Imperial College London



A Tutorial of Boiling Simulation using Coupled Molecular Dynamics and Computational Fluid Dynamics

Royal Society-DFID Africa Capacity Building Initiative 19th July Edward Smith



- Introductions to Computational Fluid Dynamics (CFD)
 - Assumptions and modelling paradigm
 - Introduction to numerical solutions
- Hands on 1
- Introductions to Molecular Dynamics (MD)
 - Assumptions and modelling paradigm
 - Introduction to numerical solutions
- Coupled Simulation
- Hands on 2

Slides and hands-on code at edwardsmith.co.uk/content/RS-DFID.zip



MOLECULAR DYNAMICS



Molecular Dynamics

Discrete molecules in continuous space

- Molecular position evolves continuously in time
- Position and velocity from acceleration

$$egin{aligned} \dot{m{r}}_i &
ightarrow \dot{m{r}}_i \ \dot{m{r}}_i &
ightarrow m{r}_i(t) \end{aligned}$$

Acceleration obtained from forces

- Governed by Newton's law for an N-body system
- · Point particles with pairwise interactions only

$$m_i \ddot{\boldsymbol{r}}_i = \mathbf{F}_i = \sum_{i \neq j}^N \boldsymbol{f}_{ij} \qquad \quad \Phi(r_{ij}) = 4\epsilon \left[\left(\frac{\ell}{r_{ij}} \right)^{12} - \left(\frac{\ell}{r_{ij}} \right)^6 \right]$$





Molecular Dynamics





Structure of Molecules

The MD models the evolving structure of the molecular lattice



Radial Distribution Function (RDF)



MD Computing

- Force Calculation
 - All pairs simulation uses local cell and neighbour lists to reduce the N² calculation to order N





• Move particles (leapfrog in time)

$$m_i \frac{dv_i}{dt} \approx m_i \frac{v_i(t + \Delta t/2) - v_i(t - \Delta t/2)}{\Delta t} = F_i$$
$$\frac{dr_i}{dt} \approx \frac{r_i(t + \Delta t) - r_i(t)}{\Delta t}$$

MD Computing – Parallel optimisations



Localisations lends itself to parallel computing using MPI

- Spatial decomposition employed as in CFD
- Halo cells (ghost molecules) are used to link adjacent regions



Halo exchange of variable amounts of data

- MPI_Send
- MPI_Probe and MPI_Recv



 $\dot{\psi} = \frac{1}{Q} \left[T - 3T_{target} \right]$

- Non Equilibrium Molecular Dynamics (NEMD) is the study of cases beyond thermodynamic equilibrium, with:
 - Temperature gradients
 - Flow of fluid (e.g. Couette or Poiseuille flow)
- We induce temperature gradients and flows
 - Thermostats (e.g. Nosé Hoover) $m_i \ddot{r}_i = F_i + F_i^{teth} \psi m_i c_i$
 - Remove heat from system
 - Tethered molecules
 - (An)harmonic spring to tether site
 - With sliding
 - Slide site and (optionally) molecules

$$oldsymbol{c}_i=\dot{oldsymbol{r}}_i-oldsymbol{u}$$

Hand-On Session

- Minimal MD solver for two molecules
 - » Includes LJ force

ules
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 $m_i \ddot{\boldsymbol{r}}_i = \mathbf{F}_i = \sum_{i \neq j}^N \boldsymbol{f}_{ij} = \sum_{i \neq j}^N \boldsymbol{\nabla} \phi_{ij}$

» Time integrations
$$m_i \frac{dv_i}{dt} \approx m_i \frac{v_i(t + \Delta t/2) - v_i(t - \Delta t/2)}{\Delta t} = F_i$$

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MATLAB code

end

for n = 1:Nsteps %Calculate forces [a,U] = Force_calculation(ri,rj,rc);

%Update molecular positions using leapfrog [ri,rj,vi,vj] = Leapfrog_int(ri,rj,vi,vj,a,delta_t);

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Molecular Dynamics – Complex Walls and Fluids

Liquid structure causes viscosity

Stick-slip near walls







Molecules of arbitrary complexity



Oil, water and textured surface



Molecular Dynamics – Shocks and Multi-Phase





Molecular Dynamics - Averaging

Refine

 0000

• Density in a cell

$$\rho = \frac{1}{V} \sum_{i=1}^{N} \langle m_i \rangle$$

Momentum in a cell

$$\rho \boldsymbol{u} = \frac{1}{V} \sum_{i=1}^{N} \langle m_i \boldsymbol{v}_i \rangle$$

