

Introduction to Molecular Dynamics simulations



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UNIVERSITY
OF MANITOBA

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□ High Performance Computing Analyst

- Grex: support for UofM users
- WestGrid and Compute Canada.
- Software and User Support.
- National teams:
 - ✓ BST: Bio-molecular Simulation Team.
 - ✓ RSNT: Research Support National Team.



□ Computational Physicist

- Monte Carlo and Molecular Dynamics codes.
- Study of the properties of materials using MD simulation.
- ❖ Metals, Glasses: Silica, Amorphous silicon, Nuclear Glasses.
- ❖ Mass transport, solid-liquid interfaces, kinetic coefficients, melting, crystallization, mechanical deformations, static and dynamical properties, He diffusion in glasses, ...

□ Classical Molecular Dynamics simulations:

- Introduction
- Classical MD: basics
- Algorithms and force fields used in MD
- Some results:
 - Crystallization of AlNi
 - Shear deformation in a-Si
 - Indentation

□ Setting and running MD simulations: LAMMPS:

- Introduction to LAMMPS
- Building LAMMPS: demonstration
- Running LAMMPS: demonstration
- Benchmarks and performance tests

Download the required material

❑ Use ssh client: PuTTy, MobaXterm, Terminal (Mac or Linux) to connect to cedar and/or graham:

- `ssh -Y username@cedar.computecanada.ca`
- `ssh -Y username@graham.computecanada.ca`

❑ Download the files using wget:

`wget https://ali-kerrache.000webhostapp.com/uofm/md.tar.gz`

`wget https://ali-kerrache.000webhostapp.com/uofm/md-slides.pdf`

❑ Unpack the archive and change the directory:

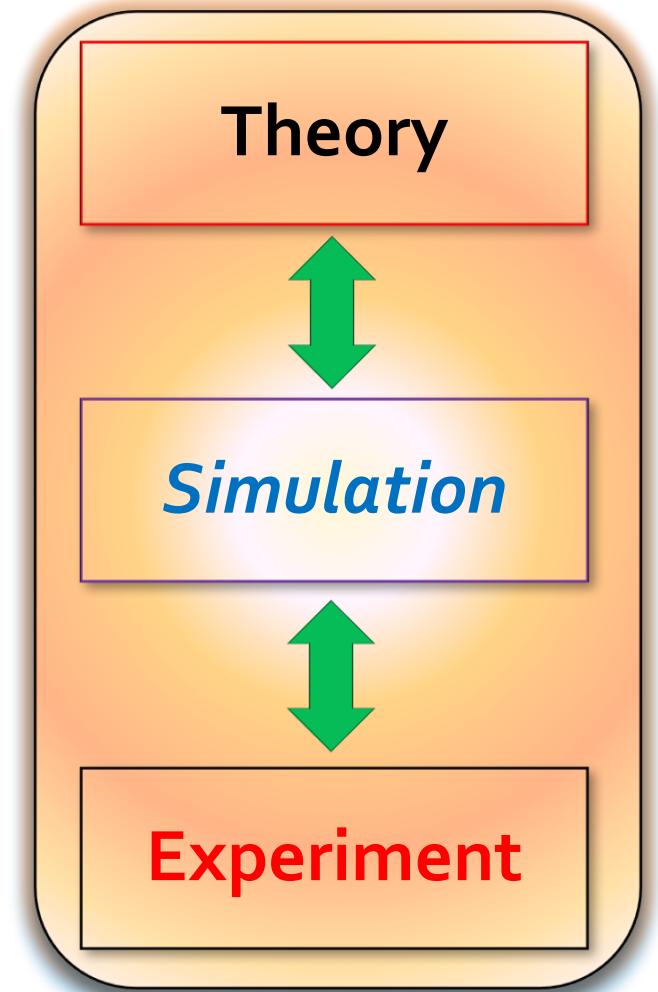
`tar -xvf md.tar.gz`

`cd UofM-Summer-School-MD`



Why do we need simulations?

- ❑ **Except for simple cases:** no analytical solutions for most of the problems.
- ❑ **In most cases, experiments are:**
 - Difficult or impossible to perform.
 - Too dangerous to ...
 - Expensive and time consuming.
 - Blind and too many parameters to control.
- ❑ **Simulation is a powerful tool:**
 - can replace some experiments.
 - provoke experiments.
 - explain and understand experiments.
 - complete the theory and experiments.

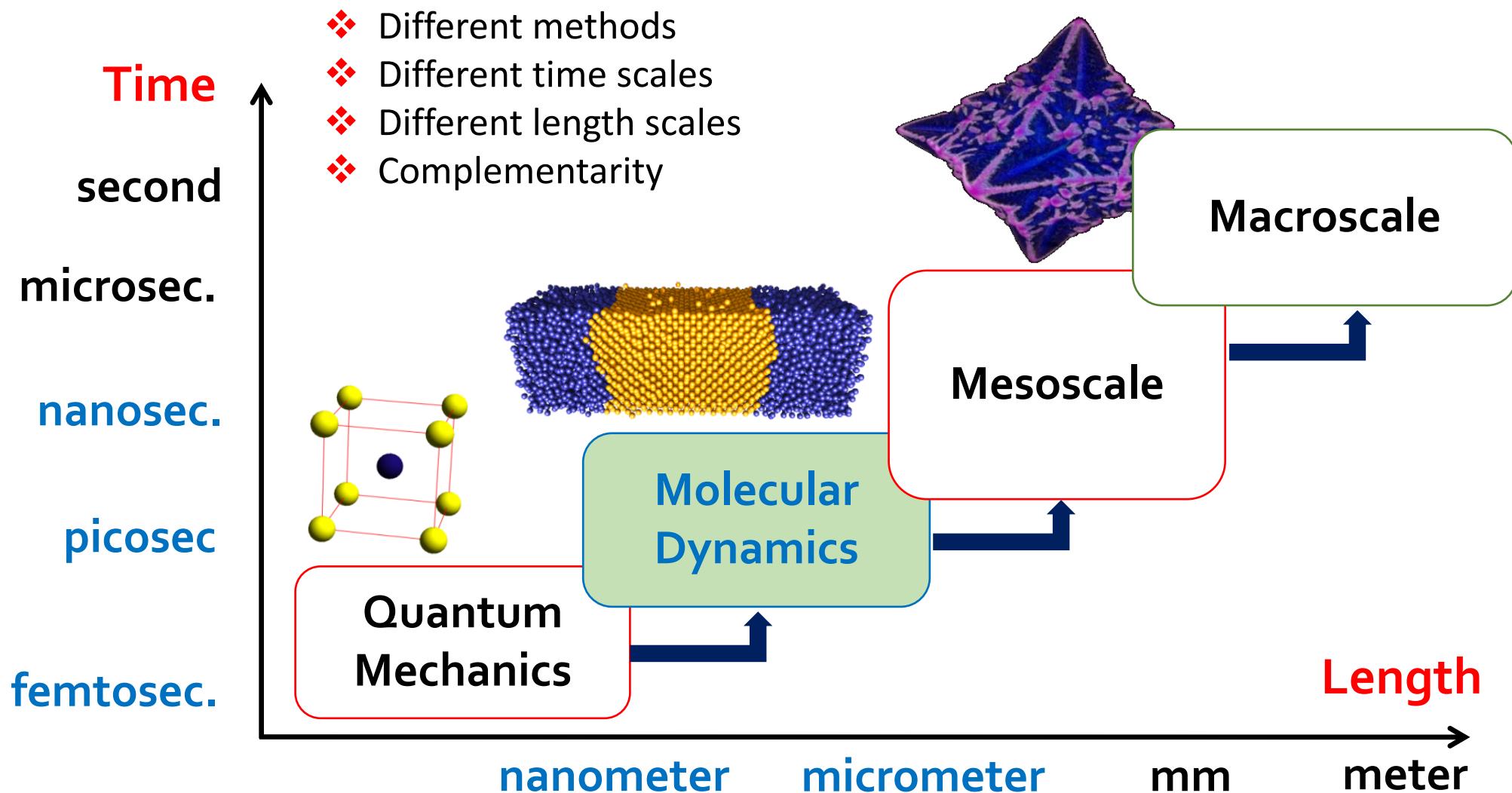


□ What are atomistic / molecular Simulation?

- a tool to get **insights** about the **properties of materials** at **atomic** or **molecular** level.
- used to predict and / or verify experiments.
- considered as a bridge between theory and experiment.
- provide a numerical solution when analytical ones are impossible.
- used to resolve the behavior of nature (the physical world surrounding us) on **different time-** and **length-scales**.

□ Applications, simulations can be applied in, **but not limited to**:

- ✓ Physics, Applied Physics, Chemistry, ...
- ✓ Materials and Engineering, ...
- ✓ and more ...



