making a system consisting of about  $10^5$  atoms, this is obviously not done manually. We have chosen to use a tool named *Moltemplate*<sup>1</sup>, which is included in the LAMMPS distribution.

The main idea is to manually enter the coordinates of only the atoms in a unit cell of the material one wish to generate, and then simply copy this unit cell wherever desired. The software will shift the coordinates of the copied unit cell by the displacement from the original image. In addition it will generate files containing data such as which atoms they share bonds with, if any, and angles between such bonds.

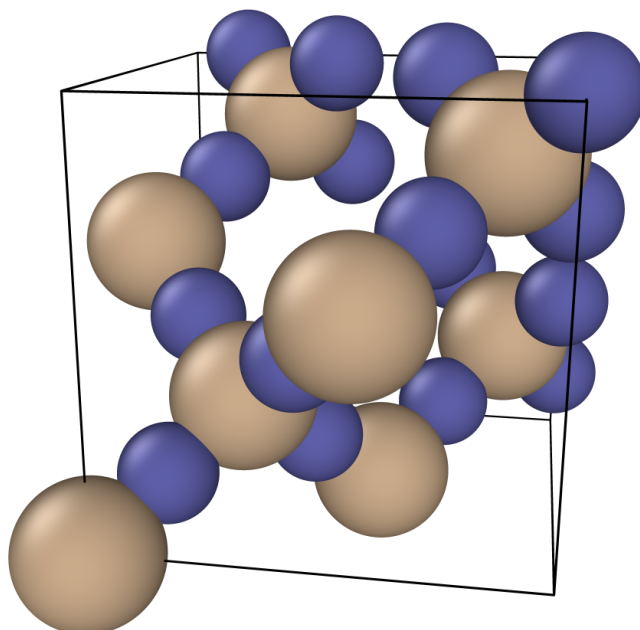
### 4.1 Silica

Silica is a chemical compound also known as Silicon dioxide, having the chemical formula  $\text{SiO}_2$ . It has several polymorph structures, the most common being quartz, which is one of the most abundant minerals in the Earth's crust. Other polymorphs include cristobalite, tridymite, coesite and more.

For our purpose it is insignificant which one we choose. Once the material is melted, it is indifferent which configuration we started from, as long as the density is correct. In this project we will build the constituents of the system from a type of cristobalite named  $\beta$ -cristobalite. This is mainly because it has a simple structure and a cubical unit cell.

---

<sup>1</sup><http://www.moltemplate.org/index.html>



**Figure 4.1:** Unit cell of  $\beta$ -cristobalite. Tan and blue spheres represent silicon and oxygen atoms respectively. The unit cell is cubical, with edges of length  $7.12\text{\AA}$ .

#### 4.1.1 Unit cell of $\beta$ -cristobalite

In order to construct the unit cell of a material, one should look up the coordinates of the atoms in a crystallography database. We have used the unit cell of  $\beta$ -cristobalite found at *Crystallography Open Database*<sup>2</sup>. At this site one can download a `.cif`-file consisting of the spatial positions of each atom, the length of the unit cell edges and angles between faces of the cell. In the case of  $\beta$ -cristobalite the unit cell is cubical with edges of length  $7.12\text{\AA}$ . It contains 8 silicon atoms and 16 oxygen atoms. The density of the unit cell can easily be computed and is  $2.2114\text{ g/cm}^3$ .

## 4.2 Building a crystal

The coordinates gotten from the `.cif`-file can now be implemented into *moltemplate* together with whatever bond and angle data required by the potential. In our simulations we will use the Vashishta potential, which does not require these.

---

<sup>2</sup><http://www.crystallography.net/cod/1010944.html>



Moltemplate has its own structure and syntax. The first step to build up a larger material is, as mentioned, to create the unit cell. Data concerning the unit cell are placed in a `.lt`-file, which is readable by Moltemplate. Such a file is shown in Listing 4.1. For a more profound understanding of the structure and syntax of these files, the reader is advised to read the moltemplate manual<sup>3</sup>.

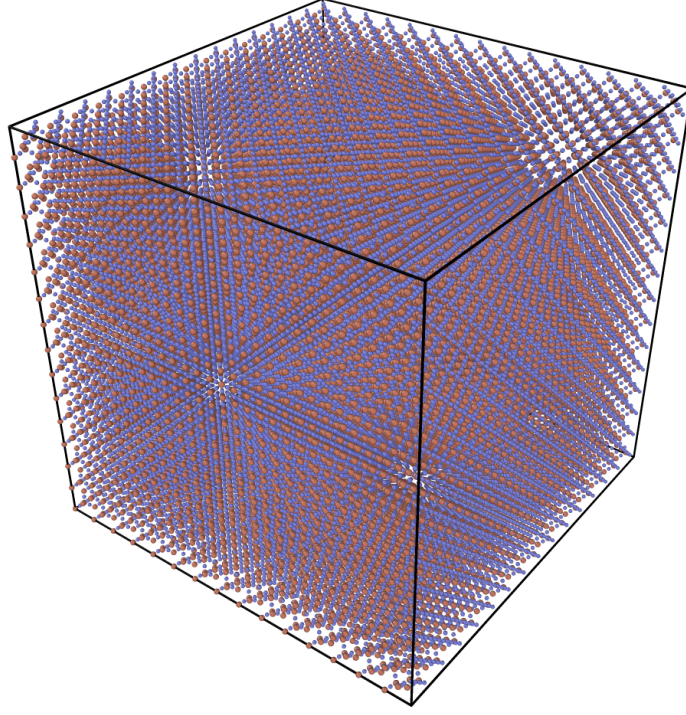
```

1  # file "beta-cristobalite.lt"
2
3  beta-cristobalite {
4    write("Data Atoms") {
5      $atom:Si1    @atom:Si    0.00    0.00    0.00
6      $atom:Si2    @atom:Si    0.00    3.56    3.56
7      $atom:Si3    @atom:Si    1.78    1.78    1.78
8      $atom:Si4    @atom:Si    3.56    0.00    3.56
9      $atom:Si5    @atom:Si    1.78    5.34    5.34
10     $atom:Si6    @atom:Si    5.34    5.34    1.78
11     $atom:Si7    @atom:Si    3.56    3.56    0.00
12     $atom:Si8    @atom:Si    5.34    1.78    5.34
13     $atom:O1     @atom:O     0.89    0.89    0.89
14     $atom:O2     @atom:O     6.23    4.45    2.67
15     $atom:O3     @atom:O     2.67    2.67    0.89
16     $atom:O4     @atom:O     4.45    0.89    4.45
17     $atom:O5     @atom:O     0.89    4.45    4.45
18     $atom:O6     @atom:O     4.45    4.45    0.89
19     $atom:O7     @atom:O     2.67    6.23    4.45
20     $atom:O8     @atom:O     2.67    0.89    2.67
21     $atom:O9     @atom:O     4.45    2.67    6.23
22     $atom:O10    @atom:O     6.23    2.67    4.45
23     $atom:O11    @atom:O     2.67    4.45    6.23
24     $atom:O12    @atom:O     0.89    6.23    6.23
25     $atom:O13    @atom:O     0.89    2.67    2.67
26     $atom:O14    @atom:O     4.45    6.23    2.67
27     $atom:O15    @atom:O     6.23    6.23    0.89
28     $atom:O16    @atom:O     6.23    0.89    6.23
29   }
30
31   write_once("Data Masses") {
32     @atom:Si 28.0855
33     @atom:O  15.9994
34   }
35
36 } # end definition of beta-cristobalite molecule type

