

# Computational Physics (PHYS6350)

Lecture 12: Classical molecular dynamics

$$m\ddot{\mathbf{r}}_{\mathbf{i}} = -\sum_{j} \nabla_{i} V_{\mathsf{LJ}}^{ij} (|\mathbf{r}_{\mathbf{i}} - \mathbf{r}_{\mathbf{j}}|)$$

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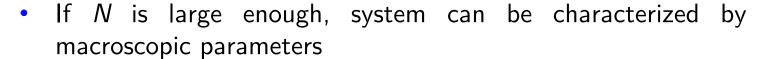
**Course materials:** <a href="https://github.com/vlvovch/PHYS6350-ComputationalPhysics">https://github.com/vlvovch/PHYS6350-ComputationalPhysics</a>

# Molecular dynamics (MD)

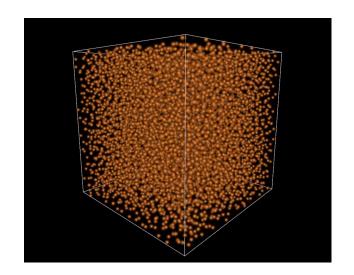
- System of N particles with a pair potential
- Newton's equations of motion (classical N-body problem)

$$m\ddot{\mathbf{r}}_{\mathbf{i}} = -\sum_{j} \nabla_{i} V_{\mathsf{LJ}}^{ij} (|\mathbf{r}_{\mathbf{i}} - \mathbf{r}_{\mathbf{j}}|)$$

- Box simulation
  - Periodic boundary conditions
  - Minimum-image convention



- Energy-Volume-Number (UVN), microcanonical ensemble
- Temperature-Volume-Number (TVN), canonical ensemble
- MD simulations give access to the equation of state



## Molecular dynamics equations

Have to solve Newton's equation of motion

$$m_i \ddot{\mathbf{r}}_i = -\sum_{j \neq i} \nabla_i V(\mathbf{r}_i, \mathbf{r}_j)$$

- Desired properties
  - Stability (long simulations)
  - Energy conservation
  - Time-reversibility
- Rewrite as system of first-order ODEs

$$\dot{\mathbf{r}}_i = \mathbf{v}_i, \ \dot{\mathbf{v}}_i = -(m_i)^{-1} \sum_{j \neq i} \nabla_i V(\mathbf{r}_i, \mathbf{r}_j),$$

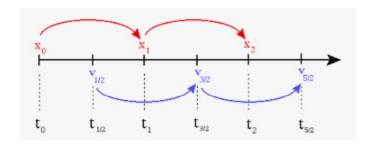
and use the leapfrog method

## **Velocity Verlet method**

We have system of equations

$$\frac{dx}{dt} = v,$$

$$\frac{dv}{dt} = f(x, t).$$



If we apply the leapfrog scheme to this system of equations, it will look like

$$x(t+h) = x(t) + hv(t+h/2),$$
  
$$v(t+3h/2) = v(t+h/2) + hf[x(t+h), t+h)],$$

i.e. the coordinates are evaluated at full steps using velocity estimates at half-steps, and vice versa. One sees that we need to keep track of coordinates at full steps only, not at half-steps. Leapfrog method here is called **Velocity Verlet method**.

### **Velocity Verlet:**

$$v(t + h/2) = v(t) + \frac{h}{2}f[x(t), t],$$
  

$$x(t + h) = x(t) + hv(t + h/2),$$
  

$$v(t + h) = v(t + h/2) + \frac{h}{2}f[x(t + h), t + h)].$$

## **Velocity Verlet method**

$$\dot{\mathbf{r}}_i = \mathbf{v}_i, \ \dot{\mathbf{v}}_i = -(m_i)^{-1} \sum_{j \neq i} \nabla_i V(\mathbf{r}_i, \mathbf{r}_j),$$

```
# Apply the velocity verlet time step
# Returns the tuple of new positions, velocities, accelerations (forces), potential energy and pressure
def velocity verlet(positions, velocities, accelerations,
                    time step, potential, potential gradient):
    # Update positions
    positions += velocities*time step + 0.5*accelerations*time step**2
    positions = positions - box length*np.floor(positions/box length)
    # Update velocities
    velocities half = velocities + 0.5*accelerations*time step
    # Compute new forces and potential energy
    accelerations, potential energy, pressure = compute forces(accelerations, positions, potential, potential gradient)
    # Update velocities using new accelerations
    velocities = velocities half + 0.5*accelerations*time step
    # Add ideal gas contribution to the pressure
    kinetic temperature = compute kinetic temperature(velocities)
    pressure += density * kinetic temperature
    return positions, velocities, accelerations, potential energy, pressure
```

