

PHASE CHANGE STUDIES WITH MOLECULAR DYNAMICS: A COMPUTER SIMULATION

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1 ABSTRACT

In this paper we include and explain in detail a computer code used to solve the molecular dynamics simulation of an evaporating droplet. In this code we use the Gear Predictor-Corrector numerical integrator and a truncated Lennard-Jones potential. However, the code can be used for different applications given some minor modifications. The scope of this paper is to give researchers a working code to study molecular dynamics and encourage other researchers to do the same.

2 INTRODUCTION

Molecular dynamics simulations could become viable as a tool for analyzing systems on a nanoscale level. This can primarily be attributed to the advanced design of high speed, large memory and/or parallel computers. Molecular dynamics formulation is deterministic and consist of simultaneously solving Newton's equations of motion for each atom, molecule or system of molecules to determine properties of the materials. Molecular dynamic studies are limited to few topics with some success. Among these the most frequent application is to simulate the nanoscale phase change phenomena through an atomic or molecular level analyses. One such application is within the metallurgical industry, an emphasis has been placed on the nanoscale phase change behavior of metals because of their relevance in many diverse nanoscale processes, such as metal powder production via nucleation from a supersaturated vapor, chemical vapor deposition processes, and the crystallization of various polymers. Pound (1952) observed the nucleation of various types of vapors and approximated that the critical nuclei consisted of only between 80 and 100 atoms. Attention has also been focused on the need for understanding the kinetics of nucleating vapor (Reiss, 1952 and Michaels, 1969). Statistical theory predicts a deviation in the behavior of droplets this small from macroscopic or continuum analyses. Hill *et al* (1963) confirmed this notion in his study of nucleating metal vapors by noting that the surface tension could be in substantial error since drops of critical size have such small radii of curvature. Nucleation phenomena are small in spatial extent in that the critical radii of the nuclei have been found to be of the order 10^{-9} m (Lothe and Pound, 1969). Furthermore, the time

required for formation of critical nuclei has been documented to be of the order 10^{-10} s (Mandell *et al*, 1976). Molecular Dynamics studies of nucleation are extended to molecular clusters undergoing phase changes with a new interaction potential by Santikara and Bartell (1997), and the crystallization of metastable fluids by Pickering and Snook (1997). Recently, molecular dynamics simulations have been used to investigate the molecular mechanism that governs many heat transfer processes such as the evaporation, condensation and melting at liquid surfaces (Chokappa and Clancy, 1988, Rey *et al* 1992, Yasuoka *et al*, 1994, Matsumoto *et al*, 1994, 1996, Kotake and Aoki, 1996, Tsuruta, Takana, Tamashima and Masuoka, 1996.) The evaporation of droplets studies are needed at supercritical conditions as it relates to combustion in cryogenic rocket motors on a microscale basis as described by Kaltz *et al* (1994). The subcritical evaporation of droplet is modeled by Long *et al* (1997), and the computed evaporation rate compared with the Knudsen aerosol theory. A molecular dynamics simulation is employed by Bhansali, Bayazitoglu and Maruyama (1998) to investigate the interfacial phenomena and to determine properties of an evaporating sodium droplet. The Lennard-Jones potential (Bhansali *et al*, 1996) and oscillatory pair potential based on Levesque *et al* (1985)'s data is studied (Bhansali and Bayazitoglu, 1996). To simulate such a problem the computational code will be presented in the following section.

Molecular dynamics simulations consist of four major phases: 1) the construction of an adequate potential that governs the intermolecular forces acting between the individual particles, 2) the initialization of the simulation and run parameters, 3) the calculation of the molecular trajectories and velocities of each particle during simulation, and 4) the analysis of the trajectories and velocities to determine the physical properties of the system.

On a different note, molecular dynamics studies have not exploded as fast as one would have originally expected. Most of the publications related to our current phase change problem have started to resemble each other very closely. It seems that this is due to the fact that writing the computer code for solving the problem is such a time consuming and daunting task that most people consider it a milestone alone when getting their code to run.

The computer codes, together with the capabilities of current and future computer technology, have the potential of solving new problems and quantifying the experiments of nano and micro-scale size. We would like to see some more collaboration in the form of making previously produced and tested computer codes available to other researchers such that they can eliminate the pain and agony of trying to write their own code from scratch. This will give people a jump start, so that they can spend their time expanding the current research or even uncover complete new areas of application. One good example is the book "Molecular Dynamics Simulation" by Haile (1992). Surely many people have put his detailed explanations of the intricacies of the problems involved in writing a molecular dynamics code to good use.

In this paper we will present our analysis of an evaporating droplet along with the code written to solve the problem. We hope other researchers will take this code and use it to their advantage. With some alterations this code can be used to simulate processes such as conduction in thin films or fluid flow in nano channels.

3 MOLECULAR DYNAMICS SIMULATION CODE

In simulation for the intermolecular forces the well-known Lennard-Jones 12-6 potential, ϕ is used,

$$\phi(r_{ij}) = 4\epsilon \left[\left(\frac{\sigma}{r_{ij}} \right)^{12} - \left(\frac{\sigma}{r_{ij}} \right)^6 \right] \quad (1)$$

where r_{ij} is the separation distance between atoms i and j , σ the first zero of the potential is the equilibrium separation parameter (\AA), and ϵ is the potential well depth (J). This potential was selected because of its simplicity, but it could easily be replaced with another potential in the code as long as it represents the physical behavior of the medium (e.g. Bhansali and Bayazitoglu, 1996).

Although the code is initially written to investigate thermal characteristics of an isolated evaporating liquid droplet at various temperatures, it can also be used for other nano-scale problems. A microcanonical ensemble was employed in which the number of particles, the volume, and the total energy of the system were the constrained constants (Rowley, 1994).

The fcc structure is used for simulations in this code. Each atom was arbitrarily assigned a velocity in each coordinate direction (v_{ik}^*) via a random number generator and then scaled to the set point temperature, T_p^* ,

$$v_{ik}^{*new} = v_{ik}^* \sqrt{T_p^*/T_{act}^*} \quad (2)$$

where subscript i corresponds to a particular atom, subscript k represents the coordinate direction. The instantaneous temperatures are time averaged during the simulation until the steady state is reached. The instantaneous temperature of the system T_{act}^* determined from the equipartition principle.

$$T_{act}^* = \frac{1}{3N} \sum_i \sum_k v_{ik}^* \cdot v_{ik}^* \quad (3)$$

where N is the number of atoms.

The velocities and the temperatures in the simulation were normalized with respect to the standard parameters used in typical soft-sphere models presented in Table 1 and are denoted as such with the * superscript (Thompson *et al.*, 1984, Allen and Tildesley, 1987).

Table 1. Reduced Parameters

<u>Quantity</u>	<u>Parameter</u>
Length	$x^* = x / \sigma$ $r^* = r / \sigma$
Pressure	$P^* = (P\sigma^3 / \epsilon)$
Temperature	$T^* = (k_B T / \epsilon)$, $k_B = 1.381 \times 10^{-23} \text{ J/K}$
Velocity	$V^* = (v / \sqrt{\epsilon / wm})$
Timestep	$\Delta t^* = (\Delta t / \sigma \sqrt{wm / \epsilon})$
Density	$\rho^* = N\sigma^3 / V$
Potential	$\phi^* = \frac{\phi}{N\epsilon}$

Since no dissipative external forces exist and since the potential was assumed pairwise additive, the force F_i , (N) on each particle i could then be related to the potential in the following manner

$$\bar{F}_i = -\sum_j \nabla \phi(r_{ij}) = m \frac{\partial^2 \bar{r}_i}{\partial t^2} \quad (4)$$

where ∇ denotes the gradient and wm , (kg) is the mass of the atom, molecule or cluster. F_i is the position vector (Armstrong), and t is the time, (sec). A 5th order Gear predictor-corrector numerical integrator algorithm was used to solve the Newton's equations of motion for each atom. This algorithm was found to have better energy conservation characteristics to the other algorithms considered previously such as the Verlet or Beeman algorithms (Swope *et al.*, 1982, Haile, 1994, Amini and Fincham, 1990).

The simulation was governed by the temperature control scheme employed in the simulation. An equilibration period was specified at each set point temperature (T_p^*) during which the velocity was scaled according to equation (2).

Thermal equilibration was monitored by using a nearest neighbor routine that tracked the number of vapor atoms with respect to time. Each atom was classified as vapor, liquid, or surface depending on the number of atoms that are within a sphere of radius 1.5σ centered at that particular atom. An atom was considered vapor if it had 1-2 neighbors, interfacial if it had 3-7 neighbors, and liquid if it had 8 or more neighbor atoms (Maruyama *et al.*, 1994). Thermal equilibrium had been reached when the number of vapor atoms had become relatively constant.

The velocity scaling was then terminated and the system was allowed to proceed in a state of constant total energy during which the trajectories and velocities were accumulated for the subsequent determination of the physical properties. The set point temperature was then reset and thermal equilibrium was achieved at the new desired state.

For a system of N atoms, there are $N(N-1)/2$ possible force interactions and the calculation of these interactions is extremely time-consuming. To calculate the force on each atom, for systems in which atoms are subjected to short range forces, a Verlet neighbor list routine was implemented to reduce the computation time (Verlet, 1967, Arnold and Mauser, 1990, Chialvo and Debenedetti, 1991). Hence, a truncated potential was used such that the force for separation distances greater than a critical cutoff distance, r_c , (A), equals zero, indicating that outside the critical radius atoms have a negligible contribution to the total force on a given atom.. Then for each atom, the routine maintains a list of neighboring atoms that lie within a distance r_L , (A) of that particular atom where typically $r_L = r_c + 0.3 \sigma$. The neighbor list for each particle was automatically updated based on a maximum particle displacement criterion as reported by Verlet.