```

**Listing 4.1:** Typical moltemplate file containing unit cell data. The columns of the "Data Atoms" section hold, from left to right, information of atom ID, atom type, x-, y- and z-position. The "Data Masses" section stores the weight of silicon and oxygen atoms in atomic mass units.

<sup>3</sup>[http://www.moltemplate.org/doc/moltemplate\\_manual.pdf](http://www.moltemplate.org/doc/moltemplate_manual.pdf)



**Figure 4.2:** System built from  $15 \times 15 \times 15$  unit cells of b-cristobalite.

We use the unit cell as building blocks, placing them concurrently until we have a crystal of the desired size. For our purpose, we generate a large cube of  $15 \times 15 \times 15$  unit cells. This is done as follows.

## 4.3 Verifications

### 4.3.1 Melting point

Finding the melting point is a very important verification of our system. There are several factors that may affect the result. For instance, if the density of the system is too high, the melting point will be at a higher temperature than it normally would. Also, errors in the potential model may affect the temperature of the melting point. When increasing the temperature of the system that is in a solid state, we will eventually reach the melting point. At the phase transition from a solid state to a liquid the atoms of the silica will have energy great enough to break the interatomic bonds. They will break loose from their regular arrangement and move about much more freely. An approach to computing the melting point is therefore to systematically increase the temperature stepwise and sample the mean square displacement of the atoms at each designated temperature. The

mean square displacement is the average of the square of the displacement every atom has from its initial position. It can be expressed as:

$$\langle r^2(t) \rangle = \frac{1}{N} \sum_{i=1}^N (\mathbf{r}_i(t) - \mathbf{r}_i(0))^2. \quad (4.1)$$

where  $\mathbf{r}_i(t)$  is the position of atom  $i$  at time  $t$  and  $N$  is the total number of atoms. In practice the mean square displacement was computed using a standard *compute* in LAMMPS, namely the *msd compute*<sup>4</sup>. At every time step it stores a vector of 4 elements; the first 3 are the squared  $dx$ ,  $dy$  and  $dz$  displacements averaged over the atoms of the specific group, while the 4th is the total mean square displacement for the specific group, i.e.  $(dx^2 + dy^2 + dz^2)$ . The  $15 \times 15 \times 15$  system is sufficient for this test. The procedure is rather simple. For  $\beta$ -cristobalite we expect the melting point to be about 1986K<sup>5</sup>, so we start out at 1500K. After equilibration the following steps are repeated until we reach a target temperature.

- equilibrate for the current temperature
- compute the msd for  $N$  time steps
- increase the temperature by a given step size

```

1  label meltingLoop
2  variable i loop 11
3      fix nvtID all nvt temp ${T} ${T} 1.0
4      run ${N}
5      compute msdID all msd
6      fix msdDumpID all ave/time 1 1 3 c_msdID[4] file
          msd_N${N}_T${T}.txt
7      run ${N}
8      uncompute msdID
9      unfix nvtID
10     unfix msdDumpID
11     variable T equal ${T}+50
12 next i
13 jump SELF meltingLoop

```

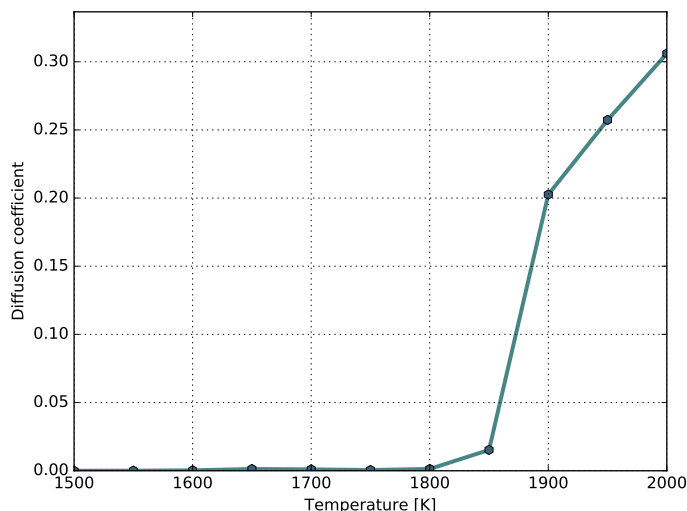
**Listing 4.2:** Main blalbabla.

