

# Direct Coupling of Computational Fluid Dynamics and Molecular Dynamics: Conservation, Computation and Timesteps

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David Trevelyan, Eduardo Fernando-Ramos,  
Omar Matar, Erich Muller and Richard Craster

## Overview

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- Introduction to Molecular Dynamics, Continuum Fluid Dynamics and Coupling
- Some Work on the Derivation of a Conservative Coupling Schemes
- Coupling Software Development

# Computational Fluid Dynamics

- Assumed continuous at every point in space
  - Mass Conservation

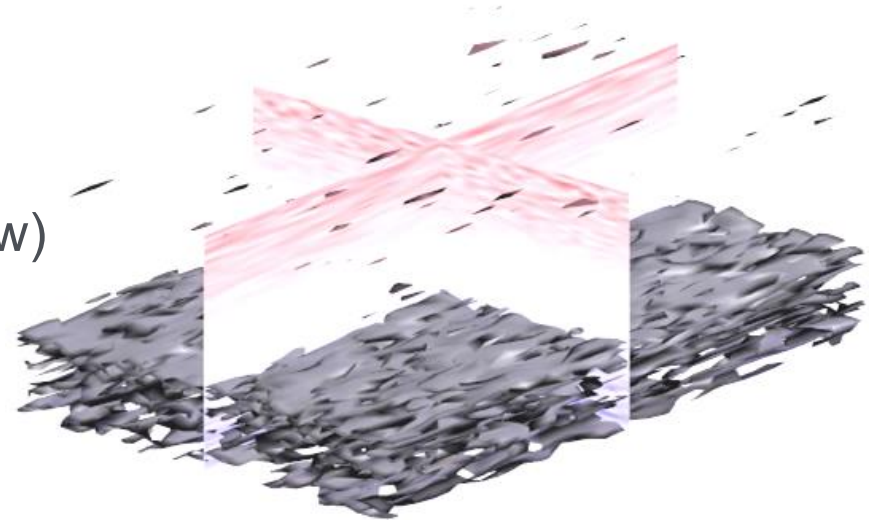
$$\frac{\partial \rho}{\partial t} = -\nabla \cdot \rho \mathbf{u}$$

- Momentum Balance (Newton's Law)

$$\frac{\partial}{\partial t} \rho \mathbf{u} + \nabla \cdot \rho \mathbf{u} \mathbf{u} = \nabla \cdot \mathbf{\Pi}$$

- Energy Conservation

$$\frac{\partial}{\partial t} \rho \mathcal{E} dV = -\nabla \cdot [\rho \mathcal{E} \mathbf{u} + \mathbf{\Pi} \cdot \mathbf{u} + \mathbf{q}]$$



Direct Numerical Simulation of  
Turbulent Couette Flow

# Computational Fluid Dynamics

- The Navier-Stokes Equation

$$\frac{\partial}{\partial t} \rho \mathbf{u} + \nabla \cdot \rho \mathbf{u} \mathbf{u} = -\nabla \cdot \Pi$$

$$\Pi = P\mathbf{I} - \mu \nabla \mathbf{u}$$

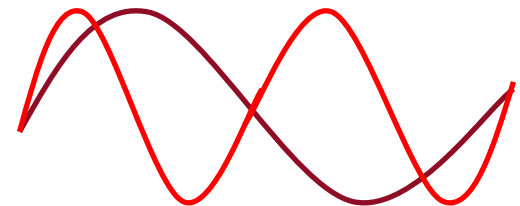
- Finite Difference Method

$$\frac{\partial u_i}{\partial x} \approx \frac{u_{i+1} - u_{i-1}}{\Delta x}$$



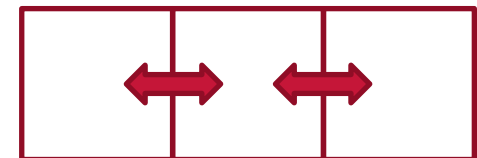
- Spectral Methods

$$u(x) = \sum_{n=1}^{X-1} \tilde{u}_n \bar{T}_n(y) e^{2\pi i(k_x x/L_x + k_z z/L_z)}$$



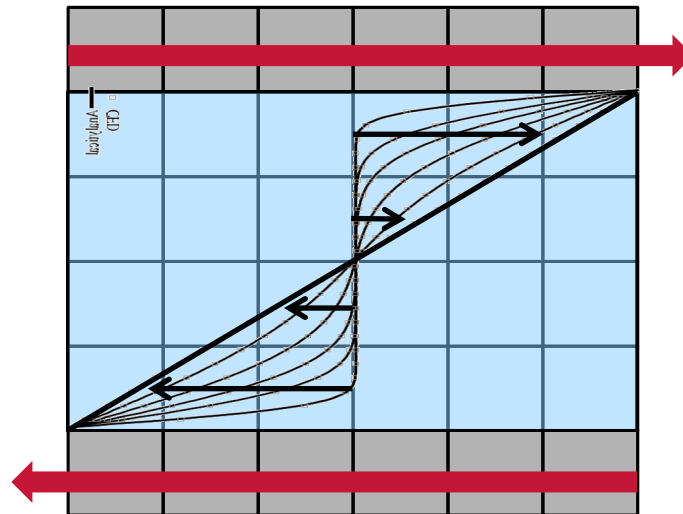
- Finite Volume (0<sup>th</sup> order element) Method

$$\frac{\partial}{\partial t} \int_V \rho \mathbf{u} dV = - \oint_S \rho \mathbf{u} \mathbf{u} \cdot d\mathbf{S} - \oint_S \Pi \cdot d\mathbf{S}$$



## Computational Fluid Dynamics

- Domain split into a number of volumes
  - Solved at every point in space before next time step
  - Boundary conditions must be specified



- Wall driven or Couette flow
  - Two infinite plates with fluid in between
  - A good model for many industrial cases of interest

## Computational Fluid Dynamics

- The Incompressible Navier-Stokes Equation

$$\frac{\partial}{\partial t} \rho \mathbf{u} + \nabla \cdot \rho \mathbf{u} \mathbf{u} = -\nabla P + \mu \nabla^2 \mathbf{u} \quad \nabla \cdot \mathbf{u} = 0$$

- Non dimensional form

$$\frac{\partial}{\partial t} \mathbf{u} + \mathbf{u} \cdot \nabla \mathbf{u} = -\nabla P + \frac{1}{Re} \nabla^2 \mathbf{u} \quad Re = \frac{\rho U L}{\mu}$$

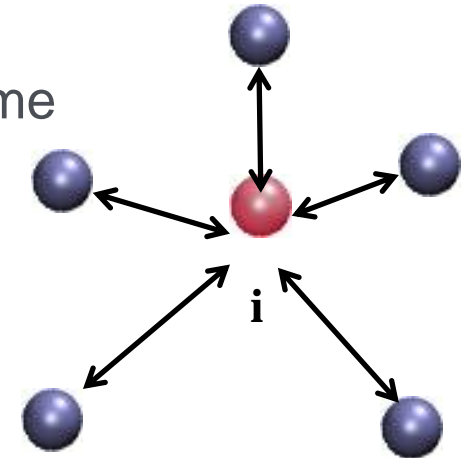
- Reynolds number
  - Scaling argument applied to any scale
- Is there a minimum?
  - Travis et al (1997) single phase valid down to nanometers
  - Theodorakis, Muller, Craster & Matar (2015) not in droplets
  - Local thermodynamic equilibrium vs. hydrodynamic scales
  - Knudsen Number

# Molecular Dynamics

## Discrete molecules in continuous space

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

$$\begin{aligned}\ddot{\mathbf{r}}_i &\rightarrow \dot{\mathbf{r}}_i \\ \dot{\mathbf{r}}_i &\rightarrow \mathbf{r}_i(t)\end{aligned}$$

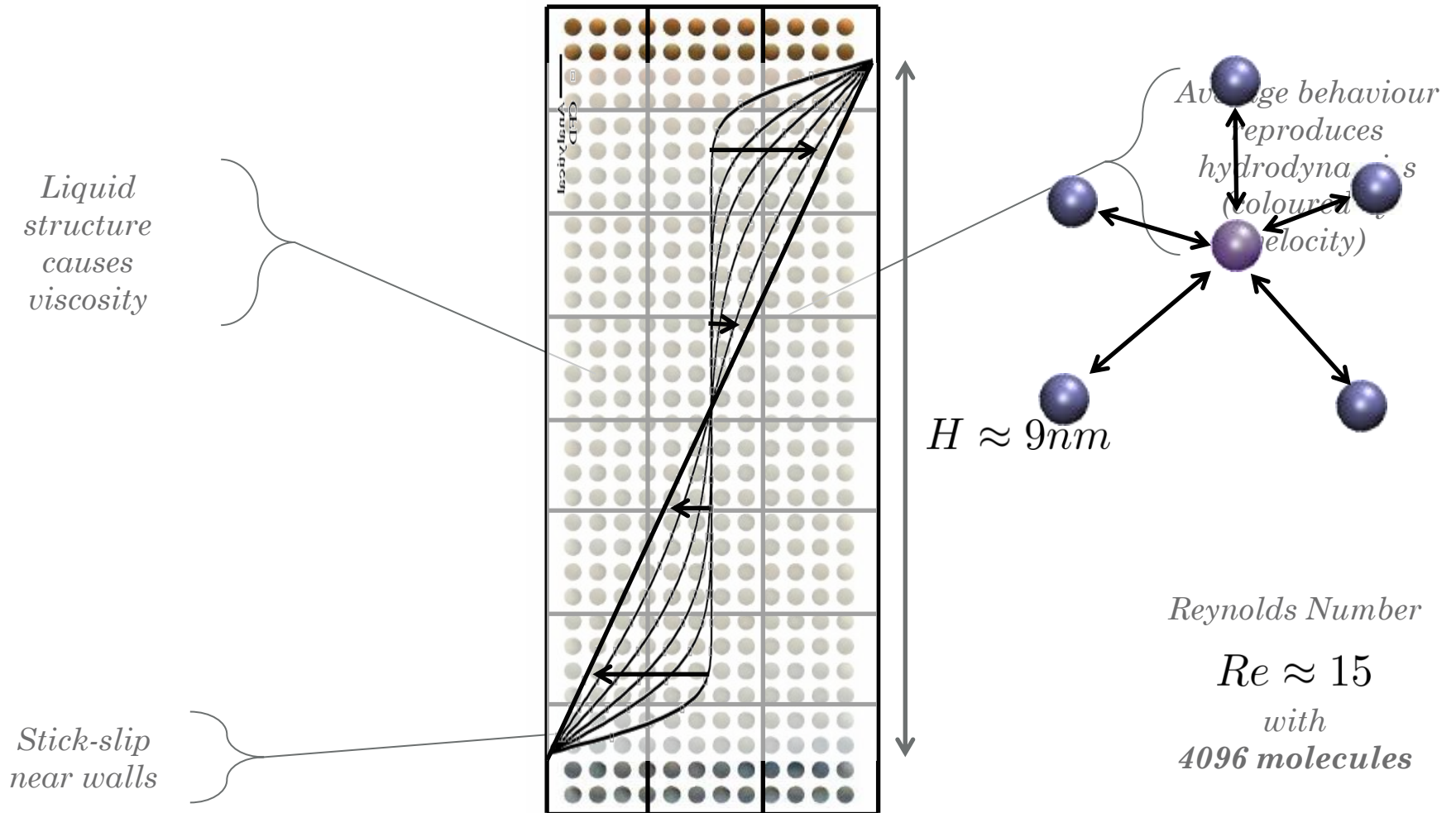


## Acceleration obtained from forces

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

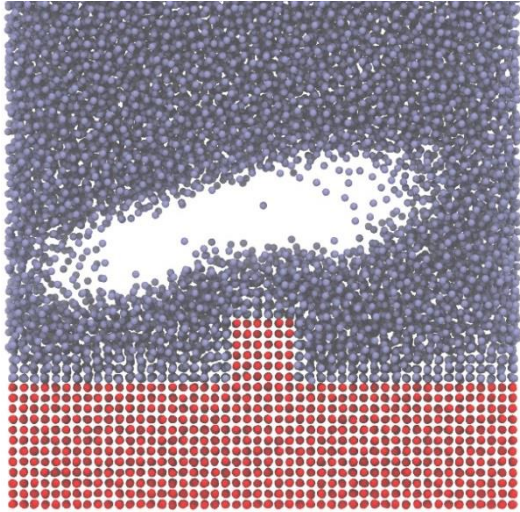
$$m_i \ddot{\mathbf{r}}_i = \mathbf{F}_i = \sum_{i \neq j}^N \mathbf{f}_{ij} \quad \Phi(r_{ij}) = 4\epsilon \left[ \left( \frac{\ell}{r_{ij}} \right)^{12} - \left( \frac{\ell}{r_{ij}} \right)^6 \right]$$

# Molecular Dynamics

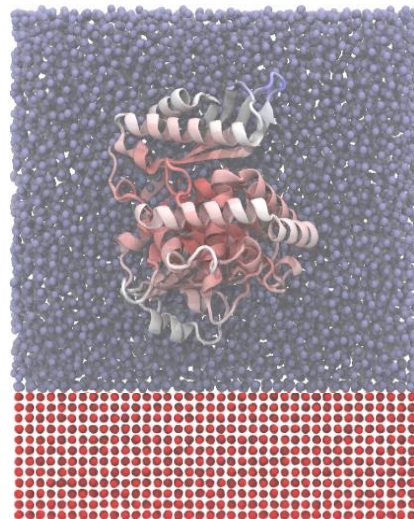
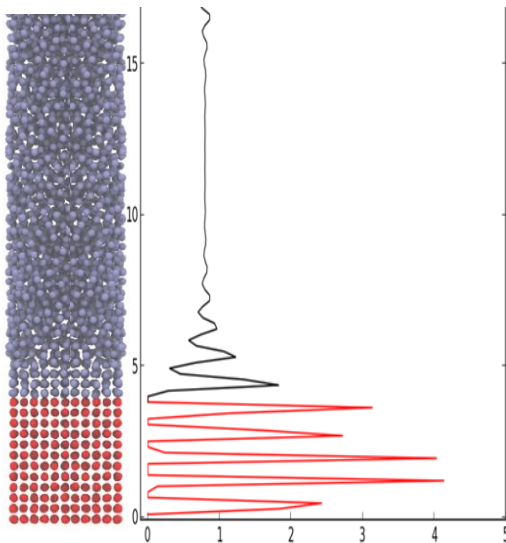
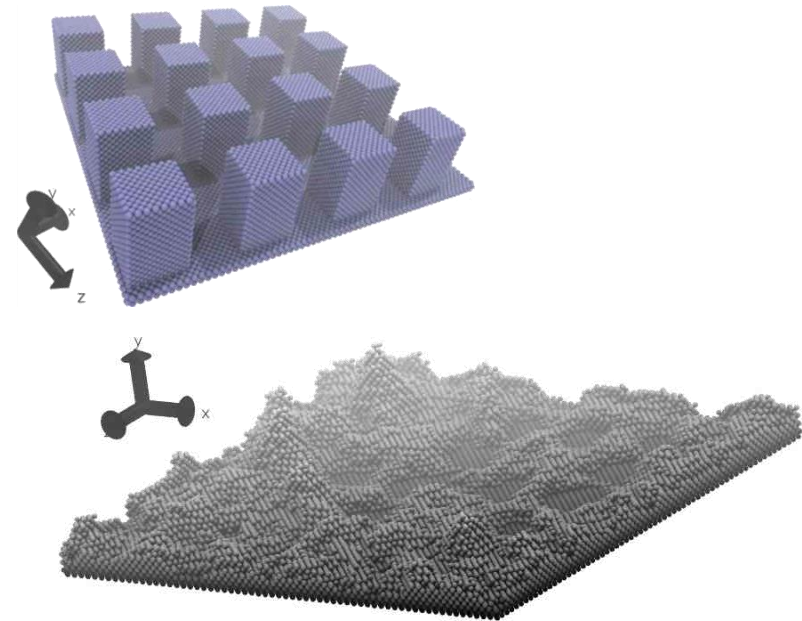
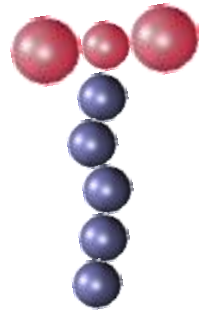