☐ Solution of Newton's equations:

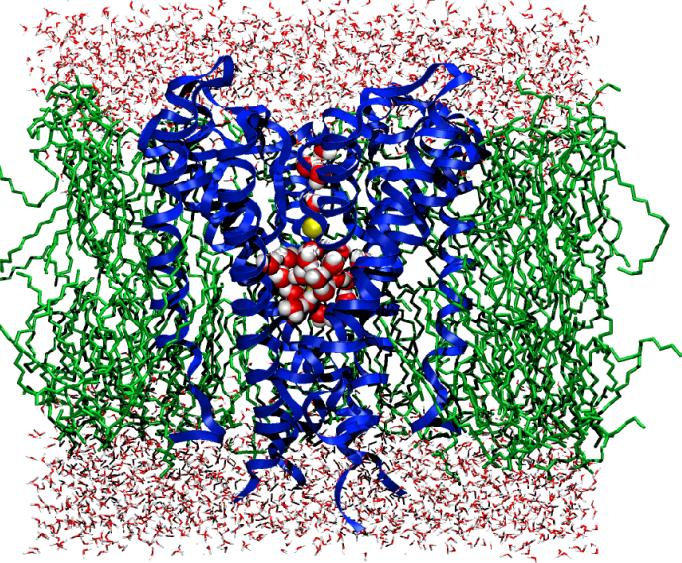
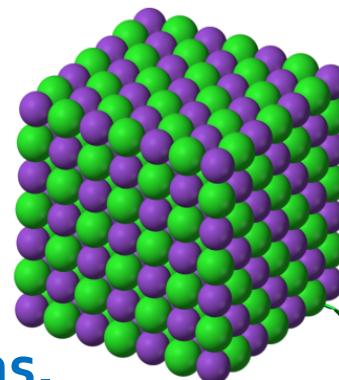
➤ MD is the **solution of the classical equations of motion** for a system of N atoms or molecules in order to obtain the time evolution of the system.

➤ Uses algorithms to integrate the equations of motion.

➤ **Applied to many-particle systems.**

➤ Requires the definition of a force field or potential to compute the forces.

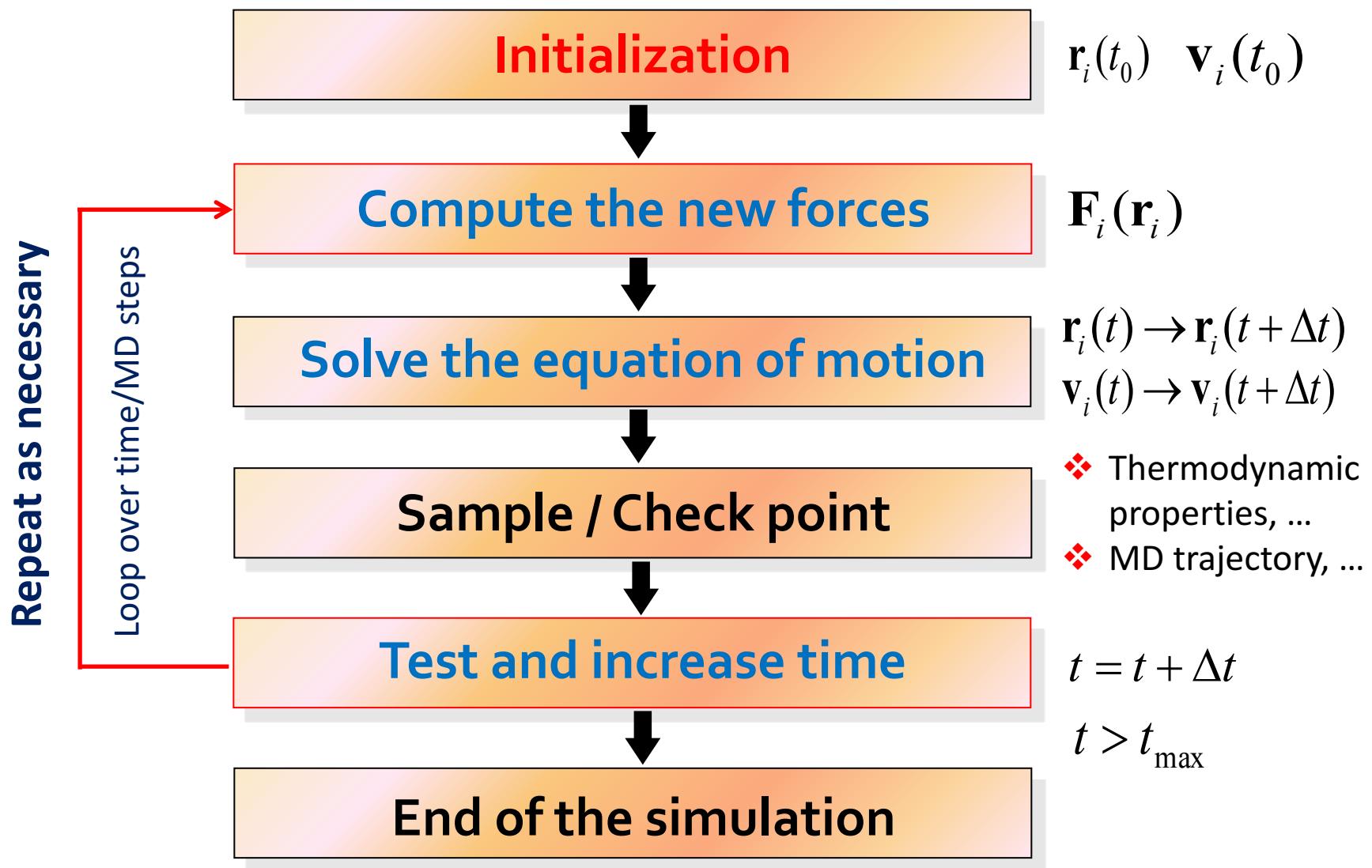
➤ **Potential fitting:** first principle calculations and experiments.



$$m_i \vec{a}_i = \vec{F}_i$$

$$\vec{F}_i = \sum_{j \neq i}^N \vec{f}_{ij}$$

$$\vec{f}_{ij} = -\vec{\nabla}_i V(r_{ij})$$



Potential function:

$$U(\mathbf{r}) = U_{bond}(\dots) + U_{non-bond}(\dots) + U_{ext}(\dots)$$

 Evaluate the forces acting on each particle:

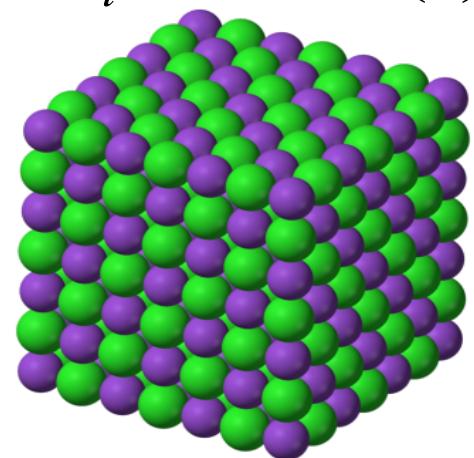
❖ The force on each atom is determined by:

- $U(\mathbf{r})$: potential function
- N : number of atoms in the system
- \mathbf{r}_{ij} : vector distance between atoms i and j

 Newton's equation of motion:

$$m_i \frac{d^2}{dt^2} \vec{x}_i = \vec{F}_i(\vec{x}_1, \dots, \vec{x}_N)$$

$$\mathbf{F}_i = -\nabla U(\mathbf{r})$$



$$i = 1 \dots N$$

Force Fields for MD simulations

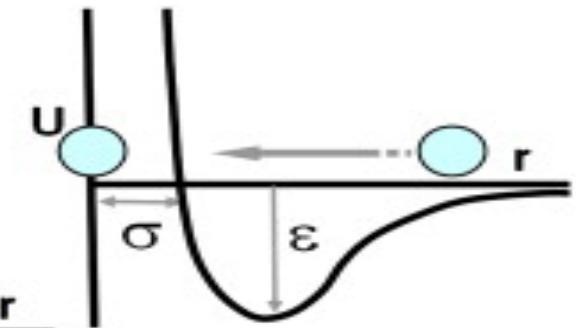
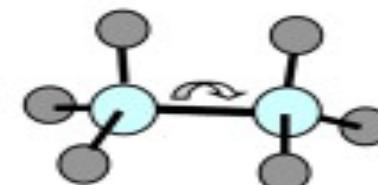
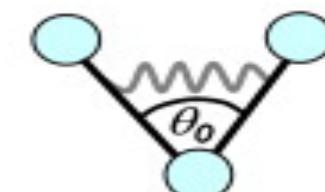
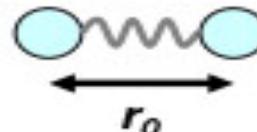
$$U = \sum_{i < j} \sum 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right]$$

$$+ \sum_{i < j} \sum \frac{q_i q_j}{4\pi\epsilon_0 r_{ij}}$$

$$+ \sum_{bonds} \frac{1}{2} k_b (r - r_0)^2$$

$$+ \sum_{angles} \frac{1}{2} k_a (\theta - \theta_0)^2$$

$$+ \sum_{torsions} k_\phi [1 + \cos(n\phi - \delta)]$$



Interactions:

- Lenard-Jones
- Electrostatic
- Bonds
- Orientation
- Rotational

Derivation of Verlet algorithm

Taylor's expansions :

$$r(t + \Delta t) = r(t) + \dot{r}(t)\Delta t + \frac{1}{2} \ddot{r}(t)\Delta t^2 + \frac{1}{6} \dddot{r}(t)\Delta t^3 + O(\Delta t^4) \quad (I)$$

$$r(t - \Delta t) = r(t) - \dot{r}(t)\Delta t + \frac{1}{2} \ddot{r}(t)\Delta t^2 - \frac{1}{6} \dddot{r}(t)\Delta t^3 + O(\Delta t^4) \quad (II)$$

Add (I) and (II):

$$r(t + \Delta t) + r(t - \Delta t) = 2r(t) + \ddot{r}(t)\Delta t^2 + O(\Delta t^4)$$

or :

$$r(t + \Delta t) = 2r(t) - r(t - \Delta t) + f(t)\Delta t^2 / m + O(\Delta t^4) \quad (II)$$

Subtract (II) from (I) :

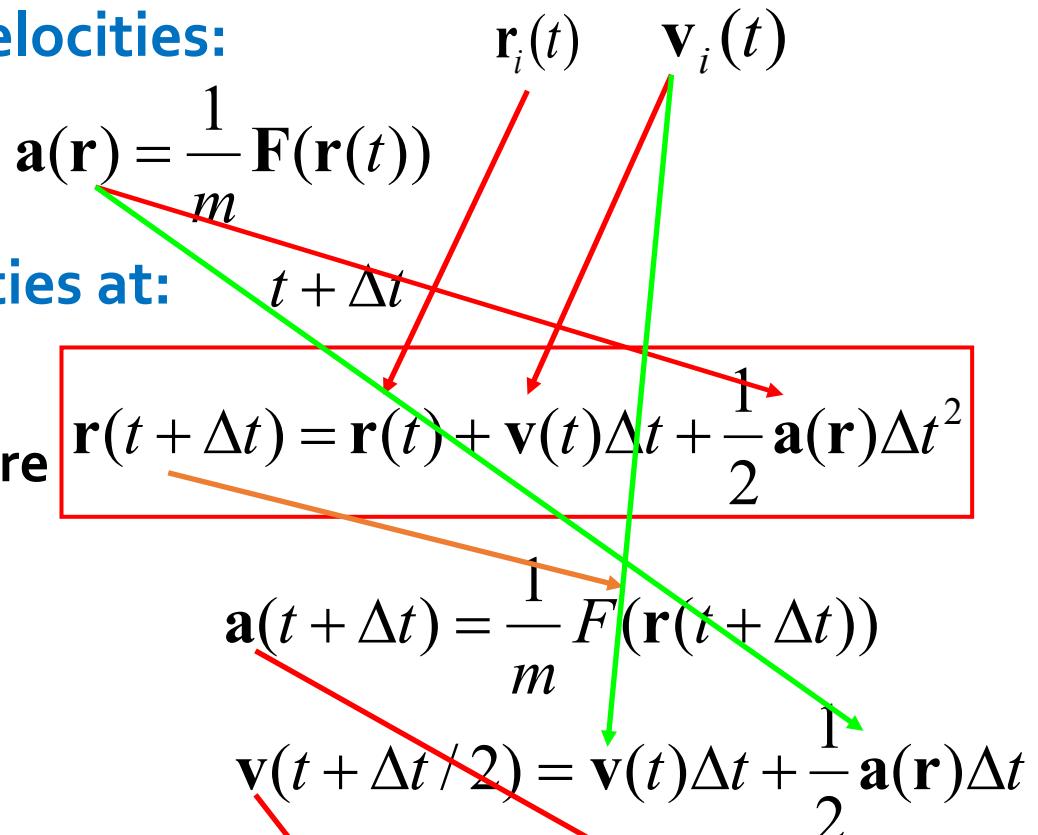
$$r(t + \Delta t) - r(t - \Delta t) = 2\dot{r}(t)\Delta t + O(\Delta t^3)$$

or :

$$v(t) = (r(t + \Delta t) - r(t - \Delta t)) / 2\Delta t + O(\Delta t^2)$$



□ From the initial positions and velocities:



□ Obtain the positions and velocities at:

- velocity calculated explicitly
- possible to control the temperature
- stable in long simulation
- most used algorithm

❖ Leap-Frog algorithm

$$\mathbf{v}(t + \frac{\Delta t}{2}) = \mathbf{v}(t - \frac{\Delta t}{2}) + \frac{\mathbf{F}(t)}{m} \Delta t$$

$$\mathbf{r}(t + \Delta t) = \mathbf{r}(t) + \mathbf{v}(t + \frac{\Delta t}{2}) \Delta t$$

□ Predictor step:

- from the initial $\mathbf{r}_i(t), \mathbf{v}_i(t)$ → $\mathbf{a}(\mathbf{r}) = \frac{1}{m} \mathbf{F}(\mathbf{r}(t))$
- predict $\mathbf{r}_i(t + \Delta t), \mathbf{v}_i(t + \Delta t)$ using Taylor's series

$$\mathbf{r}^P(t + \Delta t) \cong \mathbf{r}(t) + \mathbf{v}(t)\Delta t + \frac{\mathbf{a}(t)}{2}\Delta t^2$$

$$\mathbf{v}^P(t + \Delta t) \cong \mathbf{v}(t) + \mathbf{a}(t)\Delta t$$

$$\mathbf{a}^P(t + \Delta t) \cong \mathbf{a}(t) + \mathbf{r}^{iii}(t)\Delta t \quad \mathbf{r}^{iii}: \text{3rd order derivatives}$$

□ Corrector step:

- get corrected acceleration:

$$\mathbf{a}^C(\mathbf{r}) = \frac{\mathbf{F}(\mathbf{r}^P(t + \Delta t))}{m}$$

- using error in acceleration:

$$\Delta \mathbf{a}(t + \Delta t) \cong \mathbf{a}^C(t + \Delta t) - \mathbf{a}^P(t + \Delta t)$$

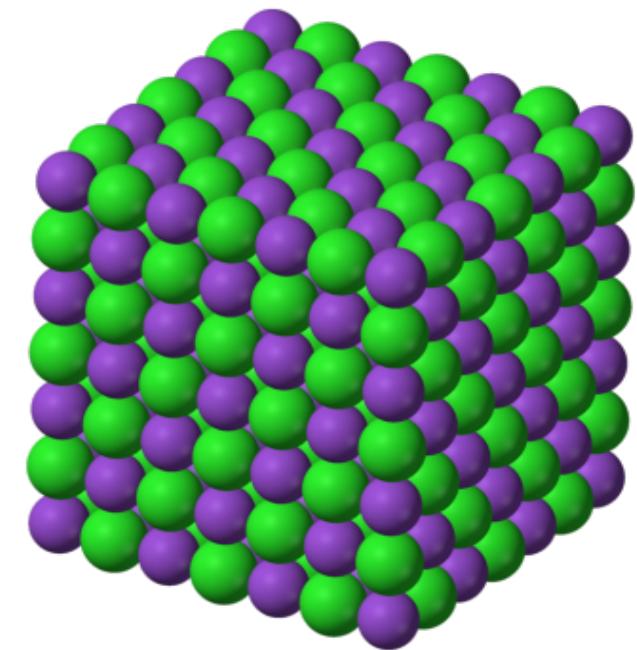
$$\mathbf{r}(t + \Delta t) \cong \mathbf{r}^P(t + \Delta t) + C_0 \frac{\Delta t^2}{2} \Delta \mathbf{a}(t + \Delta t)$$

$$\mathbf{v}(t + \Delta t) \cong \mathbf{v}^P(t + \Delta t) + C_1 \Delta t \Delta \mathbf{a}(t + \Delta t)$$