In Fig 1 we present the flow chart of the code. The code is written in FORTRAN77 and the main and the subroutines are individually explained.

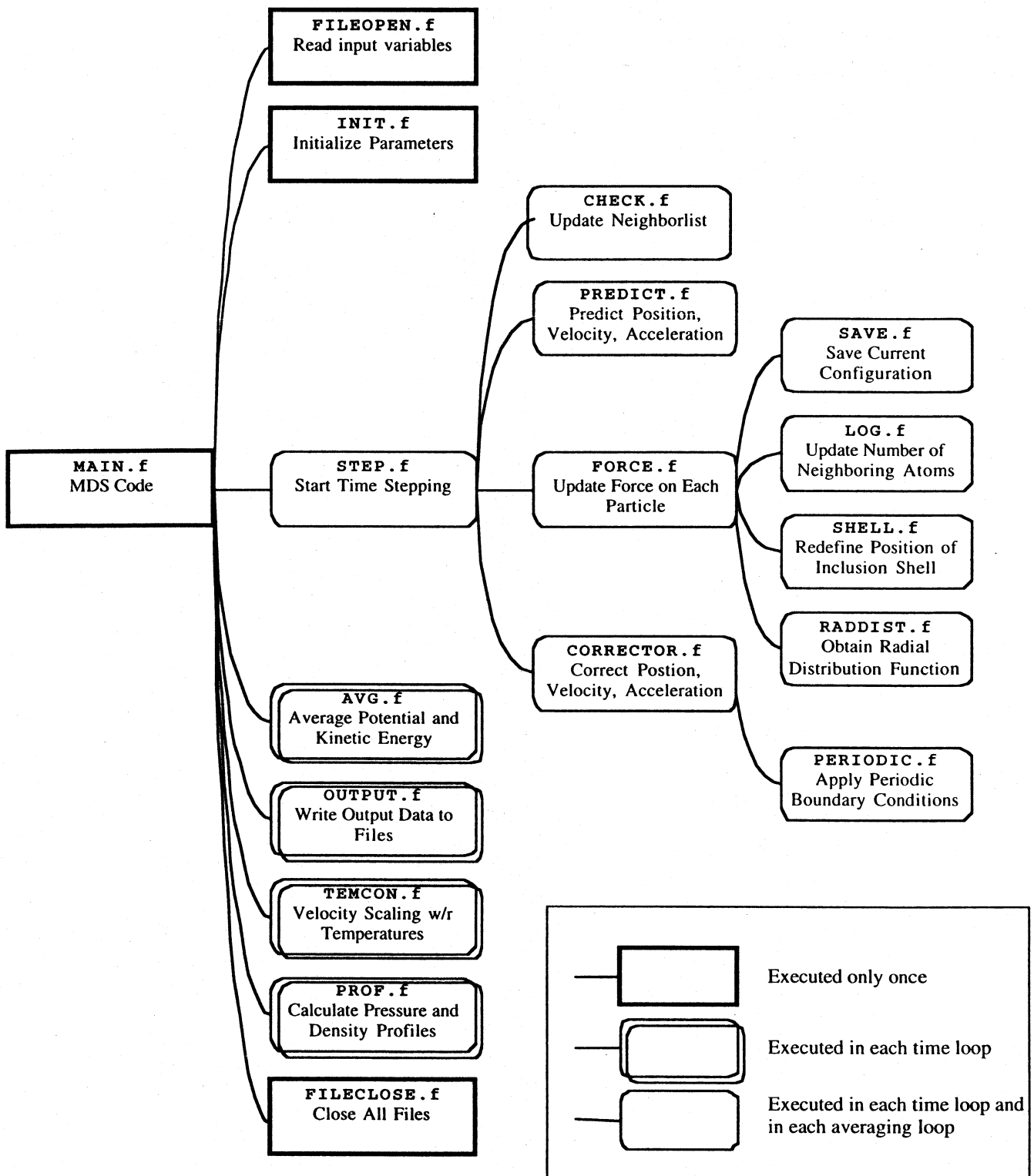


Figure 1. Flowchart

This subroutine is called by the main program once at the beginning of the code. It initializes the variables.

NOMENCLATURE

Integers :

im = atom labeling parameter
 inte = frequency that PE & KE are output
 intlg = frequency that # of neighbors is output
 intp = frequency that the position vectors are output
 intic = frequency of temperature control
 intv = frequency that the velocity is output
 k = counter
 kavg = how often averaging of properties is done
 kprnt = how often data is printed out
 lnay = how often neighbor routine is called
 lsti = listvectors for interactions
 lstj = listvectors for interactions
 nloc = # times local loop is executed
 nmax = number of particles in the simulation
 nmol = number of atoms
 nrdels = counting parameter
 nrdrn = random seed
 nrep = # times general loop is executed
 ntc = # of temperature controls imposed
 nuni = unit cells in crystal
 nvol = unit cells in volume
 upcnt = tells the number of times neighbor list is updated

Reals :

accx,accy,accz = acceleration of atom (second derivative)
 ai0 = sum of all the rotational displacements squared
 alp0,alp1,alp2,alp3,alp4 = constants of the gear-predictor algorithm
 an = Avogadro's number (6.022e23 1/mole)
 ang = random angle (similar to longitude of the earth)
 base = initial distance from the particles on the outside of the crystal structure to the periodic boundary
 bc = random magnitude
 bk = Stefan Boltzman constant (1.381e-23 J/K)
 bs = sqrt(1-bc^2)
 bx,by,bz = third derivative of atom position
 coef = scaling coefficient

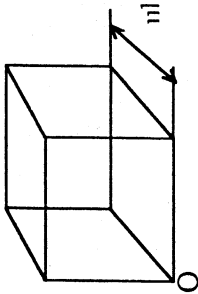
```

+      v,ve,virsum,vls,vm,wu,x)
+      end if
+      if((mod(irep,inttc).eq.0).and.(irep.le.ntc)) then
c Subroutine TEMCON corrects the velocities with temperature.
c This allows the system to equilibrate at a certain temperature.
  call temcon(irep,nmol,tins,v)
+      end if
+      if(mod(irep,inte).eq.0)then
c PROF is called once at he end of the code.( inte=2000)
  call prof(bk,eps,fnb,irep,lpo,lvo,nmol,pi,fcut,
+      sig,time,tini,tins,virsum,vl,vls,vm)
+      endif
c-----
c BOTTOM OF THE LOOP
c-----
c 100 continue
c-----
c OUTPUT FINAL CONDITION (12)
c-----
c Writes the final position vectors to a file
c-----
  write(12,*) nmol,vls,uls,time
  do 777 i = 1,nmol
    write(12,*) x(i,1),x(i,2),x(i,3)
  777 continue
  do 666 i = 1,nmol
    write(12,*) v(i,1),v(i,2),v(i,3)
  666 continue
c-----
c CLOSE FILES
c-----
c Call to subroutine "fileclose" and verify that the program
c terminated normally
c-----
  call fileclose
  write(*,*) '-- program finished normally ---'
  stop
  end

```

4.1 Subroutine INIT

(Number of atoms on the corners) \times (0.125) + (number of atoms at the faces) \times (0.5) = $8 \times (0.125) + 6 \times (0.5) = 4$

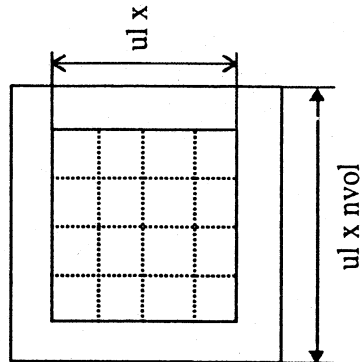


if $O(0,0,0) \Rightarrow$ The initial coordinates of 4 atoms in a cell will be: $(0, 0, 0)$; $(ul/2, ul/2, 0)$; $(0, ul/2, ul/2)$; $(ul/2, 0, ul/2)$

For this analysis the number of unit cells in a crystal is equal to $(nuni)^3$. So the number of atoms in a unit crystal is $4 \cdot (nuni)^3$, where $nuni = 4$

So the length of a crystal = $(ul) \times (nuni)$

then we define control volume as a cube having a length of vl where $vl = (ul) \times (nvol)$, where $nvol = 6$



To initialize atoms, initial distance from an atom on the outside boundary to the periodic boundary is defined as:

$$\text{base} = \frac{1}{2}(vl - (nuni) \times (ul))$$

cx,cy,cz = fourth derivative of atom position
dt = time step (sec)
dts = dimensionless time step
ek = average kinetic energy per atom per unit mass
enesum = average potential energy
eps = minimum energy (8.27e-21 J)
ffc = face centering parameter: used to define a box within the control box used to encompass only the liquid drop
gr = radial distribution function
o1,o2,o3 = angular momentum (x,y,z)
pi = 3.1415927
plr = long range pressure correction
r1,r2,r3 = position of particle minus half the box length ("init")
ra2 = sum of rotational displacements squared per atom
randf = random number generator: "FUNCTION randf"
rcut = radial distance in which forces are considered
rlist = distance larger than "rcut" including atoms that are within "rcut" before the next timestep
rdel = width of the spherical shell used in "veldist"
sig = collision diameter (potential separation distance)
time = nondimensional time
tini = initial temperature (K)
tins = nondimensional temperature
ul = crystal length
ulr = long range potential energy correction
uls = nondimensional crystal length
v1,v2,v3 = total translation
virsum = used to average virial
vl = length of the simulation box (m)
vls = nondimensional length of box
vr1,vr2,vr3 = total rotation
vsqsum = sum of kinetic energy over time
wm = mass of atom

Logicals :
update = used to decide updating the neighbor list

Initial positions of atoms are arranged based on Face Centered Cubic structure
8 atoms on the corners are common to 8 cubes and 6 atoms at the center of the faces are common to 2 cubes. So, the number of atoms for a unit cell can be calculated as follows:

After the initial positions are set, they are nondimensionalized with respect to σ .