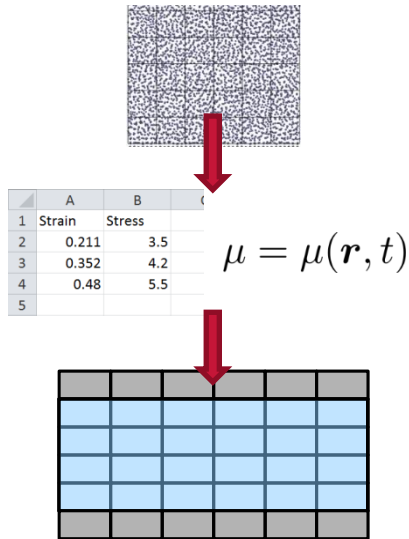
# Molecular Dynamics



*Superspreading  
Surfactant, e.g.  
Silwet-L77*

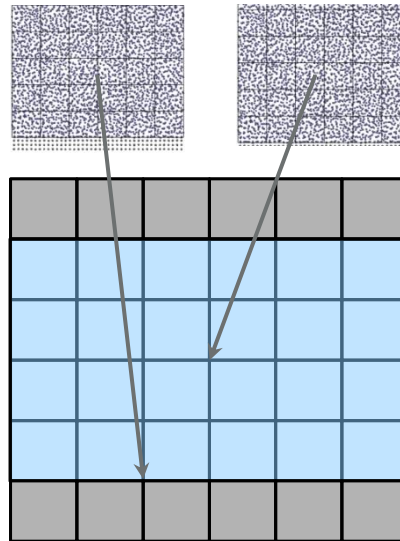


# Coupling Overview



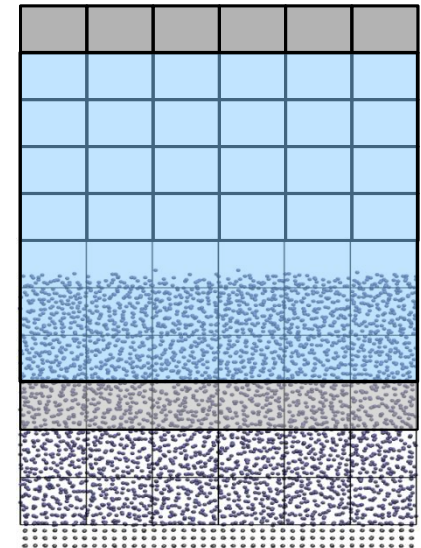
## Table Lookup or Coefficients

MD parameter study stored in table and CFD uses data



## Embedded Models (HMM)

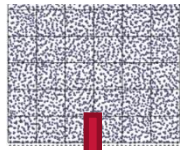
MD – embedded in a CFD simulation



## Domain Decomposition

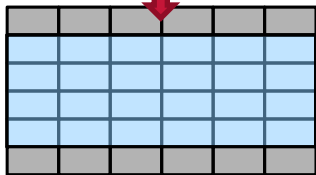
MD –CFD linked along an interface

# Coupling Assumptions



	A	B	C
1	Strain	Stress	
2	0.211	3.5	
3	0.352	4.2	
4	0.48	5.5	
5			

$$\mu = \mu(\mathbf{r}, t)$$



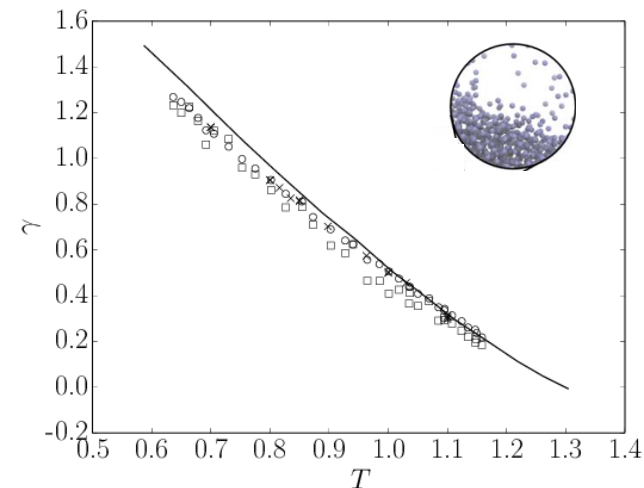
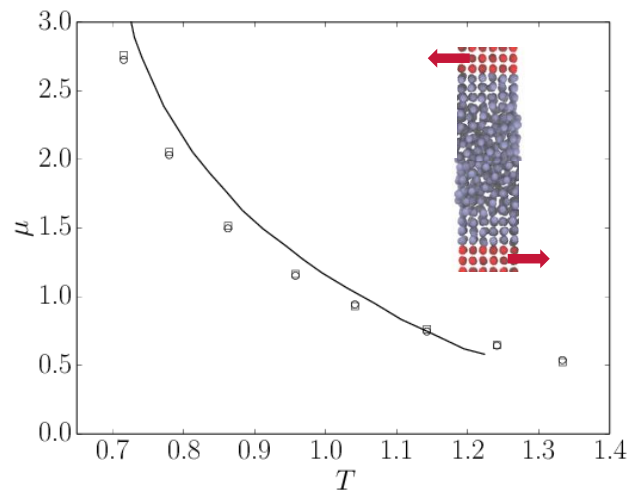
**Table Lookup or  
Coefficients**

MD parameter study  
stored in table and CFD  
uses data

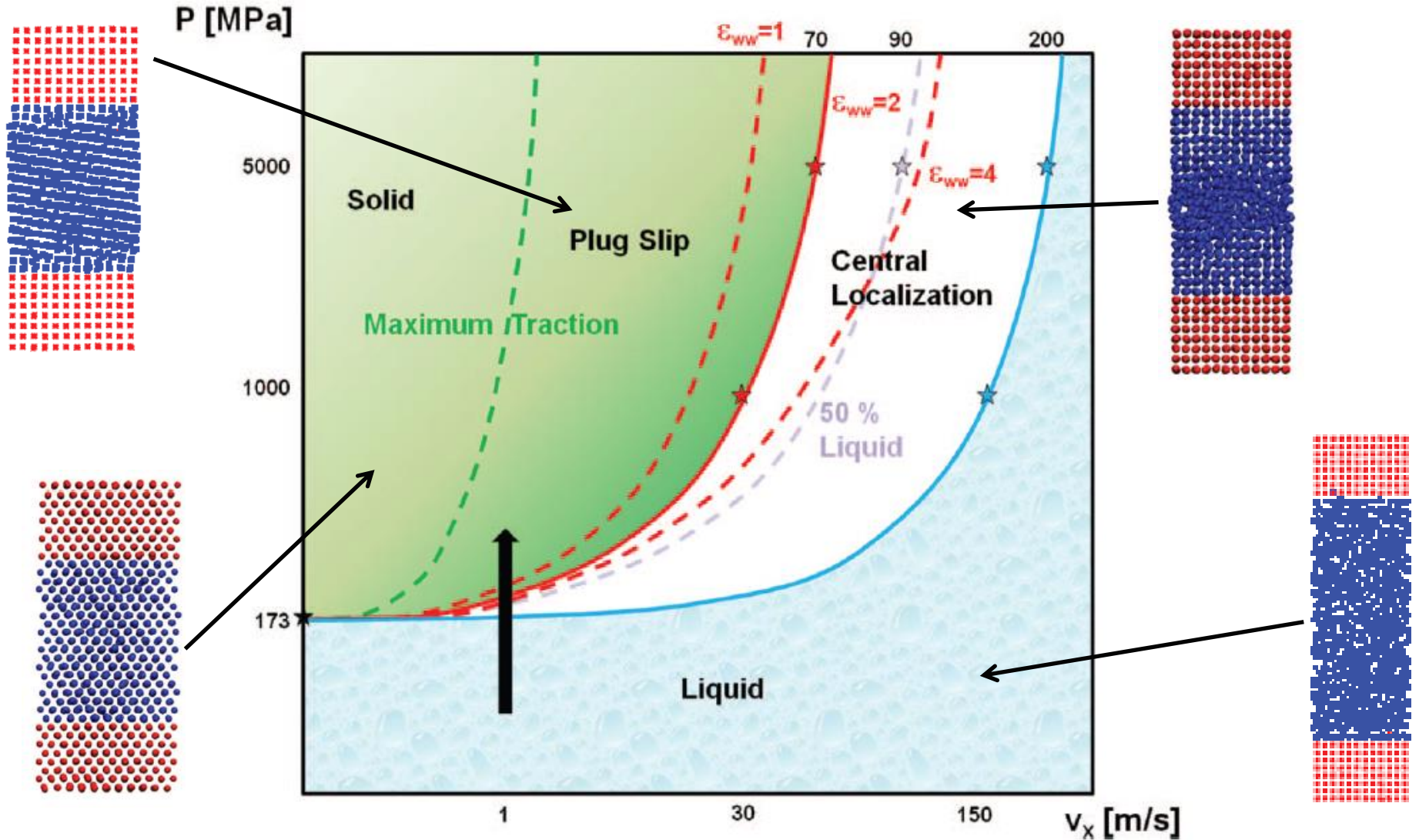
Essence of science get a relationship  
between e.g. stress and strain with MD  
simply a cheap experiment

Assumes validity of MD as representative  
for larger scale models (Similitude)

Arguably not actually coupling, simply  
“molecular fluid dynamics”



# Non-Equilibrium (Non Continuum?) Phase Map



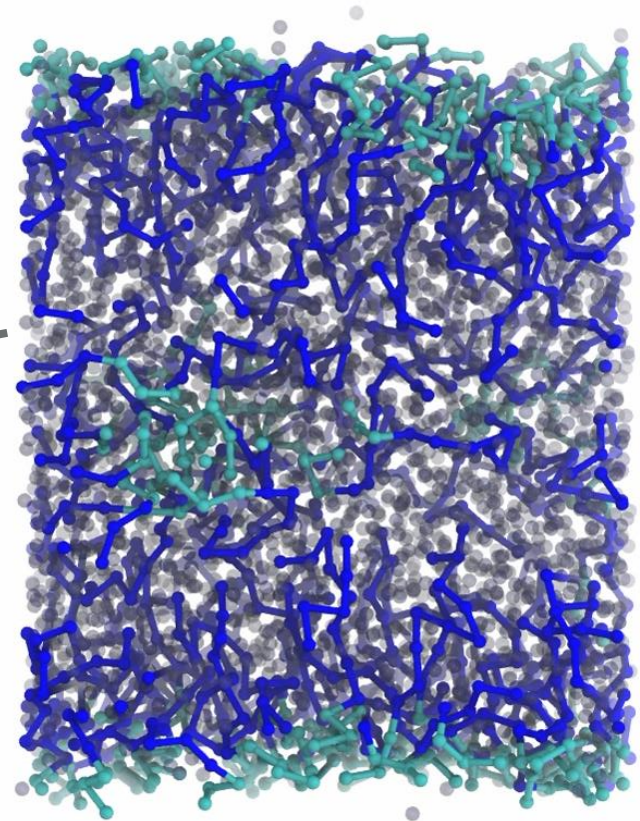
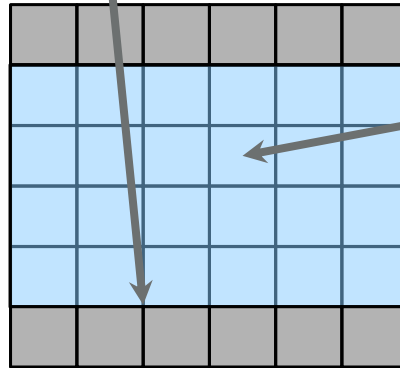
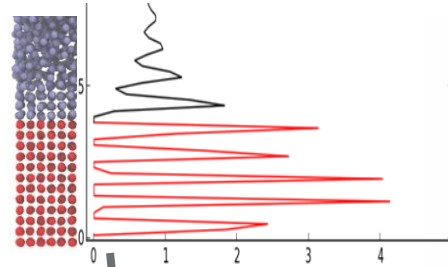


# Coupling Assumptions

When we can't  
build a table due to  
large space or  
complexity

Assume the time  
and space scales  
are decoupled

Possible to  
observe a  
relationships later  
(machine learning  
opportunity)

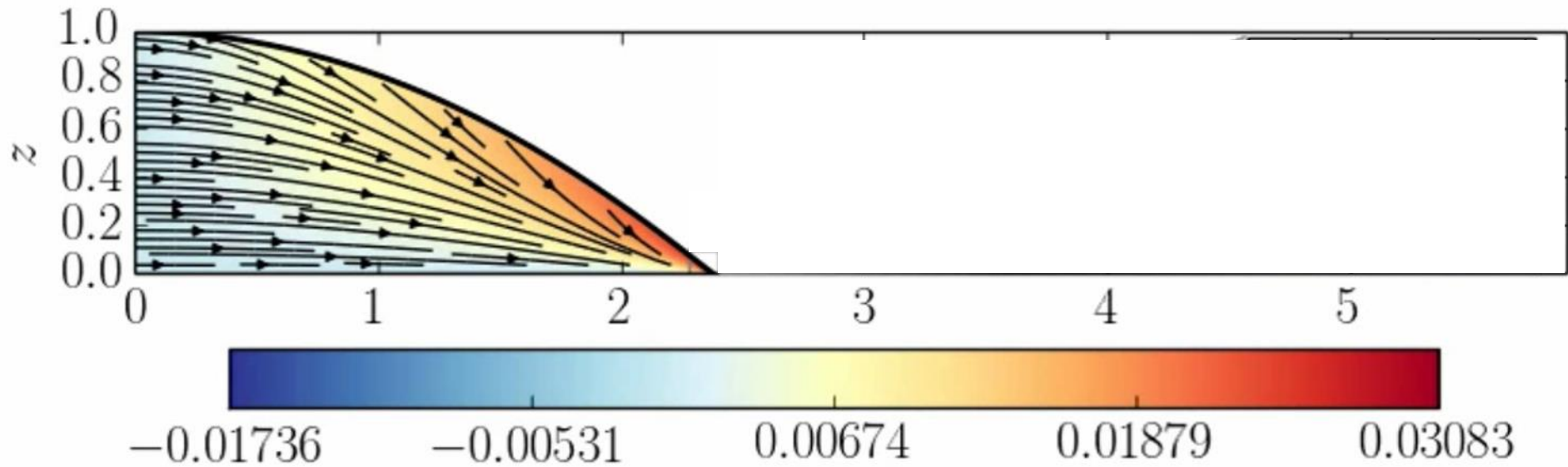


**Embedded Models (HMM)**

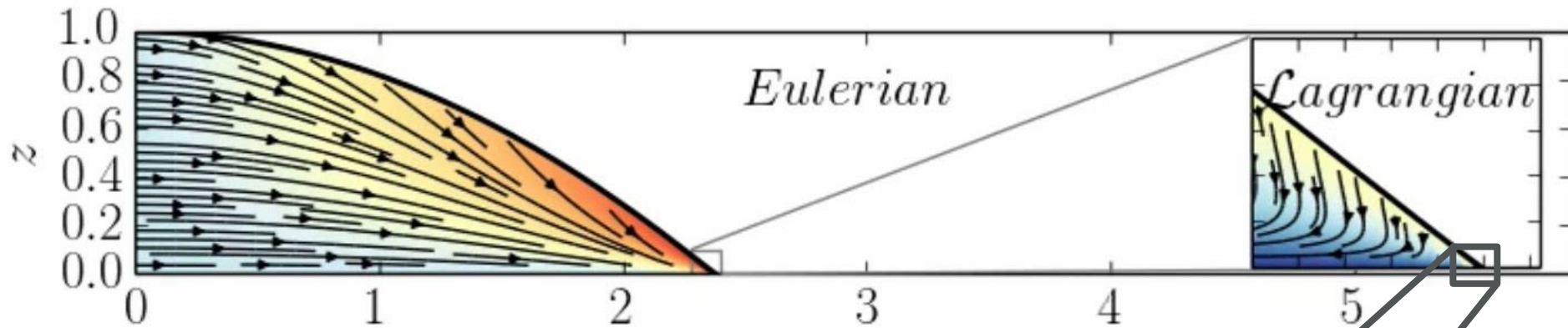
MD – embedded in a CFD  
simulation

Used for Non-Newtonian  
effects <sup>1)</sup>

# Coupled Droplet Spreading

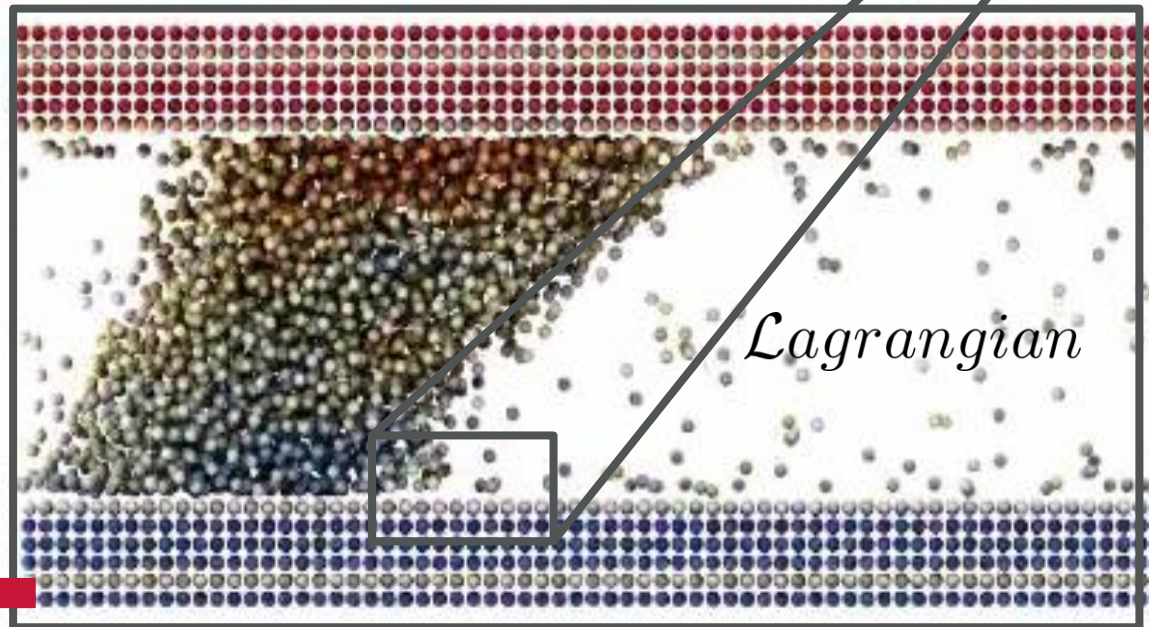


# Coupled Droplet Spreading



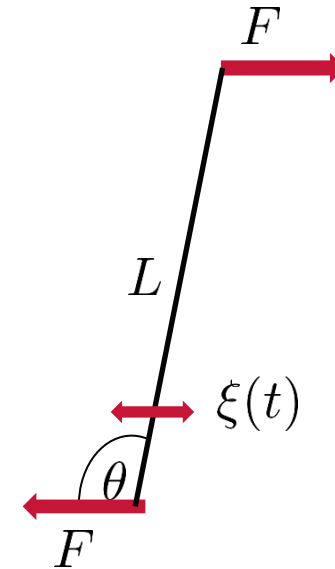
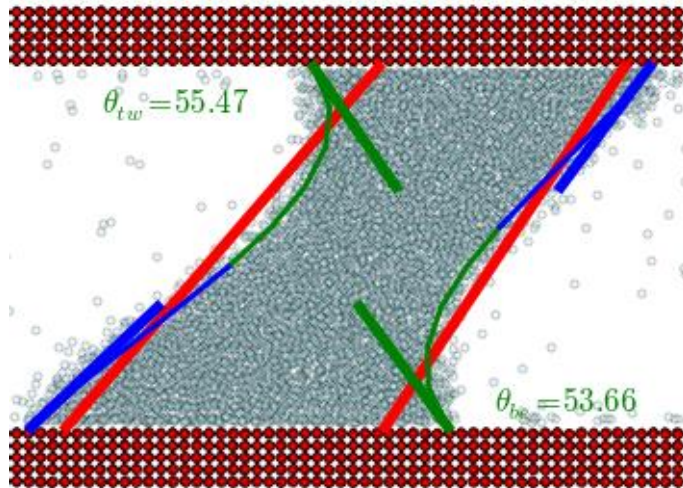
- Model the moving contact line with MD
- We want contact line speed as a function of continuum contact angle

$$\frac{dx_c}{dt}$$



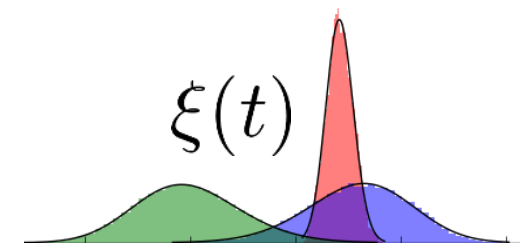
## Building this into the Continuum Model