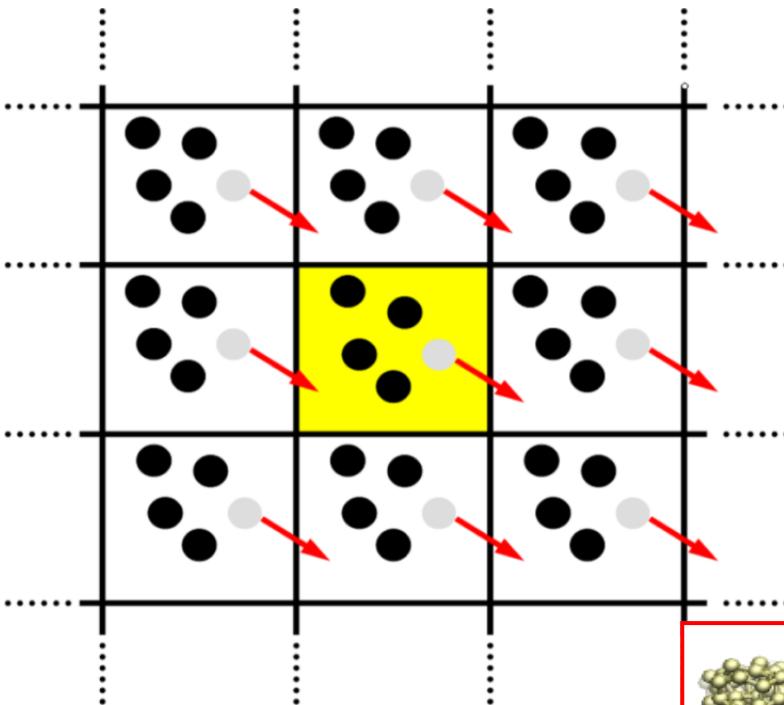
C_n : constants depending accuracy



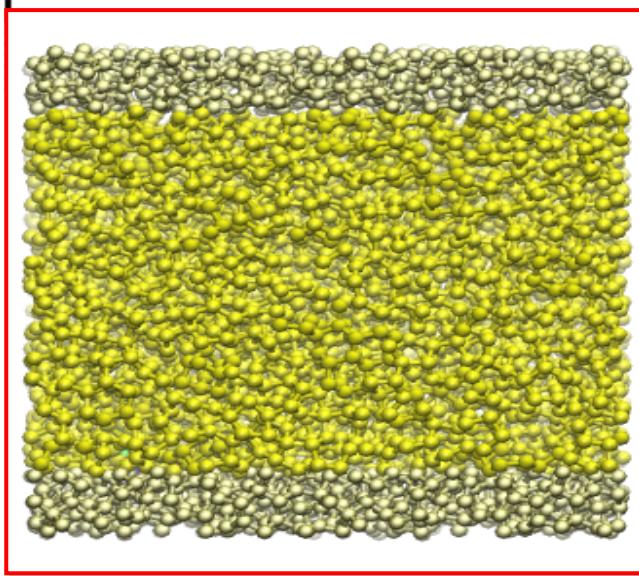
- Starting configuration:
 - Atomic positions (x,y,z)
 - density, mass, charge,
- Initial velocities: depend on temperature
- boundary conditions (PBC):
 - PBC: required to simulate bulk properties.
 - or fixed boundary conditions
- set the appropriate potential:
 - available and supported potentials
 - depend on the system to simulate (literature search).
- set the appropriate time step: should be short (order of 1fs).
- set the temperature and pressure control:
 - define the thermodynamic ensemble (NVT, NPT, NVE, ...).
- Fix run time and customize the output: depend on the software.



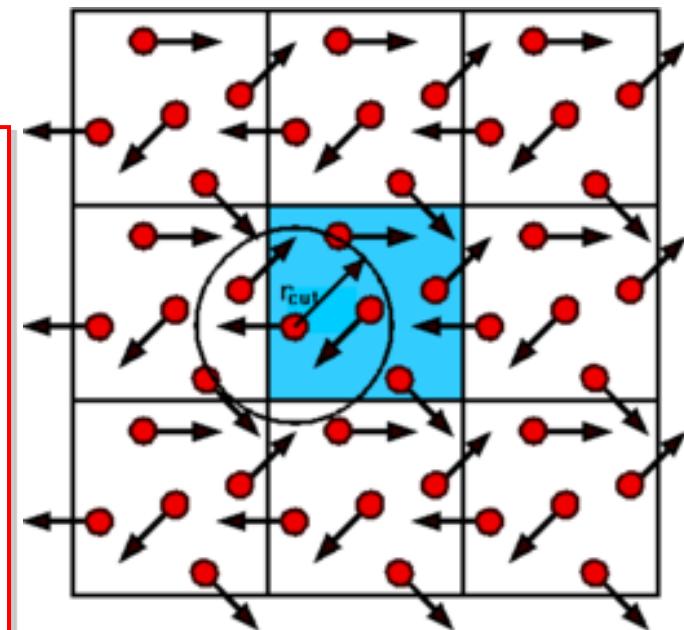
Boundary conditions



- PBC:
in x, y directions
- Walls:
fixed boundaries
in z direction.



- create **images** of the simulation box:
duplication in all directions (x, y and z)
- if an atom is moving out of boundary,
it comes from the other side.
- used also in pair interactions evaluation



- Optimization of MD algorithms:
- Evaluating the forces is **time consuming**:
 - ❖ Pair potential calculation: $\propto O(N^2)$
 - ❖ Atom moves $< 0.2 \text{ \AA}^\circ$ per time step
 - ❖ **Cutoff radius**: not necessary to include all the possible pairs.

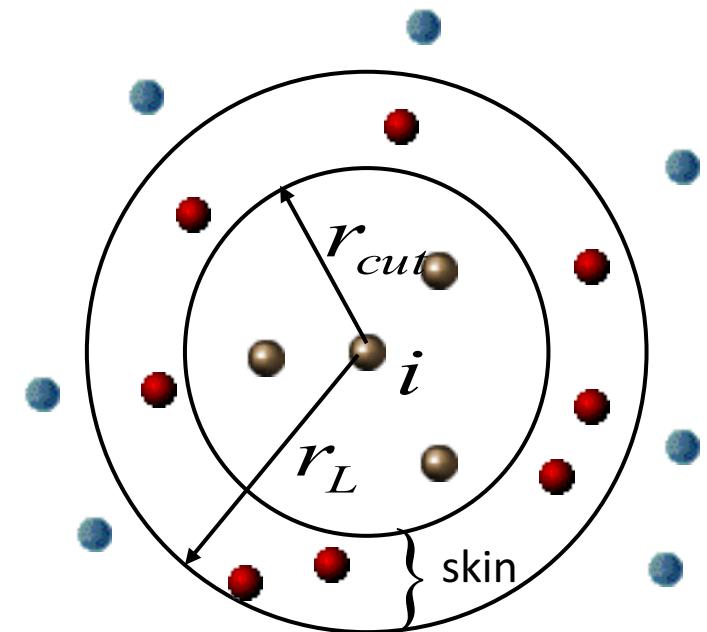
Solution: Verlet neighbor list

- Containing all neighbors of each atom

within: r_L

- Update every N_L steps

For each particle: $N-1$ pairs.
For N particles: $N(N-1)$ pairs.



$$r_L - r_{cut} > \frac{N_L \bar{v} \Delta t}{2}$$

❑ Ensembles:

- **NVE** – micro-canonical ensemble
- **NVT** – canonical ensemble
- **NPT** – grand-canonical ensemble
- others ...

Each ensemble is used for a specific simulation:

- Equilibration, ...
- Production run, ...
- Diffusion (**NVE**), ...

❑ Temperature control:

- Berendsen thermostat (velocity rescaling)
- Andersen thermostat
- Nose-Hoover chains

- ✓ Choose the ensemble that best fits your system and the properties you want to simulate
- ✓ start the simulation.
- ✓ Check the thermodynamic properties as a function of time.

❑ Pressure control:

- Berendsen volume rescaling
- Andersen piston



□ Goal of MD simulations:

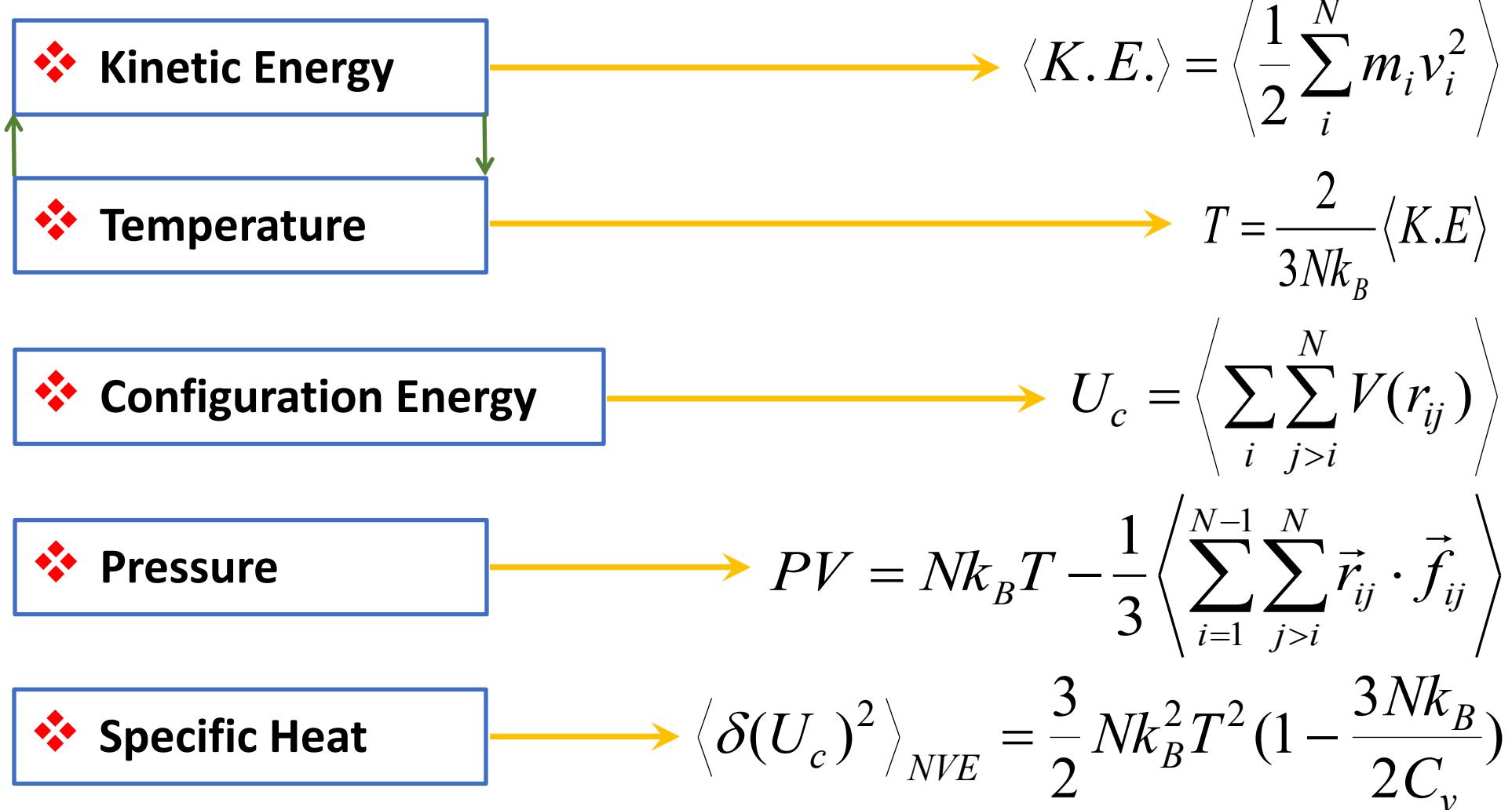
- The prime purpose of MD is to sample the *phase space* of the statistical mechanics ensemble.
- Most physical properties can be related the atomic trajectories and obtained as average as a function of time.

