

TITLE OF THE MASTER THESIS

by

Filip Henrik Larsen

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Abstract

This is an abstract text.

To someone

This is a dedication to my cat.

Acknowledgements

Flora Joelle Larsen
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.

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 that 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 page¹ 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.

¹<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*².

```
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*.

²<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 intensive³ 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.

³Physical property of a system that does not depend on the system size.

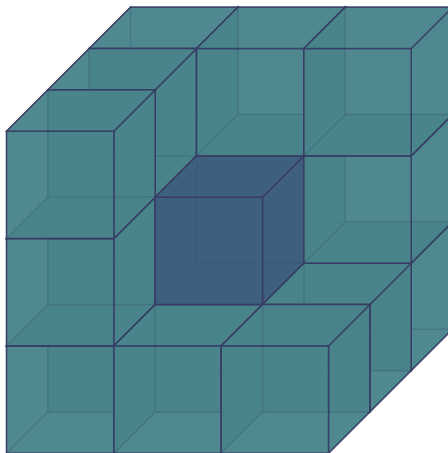


Figure 3.1: Illustrative figure of cells of concern when building the neighbor lists. The lighter cubes are neighboring cells; the darker cube is the cell containing the reference atom. The 7 cells in front of the dark cell are removed from the figure, but are also included.

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 with respect 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 speedup of parallel implementation of a code using p processors is seldom trivially $1/p$. 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 will 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 good practice to check the speedup of using several cores.

In order to compute the speedup we initialized a system containing 15×15 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 10000
6  variable T equal 293
7
8  neighbor 0.3 bin
9  neigh_modify delay 10
10
11 timestep 0.002
12
13 fix nvt all nvt temp ${T} ${T} 1.0
14 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.

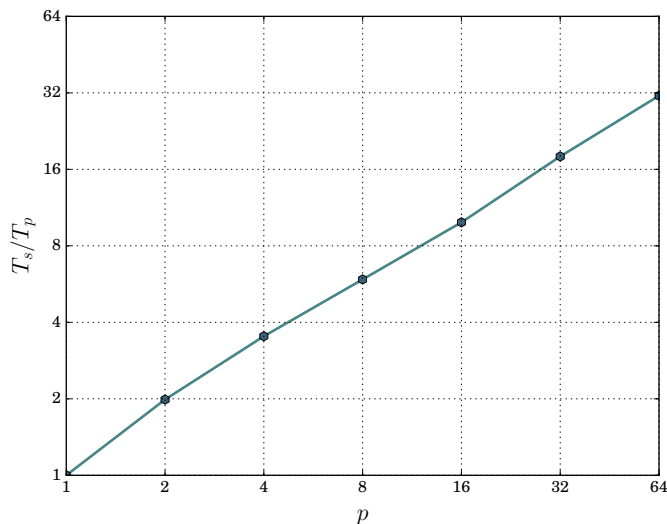


Figure 3.2: Speedup as a function of number of processors.

COMMENT ON THE RESULT ... Though we clearly see the advantage, that when using 64 processors instead of 1 we can finish a job that would have

take an hour in two minutes! Also, we can clearly see the initial argument that this is not more efficient when regarding CPU time.

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*¹, 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 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 β -cristobalite. This is mainly because it has a simple structure and a cubical unit cell.

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

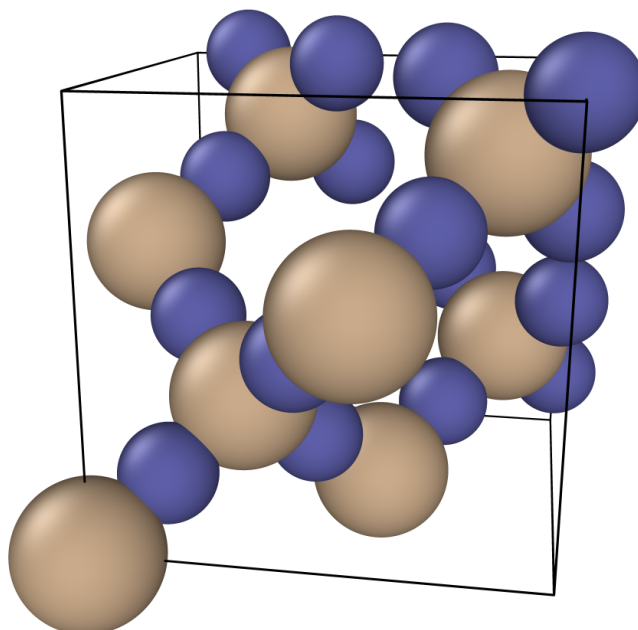


Figure 4.1: Unit cell of β -cristobalite. Tan and blue spheres represent silicon and oxygen atoms respectively.

4.1.1 Unit cell of β -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 β -cristobalite found at *Crystallography Open Database*². 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 β -cristobalite the unit cell is cubical with edges of length 7.12\AA . It contains 8 silicon atoms and 16 oxygen atoms. The density of the unit cell can easily be computed and is 2.2114 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.

Moltemplate has its own structure and syntax. The first step to build up

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

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