Set the initial velocities

Each atom is assigned to an initial velocity having a magnitude of 1.0

bc = random magnitude = $-1.0 \leq bc \leq 1.0$

a = Random angle

$$bs = \sqrt{1 - bc^2}$$

The magnitude of velocity, $|V_i| = \sqrt{(bc \cdot \sin a)^2 + (bc \cdot \cos a)^2 + bs^2} = 1.0$

The components of velocity are going to be expressed as follows in the code

$$\vec{V}_n = V(n,1) \vec{i} + V(n,2) \vec{j} + V(n,3) \vec{k}$$

$$V(n,1) = bc \sin(a)$$

$$V(n,2) = bc \cos(a)$$

$$v(n,3) = \sqrt{1 - bc^2}$$

Cancellation out of the total translation

To obtain zero total linear momentum the velocities are scaled by removing translation from the velocities.

Total translation in x, y, z directions are $V1 = \sum_{i=1}^{n_{mol}} V(i,1)$, $V2 = \sum_{i=1}^{n_{mol}} V(i,2)$

and $V3 = \sum_{i=1}^{n_{mol}} V(i,3)$. So, Average x, y, z -translations / atom are $\frac{V1}{n_{mol}}$,

$\frac{V2}{n_{mol}}$, $\frac{V3}{n_{mol}}$ respectively.

⇒ Velocities after translation :

$$V(i,1) = V(i,1) - \frac{V1}{n_{mol}}, \quad V(i,2) = V(i,2) - \frac{V2}{n_{mol}}$$

$$V(i,3) = V(i,3) - \frac{V3}{n_{mol}}$$

Cancellation out of the total rotation

Position of an atom :

$$x(i,1) \vec{i} + x(i,2) \vec{j} + x(i,3) \vec{k}$$

Velocity of an atom :

$$\vec{V}_i = V(i,1) \vec{i} + V(i,2) \vec{j} + V(i,3) \vec{k}$$

The components of the distance of an atom from the center of the control volume:

$$r_1 = x(i,1) - \frac{V1}{2}, \quad r_2 = x(i,2) - \frac{V2}{2}, \quad r_3 = x(i,3) - \frac{V3}{2}$$

then we can write angular rotation about x, y, z axes in the following form

$$O1 = \sum_{i=1}^{n_{mol}} [r_2 x V(i,3) - r_3 x V(i,2)]$$

$$O2 = \sum_{i=1}^{n_{mol}} [r_3 x V(i,1) - r_1 x V(i,3)]$$

$$O3 = \sum_{i=1}^{n_{mol}} [r_1 x V(i,2) - r_2 x V(i,1)]$$

Average angular velocities are calculated as:

$$O1 = \frac{O1}{n_{mol}}, \quad O2 = \frac{O2}{n_{mol}}, \quad O3 = \frac{O3}{n_{mol}}$$

removal of rotation

$$V(i,1) = V(i,1) - (O2 \times r_3 - O3 \times r_2)$$

$$V(i,2) = V(i,2) - (O3 \times r_1 - O1 \times r_3)$$

$$V(i,3) = V(i,3) - (O1 \times r_2 - O2 \times r_1)$$

Now, the velocities should be adjusted to match the temperature of the system.

Total kinetic energy per unit mass = $KEG = \sum_{i=1}^{nmol} V(i,1)^2 + V(i,2)^2 + V(i,3)^2$

Kinetic energy per atom = $ek = KE / nmol$

ek can also be written in terms of temperature: $ek = \frac{3k_b T}{wm}$ so, we can write the

scaling factor as, $\alpha = \sqrt{\frac{3k_b T}{wm \cdot ek}}$.

And then velocities are nondimensionalized with $\sqrt{\frac{wm}{\epsilon}}$

```

-----
c Specify the constants
c
pi = acos(-1.0)
bk = 1.381D-23
an = 6.022D23
-----
c Specify the parameters of Sodium
c
wm = 22.99D-3/an
sig = 3.240D-10
eps = 8.27D-21
-----
c read CONDITIONS (10)
c

```

```

c*****
c
subroutine init(bk,dt,dts,enesum,eps,ffc,fnb,inte,intlg,intp,
+ inttc,intv,kavg,kprnt,lhay,nloc,nmol,nrep,ntc,nuni,nvol,upcnt
+ pi,plr,rcut,rlist,sig,time,tini,tins,ulr,uls,
+ upcnt,update,virsum,vi,vls,vsum,wm,xi)
c*****
implicit none
integer nmax
parameter(nmax=865)
integer i,lm,inte,intlg,intp,inttc,intv,j,k,kavg,kprnt,
+ lhay,nloc,nmol,nrdm,nrep,ntc,nuni,nvol,upcnt
double precision x(nmax,3),v(nmax,3),xi(nmax,3)
double precision ai0,an,ang,base,bc,bk,bs,coef,dt,dts,ek,
+ enesum,eps,ffc,fnb,oi,o2,o3,pi,plr,r1,r2,
+ r3,ra2,randf,rcut,rlist,sig,time,tini,tins,ul,
+ ulr,uls,vi,v2,v3,virsum,vi,vls,vr1,vr2,vr3,
+ vsqsum,wm
double precision accx,accy,accz,alp0,alp1,alp2,alp3,alp4,
+ bx,by,bz,cx,cy,cz
c
c RDF
integer ngofr,nrdels
double precision gr,rdel
logical update
common /one/ lsti,lstj,v,x
common /gear/ accx(nmax),accy(nmax),accz(nmax),
+ bx(nmax),by(nmax),bz(nmax),
+ cx(nmax),cy(nmax),cz(nmax)
common /correct/ alp0,alp1,alp2,alp3,alp4
c RDF
common /rdf/ gr(500),rdel
common /rdf2/ nrdels,ngofr(500)

```

```

-----
c read CONDITIONS (10)
c
read(10,*) nuni
read(10,*) nvol
read(10,*) tini
read(10,*) vl
read(10,*) dt
read(10,*) nrep
read(10,*) nloc
read(10,*) intp
read(10,*) intv
read(10,*) inte
read(10,*) inttc
read(10,*) intlg
read(10,*) ntc
read(10,*) nrdm
read(10,*) fnb
read(10,*) ffc
read(10,*) kavg
read(10,*) kprnt
read(10,*) lhay
-----
c INITIALIZE POSITION AND VELOCITY
c
c READ PREVIOUS RESULT (11)
c
c read in data from file "pre.dat" to continue previous
c simulation if it exists
read(11,*,end=100) nmol,vls,uls,time
do 900 i = 1,nmol
read(11,*,end=100) x(i,1),x(i,2),x(i,3)
continue
do 901 i = 1,nmol
read(11,*,end=100) v(i,1),v(i,2),v(i,3)
continue
900
901
write(*,*) 'Continuing previous calculation.'

```

```

goto 192
-----
C START NEW CALCULATION
C
100 continue
    nmol = 4*nuni**3
    ul = vl/nvol
    uis = ul/sig
    vls = vl/sig
C POSITION (x)
C
base = 0.5*(vl-nuni*ul)
do 110 i = 0, nuni-1
  do 110 j = 0, nuni-1
    do 110 k = 0, nuni-1
      im = (k+j*nuni+i*nuni**2)*4
      x(im+1,1) = ul*(i+1.0/4)+base
      x(im+1,2) = ul*(j+1.0/4)+base
      x(im+1,3) = ul*(k+1.0/4)+base
      x(im+2,1) = ul*(i+3.0/4)+base
      x(im+2,2) = ul*(j+1.0/4)+base
      x(im+2,3) = ul*(k+3.0/4)+base
      x(im+3,1) = ul*(i+1.0/4)+base
      x(im+3,2) = ul*(j+3.0/4)+base
      x(im+3,3) = ul*(k+3.0/4)+base
      x(im+4,1) = ul*(i+3.0/4)+base
      x(im+4,2) = ul*(j+3.0/4)+base
      x(im+4,3) = ul*(k+1.0/4)+base
110 continue
C
C Nondimensionalize positions now
C
do 115 i = 1, nmol
  x(i,1) = x(i,1)/sig
  x(i,2) = x(i,2)/sig
  x(i,3) = x(i,3)/sig
  xi(i,1) = x(i,1)
  xi(i,2) = x(i,2)
  xi(i,3) = x(i,3)
115 continue
do 116 i = 1, nmol
  write(34,134) xi(i,1),xi(i,2),xi(i,3)
116 continue
134 format(f10.4,2x,f10.4,2x,f10.4)
C
C VELOCITY (v)
C
do 120 i = 1, nmol
  ang = randf(nrdm)*pi*2.0
  bc = 1.0-2*randf(nrdm)
  bs = dsqrt(1.0-bc*bc)
  v(i,1) = bc*sin(ang)
  v(i,2) = bc*cos(ang)
  v(i,3) = bs
120 continue
C
C CANCEL THE TOTAL TRANSLATION
C
v1 = 0.0
v2 = 0.0
v3 = 0.0
do 130 i = 1, nmol
  v1 = v1+v(i,1)
  v2 = v2+v(i,2)
  v3 = v3+v(i,3)
130 continue
do 140 i = 1, nmol
  v(i,1) = v(i,1)-v1
  v(i,2) = v(i,2)-v2
  v(i,3) = v(i,3)-v3
140 continue
C
C CANCEL THE TOTAL ROTATION
C
ai0 = 0.0
o1 = 0.0
o2 = 0.0
o3 = 0.0
do 150 i = 1, nmol
  r1 = x(i,1)-0.5*v1
  r2 = x(i,2)-0.5*v1
  r3 = x(i,3)-0.5*v1
  ra2 = r1*r1 + r2*r2 + r3*r3
  ai0 = ai0+ra2
  o1 = o1+(r2*v(i,3)-r3*v(i,2))
  o2 = o2+(r3*v(i,1)-r1*v(i,3))
  o3 = o3+(r1*v(i,2)-r2*v(i,1))
150 continue
  o1 = o1/ai0
  o2 = o2/ai0
  o3 = o3/ai0
do 160 i = 1, nmol
  r1 = x(i,1)-0.5*v1
  r2 = x(i,2)-0.5*v1
  r3 = x(i,3)-0.5*v1
  vr1 = o2*r3-o3*r2
  vr2 = o3*r1-o1*r3
  vr3 = o1*r2-o2*r1
  v(i,1) = v(i,1)-vr1
  v(i,2) = v(i,2)-vr2
  v(i,3) = v(i,3)-vr3