- Model the movement of the contact line as a torsional system



Spring mass + a random noise term

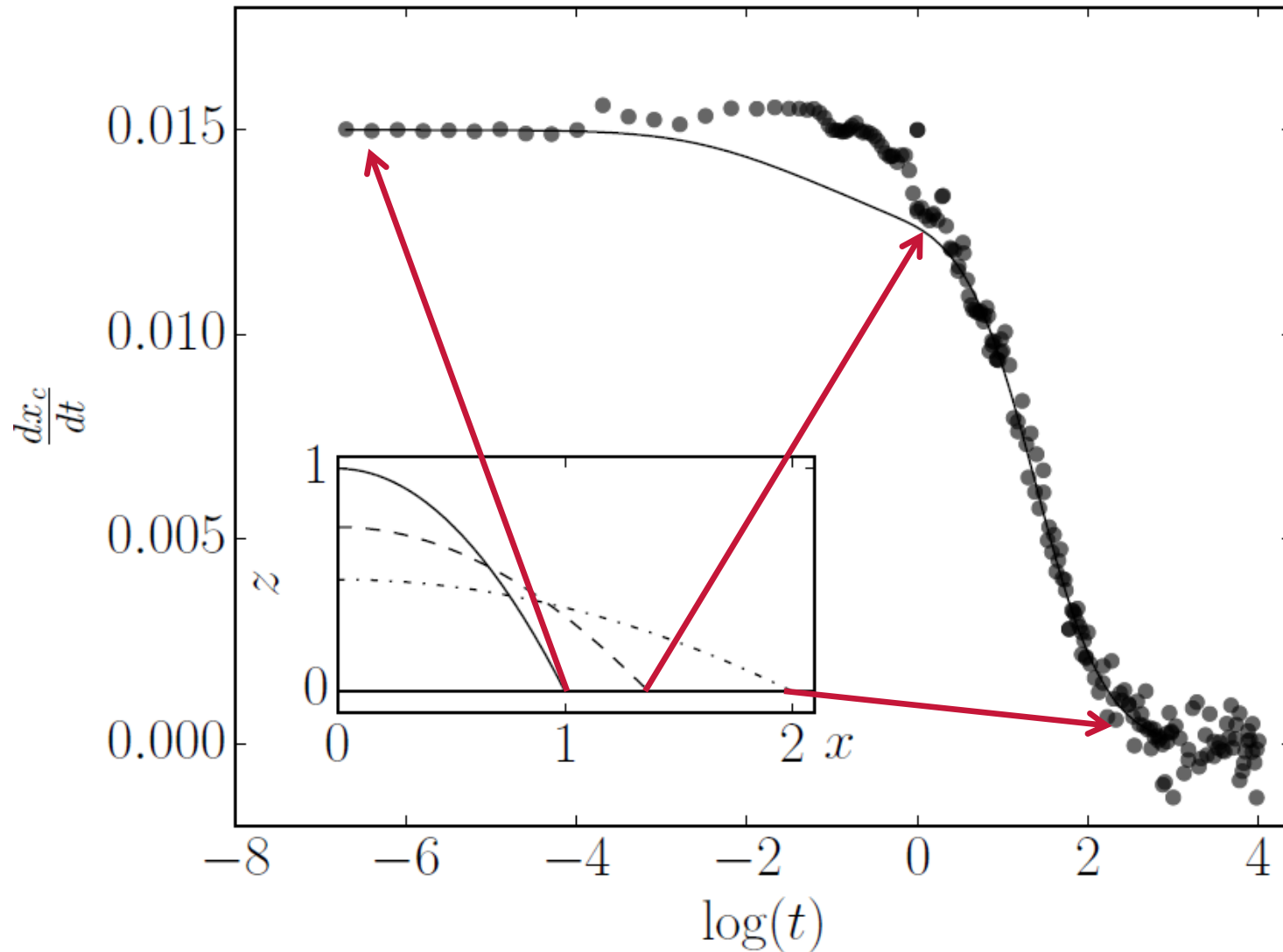
$$I\ddot{\theta} + \Gamma\dot{\theta} + k\theta - \xi = \mathcal{T}$$



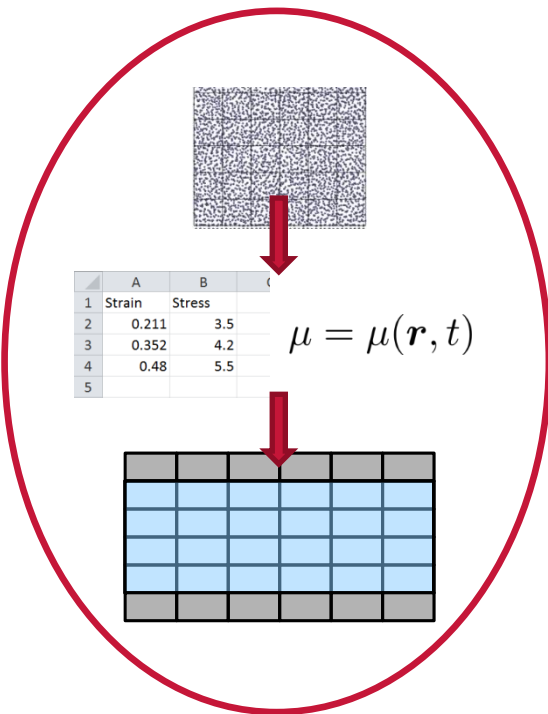
- Torque  $\mathcal{T} = F \times L$  approximately equal to wall sliding



# Building this into the Continuum Model

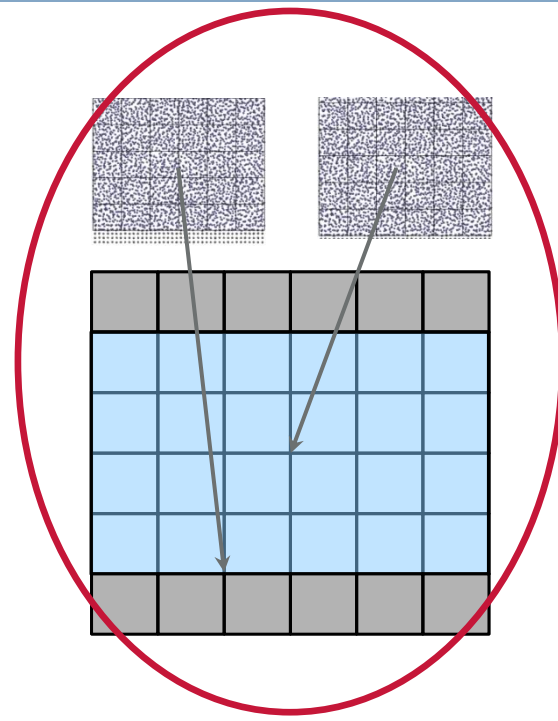


# Coupling Assumptions



**Table Lookup or Coefficients**

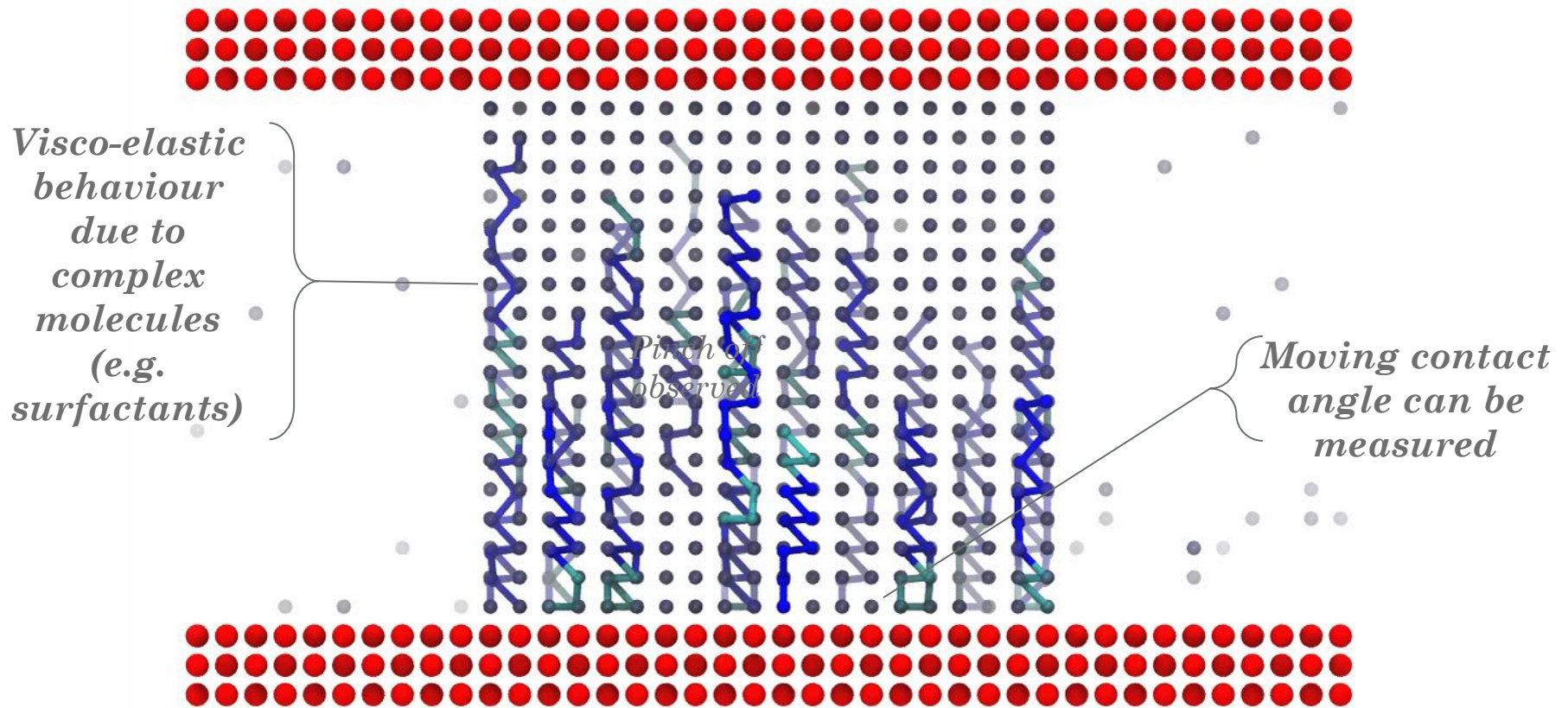
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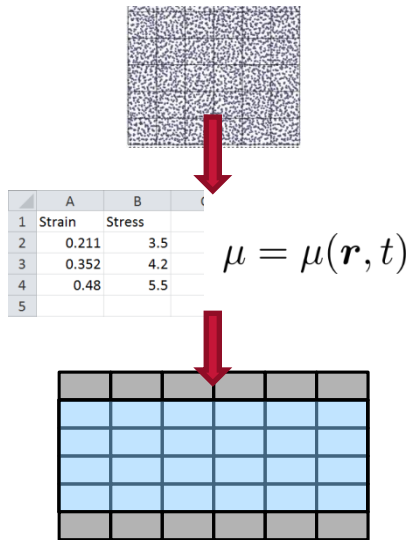
**Embedded Models (HMM)**

MD – embedded in a CFD simulation

## Extension to more complex flows

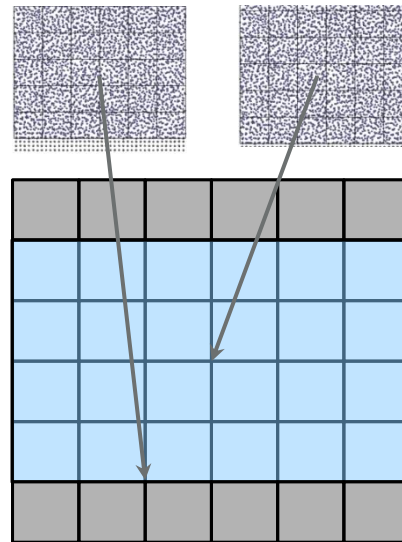


# Coupling Assumptions



**Table Lookup or Coefficients**

MD parameter study stored in table and CFD uses data



**Embedded Models (HMM)**

MD – embedded in a CFD simulation

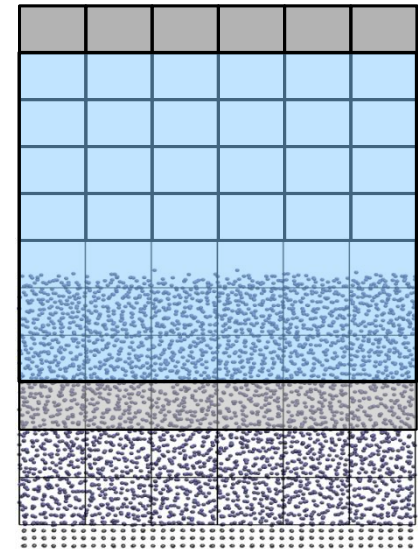
Can we really reduce all the molecular complexity down to a close form relationship, table or embedded exchange?

We don't get the true evolution of the droplet with molecular detail

**System size effects may mean similitude is not valid**

## Coupling Assumptions

- Domain decompositions makes no assumptions – full MD linked to CFD
- BUT, the length scales are the same and the timescales evolve together
- For accelerating molecular simulation NOT a boundary for CFD
- The most complex coupling
  - How to link the two descriptions of reality?
  - “Noise” in MD can cause problems (fluctuating hydrodynamic or smarter/better averaging)
  - If we solve this, we can provide insight and techniques for the other coupling



### Domain Decomposition

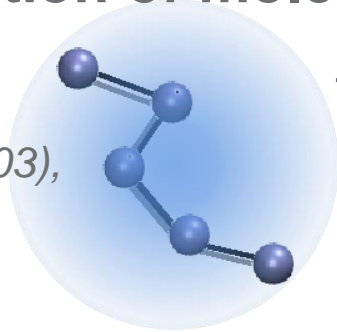
MD –CFD linked along an interface

Local features<sup>2)</sup>

# Domain Decomposition

## Boundary force and insertion of molecules

*USHER*  
(Delgado-Buscalioni 2003),  
*Fade* (Borg,  
Lockerby &  
Reese (2014)

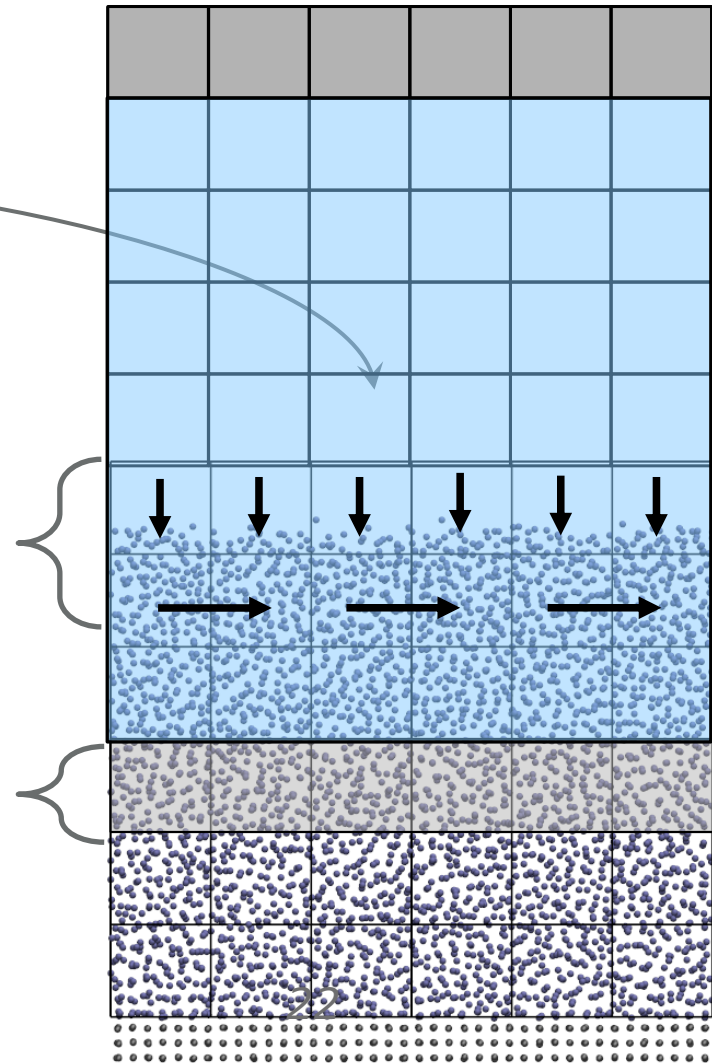


*O'Connell Thompson*  
(1995), *Hadjiconstantinou*  
(1998), *Flekkoy* (2000), *Nie*  
*et al* (2004). All since 1995,  
and we have over 100  
years of statistical  
mechanics

**CFD→MD**  
**Boundary**  
**condition**

**MD→CFD**  
**Boundary**  
**condition**

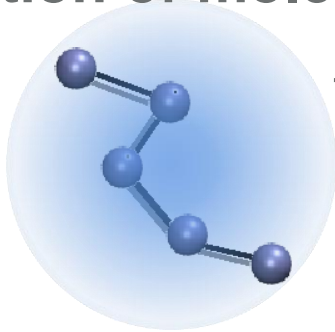
*Many tuneable parameters – an art? Overlap  
size, timestep ratio, boundary force, etc*





# Domain Decomposition

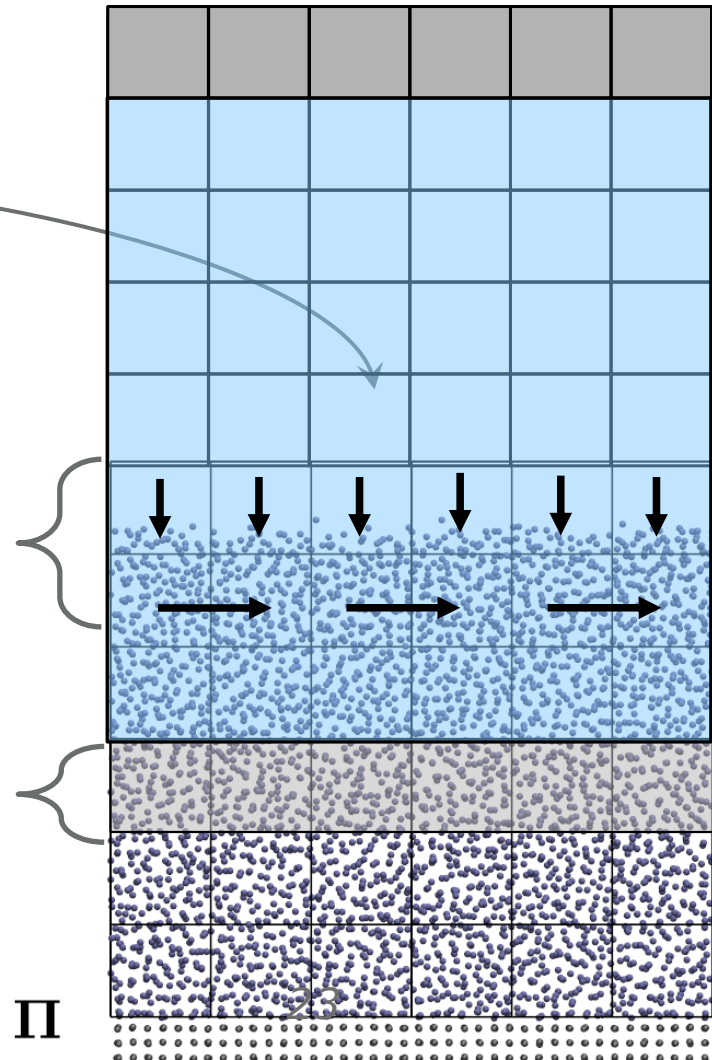
Boundary force and  
insertion of molecules