## 4.4 Shaping the silica

The huge cube of silica can be carved however we like by defining regions from which we delete the containing atoms. In LAMMPS this is done by using the

<sup>4</sup>[http://lammps.sandia.gov/doc/compute\\_msd.html](http://lammps.sandia.gov/doc/compute_msd.html)

<sup>5</sup><https://en.wikipedia.org/wiki/Cristobalite>



**Figure 4.3:** Mean square displacement as a function of temperature. The face transition occurs where we see a rapid change in the behavior.

`region`, `union`, `intersect` and `delete_atoms` commands. Our implementation is stated in Listing 4.3, which is very simple due to the way we are going to treat the boundary conditions. We start out by defining a spherical region labeled `sphereRegion`, described by the xyz-coordinates of its center and a radii. The atoms within this region are assigned to a group labeled `sphereGroup`. Next, we define a cuboid (block) region named `slabRegion`, described by the position of its faces in x-, y- and z-direction. The atoms within this region are assigned to a group, which we label `slabGroup`. We combine these two regions using the `union` command and label the region outside of these regions `outRegion`. Finally, we delete the atoms that are not in the sphere nor the slab; we delete the ones contained by `outRegion`.

```

1  region sphereRegion sphere 53.4 53.4 226.8 150
2  group sphereGroup region sphereRegion
3
4  region slabRegion block 0 INF 0 INF 0 35.6
5  group slabGroup region slabRegion
6
7  region outRegion union 2 sphereRegion slabRegion side out
8  delete_atoms region bothRegion

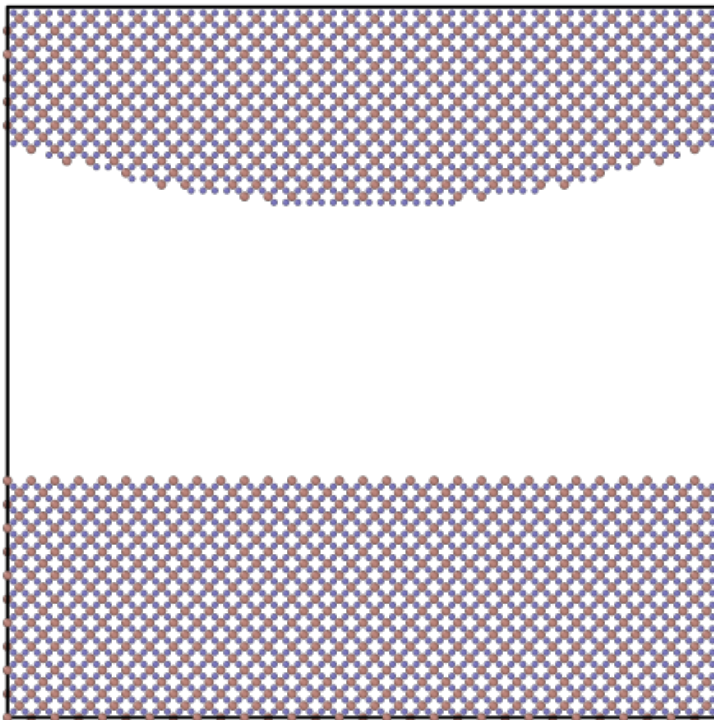
```

**Listing 4.3:** Defining regions to keep or delete from a system of dimensions  $106.8 \times 106.8 \times 106.8$  Å.

For the purpose of deleting atoms, the creation of groups is redundant. However, at a later stage we will utilize them and this is an appropriate place for

them to be defined.

The appliance of the script in Listing 4.3 on the system shown in figure 4.2 is shown in figure 4.4, where our perspective is looking along the y-axis.



**Figure 4.4:** xz-perspective on a system built from  $15 \times 15 \times 15$  unit cells of b-cristobalite, with certain regions carved out. This is a result from applying Listing 4.3 to the system shown in figure 4.2. The top shape is a sphere cap, while the bottom is a slab.

## 4.5 Moving the sphere towards the slab

We wish to push the sphere down onto the slab in order to create a deformation on the slab. There are probably a lot of smart ways to do this. The author has settled on the following strategy:

We apply periodic boundary conditions in all three dimensions. Secondly, we freeze the atoms at the bottom of the slab so that their positions are fixed. This will, due to the periodic boundary conditions, allow us to consider the sphere cap and the slab as if they are not connected to each other, but to independent blocks of silica glass. Then, for every  $N$  time steps we decrease the height of the system, while remapping the positions of the atoms. The remapping is a very important procedure. It ensures that we do not lose any atoms that otherwise would be lost when moving the z-boundary. A side-effect of the remapping is that the atoms

in the system will be somewhat compressed in the z-direction. Though, if we do the compression slowly, this will not be of any concern.

```
1 fix freezeID groupID setforce 0 0 0
2 velocity groupID set 0 0 0
```

**Listing 4.4:** LAMMPS commands for hard coding the forces and velocities of atoms within a specific group. Effectively freezing them.

```
1 fix ID all deform 1 z delta 0 -${compressionLength} remap x
```

**Listing 4.5:** LAMMPS command for changing the size of the simulation box.

# Chapter 5

## This must be sorted in designated chapters

### 5.1 Radial distribution of normal force

In order to find a radial distribution of the normal force,  $F_N$ , we partition the system into a grid in the xy-plane. We then use the command

```
1  compute chunkID all chunk/atom bin/2d x 0 7.12 y 0 7.12
2  compute stressID all stress/atom NULL
3  fix fixChunkID all ave/chunk 1 1 10 chunkID
   c_stressID[3] file forcesInChunks.txt
```

to compute the stress of every chunk in the z-direction,  $\sigma_{zz}$  (sum of every individual atom stress in the chunk).

Line 1 establishes the grid, with bin width 7.12Å.