Temperature in a cell

$$T = \frac{1}{3N} \sum_{i=1}^{N} \langle \boldsymbol{v}_i^2 \rangle$$

Work with David Heyes, Daniele Dini and Tamer Zaki



Pressure (stress) in an MD Simulation

- Pressure definition in a dense molecular system
 - Kinetic part due to fluctuations
 - Configurational part due to liquid structure



Work with David Heyes and Daniele Dini



Viscosity

Good agreement with experiments



Work with Billy Todd and Peter Daivis



Fourier's law of heat conduction

Good agreement with experiments



Work with Omar Matar, Richard Craster and Erich Muller



Results for Surface Tension

Good agreement with experiments



Work with Carlos Braga and Serrafim Kalliadasis



Results for Density





Nucleation



Isosurface of Density







Molecular Dynamics Summary

- Solving just Newton's law
 - Energy is automatically conserved \rightarrow total = kinetic + potential



- Can model complex molecules, water, polymers, biomolecules
- Pressure, viscosity, heat flux and surface tension do not need to be specified and, are in fact, all outputs of the simulation
- Solid-liquid surface constructed with molecular roughness
- Phase change (evaporation, condensation) occur with no additional models needed

* www.nd.edu/~gtryggva/MultiphaseDNS/

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Atomify at github.com/lammps/lammps-web

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COUPLING

Coupling Overview









Table Lookup or Coefficients

MD parameter study stored in table and CFD uses data

Embedded Models (HMM)

MD – embedded in a CFD simulation ¹⁾

Domain Decomposition

MD –CFD linked along an interface ²⁾

1) Ren (2007), E et al (2003), Borg et al (2013) 2) O'Connell and Thompson (1995), Flekkøy at al (2000), Nie et al (2004), Hadjiconstantinou et al (1999), Delgado-Buscalioni & Coveney, (2003), Mohamed & Mohamad, (2009)

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Coupled Simulation

Assumes a continuous field

$$\frac{\partial}{\partial t}\rho \boldsymbol{u} + \boldsymbol{\nabla} \cdot \rho \boldsymbol{u} \boldsymbol{u} = -\boldsymbol{\nabla} P + \mu \nabla^2 \boldsymbol{u}$$

• Discrete molecules

 $m_i \ddot{\boldsymbol{r}}_i = \mathbf{F}_i$ for all i in N



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Coupled Simulation



O'Connell Thompson (1995), Hadjiconstantinou (1998), Flekkoy (2000), Nie et al (2004).



Coupled Simulation Software





Coupling Results – Couette Flow





Coupling Results – Couette Flow





Coupling Results – Couette Flow





Coupling Results – Polymer Brushes





Coupled Simulation of Boiling

- Bubble nucleation occurs naturally in MD
- Density and velocity set CFD boundary conditions
- Flow in CFD carries bubble away





Hand-On Coupled Simulation





Hand-On Coupled Simulation





Hand-On Coupled Simulation



Hand-On Session

- Minimal MD solver for two molecules
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» Time integrations

 MD simulation of nucleation saved as csv data to pass to Tryggvason* CFD

» Density
$$\rho = \frac{1}{V} \sum_{i \in cell}^{N} m_i$$

» Velocity $u^{BC} = \sum_{i \in cell} v_i$

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 $\frac{dr_i}{dt_i} \approx \frac{r_i(t + \Delta t) - r_i(t)}{dt_i}$



 $\Phi(r_{ij}) = 4\epsilon \left[\left(\frac{\ell}{r_{ij}} \right)^{12} - \left(\frac{\ell}{r_{ij}} \right)^6 \right]$

 $m_i \ddot{\boldsymbol{r}}_i = \mathbf{F}_i = \sum_{i \neq j}^N \boldsymbol{f}_{ij} = \sum_{i \neq j}^N \boldsymbol{\nabla} \phi_{ij}$





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- CPL library developed under a dCSE and eCSE computing grant and used for EPSRC grant EP/P010393/1
- A recent EPSRC grant EP/S019545/1 aims to apply this technique to smart surfaces for boiling

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