□ Structural properties:

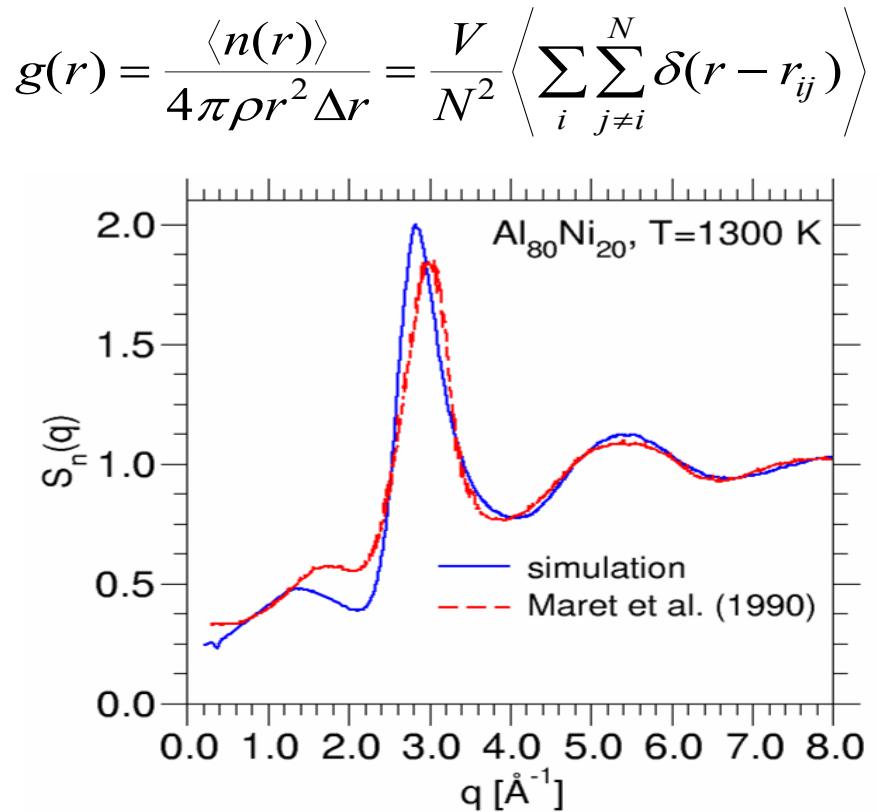
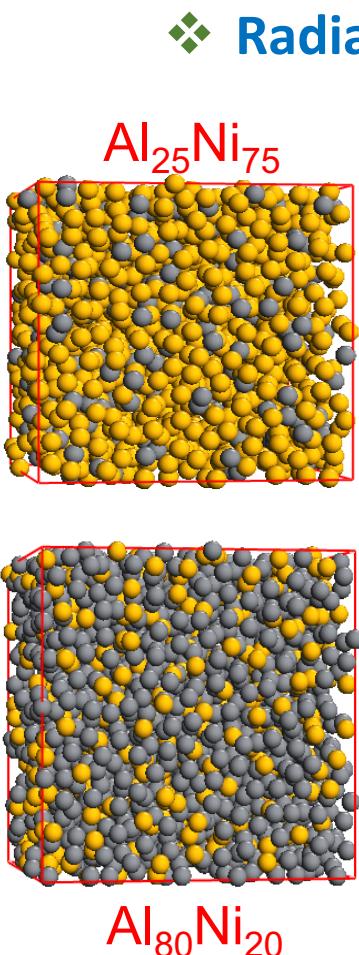
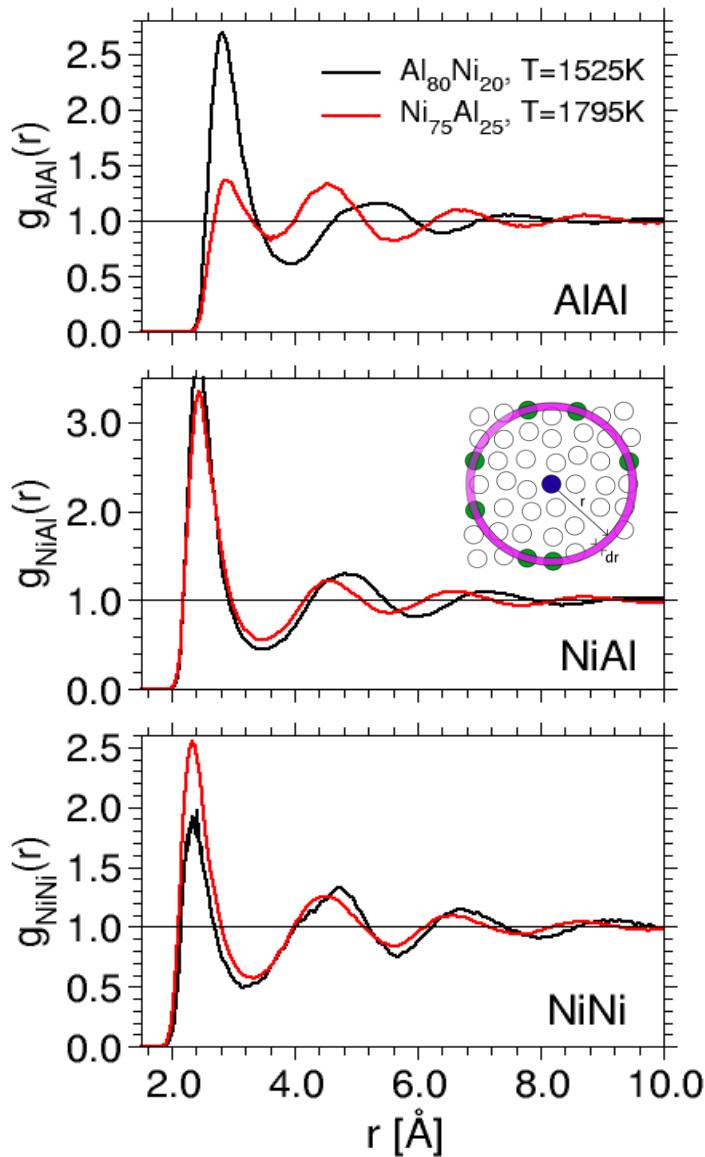
- obtained from spatial correlation functions e.g. distribution functions (RDF, S(Q), Van-Hove, ...).

□ Dynamical Properties:

- Time dependent properties (MSD, diffusion coefficients) obtained via temporal correlation functions e.g. velocity autocorrelation function, atomic displacements.