```

```

160 continue
C-----
C ADJUST THE TEMPERATURE
C Velocities will now be nondimensional
ek = 0.0
do 170 i = 1, nmol
ek = ek + v(i,1)**2 + v(i,2)**2 + v(i,3)**2
170 continue
ek = ek/nmol
coef = dsqrt(3.0*bk*tini/(wm*ek))
do 180 i = 1, nmol
v(i,1) = v(i,1)*coef*(wm/eps)**0.5
v(i,2) = v(i,2)*coef*(wm/eps)**0.5
v(i,3) = v(i,3)*coef*(wm/eps)**0.5
180 continue
write(*,*) 'Starting new calculation.'
time = 0.0
C-----
C Initialize parameters for Gear algorithm
192 do 195 i = 1, nmol
accx(i) = 0.
accy(i) = 0.
accz(i) = 0.
bx(i) = 0.
by(i) = 0.
bz(i) = 0.
cx(i) = 0.
cy(i) = 0.
cz(i) = 0.
195 continue
alp0 = 19./120.
alp1 = 3./4.
alp2 = 1.
alp3 = 1./2
alp4 = 1./12.
200 continue
C-----
C Initialize parameters for averaging properties
enesum = 0.
virsum = 0.
vsgsum = 0.
C-----
C LIST VECTORS (lsti, lstj)
k = 0
do 210 i = 1, nmol-1
do 210 j = i+1, nmol
k = k+1

```

```

lsti(k) = j-i
lstj(k) = j
210 continue
C-----
C Specify parameters for the
C Verlet Neighbor routine
update = .true.
rcut = 3.5
rlist = 3.8
C-----
C long-range correction factors
plr = 96.*pi*nmol/(3.*vls**3.)
+ (0.5/(3.*rcut**3.) - 1.)/(9.*rcut**9.)
ulr = 8.*pi*(nmol/vls**3.)
+ (1.)/(9.*rcut**9.) - 1./(3.*rcut**3.)
C-----
C Nondimensional variables
dts = dt/(sig*(wm/eps)**0.5)
tins = bk*tini/eps
C-----
C Initialize and specify params
C for rad. dist. fun.
rdel = 0.025
nrdeis = vls/(2*rdel) - 1
do 951 i = 1, 300
gr(i) = 0.
ngofr(i) = 0
951 continue
return
end

```

4.2 Subroutine STEP

This subroutine is used to move molecules. It is called by main program 10 times for each time step.

NOMENCLATURE

Integers:

iloc = counter for the execution of the local loop
irep = counter for the execution of the general loop
ixs = parameter used to update position of liquid drop

j = counter
list = list of all neighbors
lnay = how often neighbor routine is called
lsti = listvectors for interactions
lstj = listvectors for interactions
maxnab = limiting number for the neighbor list
nij = adding parameter for interactive neighbor atoms
nlist = number of atoms within the "rlist" radius
nloc = # times local loop is executed
nmax = number of particles in the simulation
nmol = number of atoms
nnb = neighbors
nrdels = counting parameter
nx = parameter used in updating position of liquid drop
point = related to list (neighbor counting parameter)
rknt = counter

Reals :
bk = Stefan Boltzman constant (1.381e-23 J/K)
dt2 = half of the dimensionless time step
dis = dimensionless time step
disq = $0.5*(dis^2)$
ek = average kinetic energy per atom per unit mass
eps = minimum energy (8.27e-21 J)
ffc = face centering parameter: used to define a box within the control box used to encompass only the liquid drop
fnb = neighbor counting parameter
gr = radial distribution function
rcut = radial distance in which forces are considered
rdel = width of the spherical shell used in "veldist"
rlist = distance larger than "rcut" including atoms that are within "rcut" before the next timestep
rxo,ryo,rzo = dummy variable used in updating neighbor list
scl = length of control box for liquid drop
sig = collision diameter (potential separation distance)
ve = nondimensional velocity
vl = length of the simulation box (m)
vli = reciprocal nodimensional length of box
vls = nondimensional length of box
wm = mass of atom
wu = used in force routine
xs1,xs2,xs3 = distance that the liquid drop is off center

with respect to the center of the control volume
gr = radial distribution function

Logicals :
update = used to decide updating the neighbor list

 First of all we check whether the neighbor list needs to be updated or not. Because, it is going to affect the number of atoms interacting the atom being considered. In other words, force domain is going to change. To check this we calculate the displacements from the current configuration and then compare those values with 0.3σ . (subroutine CHECK)

Then, we start Gear predictor-corrector scheme. First, we call subroutine PREDICT to predict the values of positions, velocities, accelerations, third and fourth derivatives of the positions. The way the method works:

- 1 Use Taylor expansions to predict the values of desired quantities at the next time step.
2. Calculate the force using predicted positions . Evaluate the acceleration from Newton's second law. Find the difference between this acceleration and acceleration from the predictor step.
3. Use this difference as a correction factor to correct the positions and velocities at the next time step.

```

c*****
c      subroutine step(bk,dts,eps,ffc,fnb,iloc,irep,lnay,nloc,
+      nmol,rcut,rlist,sig,update,upcnt,ve,
+      virsum,vi,vls,wm,wu,uls,pi,xi,rknt)
c*****
      implicit none
      integer nmax,maxnab
      parameter (nmax=865,maxnab=nmax*500)
      integer i,iloc,irep,ixs,j,list,lnay,nloc,nmol,nxs,
+      point,upcnt,rknt
      integer lsti(nmax*(nmax-1)/2),lstj(nmax*(nmax-1)/2)
      double precision fm(nmax,3),x(nmax,3),v(nmax,3),xi(nmax,3)
  
```

```

double precision bk,dts,dtsq,dt2,ek,eps,ffc,fnb,rcut,rlist,
+ rxo,ryo,rzo,scl,sig,ve,virsum,vl,vli,vls,
+ wm,wu,xs1,xs2,xs3,
+ uis,pi
c RDF
integer ngofr,nrdels
double precision gr,rdel
logical update
common /one/ lsti,lstj,v,x
common /block1/ rxo(nmax),ryo(nmax),rzo(nmax)
common /block2/ list(maxnab),point(nmax)
c RDF
common /rdf/ gr(500),rdel
common /rdf2/ nrdels,ngofr(500)
vli = 1.0/vls
dtsq = dts*dts/2.
dt2 = dts/2.
-----
c Make call to check if the Verlet
c neighbor listneeds updating
-----
c call check(iloc,irep,nmol,rcut,rlist,update,x,upcnt)
-----
c Predictor values for GPC
-----
c call predict(dts,nmol,v,x)
c Now, we have the predicted value of the position of each atom
c that will be used in the force calculations.
-----
c call force to update force on each particle
-----
c call force(fm,fnb,iloc,irep,lnay,nloc,nmol,rcut,rlist,sig,
+ ve,vl,vls,wu,update,x)
-----
c Corrector values for GPC
-----
c After force calculation positions, velocities and higher
c order derivatives of the positions should be corrected.
c CORRECTOR is used.
c call corrector(dts,fm,nmol,v,vls,x,iloc,irep)
-----
c A face centering parameter, ffc, is used that defines a box
c within the control box

```

```

c which is used to encompass only the liquid drop. This is done
c so that the new
c center of mass is fixed, based solely on the liquid droplet.
xs1=0.0
xs2=0.0
xs3=0.0
nxs=0
scl=ffc*vls*0.5
do 240 i=1,nmol
+ ix= idint(dsign(0.5D0,scl-dabs(x(i,1)-0.5*vls))+0.51)
+ *idint(dsign(0.5D0,scl-dabs(x(i,2)-0.5*vls))+0.51)
+ *idint(dsign(0.5D0,scl-dabs(x(i,3)-0.5*vls))+0.51)
c The lines provide a running total of what atoms fall inside the
c ffc box at each time step. This helps to define the center of
c mass of the droplet.