Line 2 creates a compute of the stress

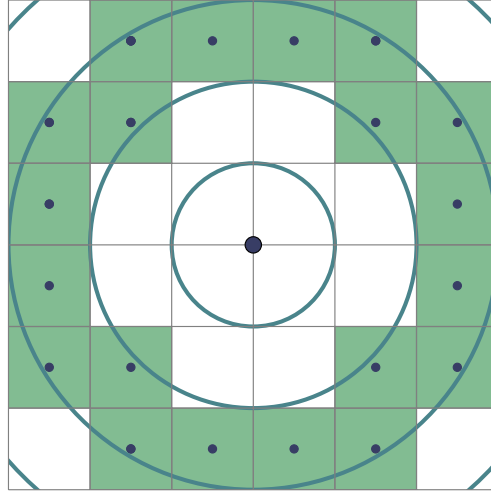
Line 3 stores the sum of individual stresses in each chunk to the file `forcesInChunks.txt`. This is done every 10 time steps in order to reduce correlation effects.

The data is stored from each time step can easily be averaged to produce a result as shown in figure X.

We can then find the radial distribution simply by binning this matrix in radial bins, and average the normal forces of the chunks within the bins.

#### 5.1.1 Radial binning

Our system is partitioned into a grid. Each cell in the grid holds an averaged value of the normal force in that cell. The radial distribution of normal force should express the averaged value of the normal force at a given radial distance from the **center of the sphere**. A coarse method of doing this is to average the weights of the cells whose center is within the bin. This is illustrated in figure 5.1. In many applications where the bin size can be large compared to the length



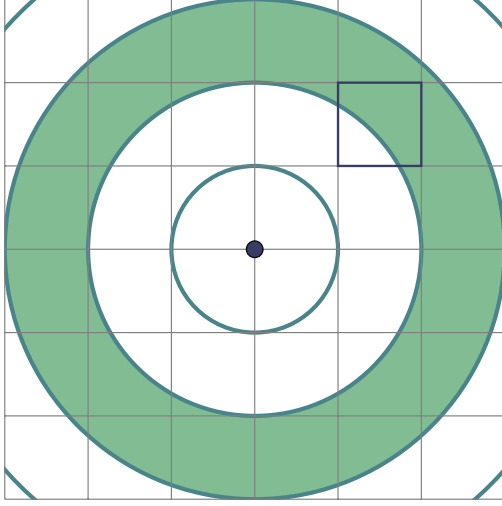
**Figure 5.1:** Coarse radial binning. The value appointed to the radial bin is the average of the weights of the cells whose center is within the bin. The cells with center within the third radial bin are colored, and their centers drawn.

of the cells, this method might suffice. However, the current radii of the contact area between the sphere and the slab is only about 10 unit cells, and therefore having a large bin width will result in very few data points.

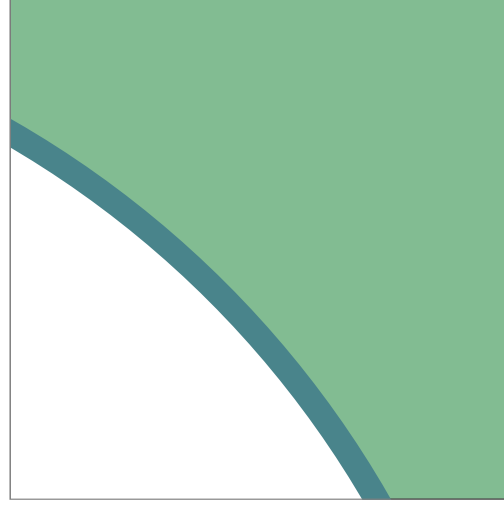
A different, slightly more sophisticated approach is to compute the fraction of the area of the cells that actually are within the bin, multiplied by the weight associated with the cell, and average these contributions. This means that even cells that do not have their center within the bin might contribute to the resulting bin value. How much, however, will depend on the fraction of the cell that is within the bin. This may be regarded as a smoothing of our coarse force distribution, and will probably give a more correct result than the coarse binning method already described. An illustration of this binning method is shown in figure 5.2 and 5.3. The figure clearly shows that some cells have a larger area within the bin than others, and thus contribute more.

Computing the area of the cell within the bin should be described here!

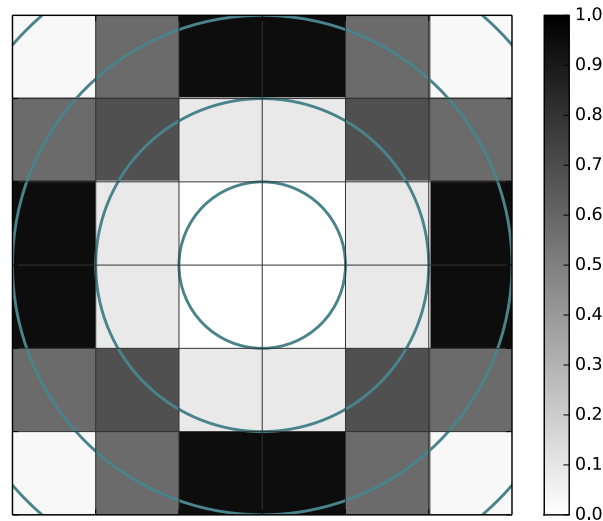




**Figure 5.2:** Radial binning based on weighted contributions of intersecting cells. The third radial bin is colored, and its value will be the average of the intersecting cells weight times the fraction of the cells area that intersects the bin. A close-up of the outlined cell, is shown in figure 5.3.



**Figure 5.3:** Close-up of outlined cell in figure 5.2. The contribution from this cell will be its weight multiplied by the fraction of its total area that is colored. I might use this figure to explain the procedure.