```

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.

We use the unit cell as building blocks, placing them concurrently until we

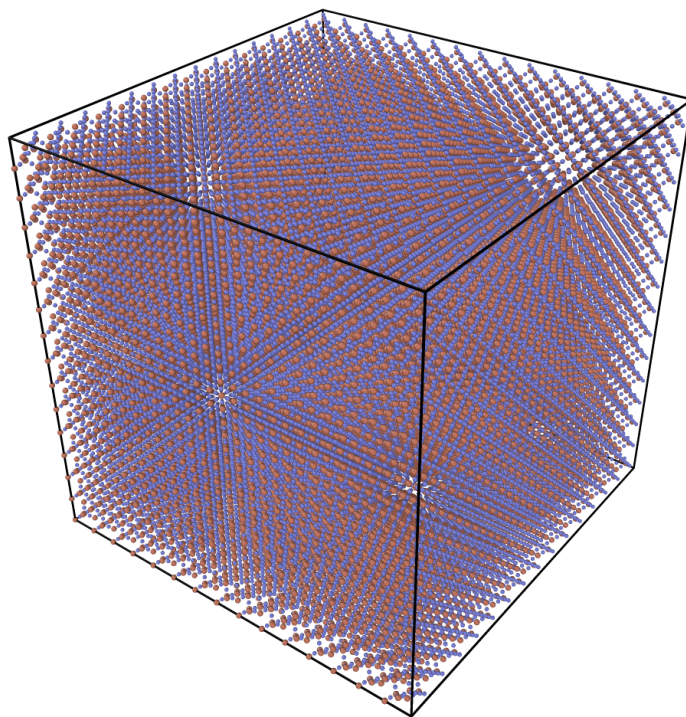


Figure 4.2: System built from $15 \times 15 \times 15$ unit cells of b-cristobalite.

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 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 `region`, `union`, `intersect` and `delete atoms` commands. Our implementation is stated in Listing 4.2, which is very simple due to the way we are going to treat the boundary conditions.

```

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 bothRegion union 2 sphereRegion slabRegion side out
8  delete_atoms region bothRegion

```

Listing 4.2: Defining regions to keep or delete from a system of dimensions $106.8 \times 106.8 \times 106.8$ Å.