**Consistent  
Framework**

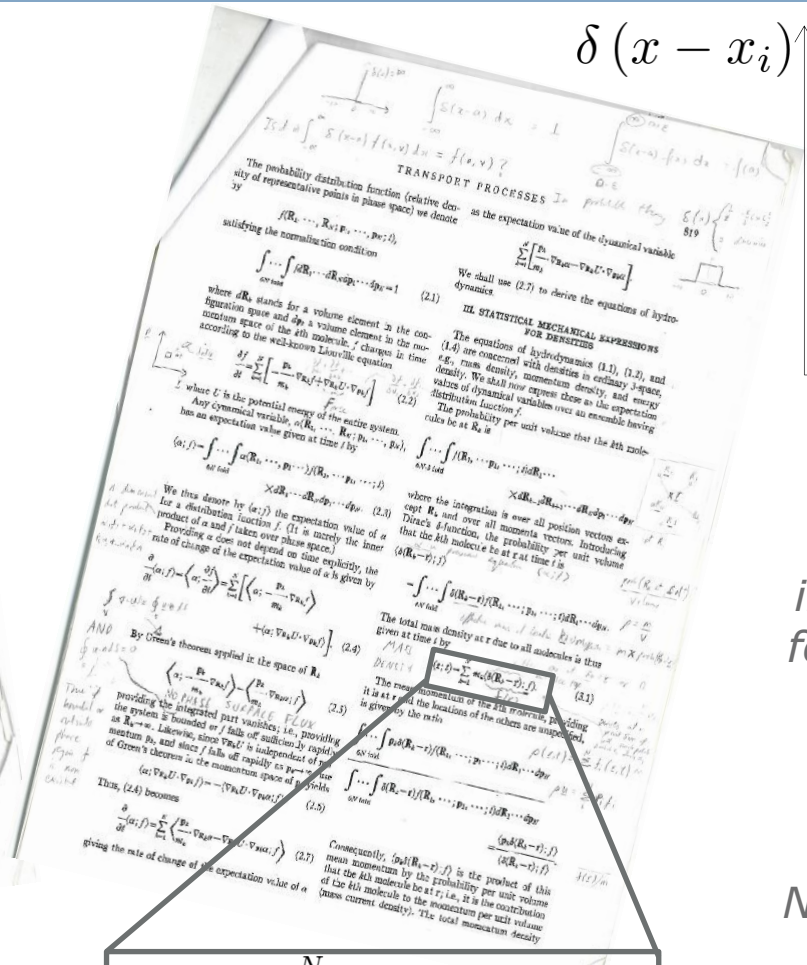
**CFD → MD  
Boundary  
condition**

**MD → CFD  
Boundary  
condition**

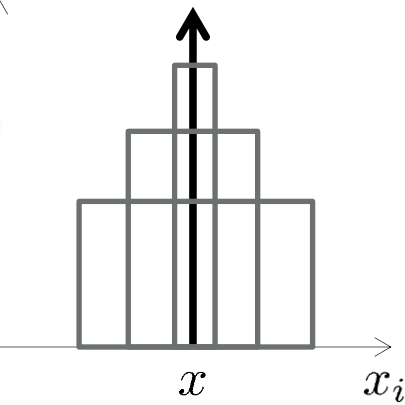


$$m_i \ddot{\mathbf{r}}_i = \mathbf{F}_i \longleftrightarrow \frac{\partial}{\partial t} \rho \mathbf{u} + \nabla \cdot \rho \mathbf{u} \mathbf{u} = \nabla \cdot \Pi$$

# Irving and Kirkwood (1950)



$$\delta(x - x_i)$$



The Dirac delta infinitely high, infinitely thin peak formally equivalent to the continuum differential formulation **BUT** No molecule is ever exactly at a point

$$\rho(\mathbf{r}, t) = \sum_{i=1}^N \left\langle m_i \delta(\mathbf{r} - \mathbf{r}_i); f \right\rangle$$



# Computational Fluid Dynamics

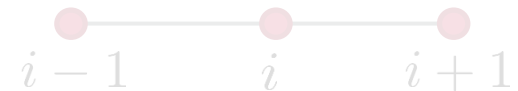
- The Navier-Stokes Equation

$$\frac{\partial}{\partial t} \rho \mathbf{u} + \nabla \cdot \rho \mathbf{u} \mathbf{u} = -\nabla \cdot \Pi$$

$$\Pi = P\mathbf{I} - \mu \nabla \mathbf{u}$$

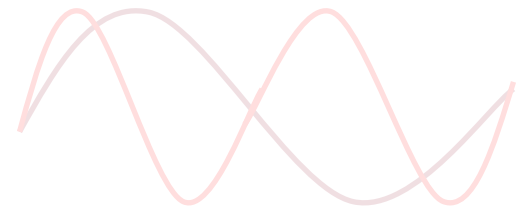
- Finite Difference Method

$$\frac{\partial u_i}{\partial x} \approx \frac{u_{i+1} - u_{i-1}}{\Delta x}$$



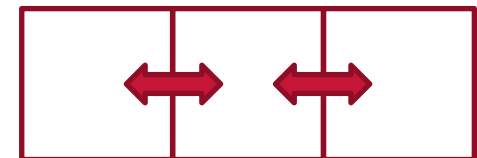
- Spectral Methods

$$u(x) = \sum_{n=1}^{X-1} \tilde{u}_n \bar{T}_n(y) e^{2\pi i(k_x x/L_x + k_z z/L_z)}$$



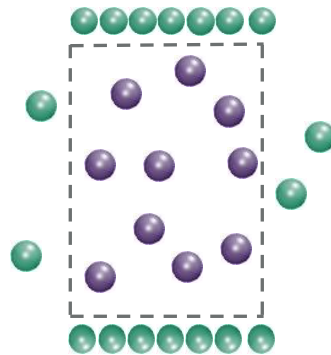
- Finite Volume (0<sup>th</sup> order element) Method

$$\frac{\partial}{\partial t} \int_V \rho \mathbf{u} dV = - \oint_S \rho \mathbf{u} \mathbf{u} \cdot d\mathbf{S} - \oint_S \Pi \cdot d\mathbf{S}$$



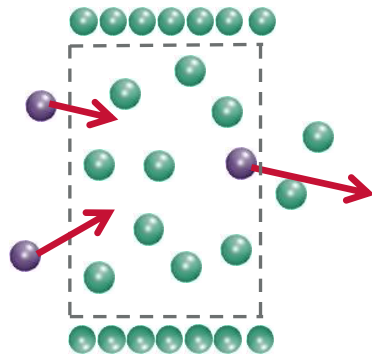
## Control Volume Functional

The Control volume function is the integral of the Dirac delta function in 3 dimensions



$$\vartheta_i \equiv \int_V \delta(\mathbf{r} - \mathbf{r}_i) dV$$

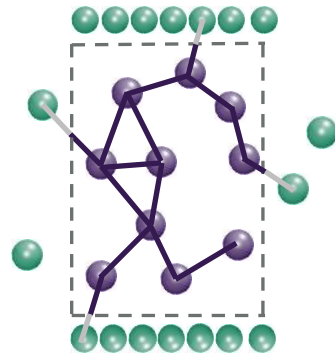
Its derivative gives the fluxes over the surface



$$dS_{ix} \equiv -\frac{\partial \vartheta_i}{\partial x_i}$$

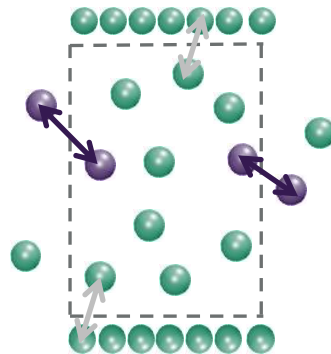
## Control Volume Functional - Forces

A CV based on the length of intermolecular interaction inside the volume (used in the volume average stress)



$$\vartheta_s \equiv \int_V \delta(\mathbf{r} - \mathbf{r}_i + s\mathbf{r}_{ij}) dV$$

Its derivative gives the forces over the surface (as in the method of planes stress)



$$dS_{xij} \equiv \int_0^1 \frac{\partial \vartheta_s}{\partial x} ds$$

# The Control Volume Equations

- Mass Conservation

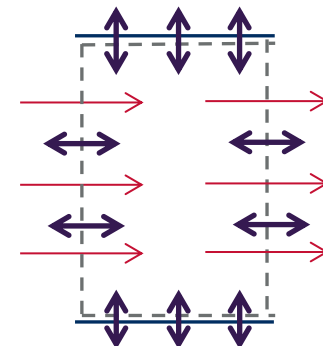
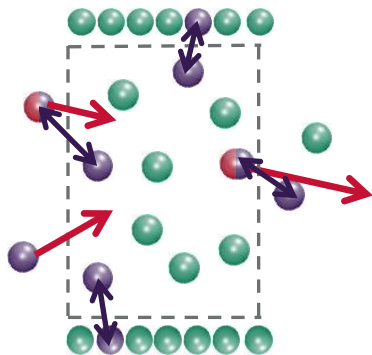
$$\frac{d}{dt} \sum_{i=1}^N m_i \vartheta_i = - \sum_{i=1}^N m_i \mathbf{v}_i \cdot d\mathbf{S}_i$$

$$\frac{\partial}{\partial t} \int_V \rho dV = - \oint_S \rho \mathbf{u} \cdot d\mathbf{S}$$

- Momentum Balance

$$\begin{aligned} \frac{d}{dt} \sum_{i=1}^N m_i \mathbf{v}_i \vartheta_i = & - \sum_{i=1}^N m_i \mathbf{v}_i \mathbf{v}_i \cdot d\mathbf{S}_i \\ & + \frac{1}{2} \sum_{i,j}^N \mathbf{f}_{ij} \mathbf{n} \cdot d\mathbf{S}_{ij} \end{aligned}$$

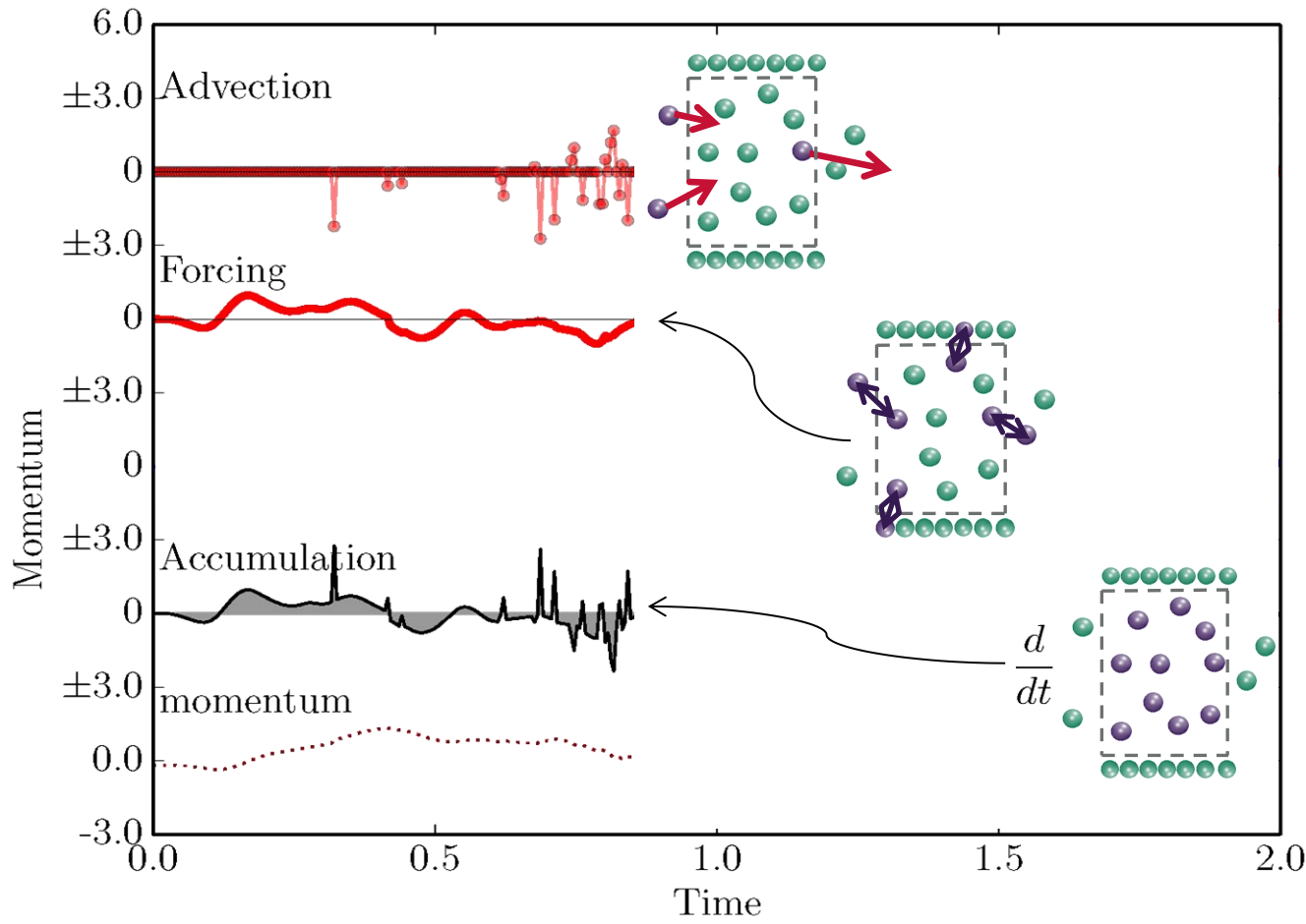
$$\begin{aligned} \frac{\partial}{\partial t} \int_V \rho \mathbf{u} dV = & - \oint_S \rho \mathbf{u} \mathbf{u} \cdot d\mathbf{S} \\ & - \oint_S \mathbf{\Pi} \cdot d\mathbf{S} \end{aligned}$$



# Exact Conservation

## Results from any arbitrary volume

- Accumulation = Forcing + Advection



$$\underbrace{\sum_{i=1}^N m_i \mathbf{v}_i \mathbf{v}_i \cdot d\mathbf{S}_i}_{\text{Advection}}$$

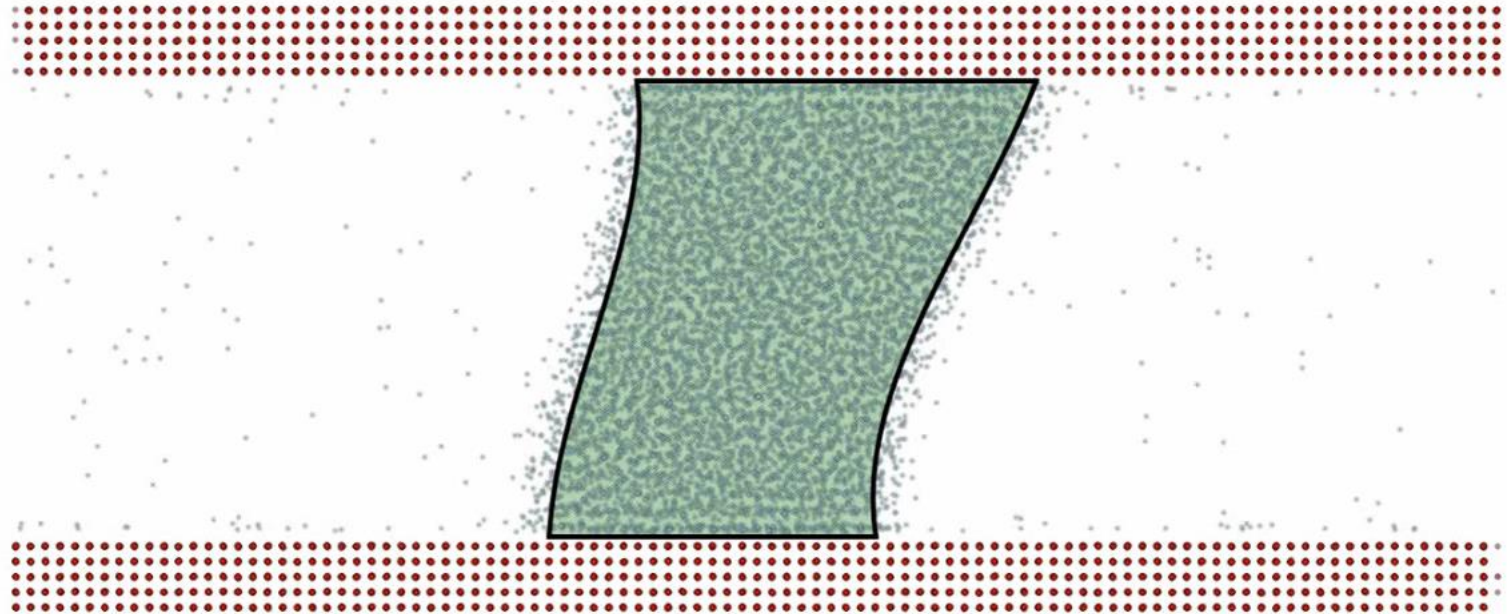
$$- \underbrace{\frac{1}{2} \sum_{i,j} \mathbf{f}_{ij} \mathbf{n} \cdot d\mathbf{S}_{ij}}_{\text{Forcing}}$$

$$= \underbrace{\frac{d}{dt} \sum_{i=1}^N m_i \mathbf{v}_i \vartheta_i}_{\text{Accumulation}}$$