```

```

xs1=xs1+x(i,1)*ix
xs2=xs2+x(i,2)*ix
xs3=xs3+x(i,3)*ix
nxs=nxs+ix

```

```

240 continue
ek = 0.0
do 290 i = 1,nmol
do 290 j = 1,3
ek = ek+v(i,j)*v(i,j)
290 continue

```

```

-----
c FIX THE TOTAL CENTER OF MASS (x)
-----

```

```

c Locate the distance in each coordinate, x, y, z that the drop
c is off center with respect to the center of the control
c volume.

```

```

xs1 = xs1/nxs - 0.5*vls
xs2 = xs2/nxs - 0.5*vls
xs3 = xs3/nxs - 0.5*vls

```

```

c So, the repositioning of each atom is completed based on the
c off center distance.

```

```

do 300 i = 1,nmol
x(i,1) = x(i,1) - xs1
x(i,2) = x(i,2) - xs2
x(i,3) = x(i,3) - xs3
if ((x(i,1).lt.0).or.(x(i,2).lt.0).or.(x(i,3).lt.0)) then
call periodic(x(i,1),x(i,2),x(i,3),vls)
end if

```

```

300 continue
return
end

```



```

accx,accy,accz = acceleration of atom (second derivative)
bx,by,bz      = third derivative of atom position
c1,c2,c3,c4   = dimensionless time parameters
cx,cy,cz      = fourth derivative of atom position
dts           = dimensionless time step
v             = velocity of particle
x,y,z         = coordinate of position vector of particle

```

4.5 Subroutine FORCE

This is the intermediate step of the Gear Algorithm. FORCE calculates the intermolecular force on each atom. We assume that the interaction energy among N atoms is a sum of isolated two body contributions which is also called pairwise additivity. FORCE is called in the subroutine STEP.

NOMENCLATURE :

Integers :

```

i           = counter
iloc       = counter for the execution of the local loop
irep       = counter for the execution of the general loop
j           = counter
jbeg       = counting parameter for neighbor atoms within "riist"
jend       = counting parameter for neighbor atoms within "riist"
jnab       = counter in "force" subroutine
list       = list of all neighbors
lnay       = how often neighbor routine is called
maxnab     = limiting number for the neighbor list
nij        = adding parameter for interactive neighbor atoms
nlist      = number of atoms within the "riist" radius
nloc       = # times local loop is executed
nmax       = number of particles in the simulation
nmol       = number of atoms
nnb        = neighbors
nrdeles    = counting parameter
point      = related to list (neighbor counting parameter)

```

Reals :

```

gr         = radial distribution function
fij        = force that atom i exerts on atom j
fm         = forces on the particle
fnb        = neighbor counting parameter
fxi,fyi,fzi = total forces on the particle
fyij,fyij,fzij = force that particle "i" exerts on "j"
rabi       = reciprocal absolute distance between two atoms
rabs       = absolute distance between two atoms
rcut       = radial distance in which forces are considered
rdel       = width of the spherical shell used in "veldist"

```

```

c*****
c      subroutine predict(dts, nmol, v, x)
c*****
c      calculate predicted values prior to force evaluation.
c
c      implicit none
c      integer nmax
c      parameter(nmax=865)
c      integer i, nmol
c      double precision dts, v(nmax, 3), x(nmax, 3)
c      double precision accx, accy, accz, bx, by, bz, cx, cy, cz, c1, c2, c3, c4
c      common /gear/ accx(nmax), accy(nmax), accz(nmax),
c      +          bx(nmax), by(nmax), bz(nmax),
c      +          cx(nmax), cy(nmax), cz(nmax)
c
c1 = dts
c2 = c1*dts/2.
c3 = c2*dts/3.
c4 = c3*dts/4.
c
c      Predicted values are obtained by expanding Taylor series.
c
do 100 i = 1, nmol
      x(i,1) = x(i,1)+c1*v(i,1)+c2*accx(i) + c3*bx(i) + c4*cx(i)
      x(i,2) = x(i,2)+c1*v(i,2)+c2*accy(i) + c3*by(i) + c4*cy(i)
      x(i,3) = x(i,3)+c1*v(i,3)+c2*accz(i) + c3*bz(i) + c4*cz(i)
      v(i,1) = v(i,1) + c1*accx(i) + c2*bx(i) + c3*cx(i)
      v(i,2) = v(i,2) + c1*accy(i) + c2*by(i) + c3*cy(i)
      v(i,3) = v(i,3) + c1*accz(i) + c2*bz(i) + c3*cz(i)
      accx(i) = accx(i) + c1*bx(i) + c2*cx(i)
      accy(i) = accy(i) + c1*by(i) + c2*cy(i)
      accz(i) = accz(i) + c1*bz(i) + c2*cz(i)
      bx(i) = bx(i) + c1*cx(i)
      by(i) = by(i) + c1*cy(i)
      bz(i) = bz(i) + c1*cz(i)
100 continue
      return
      end

```


rxj,ryj,rzj = position vectors
 rxij,ryij,rzij = distance between two atoms in x,y, and z
 rxo,ryo,rzo = dummy variable used in updating neighbor list
 sig = collision diameter (potential separation distance)
 sr2 = rabs²
 sr6 = rabs⁶
 ve = nondimensional velocity
 vij = nondimensional Lennard-Jones potential
 vli = length of the simulation box (m)
 vls = reciprocal nodimensional length of box
 wjj = nondimensional length of box
 wu = force that atom i exerts on atom j (nondimensional)
 = used in force routine

Logicals :
 update = used to decide updating the neighbor list

Now, the positions come from subroutine PREDICT. To calculate forces, one should find the distances between two atoms.

r1, r2, r3 are the x, y, z distances between two atoms respectively.

$$(r_{abs})_{ij} = \sqrt{r1^2 + r2^2 + r3^2}$$

To calculate the intermolecular forces we use Lennard-Jones (12,6) potential which is given by the expression below.

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

then the force that atom i exerts on j is =

$$df_{ij} = - \frac{d\phi_{ij}}{dr} = \frac{24\epsilon}{r_{abs}} \left[2 \left(\frac{\sigma}{r_{abs}} \right)^6 - 1 \right] \left(\frac{\sigma}{r_{abs}} \right)^6$$

x, y, z components of the force i exerts on j :

$$dfm(i,j,1) = df_{ij} \frac{r1}{(r_{abs})_{ij}}, \quad dfm(i,j,2) = df_{ij} \frac{r2}{(r_{abs})_{ij}},$$

$$dfm(i,j,3) = df_{ij} \frac{r3}{(r_{abs})_{ij}}$$

Calculate the total force on each particle:

$$fm(j,1) = \sum_{i=1}^{nmol} dfm(i,j,1), \quad fm(j,2) = \sum_{i=1}^{nmol} dfm(i,j,2),$$

$$fm(j,3) = \sum_{i=1}^{nmol} dfm(i,j,3)$$

$$\Rightarrow \text{total force on atom } j = \sqrt{fm(j,1)^2 + fm(j,2)^2 + fm(j,3)^2}$$

```

*****
subroutine force(fm,fnb,iloc,irep,irep,lnay,nloc,mmol,rcut,rlist
, sig, ve, vl, vls, wu, update, x)
+
*****
c subroutine FORCE is called to calculate the force on each
c molecule
implicit none
integer nmax, maxnab
parameter (nmax=865, maxnab=nmax*500)
integer iloc, irep, j, jbeg, jend, jnab, list, lnay, nlist, nloc,
+ nmol, point, nij (nmax*(nmax-1)/2), nrb (nmax)
double precision fm (nmax, 3), x (nmax, 3)
double precision fij, fnb, fxi, fxij, fyi, fyij, fzi, fzij, rcut,
+ rlist, rxi, rxij, rxo, ryi, ryij, ryo, rzi, rzij,
+ rzo, sig, sr2, sr6, ve, vij, vl, vli, wjj, wu
double precision vls, rabi, rabs

c RDF
integer ngofr, nrdels
double precision gr, rdel

common /block1/ rxo (nmax), ryo (nmax), rzo (nmax)
common /block2/ list (maxnab), point (nmax)
common /rdf/ gr (500), rdel
common /rdf2/ nrdels, ngofr (500)

logical update
vli = 1./vls

c zero the forces
do 10 i = 1, nmol
  fm(i,1) = 0.
  fm(i,2) = 0.
  fm(i,3) = 0.
10 continue

c Zero the virial, force, and neighbors
do 50 i = 1, nmol