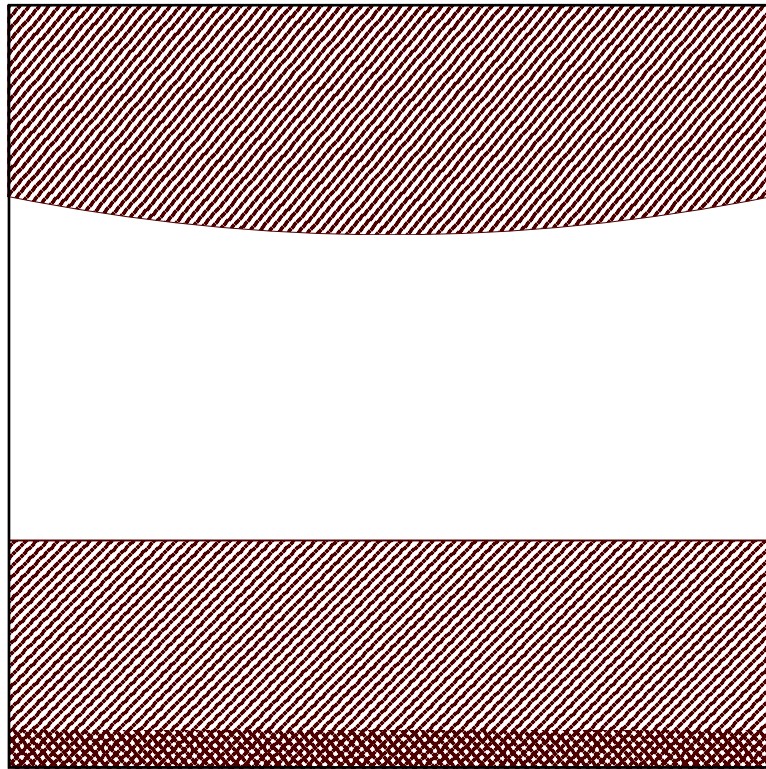


Figure 4.3: Illustrative drawing of what how the system should look. Red parallel stripes symbolize areas of silica. Red crossing stripes indicate areas of frozen silica. The boundaries are periodic in all dimensions, causing both the slab and the sphere to be connected to the frozen silica through the z-boundaries.

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, σ_{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.

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*¹ 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;

```

¹http://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 using namespace LAMMPS_NS;
21 using namespace MathConst;
22
23 #define SMALL 0.00001
24
25 ComputeGroupGroupAtom::ComputeGroupGroupAtom(LAMMPS *lmp,
26     int narg, char **arg) :
27     ComputeGroupGroup(lmp, narg, arg),
28     carray(NULL),
29     nmax(0)

```

```

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

```



```

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

```

```

121     dely = ytmp - x[j][1];
122     delz = ztmp - x[j][2];
123     rsq = delx*delx + dely*dely + delz*delz;
124     jtype = type[j];
125
126     if (rsq < cutsq[itype][jtype]) {
127         eng = pair->single(i, j, itype, jtype,
128             rsq, factor_coul, factor_lj, fpair);
129
130         // energy only computed once so tally full
131         // amount
132         // force tally is jgroup acting on igroup
133
134         if (newton_pair || j < nlocal) {
135             array_atom[i][0] += eng;
136             if (ij_flag) {
137                 array_atom[i][1] += delx*fpair;
138                 array_atom[i][2] += dely*fpair;
139                 array_atom[i][3] += delz*fpair;
140             }
141             if (ji_flag) {
142                 array_atom[j][1] -= delx*fpair;
143                 array_atom[j][2] -= dely*fpair;
144                 array_atom[j][3] -= delz*fpair;
145             }
146
147             // energy computed twice so tally half
148             // amount
149             // only tally force if I own igroup
150             atom
151
152         }
153         else {
154             array_atom[i][0] += 0.5*eng;
155             if (ij_flag) {
156                 array_atom[i][1] += delx*fpair;
157                 array_atom[i][2] += dely*fpair;
158                 array_atom[i][3] += delz*fpair;
159             }
160         }
161     }
162 }

```

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 a set of atoms. `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!

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 using namespace LAMMPS_NS;
21 using namespace MathConst;
22
23 #define SMALL 0.00001
24
25 ComputeGroupGroupAtom::ComputeGroupGroupAtom(LAMMPS *lmp,
26   int narg, char **arg) :
27   ComputeGroupGroup(lmp, narg, arg),
28   carray(NULL),
29   nmax(0)
30 {
31   if (narg < 4) error->all(FLERR, "Illegal compute
32     group/group command");
33
34   peratom_flag      = 1; // Indicating a peratom compute
35   size_peratom_cols = 4; // # of Columns per atom.
36   extarray          = 0; // 0/1 if global array is all
37     intensive/extensive
38   scalar_flag       = 0;
39   vector_flag        = 0;
40 }
41
42 ComputeGroupGroupAtom::~ComputeGroupGroupAtom()
43 {
44   memory->destroy(carray);
45 }

```