## Exact Conservation – Arbitrary Volume

### Results from any arbitrary volume

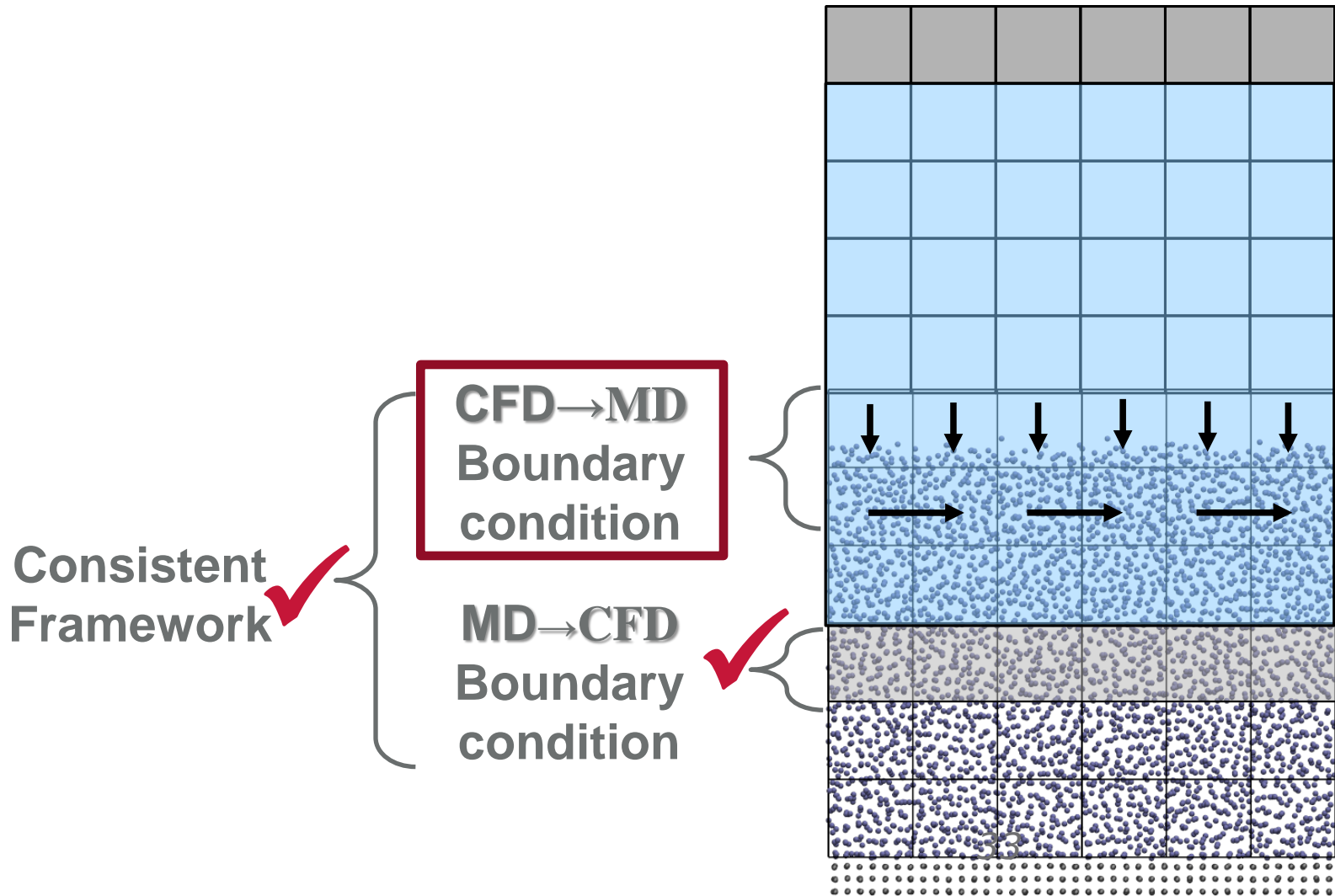
- Accumulation = Forcing + Advection



## Key Points

- We can't get molecular values at an infinitesimal point in space
- But, by integrating over a known control volume average changes inside a volume and flux over the surface can be related
- Exactly satisfaction of the conservation laws in both descriptions
- Control Volumes are the only meaningful way to relate the two systems

# Domain Decomposition





# Constrained Control Volume

## Non-unique solution

- Continuum field properties must specify dynamics of N molecules
- Hamilton's principle (subject to a constraint) used in the first fluids coupling scheme (O'Connell and Thompson 1995)

## We apply a constraint localised using the control volume function

- CV function takes care of the localisation for us
- Non-holonomic constraint

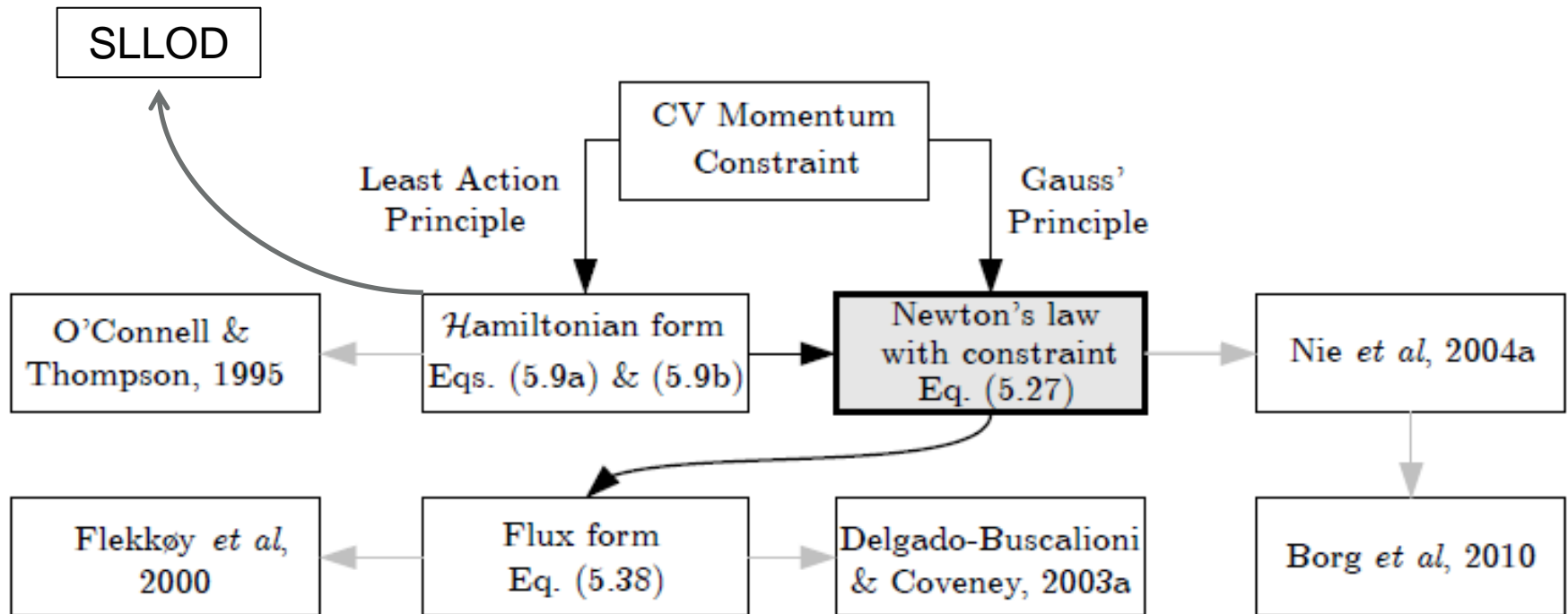
$$g(\mathbf{r}_i, \dot{\mathbf{r}}_i) = \sum_{i=1}^N m_i \dot{\mathbf{r}}_i \vartheta_i - \int_V \rho \mathbf{u} dV = 0$$

## Gauss Principle of Least Constraint Applied

- Valid for any form of constraint

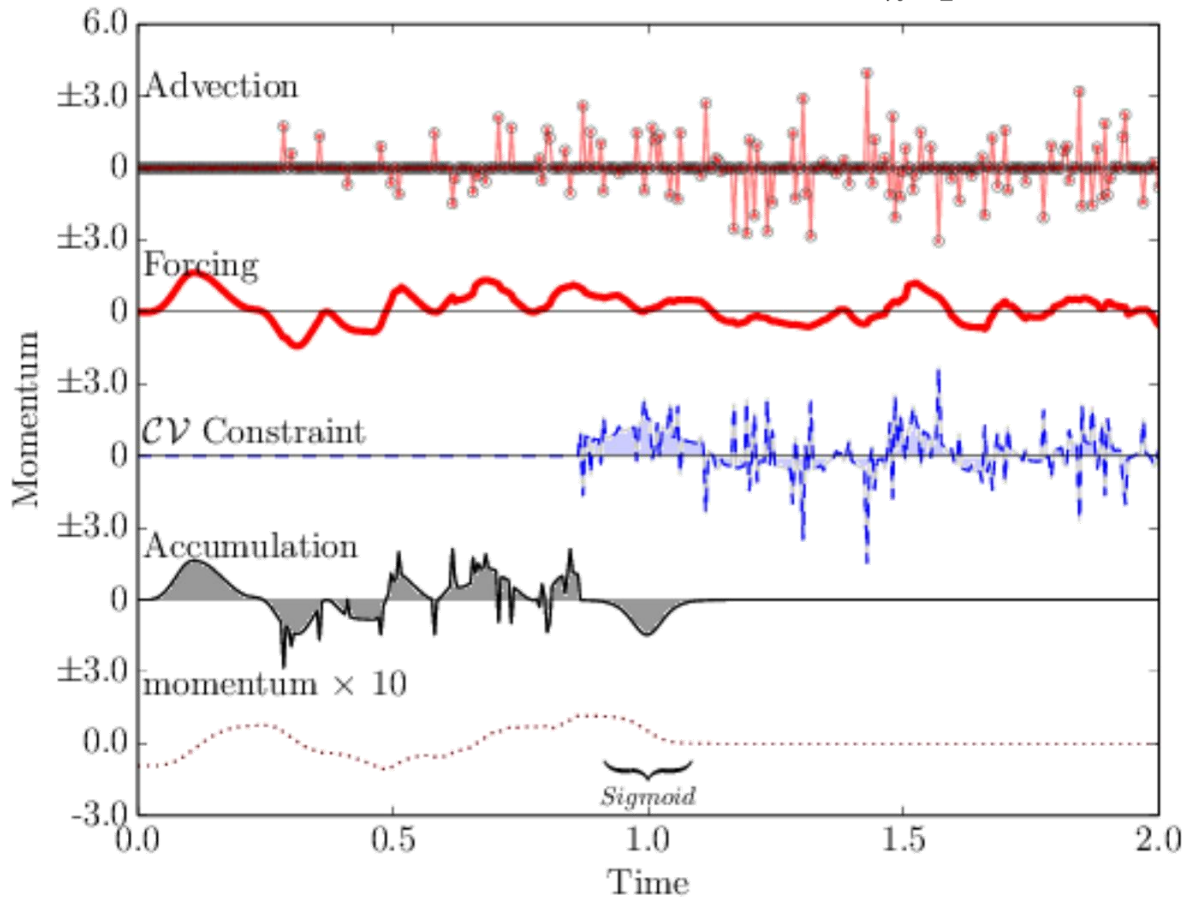
$$\frac{\partial}{\partial \mathbf{r}_{ij}} \sum_{i=1}^N [\mathbf{F}_i - \mathbf{r}_{ij}]^2 - \lambda \cdot \mathbf{g} = 0$$

# Constrained Control Volume

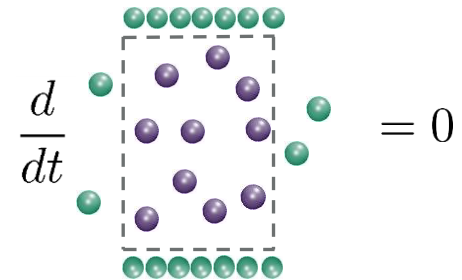


# Constrained Control Volume

$$m_i \ddot{\mathbf{r}}_i = \mathbf{F}_i + \frac{m_i \vartheta_i}{M_I} \left[ \frac{d}{dt} \int_V \rho \mathbf{u} dV + \overbrace{\sum_{n=1}^N m_i \dot{\mathbf{r}}_n \dot{\mathbf{r}}_n \cdot d\mathbf{S}_n}^{\text{Advection}} - \overbrace{\sum_{n,m}^N \mathbf{f}_{nm} \mathbf{n} \cdot dS_{nm}}^{\text{Forcing}} \right]$$

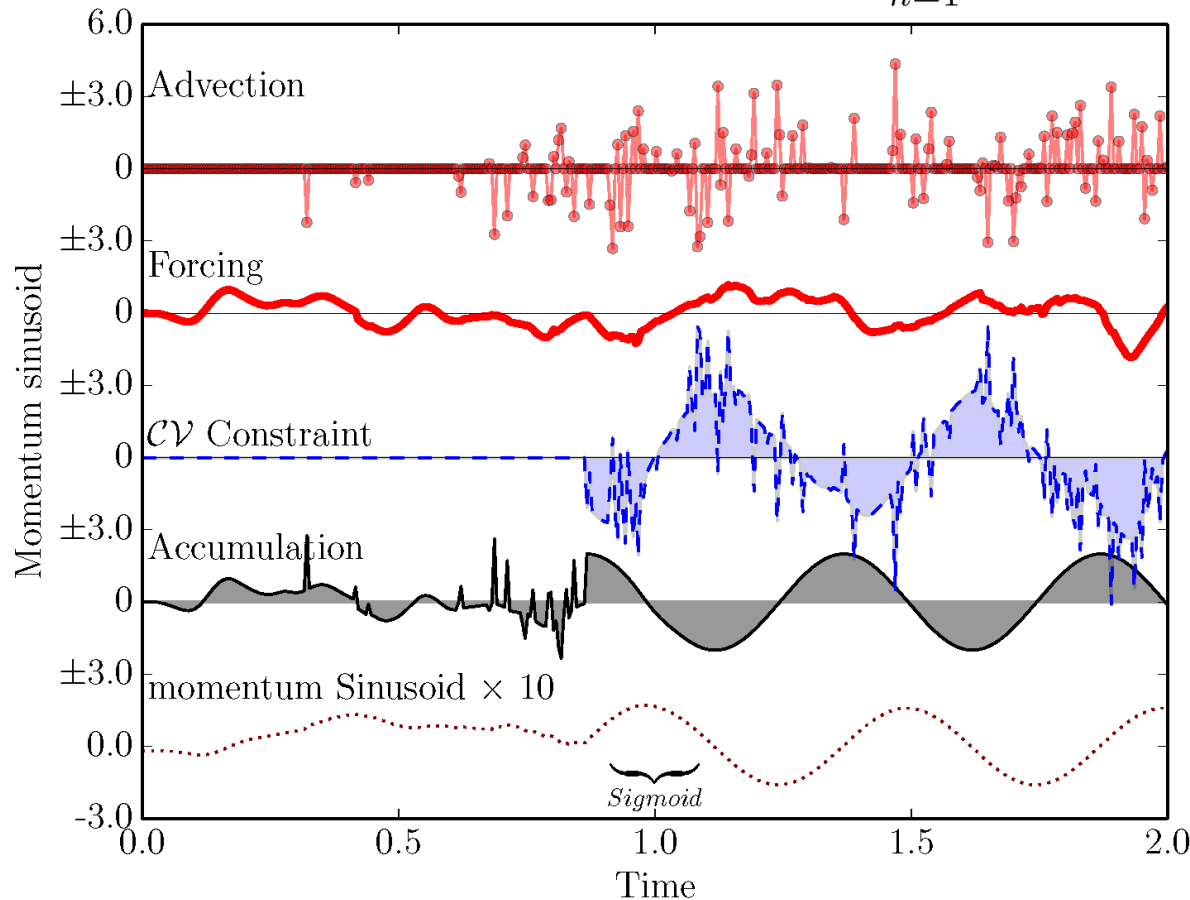


- Zero time evolution applied
- No velocity evolution results
- Exact control of momentum using iteration to cancel both Forcing and Advection



# Constrained Control Volume

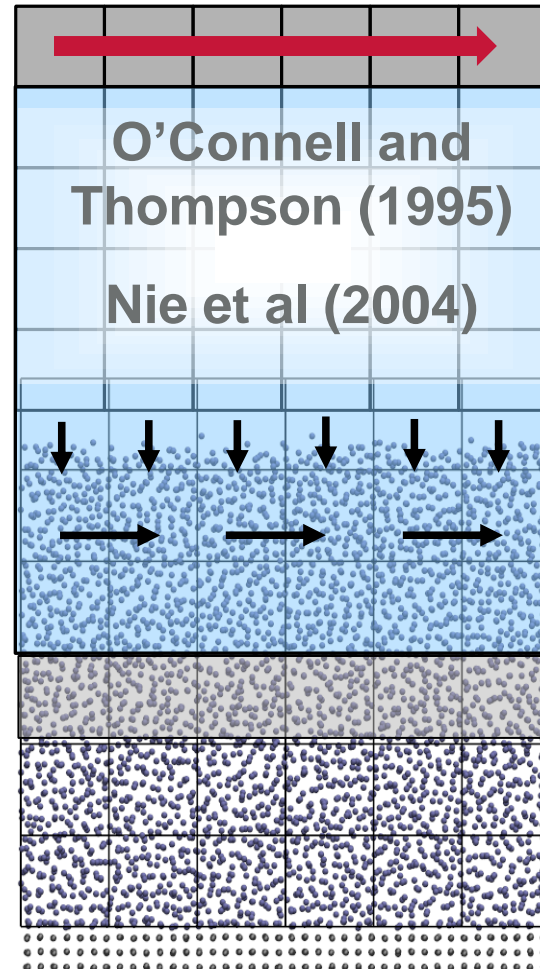
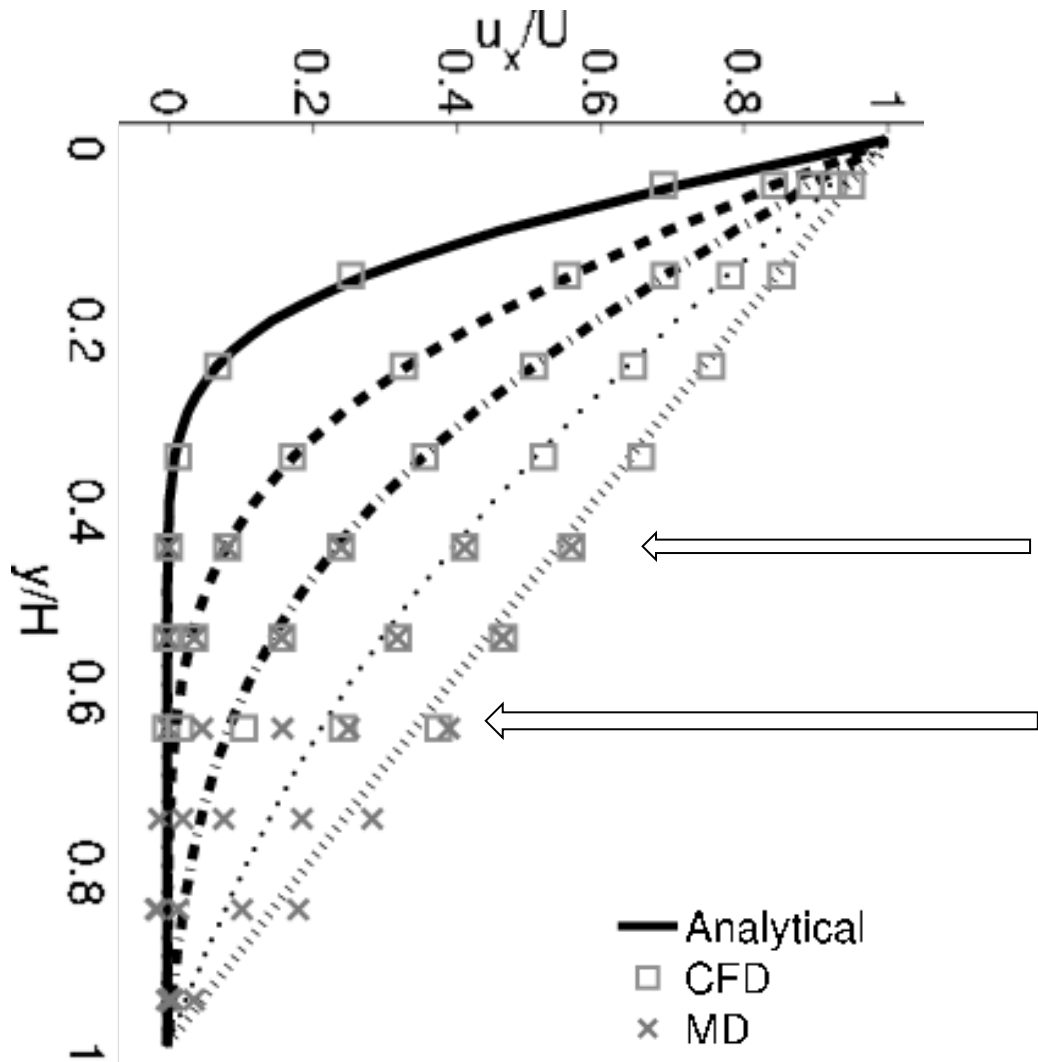
$$m_i \ddot{\mathbf{r}}_i = \mathbf{F}_i + \frac{m_i \vartheta_i}{M_I} \left[ \underbrace{\frac{d}{dt} \int_V \rho \mathbf{u} dV}_{\text{Advection}} + \underbrace{\sum_{n=1}^N m_i \dot{\mathbf{r}}_n \dot{\mathbf{r}}_n \cdot d\mathbf{S}_n}_{\text{Forcing}} - \sum_{n,m} \mathbf{f}_{nm} \mathbf{n} \cdot d\mathbf{S}_{nm} \right]$$