**Figure 5.4:** Fraction of cell's area that are within the third radial bin.



## Chapter 6

# Computing the normal force distribution

The normal force is defined as the force exerted on an object that is perpendicular to the contact surface. In this chapter we will make an attempt to find the distribution of the normal forces. This is not a trivial thing to compute in LAMMPS. As a matter of fact, to achieve this we have expanded the LAMMPS library by creating a custom compute class. The details of that procedure will be described.

Our strategy is simple, but not necessarily easy. First of, we divide the system into a grid. Secondly, we compute the average force exerted on one body from another within each cell. We approximate the slope of the contact surface within the cells using a least squares regression method. Finally, we project the average force of the atoms in a cell onto the normal vector of the cell.

### 6.1 Creating a custom compute

A *compute* is a LAMMPS command that defines a computation that will be performed on a group of atoms. The *computes* produce instantaneous values, using information about the atoms on the current time step.

In LAMMPS there are more than 100 computes already, and chances are they have what you're looking for. If not, one might treat the data from other computes in some way to get the desired information. However, if there are no compute command that does the desired task, it is possible to create an own custom class.

In order to compute the normal forces acting on the sphere, we have written a custom compute class. The purpose of the class was to save the forces acting on atoms in one group from atoms of another group. In this section we will try to give brief instructions on how this was done.

[MAYBE AN ILLUSTRATIVE FIGURE HERE]

### 6.1.1 Find a similar compute

Obviously, before writing any code we should know what we want the compute to calculate and how this should be done. Before starting off with a blank sheet in the editor, one should definitely search for similar computes in LAMMPS. This can potentially save hours of hard work!

For instance there is a compute named *group/group*<sup>1</sup> which computes the total energy and force interaction between two groups of atoms. This is almost what we want, but we need to know the total force acting on all atoms from atoms of other groups. **It should also work with the Vashishta potential.**

Thus, there are minor modifications needed and because of the similarities we chose to make our compute a subclass of this one.

### 6.1.2 Creating the class

All computes in LAMMPS are subclasses of the class named *compute*. From this superclass they inherit a bunch of variables, functions and flags, which the user may decide to set. Functions are of course declared in the header file, while variables and flags are set in the source file. The source code of the *group/group* compute is shown in Appendix A.1. Since we will be making a subclass of it, we change the *private* property to *protected* so that we have access to all the variables and functions.

We start out by creating a header file and decide upon a name for our class. We have chosen the name *group/group/atom* since it is basically a per-atom version of the already existing compute *group/group*. A complete header file is shown in Listing 6.2 and explained in detail below.

```

1  #ifdef COMPUTE_CLASS
2  ComputeStyle(group/group/atom, ComputeGroupGroupAtom)
3  #else
4
5  #ifndef LMP_COMPUTE_GROUP_GROUP_ATOM_H
6  #define LMP_COMPUTE_GROUP_GROUP_ATOM_H
7
8  #include "compute.h"
9  #include "compute_group_group.h"
10
11 namespace LAMMPS_NS {
12
13 class ComputeGroupGroupAtom : public ComputeGroupGroup {
14 public:
15     ComputeGroupGroupAtom(class LAMMPS *, int, char **);
16     ~ComputeGroupGroupAtom();
17     void compute_peratom() override;
18     int nmax;

```

<sup>1</sup>[http://lammps.sandia.gov/doc/compute\\_group\\_group.html](http://lammps.sandia.gov/doc/compute_group_group.html)

```

19     double **carray;
20
21     private:
22     void pair_contribution() override;
23 };
24 }
25 #endif
26 #endif

```

**Listing 6.1:** Header file of our new compute: `compute_group_group_atom.h`.

`ComputeStyle` defines the command to be used in the LAMMPS input script to be `group/group/atom`, and the name to be *ComputeGroupGroupAtom*. The name will be redundant to us.

`nmax` is the number of atoms which are subject to a non zero force from atoms of another group at the current time step; it may vary.

`carray` is a two dimensional array containing the force on atoms in one group induced by atoms of another group. Its dimension will necessarily be  $nmax \times 3$ .

`compute_peratom()` and `pair_contribution()` are functions which will be described below the corresponding source file.

```

1  #include <mpi.h>
2  #include <string.h>
3  #include "compute_group_group_atom.h"
4  #include "atom.h"
5  #include "update.h"
6  #include "force.h"
7  #include "pair.h"
8  #include "neighbor.h"
9  #include "neigh_request.h"
10 #include "neigh_list.h"
11 #include "group.h"
12 #include "kspace.h"
13 #include "error.h"
14 #include <math.h>
15 #include "comm.h"
16 #include "domain.h"
17 #include "math_const.h"
18 #include "memory.h"
19
20 #include <iostream>
21 using namespace LAMMPS_NS;
22 using namespace MathConst;
23
24 #define SMALL 0.00001
25
26 ComputeGroupGroupAtom::ComputeGroupGroupAtom(LAMMPS *lmp,
27     int narg, char **arg) :
28     ComputeGroupGroup(lmp, narg, arg),
29     carray(NULL),

```

```

29     nmax(0)
30 {
31     if (narg < 4) error->all(FLEERR,"Illegal compute
        group/group command");
32
33     peratom_flag      = 1; // Indicating a peratom compute
34     size_peratom_cols = 4; // # of Columns per atom.
35     extarray          = 0; // 0/1 if global array is all
        intensive/extensive
36     scalar_flag       = 0;
37     vector_flag       = 0;
38 }
39
40
41 ComputeGroupGroupAtom::~~ComputeGroupGroupAtom()
42 {
43     memory->destroy(carray);
44 }
45
46
47 void ComputeGroupGroupAtom::compute_peratom()
48 {
49     // grow array if necessary
50     if (atom->nmax > nmax) {
51
52         memory->destroy(carray);
53         nmax = atom->nmax;
54         memory->create(carray, nmax, size_peratom_cols,
            "group/group/atom:carray");
55         array_atom = cararray;
56
57     }
58
59     if (pairflag) pair_contribution();
60     if (kspacelflag) kspace_contribution(); // This doesn't
        happen though. See compute_group_group.cpp
        constructor.
61 }
62
63
64 void ComputeGroupGroupAtom::pair_contribution()
65 {
66     int i,j,ii,jj,inum,jnum,itype,jtype;
67     double xtmp,ymtp,ztmp,dex,dely,dely;
68     double rsq,eng,fpair,factor_coul,factor_lj;
69     int *ilist,*jlist,*numneigh,**firstneigh;
70
71     double **x = atom->x;
72     int *type = atom->type;
73     int *mask = atom->mask;
74     int nlocal = atom->nlocal;