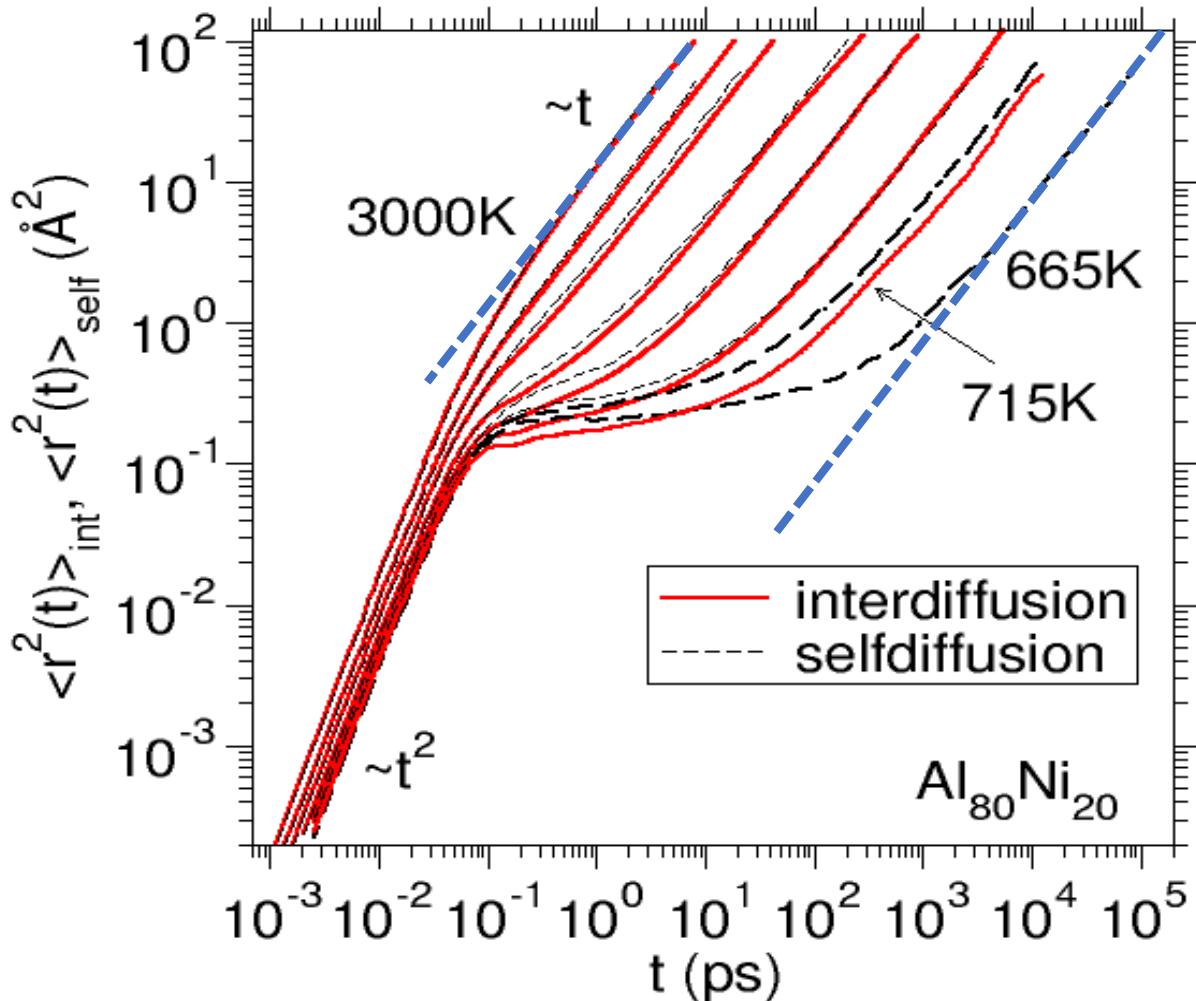
Structural properties



$$S(k) = 1 + 4\pi\rho \int_0^\infty \frac{\sin(kr)}{kr} (g(r) - 1) r^2 dr$$

➤ Structure Factor (experiments)

MSD: Mean Square Displacement (Einstein relation)



$$2Dt = \frac{1}{3} \left\langle |\mathbf{r}_i(t) - \mathbf{r}_i(0)|^2 \right\rangle$$

$$\text{MSD} = c_{\text{Al}} \left\langle (\vec{r}_{\text{s},\text{Ni}}(t) - \vec{r}_{\text{s},\text{Ni}}(0))^2 \right\rangle + c_{\text{Ni}} \left\langle (\vec{r}_{\text{s},\text{Al}}(t) - \vec{r}_{\text{s},\text{Al}}(0))^2 \right\rangle$$

Diffusion constants

$$D = \lim_{t \rightarrow \infty} \frac{1}{N} \sum_{i=1}^N \frac{\left\langle (r_i(t) - r_i(0))^2 \right\rangle}{6t}$$

- **The Art of Molecular Dynamics Simulation**, D.C. Rapaport, Camb. Univ. Press (2004)
- **Understanding Molecular Simulation**, D. Frenkel and B. Smit, Academic Press (2002).
- **Computer Simulation of Liquids**, M.P. Allen and D.J. Tildesley, Oxford (1989).
- **Theory of Simple Liquids**, J.-P. Hansen and I.R. McDonald, Academic Press (1986).
- **Classical Mechanics**, H. Goldstein, Addison Wesley (1980).
- **Glassy Materials and Disordered Solids, An Introduction to their Statistical Mechanics**, 2nd edition, Kob, Walter and Binder, K., 2011

Open source: free access

- ✓ **LAMMPS:** <http://lammps.sandia.gov/index.html>
- ✓ **DL_POLY:** <http://www.scd.stfc.ac.uk/SCD/44516.aspx>
- ✓ **CP2K:** <https://www.cp2k.org/about>
- ✓ **NAMD:** <http://www.ks.uiuc.edu/Research/namd/>
- ✓ **GROMACS:** <http://www.gromacs.org/>
- ✓

Commercial software: Amber

- ✓ **Amber:** <http://ambermd.org/>

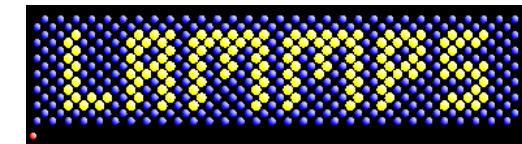
Home made codes:

- ✓ **C, C++**
- ✓ **Fortran, ... etc.**
- ✓ **Python, ... etc.**

Visualization:

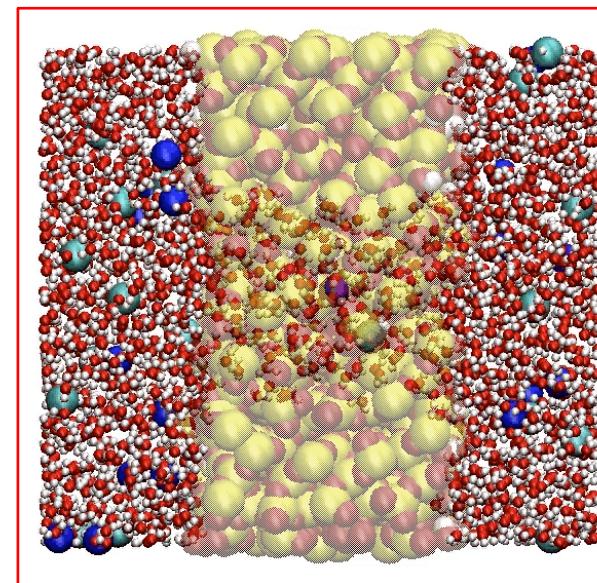
- **VMD**
- **OVITO, ...**

Analysis?



GROMACS
FLEXIBLE

NAMD
Scalable Molecular Dynamics



Flow of
water
and
ions
thru a
silica
pore

□ Binary Metallic alloys:

- Melting and crystallization.
- Solid-Liquid interfaces.
- Crystal growth from melt.
- Crystal growth is diffusion limited process.



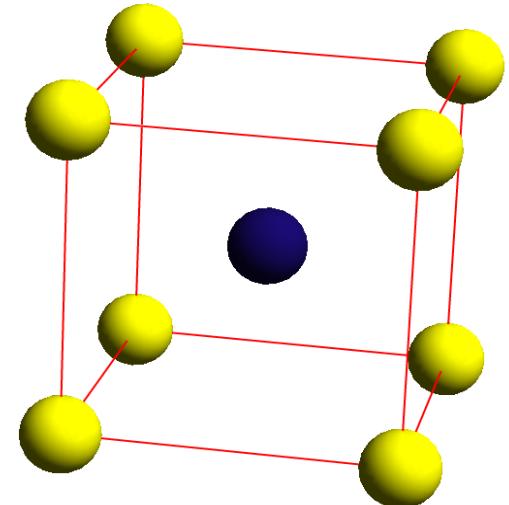
□ Glasses:

- Shear deformations in amorphous materials
- How to prepare a glass using MD simulation?
- Glass Indentation using MD.



Why $B_2\text{-Al}_{50}\text{Ni}_{50}$?

- ✓ $B_2\text{-Al}_{50}\text{Ni}_{50}$: prototype of binary ordered metals
- ✓ simulations of interfacial growth in binary systems rare
- ✓ growth kinetics of binary metals: diffusion limited?
- ✓ crystal growth slower than in one-component metals
- ✓ understand crystal growth of alloys on microscopic level



Questions:

- crystal growth & accurate estimation of T_m ?
- solid-liquid interface velocity from interface motion?
- kinetic coefficients and their anisotropy?
- solid-liquid interface motion controlled by mass diffusion?
- solid-liquid coexistence, interface structure?
- how to distinguish between solid-like & liquid-like particles?