- Cosinusoidal time evolution applied
- Sinusoidal velocity evolution results
- Exact control of momentum using iteration to cancel both Forcing and Advection

$$\frac{d}{dt} \int_V \rho \mathbf{u} dV$$

# Coupling Results – Couette Flow



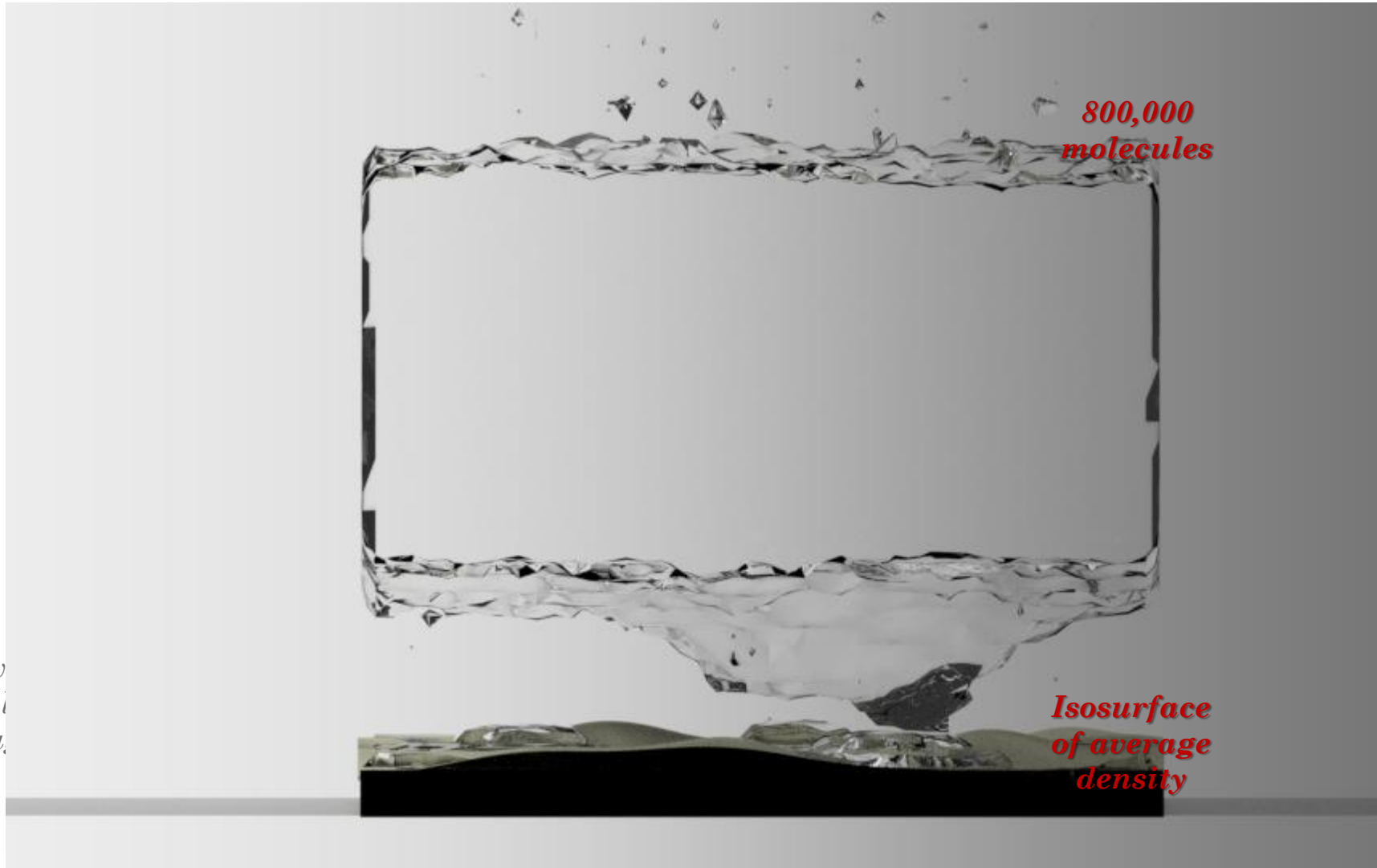
## Key Points

---

- How do we ensure conservation equations are satisfied between domains
- A consistent framework and exact constraints derived from sound physical theories help
- Still lots of work needed to elevate from an art to a science (pressure solver, order of accuracy, complex molecules, interfaces, etc)

# Some Examples

# Molecular Dynamics simulation of Nucleation





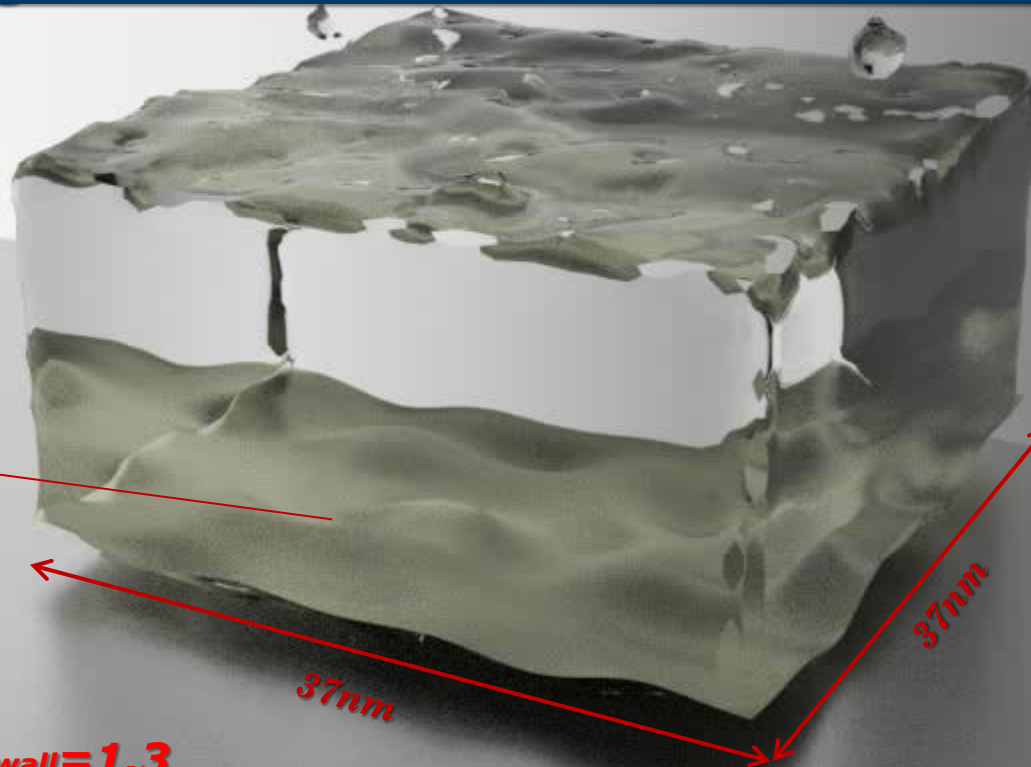
# Isosurface of Density

For video, see:  
<https://doi.org/10.1103/APS.DFD.2016.GFM.V0081>

800,000  
molecules

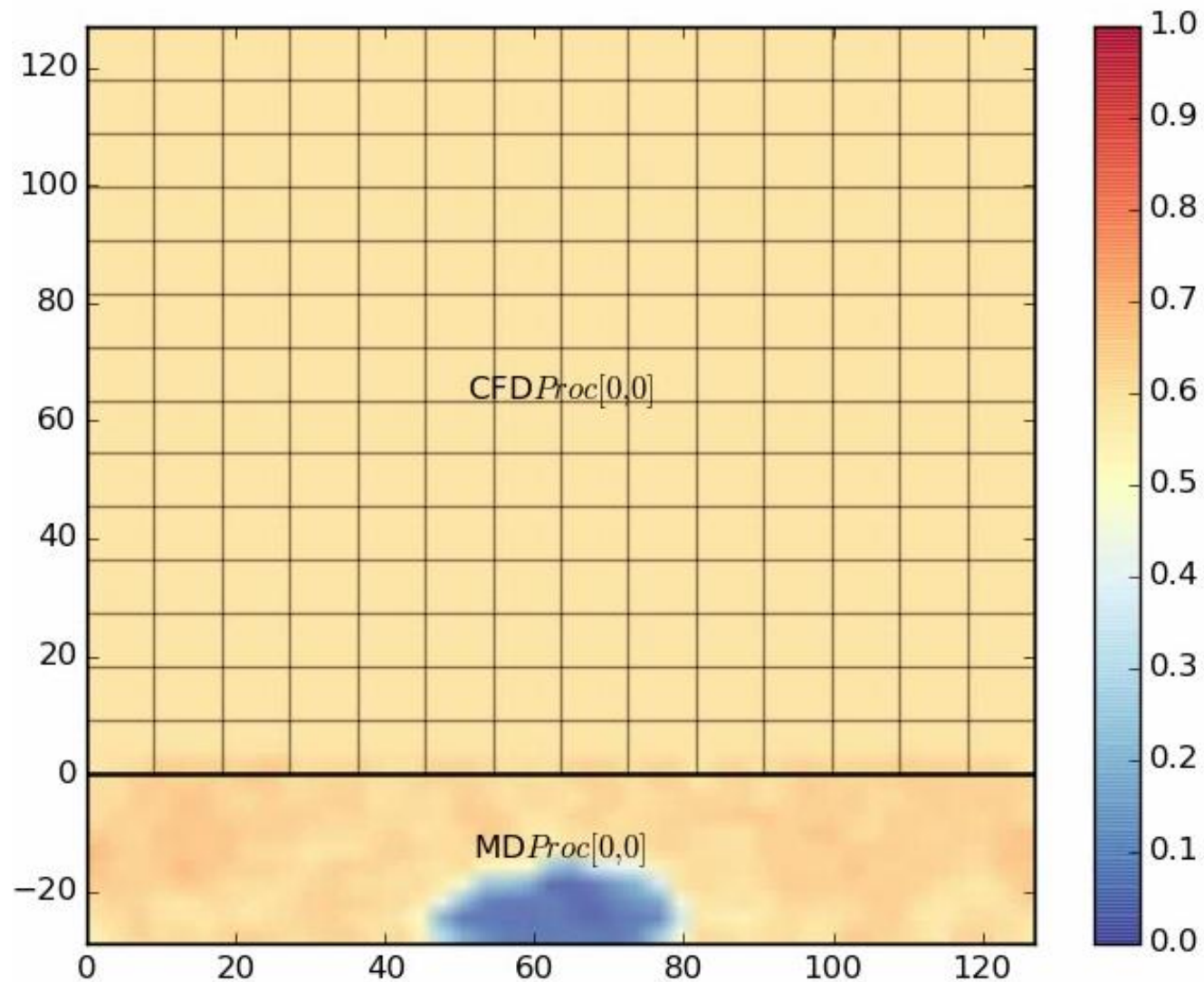
Bubbles grow,  
coalesce and  
eventually  
form a film

$T_{\text{wall}}=1.3$



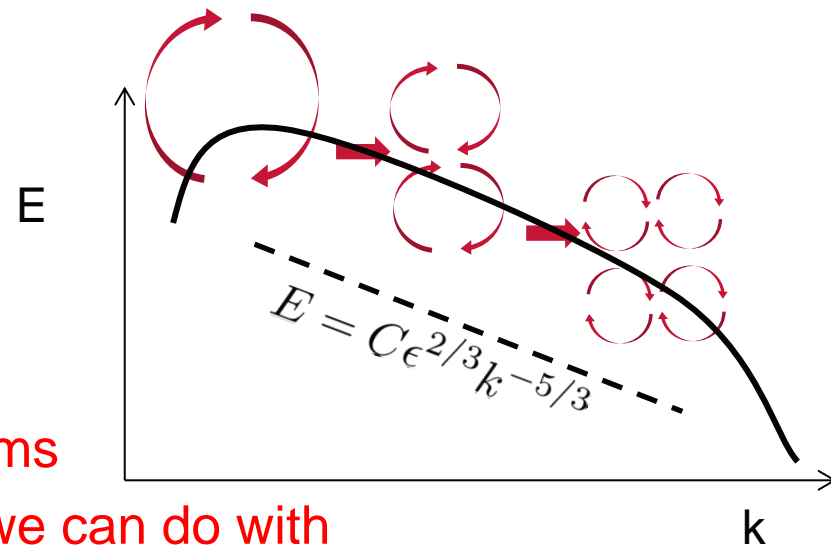
Isosurface  
of average  
density

# Coupled Simulation of Boiling



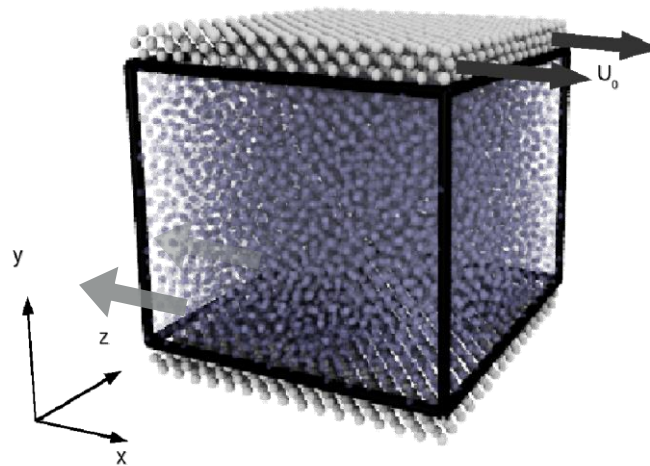
# Molecular Simulation of Turbulence

- Turbulent flow
  - Fluid flow which is spatially and temporally varying
  - Inertial effects dominate viscous
  - No clear order and not simply chaotic motions
- Some standard characteristics
  - Statistics are reproducible
  - The law of the wall
  - Range of scales
- Minimal Channel flow
  - Insight into fundamental mechanisms
  - For molecular dynamics this is all we can do with current computers



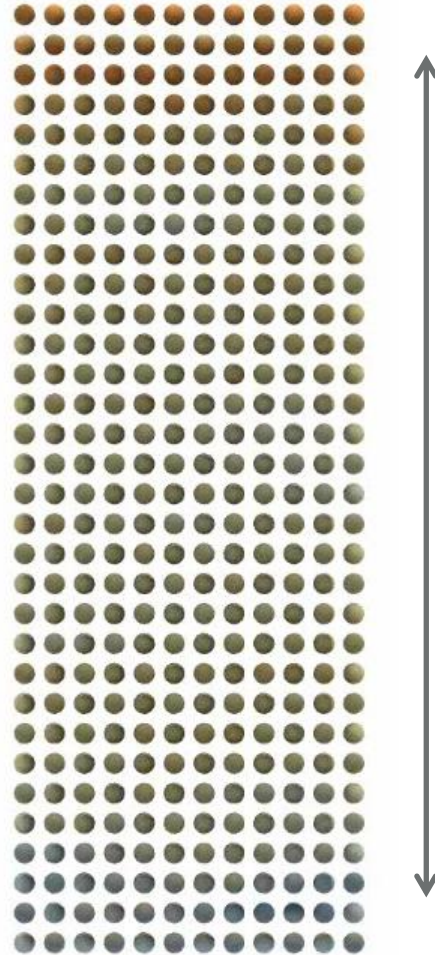
## Domain Overview

- Simulation Setup
  - All Molecular Dynamics (not coupled)
  - Sliding top and bottom walls in  $y$  with  $u = \pm 1$
  - Periodic in  $x$  and  $z$  directions
  - Walls are tethered, sliding molecules with NH thermostat with  $T=0.4$