### **Forces**

We will assume all masses are equal to unity,  $m_{\rm i}=1$  (dimensionless time) and that the pair potential depends on the distance only. Then

$$\ddot{\mathbf{r}}_i = -\sum_{j\neq i} \frac{dV(r_{ij})}{dr_{ij}} \frac{\mathbf{r}_i - \mathbf{r}_j}{r_{ij}}$$
.

```
# Computes forces for a given vector of positions, interaction potential and its gradient
# Return a tuple: positions, total potential energy, and the virial part of the pressure
def compute forces(forces, positions, potential, potential gradient):
    # forces = np.zeros like(positions)
    forces.fill(0.)
    potential energy = 0.0
    virial = 0.0
    for i in range(n particles):
        for j in range(i+1, n_particles):
            # Vector of relative distance
            r ij = positions[i] - positions[j]
            # Periodic boundary conditions (minimum-image convention)
            r_ij = r_ij - box_length*np.round(r_ij/box_length)
            r sq = np.sum(r ij**2)
            f ij = -potential gradient(r sq) * r ij
            forces[i] += f ij
            forces[i] -= f ii
            potential energy += potential(r sq)
            virial += np.dot(f_ij, r_ij)
    virial = virial/(3.0*box length**3)
    return forces, potential energy, virial
```

### **Example: Lennard-Jones fluid**

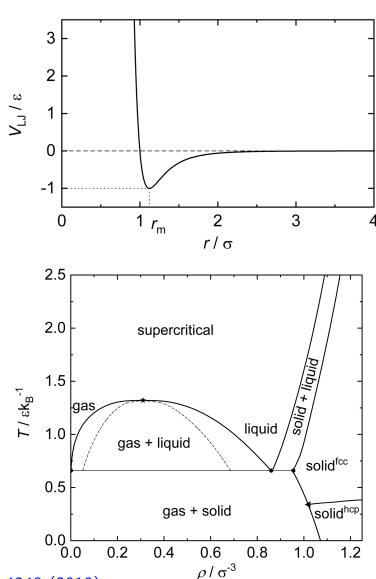
$$V_{
m LJ}(r) = 4arepsilon \left[ \left(rac{\sigma}{r}
ight)^{12} - \left(rac{\sigma}{r}
ight)^{6}
ight]$$

#### Reduced variables:

$$\tilde{r} = r/\sigma$$
  $\tilde{T} = T/(k_B \varepsilon)$   $\tilde{n} = n\sigma^3$ 

### Properties:

- Multiple phase transitions, including critical point
- Cannot be solved analytically
- Tractable with molecular dynamics simulations



## **Example: Lennard-Jones fluid**

$$\ddot{\mathbf{r}}_i = -\sum_{j\neq i} \frac{dV(r_{ij})}{dr_{ij}} \frac{\mathbf{r}_i - \mathbf{r}_j}{r_{ij}}$$
.

```
# Lennard-Jones potential as a function of squared distance
def lj_potential(r_sq):
    r6 = r_sq**3
    r12 = r6**2
    return 4.0*(1./r12 - 1./r6)

# The grandient term dV/dr / r in the rhs of Newton's equations
# for the LJ potential
def lj_potential_gradient(r_sq):
    r6 = r_sq**3
    r12 = r6**2
    return -24.0*(2./r12 - 1./r6) / r_sq
```

Both the potential and the gradient term can be expressed in terms of  $|\mathbf{r}_i-\mathbf{r}_j|^2$ , saves the unnecessary computation of the square root

### Simulation: Initial conditions

We have to initialize the system with initial positions and velocities

- Coordinates
  - Put particles in a grid
  - Avoids particle overlap (mind the  $r^{12}$  term)

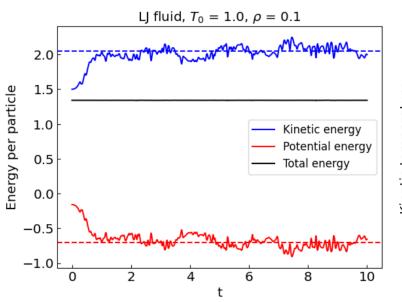
- Velocities
  - Sample each component from Gaussian (Maxwell-Bolztmann) distribution

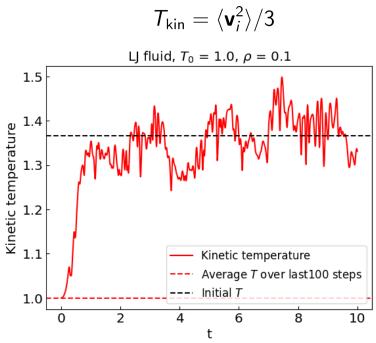
```
positions = initial_positions()
velocities = np.random.normal(loc=0.0, scale=np.sqrt(temperature0), size=(n particles, 3))
```