- Frenkel J., Phys. Z. Sowjetunion, **1** (1932) 498.
- Wilson H.A., Philos. Mag., **50** (1900) 238.

solve Newton's equation of motion for system of N particles:

- velocity Verlet algorithm (time step = 1 fs)

- NPT ensemble:

 - constant pressure (Anderson algorithm): $p = 0$

 - constant temperature: stochastic heat bath

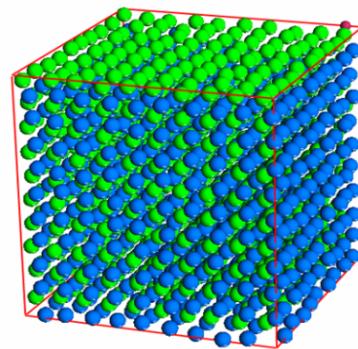
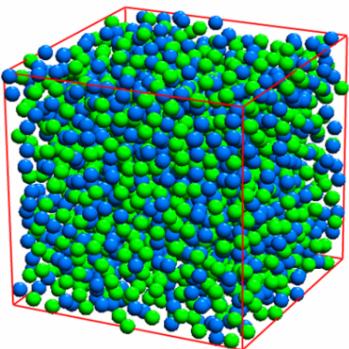
- periodic boundary conditions in all directions

Allen M.P. and Tildesley D.J.,

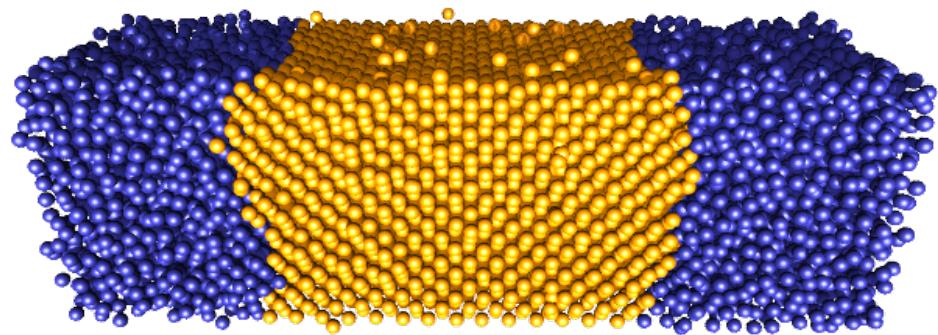
Computer simulation of liquids, 1987

Anderson H.C., JCP 72 (1980) 2384

MD of pure systems



MD of inhomogeneous systems



- lattice properties
- T dependence of density
- Structural quantities
- Self-diffusion constant

- accurate melting temperature T_m
- kinetic coefficients & their anisotropy
- solid-melt interface structure
- crystal growth

- ❑ Binary metallic mixtures - simple: Lennard-Jones potential
- better: EAM
- ❑ EAM potential:

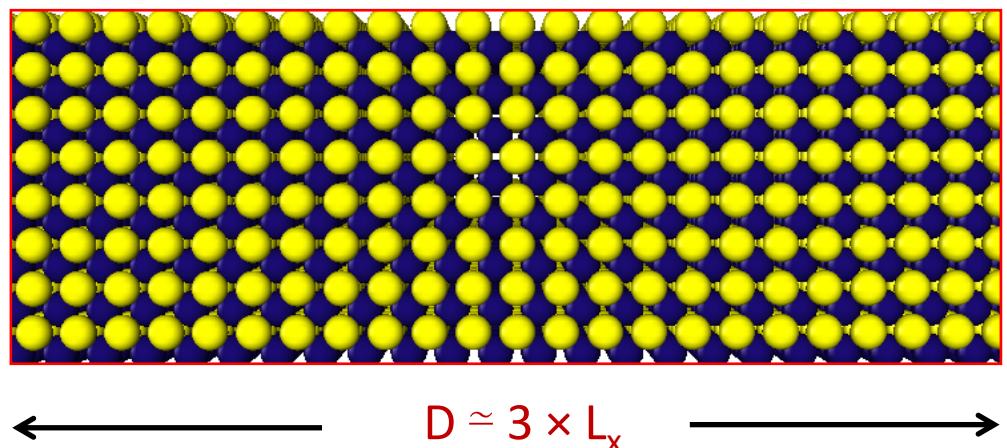
- two body interactions.
- many body interactions (e-density).
- fitting to both experimental and *ab-initio* data.
- reproduces the lattice properties & point defects.
- structure and dynamics of AlNi melts.

$$U_{\text{pot}} = \frac{1}{2} \sum_{k,l} u(r_{kl}) + \sum_k F(\bar{\rho}_k)$$

$$\bar{\rho}_k = \sum_{l \neq k} \rho_l(r_{kl})$$

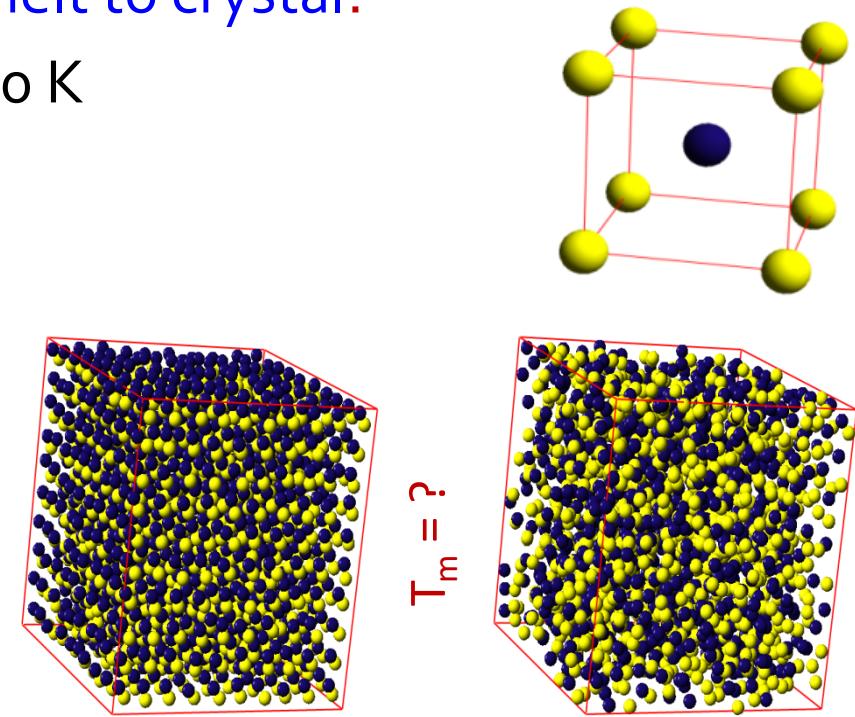
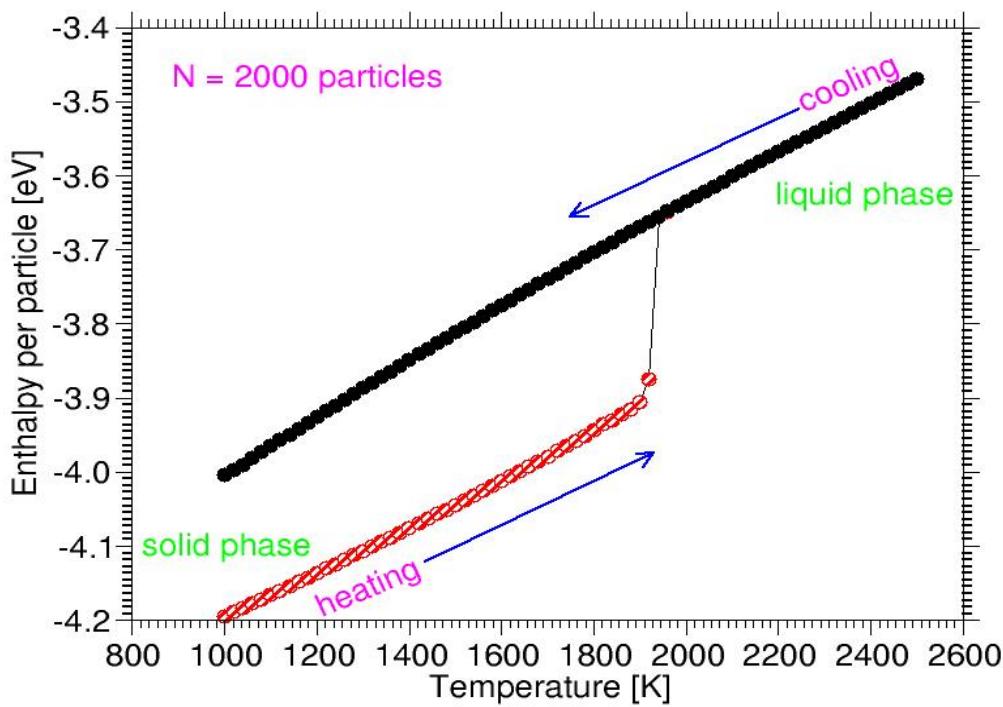
Y. Mishin *et al.*, PRB **65**, (2002) 224114.
J. Horbach *et al.*, PRB **75**, (2007) 174304.