```

```

50 nnb(i) = 0
    continue
    ve = 0.
    wu = 0.

c first of all we look at the result of subroutine CHECK. If the
c neighbor list needs to
c be updated we save the current configuration and reconstruct
c the neighbor list. to save the current configuration,
c subroutine SAVE is called
    if (update) then
        call save(fm,nmol,x)
        nlist = 0
        do 100 i = 1,nmol-1
            point(i) = nlist + 1
            rxi = x(i,1)
            ryi = x(i,2)
            rzi = x(i,3)
            fxi = fm(i,1)
            fyi = fm(i,2)
            fzi = fm(i,3)
        do 99 j = i+1,nmol
            rxij = rxi - x(j,1)
            ryij = ryi - x(j,2)
            rzij = rzi - x(j,3)
            rxij = rxij - dntint(rxij*vli)*vls
            ryij = ryij - dntint(ryij*vli)*vls
            rzij = rzij - dntint(rzij*vli)*vls
            rabs = dsqrt(rxij*rxij + ryij*ryij + rzij*rzij)
            rabi = 1/rabs
            if (rabs.lt.rlist) then
                nlist = nlist + 1
                list(nlist) = j
            if (mod(irep,lnay).eq.0).and.(mod(iloc,nloc).eq.0))then
                call log(fnb,nij,nlist,rxij,ryij,rzij)
                call shell(rxij,ryij,rzij)
                call raddist(irep,lnay,nmol,sig,vl)
            end if
            if (nlist.eq.maxnab) stop 'list too small'
            if (rabs.lt.rcut) then
                sr2 = rabi**2
                sr6 = sr2*sr2*sr2
                vij = 4*sr6*(sr6 - 1.)
                c Nondimensional potential
                wij = 48*sr6*(sr6 - 0.5)
                c Nondimensional force
                ve = ve + vij
                wu = wu + wij
                fij = wij*rabi**2
                fxij = rxij*fij
                fyi = ryij*fij
                fzij = rzij*fij
                fxi = fxi + fxij
                fyi = fyi + fyij
                fzi = fzi + fzij
                fm(j,1) = fm(j,1) - fxij
                fm(j,2) = fm(j,2) - fyi
                fm(j,3) = fm(j,3) - fzij
            end if
        end if
    99 continue
    100 continue
        point(nmol) = nlist + 1
    else
        c If neighbor list does not need to be updated, we don't SAVE
        c the current configuration. (But again We use predicted
        c positions) Then the same force calculations are done.
        nlist = 0
        do 200 i = 1,nmol-1
            jbeg = point(i)
            jend = point(i+1) - 1
            c check that atom i has neighbors
            if (jbeg.le.jend) then
                rxi = x(i,1)
                ryi = x(i,2)
                rzi = x(i,3)
                fxi = fm(i,1)

```

```

c      Calculate number of neighboring particles
c      -----
      if((mod(irep,lnay).eq.0).and.(mod(iloc,nloc).eq.0)) then
          do 987 i = 1,nmol-1
              do 988 jnab = point(i),point(i+1)-1
                  nlist = nlist + 1
                  j = list(jnab)
                  nnb(i) = nnb(i) + nij(nlist)
                  nnb(j) = nnb(j) + nij(nlist)
              988      continue
              987      continue
          do 986 i = 1,nmol
              write(99,178) nnb(i)
          986      continue
      end if
      178 format(i5)
      return
      end

```

4.6 Subroutine SAVE

Saves the current configuration for future checking. It is called in subroutine FORCE.

NOMENCLATURE

Integers :

- i = counter
- nmax = number of particles in the simulation
- nmol = number of atoms

Reals :

- fm = forces on the particle
- rxo,ryo,rzo = dummy variable used in updating neighbor list
- x,y,z = coordinate of position vector of particle

```

fyi = fm(i,2)
fzi = fm(i,3)
do 199 jnab = jbeg,jend
    j = list(jnab)
    nlist = nlist + 1
    rxij = rxi - x(j,1)
    ryij = ryi - x(j,2)
    rzij = rzi - x(j,3)
    rxij = rxij - dnint(rxij*vli)*vls
    ryij = ryij - dnint(ryij*vli)*vls
    rzij = rzij - dnint(rzij*vli)*vls
    rabs = dsqrt(rxij*rxij + ryij*ryij + rzij*rzij)
    rabi = 1/rabs
    if((mod(irep,lnay).eq.0).and.(mod(iloc,nloc).eq.0)) then
        call log(fnb,nij,nlist,rxij,ryij,rzij)
        call shell(rxij,ryij,rzij)
        call raddist(irep,lnay,nmol,sig,vl)
    end if
    if(rabs.lt.rcut) then
        sr2 = rabi**2
        sr6 = sr2*sr2*sr2
        vij = 4*sr6*(sr6 - 1.)
        wij = 48*sr6*(sr6 - 0.5)
        ve = ve + vij
        wu = wu + wij
        fij = wij*rabi**2
        fxi = rxij*fij
        fyi = ryij*fij
        fzij = rzij*fij
        fxi = fxi + fxi
        fyi = fyi + fyi
        fzi = fzi + fzij
        fm(j,1) = fm(j,1) - fxi
        fm(j,2) = fm(j,2) - fyi
        fm(j,3) = fm(j,3) - fzij
    end if
199      continue
    fm(i,1) = fxi
    fm(i,2) = fyi
    fm(i,3) = fzi
end if
wu = wu/3.
nlist = 0

```

```

c*****
c      subroutine save(fm,nmol,x)
c*****
c      implicit none
c      integer nmax

```

```

parameter (nmax=865)
integer i, nmol
double precision rxo, ryo, rzo
double precision fm(nmax,3), x(nmax,3)

common /block1/rxo(nmax), ryo(nmax), rzo(nmax)

do 100 i = 1, nmol
  rxo(i)=x(i,1)
  ryo(i)=x(i,2)
  rzo(i)=x(i,3)
100 continue

return
end

```

4.7 Subroutine LOG

LOG is called by FORCE to update the number of atoms in the neighbor list.

NOMENCLATURE

Integers :
 nij = adding parameter for interactive neighbor atoms
 nlist = number of atoms within the "rlist" radius
 nmax = number of particles in the simulation

Reals :
 fnb = neighbor counting parameter
 rij = absolute distance between atoms i and j
 rxdum, rydum, rzdum = distance between two atoms

```

c*****
c      subroutine log(fnb,nij,nlist,rxdum,rydum,rzdum)
c*****
implicit none
integer nmax
parameter (nmax=865)
integer nlist,nij(nmax*(nmax-1)/2)
double precision fnb,rij,rxdum,rydum,rzdum
rij = (rxdum*rxdum + rydum*rydum + rzdum*rzdum)**0.5
nij(nlist) = idint(dsign(1.0D0,fnb-rij)+1.1)/2

return
end

```

4.8 Subroutine SHELL

NOMENCLATURE

Integers :
 c nrdels = counting parameter
 c nshell = number of shells

Reals :
 gr = radial distribution function
 rdel = width of the spherical shell used in "veldist"
 rij = absolute distance between atoms i and j
 rxij,ryij,rzij = distance between two atoms in x, y, and z

```

c*****
c      subroutine shell(rxij,ryij,rzij)
c*****
implicit none
integer nrdels,nshell,ngofr
double precision gr,rdel,rij,rxij,ryij,rzij

common /rdf/ gr(500),rdel
common /rdf2/ nrdels,ngofr(500)

rij = (rxij*rxij + ryij*ryij + rzij*rzij)**0.5
nshell = rij/rdel + 0.5
ngofr(nshell) = ngofr(nshell) + 1

return
end

```

4.9 Subroutine CORRECTOR

After intermolecular forces are calculated, subroutine CORRECTOR is called to correct positions, velocities and higher order derivatives of the positions. These values are then used to update the configuration of molecules.

NOMENCLATURE

```

Integer i,nmol,iloc,irep
double precision dts,v(nmax,3),x(nmax,3)
double precision accx,accy,accz,alp0,alp1,alp2,alp3,alp4,
+ axi,ayi,azi,bx,by,bz,c1,c2,c3,c4,corr,
+ corrx,corry,corrz,cx,cy,cz,cb,cc,cex,cv,vls,
+ vs1,vs2,vs3
+ double precision fm(nmax,3)
common /gear/ accx(nmax),accy(nmax),accz(nmax),
+ bx(nmax),by(nmax),bz(nmax),
+ cx(nmax),cy(nmax),cz(nmax)
common /correct/ alp0,alp1,alp2,alp3,alp4

C Coefficients of corrector step
c1 = dts
c2 = c1*dts/2.
c3 = c2*dts/3.
c4 = c3*dts/4.

cex = alp0*c2
cv = alp1*c2/c1
cb = alp3*c2/c3
cc = alp4*c2/c4

do 200 i = 1,nmol

C Accelerations calculated from Newton' s second law.
axi = fm(i,1)
ayi = fm(i,2)
azi = fm(i,3)

C Corrector factor for Gear predictor - corrector algorithm.
corrx = axi - accx(i)
corry = ayi - accy(i)
corrz = azi - accz(i)

C Corrected values for positions.
x(i,1) = x(i,1) + cex*corrx
x(i,2) = x(i,2) + cex*corry
x(i,3) = x(i,3) + cex*corrz

C Corrected values for velocities.
v(i,1) = v(i,1) + cv*corrx
v(i,2) = v(i,2) + cv*corry
v(i,3) = v(i,3) + cv*corrz

C Total translation.
vs1=vs1+v(i,1)
vs2=vs2+v(i,2)
vs3=vs3+v(i,3)

accx(i) = axi
accy(i) = ayi

```

```

= counter
= counter for the execution of the local loop
= counter for the execution of the general loop
= number of particles in the simulation
= number of atoms

```

```

Reals :
accx,accy,accz
alp0,alp1,alp2,alp3,alp4
axi,ayi,azi
subroutine)
bx,by,bz
c1,c2,c3,c4
corr,corrx,corry,corrz

"force"
cx,cy,cz
cb
subroutine (alpha2)
cc
subroutine (alpha3)
cex
subroutine (alpha0)
cv
subroutine (alpha1)
dts
fm
v
vls
vs1,vs2,vs3

```

```

C*****
C subroutine corrector(dts,fn,nmol,v,vls,x,iloc,irep)
C*****
C calculate corrected values after force evaluation.
implicit none
integer nmax
parameter(nmax=865)

```

```

accz(i) = azi
c Corrected values for the third derivatives of the positions.
  bx(i) = bx(i) + cb*corrxx
  by(i) = by(i) + cb*corrxy
  bz(i) = bz(i) + cb*corrzz
c Corrected values for the fourth derivatives of the positions.
  cx(i) = cx(i) + cc*corrxx
  cy(i) = cy(i) + cc*corrxy
  cz(i) = cz(i) + cc*corrzz
call periodic(x(i,1),x(i,2),x(i,3),vls)
200 continue
c Total translation is gradually removed
do 280 i = 1,nmol
  v(i,1)=v(i,1)-vs1/nmol*0.01
  v(i,2)=v(i,2)-vs2/nmol*0.01
  v(i,3)=v(i,3)-vs3/nmol*0.01
280 continue
return
end

```

4.10 Subroutine PERIODIC

This subroutine applies periodic boundary conditions. It is called by both subroutines STEP and CORRECTOR.