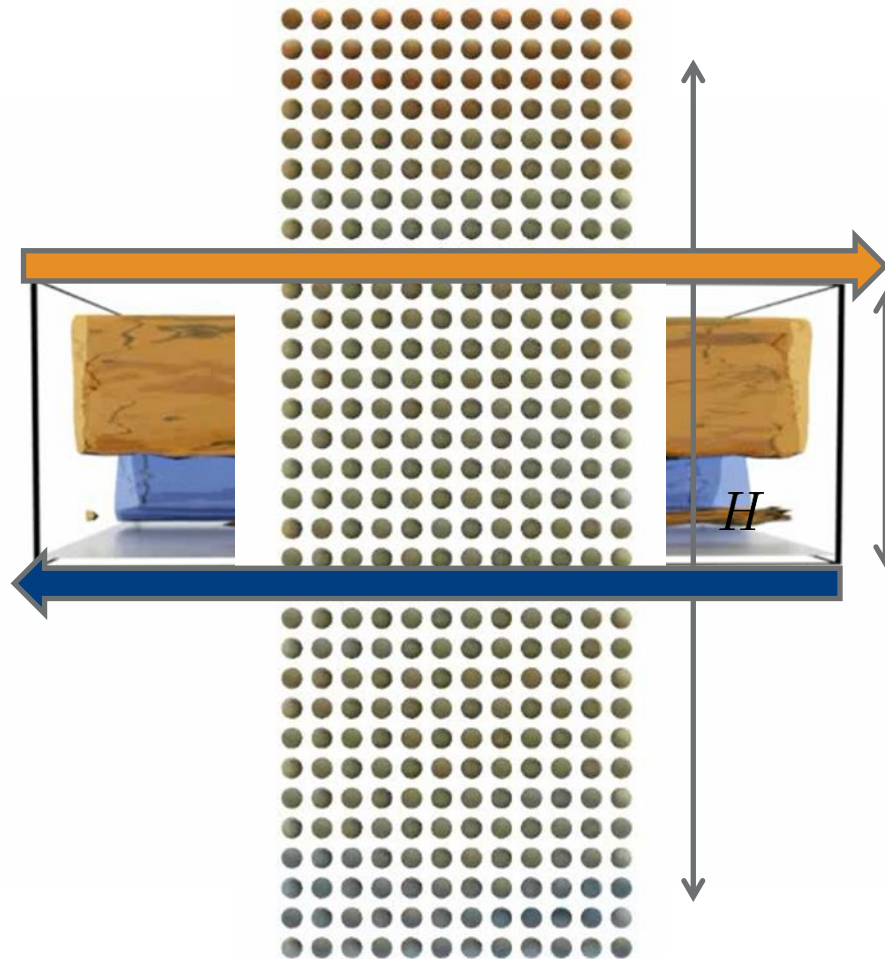


- Domain in reduced units:  $x = 1560.4$ ,  $y = 566.7$ ,  $z = 1069.9$   
at density=0.3, ~300 million molecules on 256+ processors

# Molecular Simulation of Turbulence



# Molecular Simulation of Turbulence



*Reynolds Number*

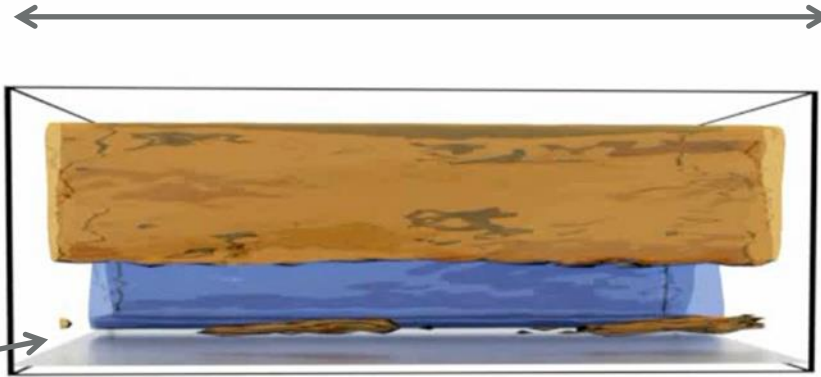
$Re \approx 400$

*with  
300 million  
molecules*

# Molecular Simulation of Turbulence

*Minimal channel Couette  
flow*

$$L \approx 523nm$$



$$H \approx 190nm$$

$$W \approx 359nm$$

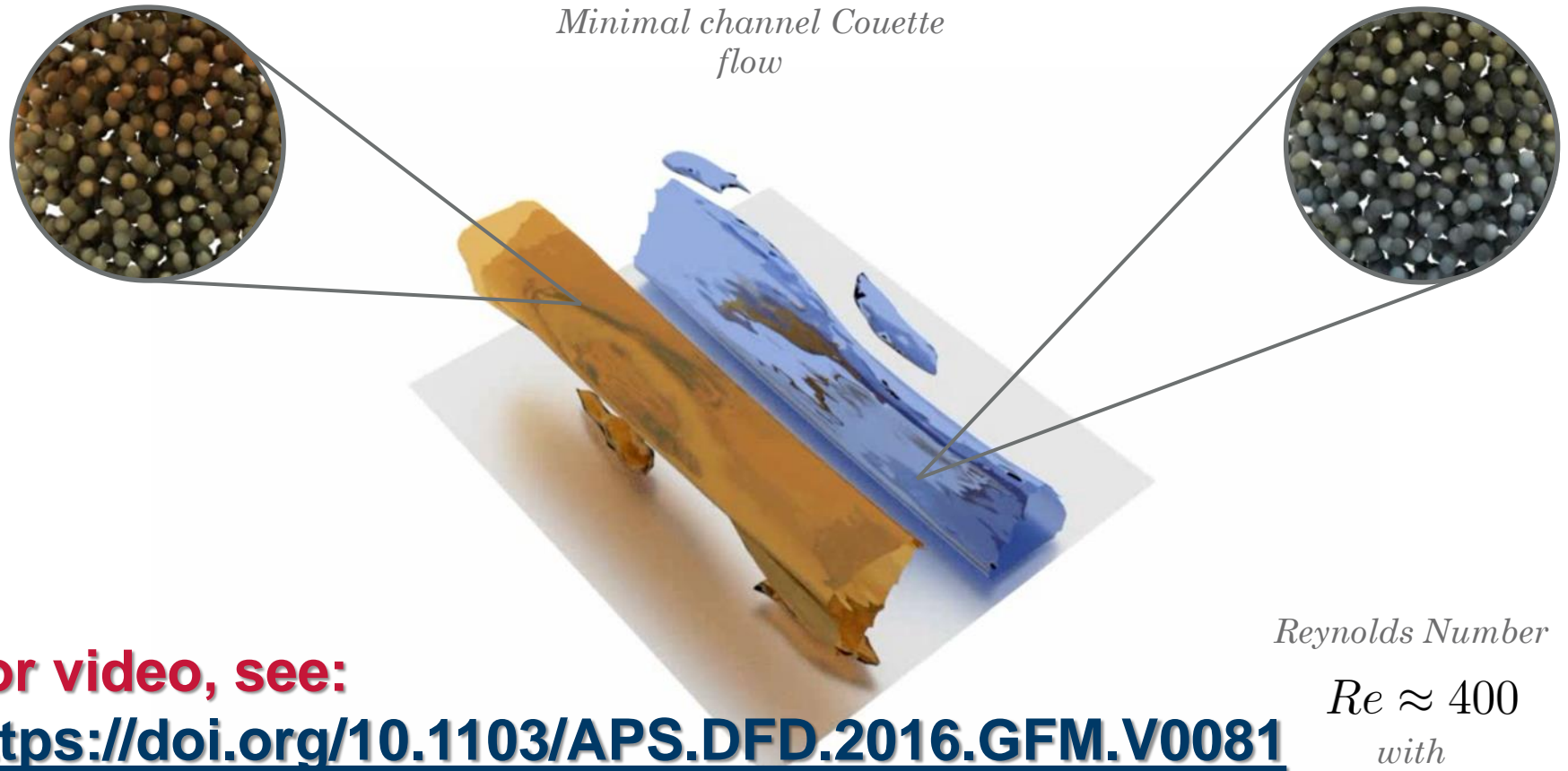
*Reynolds Number*

$$Re \approx 400$$

*with  
300 million  
molecules*

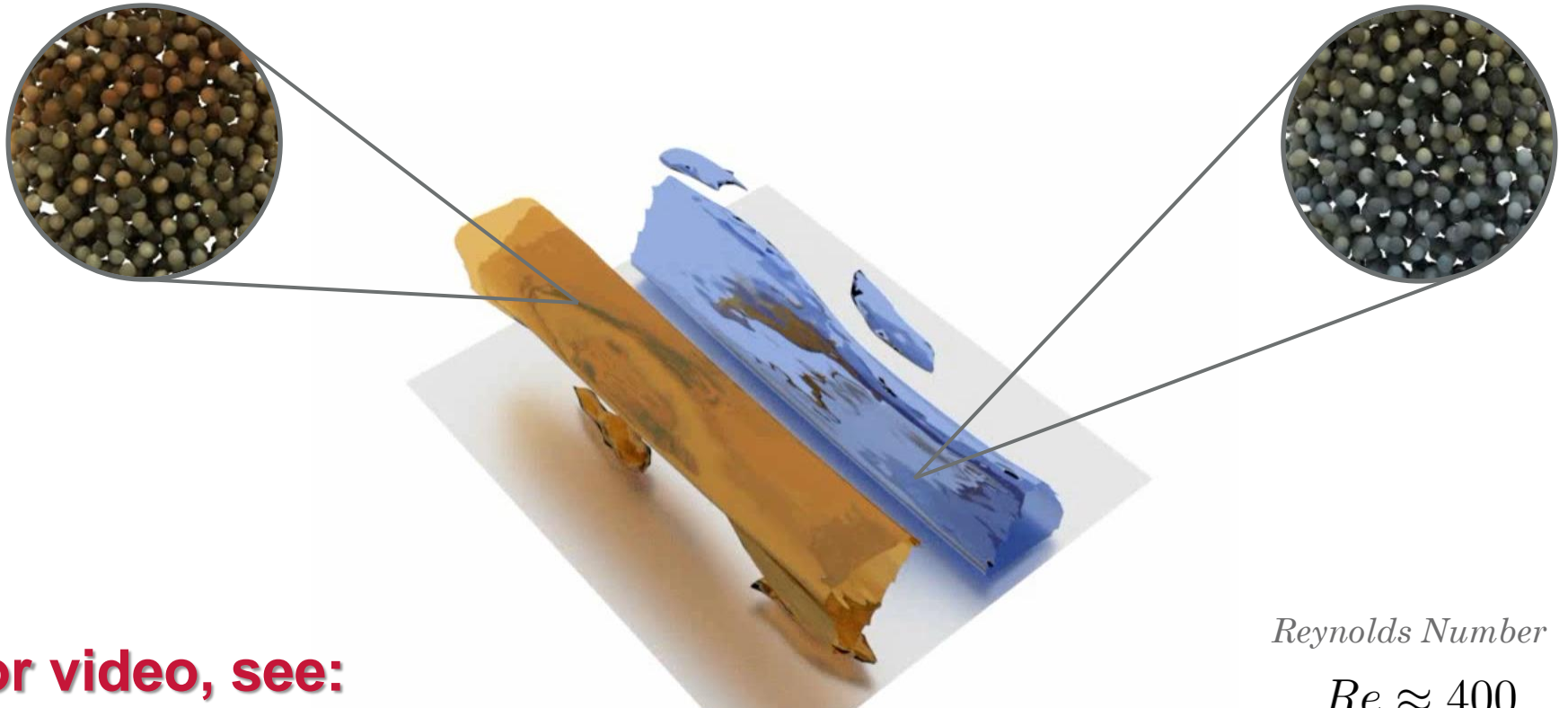


# Molecular Simulation of Turbulence



*Isosurfaces of turbulent kinetic energy coloured by velocity*

# Molecular Simulation of Turbulence



*Reynolds Number*

$Re \approx 400$

*with  
300 million  
molecules*

*Isosurfaces of turbulent kinetic  
energy coloured by velocity*

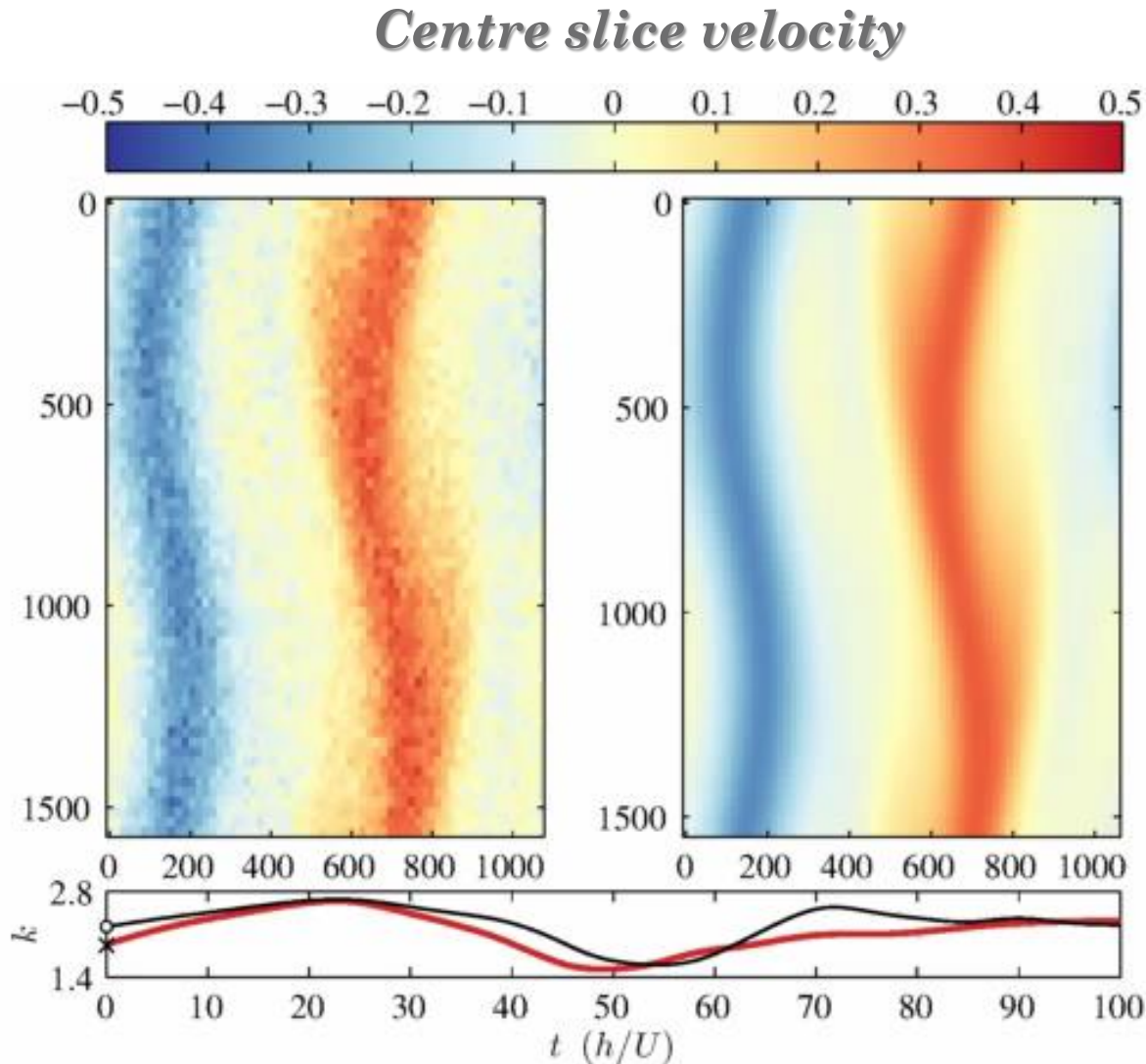
**For video, see:**

**<https://doi.org/10.1103/APS.DFD.2016.GFM.V0081>**

# Molecular Simulation of Turbulence

## MD

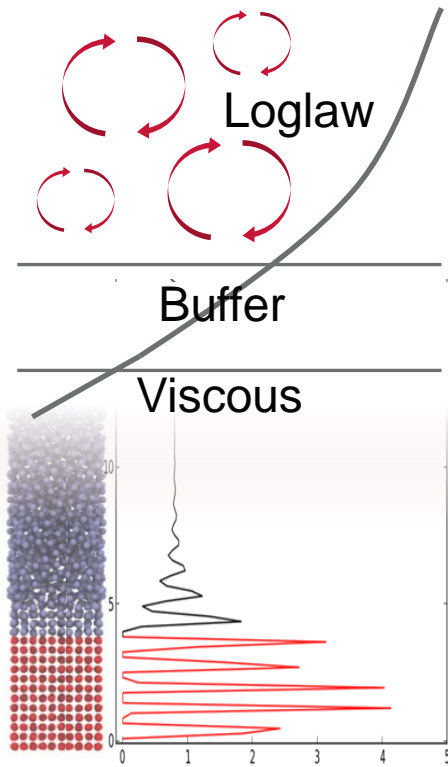
Own code written in Fortran and parallelised using MPI



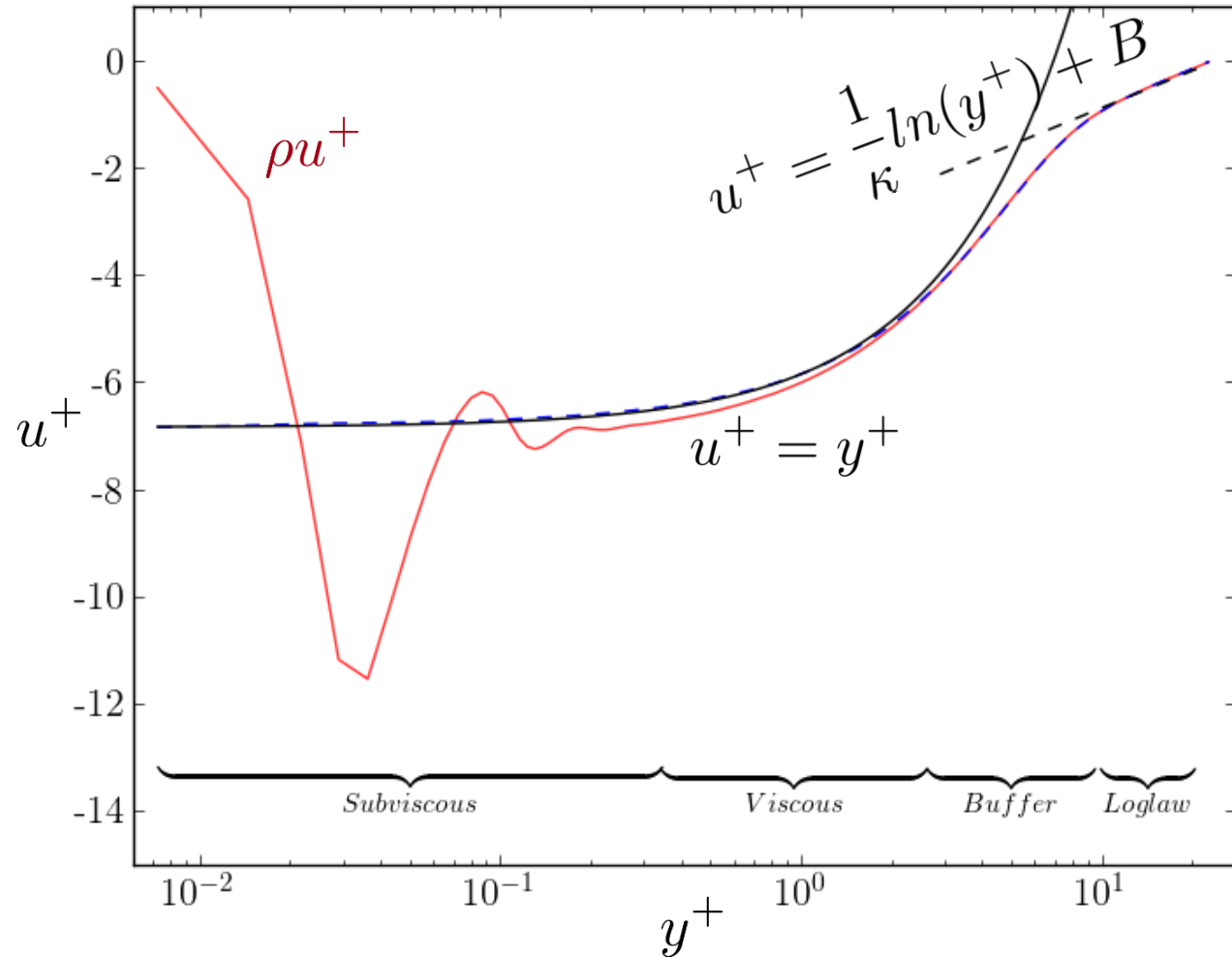
## CFD (Channelflow)

F. Gibson.  
Channelflow: A spectral Navier-Stokes simulator in C++.  
Technical report, U. New Hampshire, 2012.  
Channelflow.org.