```

```

75     double *special_coul = force->special_coul;
76     double *special_lj = force->special_lj;
77     int newton_pair = force->newton_pair;
78     double *columns;
79
80     // invoke half neighbor list (will copy or build if
      necessary)
81
82     neighbor->build_one(list);
83
84     inum = list->inum;
85     ilist = list->ilist;
86     numneigh = list->numneigh;
87     firstneigh = list->firstneigh;
88
89     // loop over neighbors of my atoms
90     // skip if I,J are not in 2 groups
91
92
93     for (ii = 0; ii < inum; ii++) {
94         i = ilist[ii];
95
96         array_atom[i][0] = 0;
97         array_atom[i][1] = 0;
98         array_atom[i][2] = 0;
99         array_atom[i][3] = 0;
100     }
101
102     for (ii = 0; ii < inum; ii++) {
103         i = ilist[ii];
104
105         // skip if atom I is not in either group
106         if (!(mask[i] & groupbit || mask[i] & jgroupbit))
            continue;
107
108         xtmp = x[i][0];
109         ytmp = x[i][1];
110         ztmp = x[i][2];
111         itype = type[i];
112         jlist = firstneigh[i];
113         jnum = numneigh[i];
114
115         for (jj = 0; jj < jnum; jj++) {
116             j = jlist[jj];
117             factor_lj = special_lj[sbmask(j)];
118             factor_coul = special_coul[sbmask(j)];
119             j &= NEIGHMASK;
120
121             // skip if atom J is not in either group
122             if (!(mask[j] & groupbit || mask[j] &
                  jgroupbit)) continue;

```

```

123
124     int ij_flag = 0;
125     int ji_flag = 0;
126     if (mask[i] & groupbit && mask[j] & jgroupbit)
127         ij_flag = 1;
128     if (mask[j] & groupbit && mask[i] & jgroupbit)
129         ji_flag = 1;
130
131     // skip if atoms I,J are only in the same group
132     if (!ij_flag && !ji_flag) continue;
133
134     delx = xtmp - x[j][0];
135     dely = ytmp - x[j][1];
136     delz = ztmp - x[j][2];
137     rsq = delx*delx + dely*dely + delz*delz;
138     jtype = type[j];
139
140     if (rsq < cutsq[itype][jtype]) {
141         eng = pair->single(i, j, itype, jtype,
142             rsq, factor_coul, factor_lj, fpair);
143
144         // energy only computed once so tally full
145         // amount
146         // force tally is jgroup acting on igrp
147
148         if (newton_pair || j < nlocal) {
149             array_atom[i][0] += eng;
150             if (ij_flag) {
151                 array_atom[i][1] += delx*fpair;
152                 array_atom[i][2] += dely*fpair;
153                 array_atom[i][3] += delz*fpair;
154             }
155             if (ji_flag) {
156                 array_atom[j][1] -= delx*fpair;
157                 array_atom[j][2] -= dely*fpair;
158                 array_atom[j][3] -= delz*fpair;
159             }
160
161             // energy computed twice so tally half
162             // amount
163             // only tally force if I own igrp
164             // atom
165             }
166         else {
167             array_atom[i][0] += 0.5*eng;
168             if (ij_flag) {
169                 array_atom[i][1] += delx*fpair;
170                 array_atom[i][2] += dely*fpair;
171                 array_atom[i][3] += delz*fpair;
172             }
173         }
174     }

```



```
168         }  
169     }  
170 }  
171 }
```

**Listing 6.2:** Source file of compute: `compute_group_group_atom.cpp`.

In the constructor we set specific flags that LAMMPS uses to interpret what structure our data should have, and how to store them. We set the `peratom_flag` to be `True`, which indicates that we desire to store some data for each atom. `size_peratom_cols` defines the number of data values to store for each atom. Also, we set the `scalar_flag` and `vector_flag` to `False`, since we do not wish to return a vector or scalar value.

Following the constructor is the destructor on line 40. Its only task is to free the memory occupied by the array once it is no longer needed.

`compute_peratom()` will resize the array to the number of atoms of concern, `nmax`. It does this using LAMMPS internal functions, which we will not care to describe here. Finally it calls upon functions

I ENDED HERE  
LAST TIME!

Note that we should only compute the force for one of the groups. factor 2...

## 6.2 Least squares regression

The method of least squares aims to find parameters which minimize the sum of the squared residuals, where residuals are the difference between observed values and the approximated value. We will use this method to approximate the slope of the surface of the substrate. This will be done by partitioning the system in a grid and do a plane approximation on each cell of the grid. In other words, we seek the coefficients in the plane equation

$$z = ax + by + c \quad (6.1)$$

that minimizes the sum of the squared residuals

$$S = \sum_{i=1}^n r_i^2 = \sum_{i=1}^n (z_i - f(x_i, y_i, \boldsymbol{\beta}))^2, \quad (6.2)$$

where  $f(x_i, y_i, \boldsymbol{\beta})$  is the right hand side of the plane equation and  $\boldsymbol{\beta}$  is the set of coefficients. The minima has the property that the differential with respect to any coefficient is zero.