NOMENCLATURE

Reals :
 vls = nondimensional length of box
 x,y,z = coordinate of position vector of particle

Periodic boundary conditions are applied under the following conditions:

1. If $x(i,j) < 0$ then $x(i,j) = x(i,j) + vl$
2. If $x(i,j) > vl$ then $x(i,j) = x(i,j) - vl$

```

c*****
c

```

```

subroutine periodic(x,y,z,vls)
c*****
c Apply pbc to particle in cubic box with the origin
c of the coordinate system being at (0,0,0). The length
c of the boundary is "vls" in dimensionless units.
implicit none
double precision vls,x,y,z
if(x.lt.0.0) then
  x = x + vls
elseif (x.gt.vls) then
  x = x - vls
end if
if(y.lt.0.0) then
  y = y + vls
elseif (y.gt.vls) then
  y = y - vls
end if
if(z.lt.0.0) then
  z = z + vls
elseif (z.gt.vls) then
  z = z - vls
end if
return
end

```

4.11 Subroutine AVG

AVG is used to calculate average potential and kinetic energy. It called in the main program after local loop is completed.

NOMENCLATURE

Integers :
 i = counter
 nmax = number of particles in the simulation
 nmol = number of atoms

Reals :
 enesum = average potential energy
 v = velocity of particle
 ve = nondimensional velocity

velsq = used to average kinetic energy
 virsum = used to average virial
 vsqsum = sum of kinetic energy over time
 wu = used in force routine

lnay
 nloc
 nmax
 nmol
 nrrels

= how often neighbor routine is called
 = # times local loop is executed
 = number of particles in the simulation
 = number of atoms
 = counting parameter

Reals :

bk = Stefan Boltzman constant (1.381e-23 J/K)
 denom = averaging parameter
 ek = average kinetic energy per atom per unit mass
 ekavg = average kinetic energy
 enesum = average potential energy
 epavg = average potential energy
 eps = minimum energy (8.27e-21 J)
 etot = average total energy
 gr = radial distribution function
 plr = long range pressure correction
 preavg = average pressure
 press = pressure
 radius = radial distance between two atoms
 rdel = width of the spherical shell used in "veldist"
 time = nondimensional time
 tmp = nondimensional absolute temperature
 tmpavg = average temperature
 ulr = long range potential energy correction
 ve = nondimensional velocity
 velsq = used to average kinetic energy
 virsum = used to average virial
 vls = nondimensional length of box
 vsqsum = sum of kinetic energy over time
 wm = mass of atom
 wu = used in force routine

Logicals :

lpo = controls position vector output
 lvo = controls velocity vector output

```

c*****
c      subroutine output(bk,enesum,eps,irep,kavg,lnay,lpo,lvo,
+      nloc,nmol,plr,sig,time,ulr,velsq,
+      vsqsum,v,ve,virsum,vls,wm,wu,x)
c*****

```

implicit none
 integer nmax

```

c*****
c      subroutine avg(enesum,nmol,velsq,vsqsum,v,ve,virsum,wu)
c*****
c      Average potential and kinetic energy are calculated by
c      subroutine AVG
c      implicit none
c      integer nmax
c      parameter (nmax=865)
c      integer i,nmol
c      double precision enesum,ve,velsq,vsqsum,virsum,wu
c      double precision v(nmax,3)
c      velsq = 0.
c      do 109 i = 1,nmol
c        velsq = velsq + v(i,1)**2. + v(i,2)**2. + v(i,3)**2.
c      109 continue
c      enesum = enesum + ve
c      virsum = virsum + wu
c      vsqsum = vsqsum + velsq
c      return
c      end

```

4.12 Subroutine OUTPUT

Positions, velocities, energies and average properties are output by this subroutine. it is called in the main program.

NOMENCLATURE

Integers :

i = counter
 irep = counter for the execution of the general loop
 j = counter
 kavg = how often averaging of properties is done

```

parameter (nmax=865)
integer i, irep, j, kavg, nloc, nmol, lnavy
integer nrdels, ngofr
double precision v(nmax,3), x(nmax,3)
double precision bk, denom, ek, ekavg, enesum, epot, epavg, eps,
+ etot, plr, preavg, press, sig, tmp, time,
+ tmpavg, ulr, ve, velsq, virsum, vsqsum,
+ vls, wv, wu
double precision gr, rdel, radius
logical lpo, lvo
common /rdf/ gr(500), rdel
common /rdf2/ nrdels, ngofr(500)
c instantaneous properties
ek = 0.5*velsq
epot = ve/nmol + ulr
etot = ek + epot
tmp = 2.*ek/(3.*nmol)
press = (wu + tmp*nmol)/vls**3 - plr*nmol*(1./vls)**3.
c average properties
denom = dfloat(irep/kavg)
ekavg = 0.5*vsqsum/denom
epavg = enesum/(denom*nmol) + ulr
tmpavg = 2.*ekavg/(3.*nmol)
preavg = (virsum/denom + tmpavg*nmol)/vls**3.
+ - plr*nmol*(1./vls)**3.
c
c-----
c OUTPUT POSITION (x) (13)
c-----
if(lpo)then
do 510 i = 1, nmol
write(13, '(3F8.3)') (x(i,j)*sig*1.0D10, j=1,3)
510 continue
endif
c-----
c OUTPUT VELOCITY (v) (14)
c-----
if(lvo)then
do 550 i = 1, nmol
write(27, '(3F10.3)') (v(i,j)/(wm/eps)**0.5, j=1,3)
550 continue
endif
c-----
c OUTPUT INSTANTANEOUS PROPERTIES (16)
c-----
write(16, '(F8.3,2x,F8.3,2x,f10.3,2x,f10.3,2x,f12.7)')
+ time*sig*(wm/eps)**0.5*1.0D12,

```

```

+ tmp, ek,
+ epot, press
c-----
c OUTPUT INSTANTANEOUS PROPERTIES (30)
c-----
write(30, '(F8.3,2x,F8.3,2x,f10.3,2x,f10.3,2x,f10.3,2x,f12.7)')
+ time*sig*(wm/eps)**0.5*1.0D12,
+ tmpavg, ekavg,
+ epavg, preavg
if (mod(irep,lnay).eq.0) then
do 800 j = 1, nrdels
radius = rdel*dfloat(j)
write(88,133) radius, gr(j)
800 continue
end if
133 format (f8.3,2x,f8.3)
return
end

```

4.13 Subroutine TEMCON

Subroutine TEMCON corrects the velocities with temperature. It is called by the main program.

$$V(i,j) = V(i,j) \sqrt{\frac{T_{ins}}{T_{mp}}} \text{ where}$$

$$T_{ins} = \frac{bk \cdot T_{ini}}{\epsilon}$$

This allows the system to equilibrate at a certain temperature which is initial temperature here.

NOMENCLATURE

Integers :

i = counter
irep = counter for the execution of the general loop
j = counter
nmax = number of particles in the simulation

nmol = number of atoms

Reals :

ek = average kinetic energy per atom per unit mass
st = temperature control scalar
tins = nondimensional temperature
tmp = nondimensional absolute temperature
v = velocity of particle

```
C*****  
C subroutine temcon(irep,nmol,tins,v)  
C*****  
implicit none  
integer nmax  
parameter(nmax=865)  
integer i,irep,j,nmol  
double precision ek,st,tins,tmp,v(nmax,3)
```

```
open (33,file='tempcon.dat')  
write (33,*) irep  
close (33)
```

ek = 0.

```
do 110 i = 1,nmol  
ek = ek+v(i,1)*v(i,1) + v(i,2)*v(i,2) + v(i,3)*v(i,3)  
110 continue
```

```
tmp = ek/(3.*nmol)  
st = dsqrt(tins/tmp)
```

```
do 120 i = 1,nmol  
do 120 j = 1,3  
v(i,j) = v(i,j)*st  
120 continue
```

```
return  
end
```

4.14 Subroutine PROF

Pressure and density profiles are calculated in this routine. It is called in the main program.