```

46 void ComputeGroupGroupAtom::compute_peratom()
47 {
48     // grow array if necessary
49     if (atom->nmax > nmax) {
50         memory->destroy(carray);
51         nmax = atom->nmax;
52         memory->create(carray, nmax, size_peratom_cols,
53             "group/group/atom:carray");
54         array_atom = cararray;
55     }
56
57     if (pairflag) pair_contribution();
58     if (kpaceflag) kspace_contribution(); // This doesn't
59     happen though. See compute_group_group.cpp
60     constructor.
61 }
62
63 void ComputeGroupGroupAtom::pair_contribution()
64 {
65     int i,j,ii,jj,inum,jnum,itype,jtype;
66     double xtmp,ymtp,ztmp,dex,dely,delz;
67     double rsq,eng,fpair,factor_coul,factor_lj;
68     int *ilist,*jlist,*numneigh,**firstneigh;
69
70     double **x = atom->x;
71     int *type = atom->type;
72     int *mask = atom->mask;
73     int nlocal = atom->nlocal;
74     double *special_coul = force->special_coul;
75     double *special_lj = force->special_lj;
76     int newton_pair = force->newton_pair;
77     double *columns;
78
79     // invoke half neighbor list (will copy or build if
80     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     for (ii = 0; ii < inum; ii++) {
93         i = ilist[ii];

```

```

93 // skip if atom I is not in either group
94 if (!(mask[i] & groupbit || mask[i] & jgroupbit))
95     continue;
96
97 xtmp = x[i][0];
98 ytmp = x[i][1];
99 ztmp = x[i][2];
100 itype = type[i];
101 jlist = firstneigh[i];
102 jnum = numneigh[i];
103
104 for (jj = 0; jj < jnum; jj++) {
105     j = jlist[jj];
106     factor_lj = special_lj[sbmask(j)];
107     factor_coul = special_coul[sbmask(j)];
108     j &= NEIGHMASK;
109
110     // skip if atom J is not in either group
111     if (!(mask[j] & groupbit || mask[j] &
112         jgroupbit)) continue;
113
114     int ij_flag = 0;
115     int ji_flag = 0;
116     if (mask[i] & groupbit && mask[j] & jgroupbit)
117         ij_flag = 1;
118     if (mask[j] & groupbit && mask[i] & jgroupbit)
119         ji_flag = 1;
120
121     // skip if atoms I,J are only in the same group
122     if (!ij_flag && !ji_flag) continue;
123
124     delx = xtmp - x[j][0];
125     dely = ytmp - x[j][1];
126     delz = ztmp - x[j][2];
127     rsq = delx*delx + dely*dely + delz*delz;
128     jtype = type[j];
129
130     if (rsq < cutsq[itype][jtype]) {
131         eng = pair->single(i, j, itype, jtype,
132             rsq, factor_coul, factor_lj, fpair);
133
134         // energy only computed once so tally full
135         // amount
136         // force tally is jgroup acting on igroup
137
138         if (newton_pair || j < nlocal) {
139             array_atom[i][0] += eng;
140             if (ij_flag) {
141                 array_atom[i][1] += delx*fpair;
142                 array_atom[i][2] += dely*fpair;
143                 array_atom[i][3] += delz*fpair;
144             }
145         }
146     }
147 }

```

```
138         }
139         if (ji_flag) {
140             array_atom[j][1] -= delx*fpair;
141             array_atom[j][2] -= dely*fpair;
142             array_atom[j][3] -= delz*fpair;
143         }
144
145         // energy computed twice so tally half
146         // amount
147         // only tally force if I own igroup
148         // atom
149         }
150         else {
151             array_atom[i][0] += 0.5*eng;
152             if (ij_flag) {
153                 array_atom[i][1] += delx*fpair;
154                 array_atom[i][2] += dely*fpair;
155                 array_atom[i][3] += delz*fpair;
156             }
157         }
158     }
159 }
```


Bibliography

- [1] Bin Luan and Mark O Robbins. The breakdown of continuum models for mechanical contacts. *Nature*, 435(7044):929–932, 2005.