$$\frac{\partial S}{\partial \beta_j} = \sum_{i=1}^n \frac{\partial r_i^2}{\partial \beta_j} = \sum_{i=1}^n \frac{\partial r_i^2}{\partial r_i} \frac{\partial r_i}{\partial \beta_j} = -2 \sum_{i=1}^n r_i \frac{\partial f(x_i, y_i, \boldsymbol{\beta})}{\partial \beta_j} = 0, \quad \forall \beta_j \in \boldsymbol{\beta} \quad (6.3)$$

When approximating a plane we have three coefficients to account for:  $a$ ,  $b$  and  $c$ . This leaves us with the following set of equations:

$$-2 \sum_{i=1}^n (z_i - ax_i - by_i - c) \frac{\partial}{\partial a} (ax_i + by_i + c) = 0 \quad (6.4)$$

$$-2 \sum_{i=1}^n (z_i - ax_i - by_i - c) \frac{\partial}{\partial b} (ax_i + by_i + c) = 0 \quad (6.5)$$

$$-2 \sum_{i=1}^n (z_i - ax_i - by_i - c) \frac{\partial}{\partial c} (ax_i + by_i + c) = 0, \quad (6.6)$$

which corresponds to

$$\sum_{i=1}^n z_i x_i = a \sum_{i=1}^n x_i^2 + b \sum_{i=1}^n x_i y_i + c \sum_{i=1}^n x_i \quad (6.7)$$

$$\sum_{i=1}^n z_i y_i = a \sum_{i=1}^n x_i y_i + b \sum_{i=1}^n y_i^2 + c \sum_{i=1}^n y_i \quad (6.8)$$

$$\sum_{i=1}^n z_i = a \sum_{i=1}^n x_i + b \sum_{i=1}^n y_i + nc. \quad (6.9)$$

This can be expressed as a matrix equation.

$$\begin{bmatrix} \sum x_i^2 & \sum x_i y_i & \sum x_i \\ \sum x_i y_i & \sum y_i^2 & \sum y_i \\ \sum x_i & \sum y_i & n \end{bmatrix} \begin{bmatrix} a \\ b \\ c \end{bmatrix} = \begin{bmatrix} \sum x_i z_i \\ \sum y_i z_i \\ \sum z_i \end{bmatrix} \quad (6.10)$$

where we have omitted the indices to better readability. Solving this linear system retrieves the optimal coefficients in the sense of the least squares method. The normal vector of the plane will be  $\mathbf{n} = [1, a, b]$ . This vector will be used to compute the size of the normal force. Since we know the average force on an atom in the chunk, and the normal vector from the approximated slope of the surface, we can compute the normal force simply as

$$\mathbf{F}_N = |\mathbf{F}| \cos \theta \frac{\mathbf{n}}{|\mathbf{n}|}. \quad (6.11)$$

The cosine of the angle between the two vectors is given as

$$\cos \theta = \frac{\mathbf{F} \cdot \mathbf{n}}{|\mathbf{F}| \cdot |\mathbf{n}|}, \quad (6.12)$$

meaning that the normal force may be expressed as

$$\mathbf{F}_N = (\mathbf{F} \cdot \mathbf{n}) \frac{\mathbf{n}}{|\mathbf{n}|^2}. \quad (6.13)$$

We will assume that the normal vector  $\mathbf{n}$  is always in the same general direction as the average force, though obviously it may just as well point in the opposite direction and still be a normal vector to the plane. Programatically this was done in python as shown in Listing 6.3.

```

1     def getAngle(self, v1, v2):
2         'Computes angle between a vector and a line
          parallel to another vector'
3
4         lv1 = np.linalg.norm(v1)
5         lv2 = np.linalg.norm(v2)
6
7         angle = np.arccos(np.dot(v1, v2)/(lv1*lv2))
8         angle = min(angle, abs(np.pi-angle))

```

**Listing 6.3:** Python function to compute the smallest angle between a vector and a line parallel to another vector.



# Appendix A

## Source code

## A.1 compute\_group\_group.h

```

1  #ifdef COMPUTE_CLASS
2  ComputeStyle(group/group, ComputeGroupGroup)
3  #else
4
5  #ifndef LMP_COMPUTE_GROUP_GROUP_H
6  #define LMP_COMPUTE_GROUP_GROUP_H
7
8  #include "compute.h"
9
10 namespace LAMMPS_NS {
11
12 class ComputeGroupGroup : public Compute {
13 public:
14     ComputeGroupGroup(class LAMMPS *, int, char **);
15     ~ComputeGroupGroup();
16     void init();
17     void init_list(int, class NeighList *);
18     double compute_scalar();
19     void compute_vector();
20
21 protected: // private
22     char *group2;
23     int jgroup, jgroupbit, othergroupbit;
24     double **cutsq;
25     double e_self, e_correction;
26     int pairflag, kspaceflag, boundaryflag;
27     class Pair *pair;
28     class NeighList *list;
29     class KSpace *kspace;
30
31     virtual void pair_contribution();
32     void kspace_contribution();
33     void kspace_correction();
34 };
35
36 }
37
38 #endif
39 #endif

```

## A.2 compute\_group\_group\_atom.h

```
1  #ifndef COMPUTE_CLASS
2  ComputeStyle(group/group/atom,ComputeGroupGroupAtom)
3  #else
4
5  #ifndef LMP_COMPUTE_GROUP_GROUP_ATOM_H
6  #define LMP_COMPUTE_GROUP_GROUP_ATOM_H
7
8  #include "compute.h"
9  #include "compute_group_group.h"
10
11 namespace LAMMPS_NS {
12
13 class ComputeGroupGroupAtom : public ComputeGroupGroup {
14 public:
15     ComputeGroupGroupAtom(class LAMMPS *, int, char **);
16     ~ComputeGroupGroupAtom();
17     void compute_peratom() override;
18     int nmax;
19     double **carray;
20
21 private:
22     void pair_contribution() override;
23 };
24 }
25 #endif
26 #endif
```