NOMENCLATURE

Integers :

i = counter
ij = counter
im = atom labeling parameter
irep = counter for the execution of the general loop
j = counter
jm = atom labeling parameter
k = parameter that places the atom in the correct radial increment or interval ("prof")
kk = counter
lsti = listvectors for interactions
lstj = listvectors for interactions
ndr = number of radial intervals ("prof")
nmax = number of particles in the simulation
nmol = number of atoms
nr1 = parameter which decides whether an atom is used in the calculation of the density profile

Reals :

bk = Stefan Boltzman constant (1.381e-23 J/K)
drp = size of the radial grid
dv = volume of the region ("prof")
epm = total potential energy
epm1 = half of epj
eps = minimum energy (8.27e-21 J)
fij = force that atom i exerts on atom j
fnb = neighbor counting parameter
fs = total force exerted on atom i per unit distance
fsij = force that atom i exerts on atom j per unit distance
pi = 3.1415927
pr = pressure
pr1 = parameter used to construct the pressure distribution
prb = pressure distribution
r1,r2,r3 = position of particle minus half the box length ("init")
rabs = distance between atom i and j ("prof")
rcut = positions atom i w.r.t center of control volume ("prof")
r1,r2,r3 = absolute distance between two atoms
rj1,rj2,rj3 = absolute position w.r.t center of control volume ("prof")
rij = radial distance in which forces are considered
rj1,rj2,rj3 = position of i molecule
rij = position of j molecule
rij = absolute distance between atoms i and j

```

do 912 kk = 1, nmol
  if (x(kk,1).lt.0.or.x(kk,2).lt.0.or.x(kk,3).lt.0.) then
    print *, irep, "hold it right here"
  end if
912 continue

vli = 1/vls
rp0 = 3.5D-10/sig
drp = .1

C-----POTENTIAL ENERGY AND PRESSURE
C-----
ep = 0.0
vi = 0.0
do 150 i = 1, nmol
  fs(i) = 0.0
  epm(i) = 0.0
150 continue
do 160 i = 1, ndr
  pr(i) = 0.0
  prb(i) = 0.0
  nr(i) = 0
160 continue
do 210 ij = 1, (nmol-1)*nmol/2
  im = lsti(ij)
  jm = lstj(ij)
C-----i-j DISTANCE
C-----
ri1 = x(im,1) - vls*0.5
ri2 = x(im,2) - vls*0.5
ri3 = x(im,3) - vls*0.5
rj1 = x(jm,1) - vls*0.5
rj2 = x(jm,2) - vls*0.5
rj3 = x(jm,3) - vls*0.5
riq = ri1*ri1 + ri2*ri2 + ri3*ri3
ri(ij) = dsqrt(riq)
rjq = rj1*rj1 + rj2*rj2 + rj3*rj3
rj(ij) = dsqrt(rjq)
r1 = x(im,1) - x(jm,1)
r2 = x(im,2) - x(jm,2)
r3 = x(im,3) - x(jm,3)
rijq(ij) = r1*r1 + r2*r2 + r3*r3
rij = dsqrt(rijq(ij))
r1 = r1 - dnint(ri*vli)*vls
r2 = r2 - dnint(r2*vli)*vls
r3 = r3 - dnint(r3*vli)*vls
rabs = dsqrt(r1*r1 + r2*r2 + r3*r3)

```

```

= absolute position of i,j molecules squared
= point on grid midway between rk1 and rk2
= first grid point before and after position "rk"
= radial position of the first grid
= rabs^(6)
= collision diameter (potential separation distance)
= volume at grid position
= adding parameter for interactive neighbor atoms
= parameter used to construct the pressure distribution
= nondimensional time
= initial temperature (K)
= nondimensional temperature
= parameter used in calculating pressure
= parameter used to construct the pressure distribution
= parameter used to construct the pressure distribution
= parameter used to construct the pressure distribution
= virial
= used to average virial
= length of the simulation box (m)
= reciprocal nodimensional length of box
= nondimensional length of box
= mass of atom

C-----
C-----
subroutine prof(bk, eps, fnb, irep, lpo, lvo, nmol, pi, rcut,
  sig, time, tini, tins, virsum, vl, vls, wm)
C-----
implicit none
integer nmax, ndr
parameter (nmax=865, ndr=110)
integer i, ij, im, irep, j, jm, k, kk, nmol, nr1
integer lsti(nmax*(nmax-1)/2), lstj(nmax*(nmax-1)/2),
  nr(ndr)
double precision epm(nmax), fij(nmax*(nmax-1)/2),
  epij(nmax*(nmax-1)/2), fsij(nmax*(nmax-1)/2),
  fs(nmax), pr(ndr), prb(ndr),
  ri(nmax*(nmax-1)/2), rj(nmax*(nmax-1)/2),
  rijq(nmax*(nmax-1)/2), v(nmax,3), x(nmax,3)
double precision bk, drp, dv, ep, epmi, eps, fnb,
  pi, pr1, r1, r2, r3, rabs, rcut, ri1, ri2, ri3, rij,
  riq, rj1, rj2, rj3, rjq, rk, rk1, rk2, rp0, sbr6,
  sig, sk, sl, sv1, sv2, time, tini, v0,
  v1, v2, vd, vd2, vi, vli, vlii, wm
double precision tins, virsum, vls
common /one/ lsti, lstj, v, x
logical lpo, lvo

```

```

260 continue
-----
C  OUTPUT PRESSURE AND NEAREST NEIGHBOR RESULTS
C  -----
do 310 k = 1, ndr
  rk = (rp0+drp*(k*1.0-0.5))*sig
  sk = 4*pi*rk*rk
  rk1 = (rp0+drp*(k-1))*sig
  rk2 = rk1 + drp*sig
  dv = 4*pi*(rk2**3-rk1**3)/3
  write(15, '(3D12.3,2x,f10.3)') rk,pr(k)*eps/(sk*rk),
+      prb(k)*eps/(sk*rk),
+      nr(k)*wm/dv
310 continue
-----
C  OUTPUT INDIVIDUAL PE and KE/atom
C  -----
do 520 ij = 1, (nmol-1)*nmol/2
  im = lsti(ij)
  jm = lstj(ij)
  epm1 = epij(ij)*0.5
  epm(im) = epm(im) + epm1
  epm(jm) = epm(jm) + epm1
520 continue
return
end

```

```

sbr6 = (1/rabs)**6
sl = dsign(0.5D0,vls*0.5-rabs)+0.5
epij(ij) = 4*(sbr6 - 1.0)*sbr6
ep = ep + epij(ij)*sl
sbr6 = (1/rij)**6
sl = dsign(0.5D0,vls*0.5-rij)+0.5
fij(ij) = 48*(sbr6-0.5)*sbr6*sl
fsij(ij) = dabs(fij(ij)/rij)

210 continue
-----
C  PRESSURE
C  -----
do 220 k = 1, ndr
  rk = rp0 + drp*(k*1.0-0.5)
  do 230 ij = 1, (nmol - 1)*nmol/2
    riq = ri(ij)*ri(ij)
    rjq = rj(ij)*rj(ij)
    v0 = (riq - rjq)/rijq(ij)
    vd2 = dmax1(0.0D0,v0+v0+1.0-2*(riq+rjq-2*rk*rk)/rijq(ij))
    vd = dsqrt(vd2)
    v1 = v0 - vd
    v2 = v0 + vd
    sv1 = dsign(0.5D0,1.0 - dabs(v1)) + 0.5
    sv2 = dsign(0.5D0,1.0 - dabs(v2)) + 0.5
    pr1 = 0.5*fij(ij)*vd*(sv1 + sv2)
    pr(k) = pr(k) + (dsign(0.5D0,-pr1)+0.5)*pr1
    prb(k) = prb(k) + (dsign(0.5D0, pr1)+0.5)*pr1
220 continue
230 continue

```

```

-----
C  DENSITY PROFILE
C  -----
do 250 i = 1, nmol
  r1 = x(i,1) - vls*0.5
  r2 = x(i,2) - vls*0.5
  r3 = x(i,3) - vls*0.5
  rabs = dsqrt(r1*r1 + r2*r2 + r3*r3)
  k = idint((rabs-rp0)/drp) + 1
  nr1=(dsign(1D0,rabs-rp0)+1)*(dsign(1D0,rp0+ndr*drp-rabs)+1)/4
  k = max(k,1)
  k = min(k,ndr)
  nr(k) = nr(k) + nr1
250 continue
do 260 i = 1, nmol-1
  do 260 j = i+1, nmol
    k = j-i-1
    ij = i+k*nmol - (1+k)*k/2b
    fs(i) = fs(i) + fsij(ij)
    fs(j) = fs(j) + fsij(ij)

```

5 DATA REDUCTION

Once thermal equilibrium had been reached at a desired temperature, the density profile throughout the drop could be calculated by determining the number of atoms, $N(r)$, in differential spherical shells of equal width, $\Delta r = 0.1 \sigma$, through the following equation

$$\rho(r) = \langle N(r) \rangle / v(r) \quad (5)$$

where $\langle \rangle$ denotes an ensemble average taken over the duration of the simulation for which thermal equilibrium exists. The shell volume $v(r)$, (A^3) is simply represented by:

$$v(r) = \frac{4\pi\Delta r}{3} (3r^2 + \Delta r^2/4) \quad (6)$$

where r denotes the midpoint of the shell as measured from the center of the drop. The center of the drop coincided with the center of the simulation box because the center of mass of the drop was recalculated at each time step to compensate for any bulk motion of the drop. A regression analysis was then performed (Thompson *et al*, 1984) to fit the density data with the commonly used hyperbolic tangent function such that

$$\rho(r) = \frac{1}{2}(\rho_\ell + \rho_v) - \frac{1}{2}(\rho_\ell - \rho_v) \tanh \left[\frac{2(r - r_0)}{d_s} \right] \quad (7)$$

where ρ_ℓ , (kg/m^3) and ρ_v , (kg/m^3) are the local liquid density at the center of the drop and the local vapor density at the boundary of the container, respectively and r_0 (A) is a coefficient designating estimate of the drop radius. The parameter d_s is a measure of the thickness of the surface layer about the equimolar plane at $r = r_0$.

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