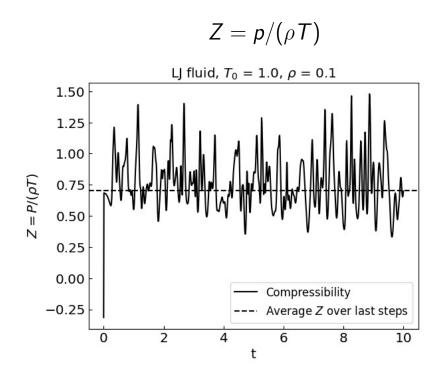
```
def initial_positions():
    ret = np.zeros((n_particles,3))
    Nsingle = np.ceil(n_particles**(1/3.))
    dL = box_length / Nsingle
    for i in range(n_particles):
        ix = i % Nsingle
        iy = (np.trunc(i / Nsingle)) % Nsingle
        iz = np.trunc(i / (Nsingle * Nsingle))
        ret[i][0] = (ix + 0.5) * dL;
        ret[i][1] = (iy + 0.5) * dL;
        ret[i][2] = (iz + 0.5) * dL;
    return ret
```

### **Simulation**

$$T = 1$$
,  $\rho = 0.1$ ,  $N = 64$ 







Kinetic temperature drifts away from initial value!

Reason: system takes time to equilibrate, and temperature is not conserved in microcanonical ensemble

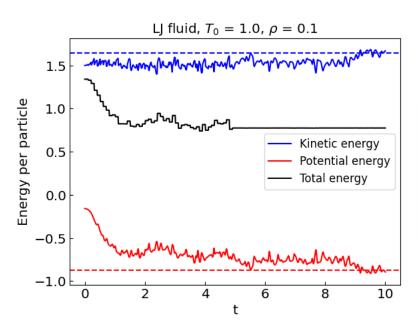
## Simulation: Keep the temperature fixed

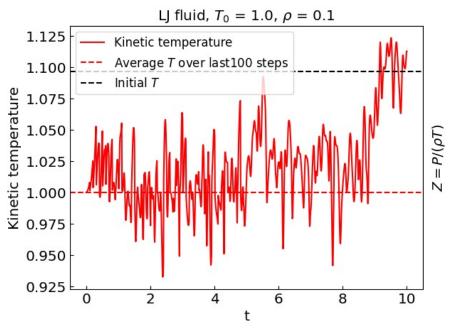
Keep the temperature fixed during the equilibration phase by preioducally rescaling the velocities to have desired temperature

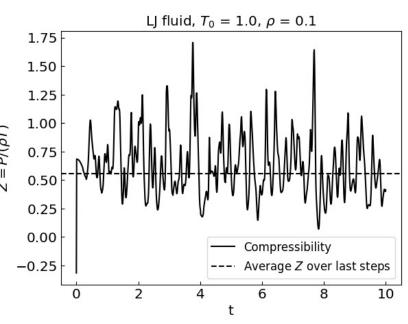
$$T = 1$$
,  $\rho = 0.1$ ,  $N = 64$ 

$$T_{\rm kin} = \langle {\bf v}_i^2 \rangle / 3$$

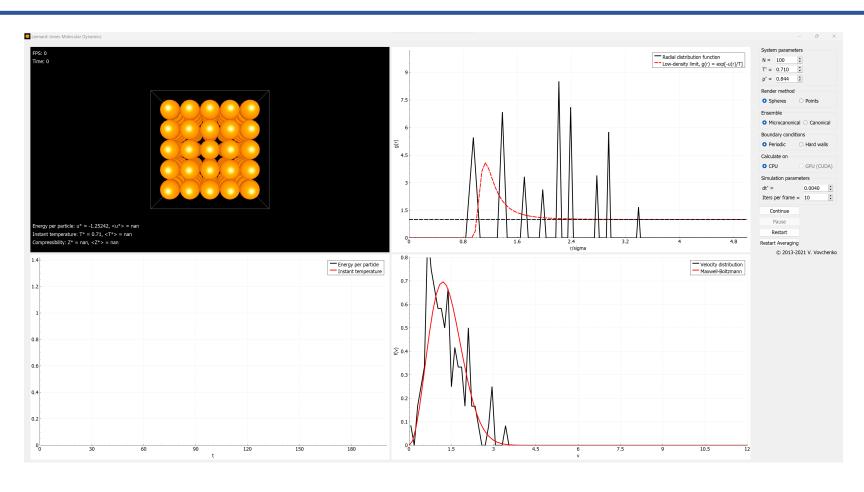
$$Z = p/(\rho T)$$







## Lennard-Jones fluid: C++/GPU implementation



### Implementation:

Velocity Verlet integration scheme implemented on CUDA-GPU (x100-200 speed-up\*)

open source: <a href="https://github.com/vlvovch/lennard-jones-cuda">https://github.com/vlvovch/lennard-jones-cuda</a>