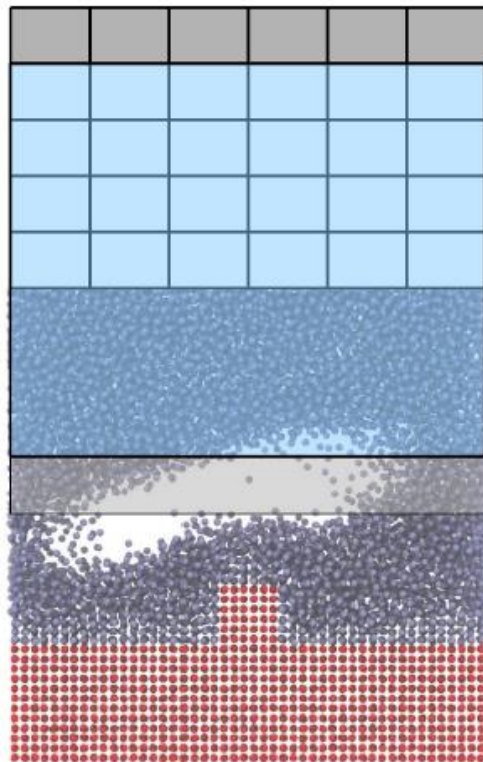
# Law of the wall



Subviscous? (MD)



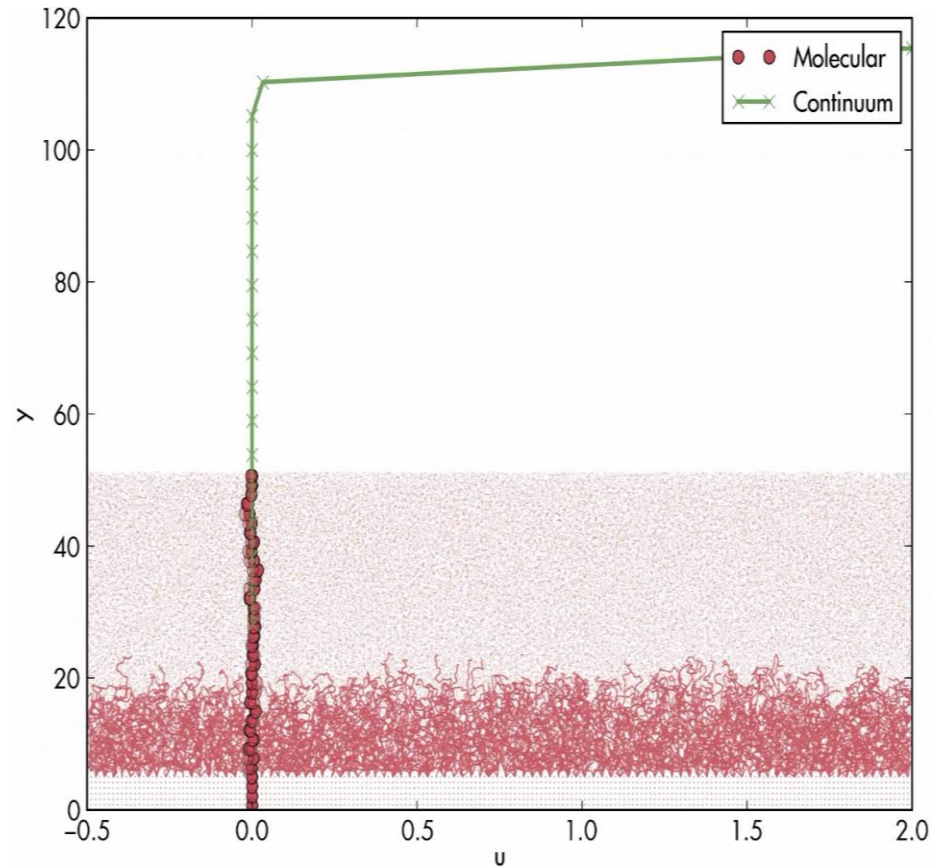
# Coupled Simulation (The Extension to Coupling)



CFD  
Region

Overlap  
Region

MD  
Region



With David Trevelyan, Lucian Anton, Eduardo Fernando-Ramez, David Heyes and Daniele Dini



## Coupled Simulation

- For turbulent flow, the timescales must evolve together; We cannot separate into pseudo-steady cases
- For nucleation the molecular provides an instance of an evolving bubble to the continuum
- Gain unique insight into the effect of wall textures, chemical coatings, effects of fouling, etc
- The timescales are very far from industrial, but validity of dimensionless analysis means we gain insight
- This assumption is the same in all types of coupled simulation – MD is representative of larger scale
- We still need large scale simulations and coupling allows system sizes which would be too expensive with MD

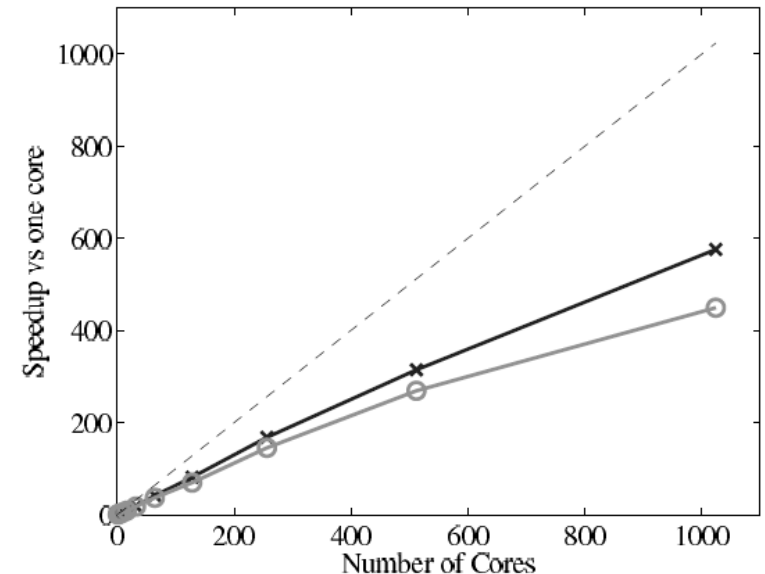
# Large Scale Simulation : CPL library

- Open Source ([www.cpl-library.org](http://www.cpl-library.org)) Fortran, C, C++ and Python bindings
- Designed to facilitate the linking of massively parallel codes with minimal impact on performance of each code
- Continuous integration testing, no external dependencies beyond standard packages and suite of Python and google tests
- Minimal set of functions and examples to lower barrier to entry for coupled simulation

## CPL LIBRARY

[ABOUT](#) [DOWNLOAD](#) [DOCUMENTATION](#) [FAQ](#) [CONTACT](#)

	Fluid Dynamics					cpl
					Coupled Simulation	

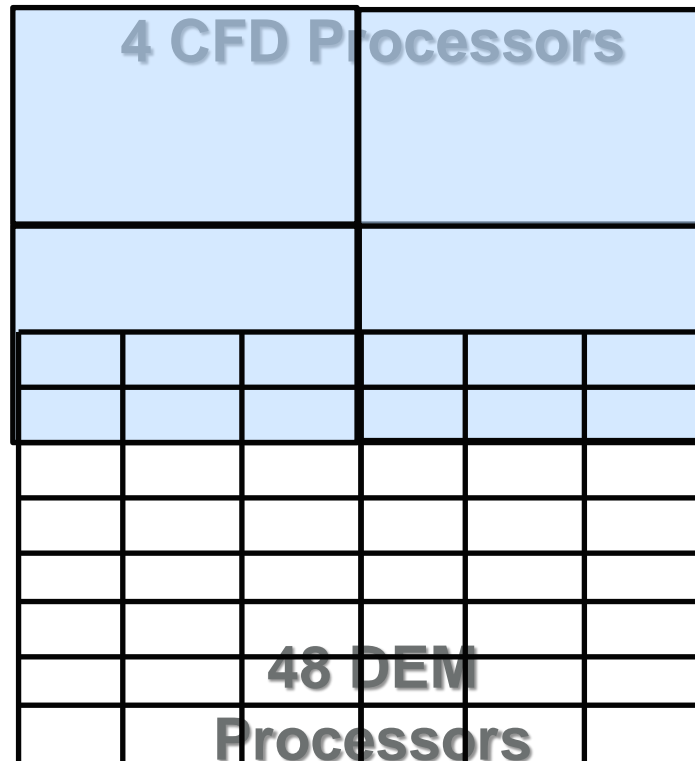


(a) Parallel speedup of the MD solver only (x), coupled code (o) against the ideal speedup (---)

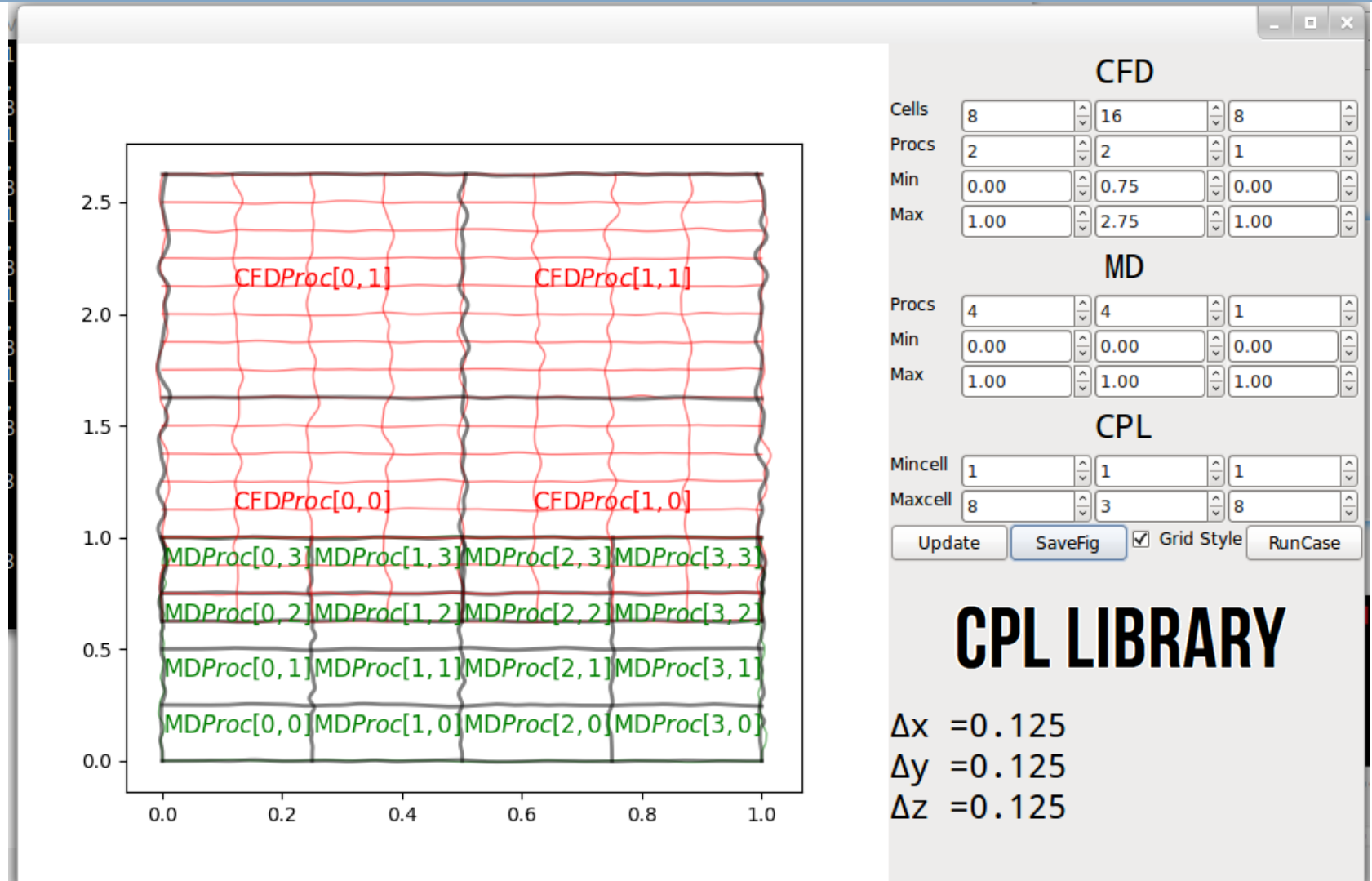




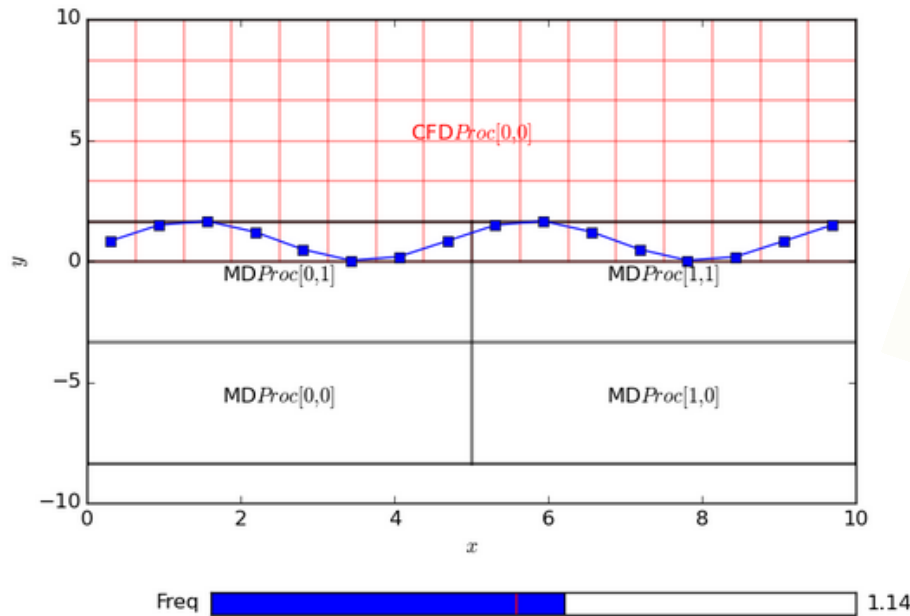
# Granular Mechanics



# Topology Design Tool



# Minimal Examples to Lower Barrier to Entry



**CPL LIBRARY**

## MINIMAL CFD AND MD CODE WITH COUPLING

Bringing the previous examples of topological setup and data exchange, along with a minimal CFD solver for the 2D unsteady diffusive equation,

$$\frac{\partial u}{\partial t} = \nu \left[ \frac{\partial^2 u}{\partial x^2} + \frac{\partial^2 u}{\partial y^2} \right]$$

## Key Points

- We need easy to use, well tested and highly scalable computing to lower barrier to entry
- Molecular Fluid Dynamics has the potential to be a rich area of research at the molecular **timescale!**
- Domain decomposition is NOT a boundary for CFD, it is for accelerating molecular simulation
- Molecular details are not simply an inconvenience to be ignored, many important insights
- Direct benefits to industry both from the new cases which are only possible with coupled simulation and from development of new closure relationships

# Coupling Overview

	A	B	C
1	Strain	Stress	
2	0.211	3.5	
3	0.352	4.2	
4	0.48	5.5	
5			

$$\mu = \mu(\mathbf{r}, t)$$

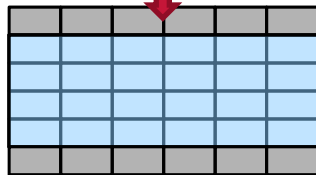
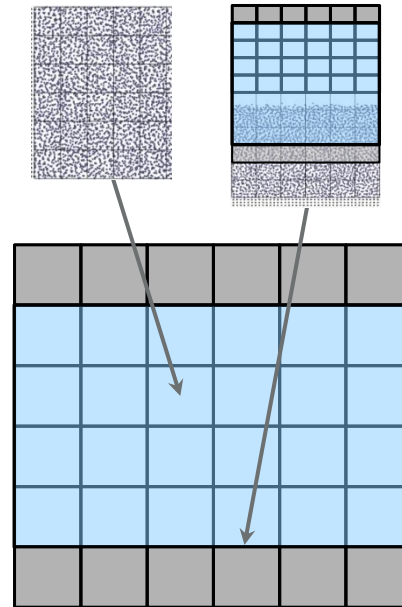
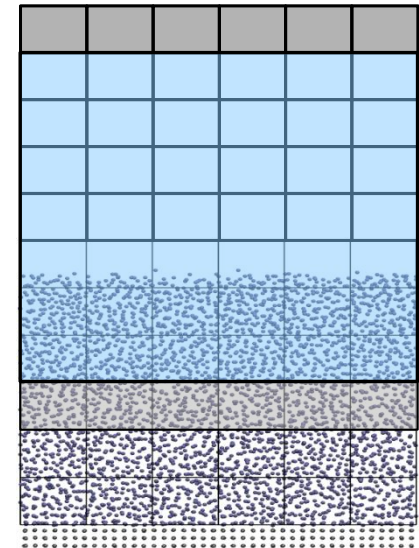


Table Lookup or Coefficients



Embedded Models (HMM)



Domain Decomposition

- Assumes phenomenon can be parameterised
- By using coupling we gain new data and new ways of doing this

- Separate **timescales** and lengthscales
- Assumes phenomenon can be modelled using steady state cases

- Same **timescale**
- Systems evolve together
- Limited to molecular scale studies but similarity is valid

**Thank you – Any Questions?**

Collaborations with David Heyes, Daniele Dini, Tamer Zaki,  
David Trevelyan, Eduardo Fernando-Ramos,  
Omar Matar, Erich Muller and Richard Craster