### A.3 compute\_group\_group\_atom.cpp

```

1  #include <mpi.h>
2  #include <string.h>
3  #include "compute_group_group_atom.h"
4  #include "atom.h"
5  #include "update.h"
6  #include "force.h"
7  #include "pair.h"
8  #include "neighbor.h"
9  #include "neigh_request.h"
10 #include "neigh_list.h"
11 #include "group.h"
12 #include "kspace.h"
13 #include "error.h"
14 #include <math.h>
15 #include "comm.h"
16 #include "domain.h"
17 #include "math_const.h"
18 #include "memory.h"
19
20 #include <iostream>
21 using namespace LAMMPS_NS;
22 using namespace MathConst;
23
24 #define SMALL 0.00001
25
26 ComputeGroupGroupAtom::ComputeGroupGroupAtom(LAMMPS *lmp,
27   int narg, char **arg) :
28   ComputeGroupGroup(lmp, narg, arg),
29   carray(NULL),
30   nmax(0)
31 {
32   if (narg < 4) error->all(FLERR, "Illegal compute
33     group/group command");
34
35   peratom_flag      = 1; // Indicating a peratom compute
36   size_peratom_cols = 4; // # of Columns per atom.
37   extarray          = 0; // 0/1 if global array is all
38     intensive/extensive
39   scalar_flag       = 0;
40   vector_flag       = 0;
41 }
42
43 ComputeGroupGroupAtom::~ComputeGroupGroupAtom()
44 {
45   memory->destroy(carray);
46 }

```



```

46
47 void ComputeGroupGroupAtom::compute_peratom()
48 {
49     // grow array if necessary
50     if (atom->nmax > nmax) {
51
52         memory->destroy(carray);
53         nmax = atom->nmax;
54         memory->create(carray, nmax, size_peratom_cols,
55             "group/group/atom:carray");
56         array_atom = cararray;
57     }
58
59     if (pairflag) pair_contribution();
60     if (kspaceflag) kspace_contribution(); // This doesn't
        happen though. See compute_group_group.cpp
        constructor.
61 }
62
63
64 void ComputeGroupGroupAtom::pair_contribution()
65 {
66     int i,j,ii,jj,inum,jnum,itype,jtype;
67     double xtmp,ymtp,ztmp,dex,dely,dely;
68     double rsq,eng,fpair,factor_coul,factor_lj;
69     int *ilist,*jlist,*numneigh,**firstneigh;
70
71     double **x = atom->x;
72     int *type = atom->type;
73     int *mask = atom->mask;
74     int nlocal = atom->nlocal;
75     double *special_coul = force->special_coul;
76     double *special_lj = force->special_lj;
77     int newton_pair = force->newton_pair;
78     double *columns;
79
80     // invoke half neighbor list (will copy or build if
        necessary)
81
82     neighbor->build_one(list);
83
84     inum = list->inum;
85     ilist = list->ilist;
86     numneigh = list->numneigh;
87     firstneigh = list->firstneigh;
88
89     // loop over neighbors of my atoms
90     // skip if I,J are not in 2 groups
91
92

```

```

93     for (ii = 0; ii < inum; ii++) {
94         i = ilist[ii];
95
96         array_atom[i][0] = 0;
97         array_atom[i][1] = 0;
98         array_atom[i][2] = 0;
99         array_atom[i][3] = 0;
100     }
101
102     for (ii = 0; ii < inum; ii++) {
103         i = ilist[ii];
104
105         // skip if atom I is not in either group
106         if (!(mask[i] & groupbit || mask[i] & jgroupbit))
107             continue;
108
109         xtmp = x[i][0];
110         ytmp = x[i][1];
111         ztmp = x[i][2];
112         itype = type[i];
113         jlist = firstneigh[i];
114         jnum = numneigh[i];
115
116         for (jj = 0; jj < jnum; jj++) {
117             j = jlist[jj];
118             factor_lj = special_lj[sbmask(j)];
119             factor_coul = special_coul[sbmask(j)];
120             j &= NEIGHMASK;
121
122             // skip if atom J is not in either group
123             if (!(mask[j] & groupbit || mask[j] &
124                 jgroupbit)) continue;
125
126             int ij_flag = 0;
127             int ji_flag = 0;
128             if (mask[i] & groupbit && mask[j] & jgroupbit)
129                 ij_flag = 1;
130             if (mask[j] & groupbit && mask[i] & jgroupbit)
131                 ji_flag = 1;
132
133             // skip if atoms I,J are only in the same group
134             if (!ij_flag && !ji_flag) continue;
135
136             delx = xtmp - x[j][0];
137             dely = ytmp - x[j][1];
138             delz = ztmp - x[j][2];
139             rsq = delx*delx + dely*dely + delz*delz;
140             jtype = type[j];
141
142             if (rsq < cutsq[itype][jtype]) {
143                 eng = pair->single(i, j, itype, jtype,

```

```
140         rsq, factor_coul, factor_lj, fpair);
141
142         // energy only computed once so tally full
143         // amount
144         // force tally is jgroup acting on igroup
145
146         if (newton_pair || j < nlocal) {
147             array_atom[i][0] += eng;
148             if (ij_flag) {
149                 array_atom[i][1] += delx*fpair;
150                 array_atom[i][2] += dely*fpair;
151                 array_atom[i][3] += delz*fpair;
152             }
153             if (ji_flag) {
154                 array_atom[j][1] -= delx*fpair;
155                 array_atom[j][2] -= dely*fpair;
156                 array_atom[j][3] -= delz*fpair;
157             }
158
159             // energy computed twice so tally half
160             // amount
161             // only tally force if I own igroup
162             // atom
163         }
164         else {
165             array_atom[i][0] += 0.5*eng;
166             if (ij_flag) {
167                 array_atom[i][1] += delx*fpair;
168                 array_atom[i][2] += dely*fpair;
169                 array_atom[i][3] += delz*fpair;
170             }
171         }
172     }
173 }
```