- Solid and liquid properties:
2000 particles ($L_x = L_y = L_z = 24.6 \text{ \AA}$)
- Solid-liquid interfaces (N particles):
 $N_{\text{Al}} = N_{\text{ni}} \Rightarrow D = L_z \simeq 3 \times L_x \simeq 3 \times L_y$
10386 and 12672 particles, ... or more



Heating and cooling: pure phases

- How to go from crystal to melt & from melt to crystal?
- ✓ start from B₂ phase: equilibration at 1000 K
- ✓ try to melt the crystal: heating process
- ✓ cool down the melt: cooling process

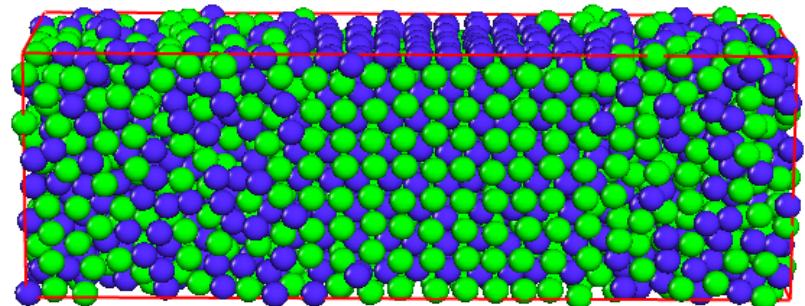


- binary alloys: glass formers.
- crystallization: process too slow
- brute force method:
not appropriate to estimate T_M

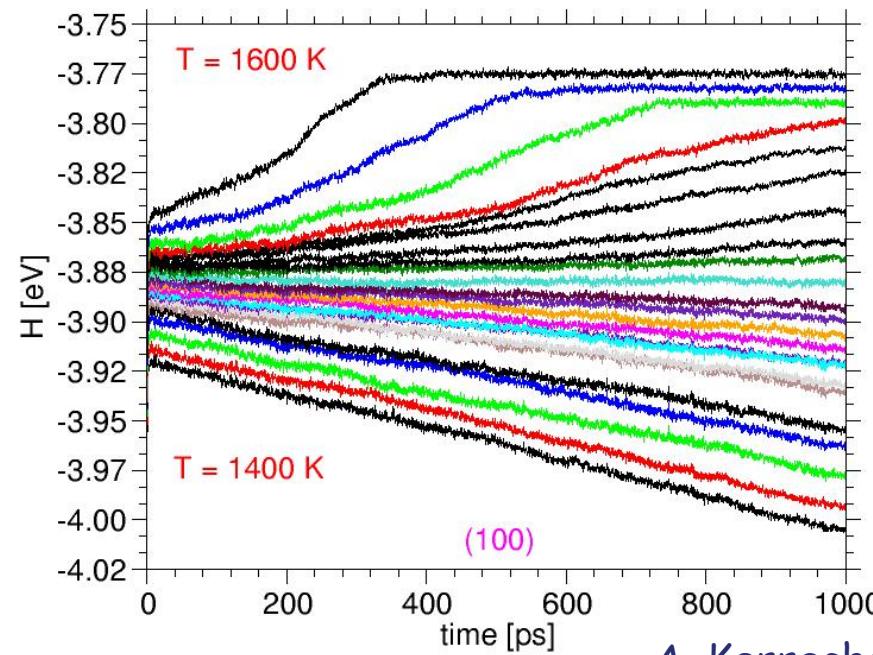
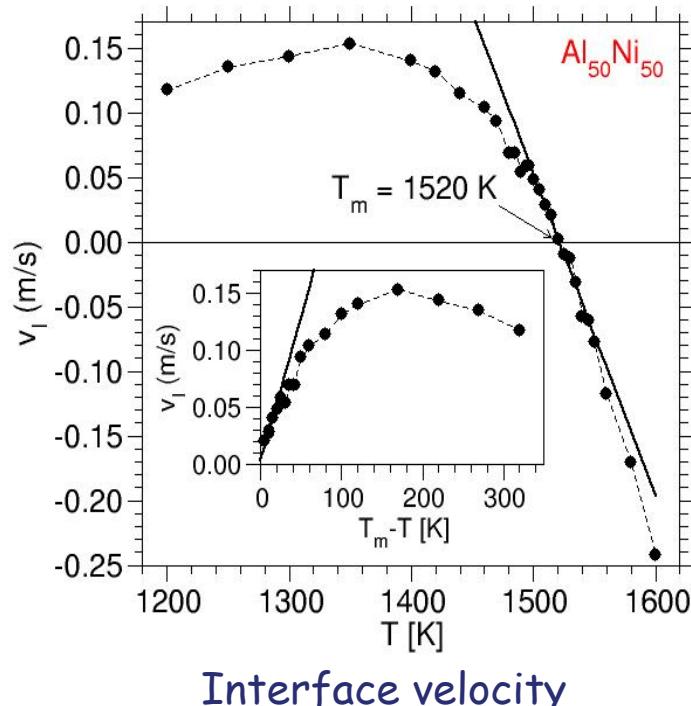
- How to study crystallization?

Estimation of melting temperature

- ❑ How to prepare a system with two phases?
- Equilibrate a crystal (NPT, $p=0$)
- Fix the particles in the middle of the box
- Heat away the two other regions
- Quench at the target temperature



Estimation of the melting temperature T_M from solid-liquid interface motion



$T > T_M$:
Melting

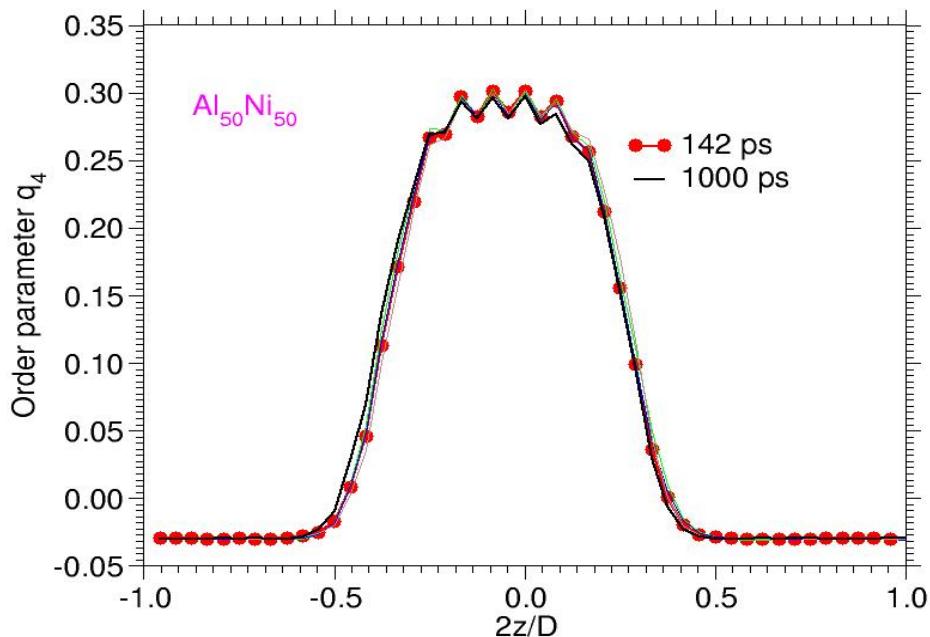
$T = T_M$:
coexistence

$T < T_M$:
crystallization

A. Kerrache et al., EPL 2008.

Enthalpy as a function of time

Bond order parameter profile

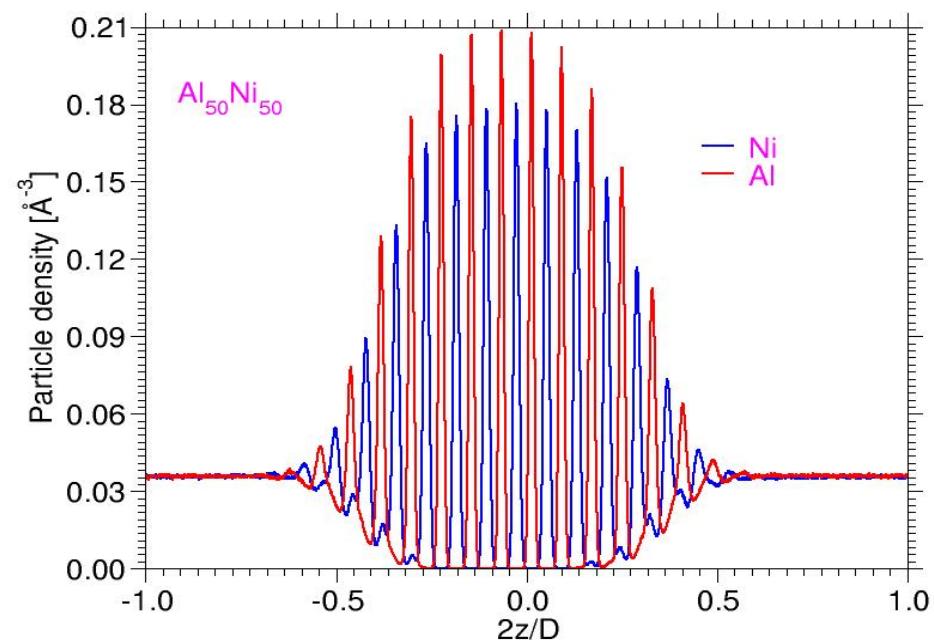


$$q_n = \left\langle \frac{1}{N} \sum_{i,j,k} \cos(n\theta_{xy}(i,j,k)) \right\rangle$$

$$n = 1, 2, \dots, 6$$

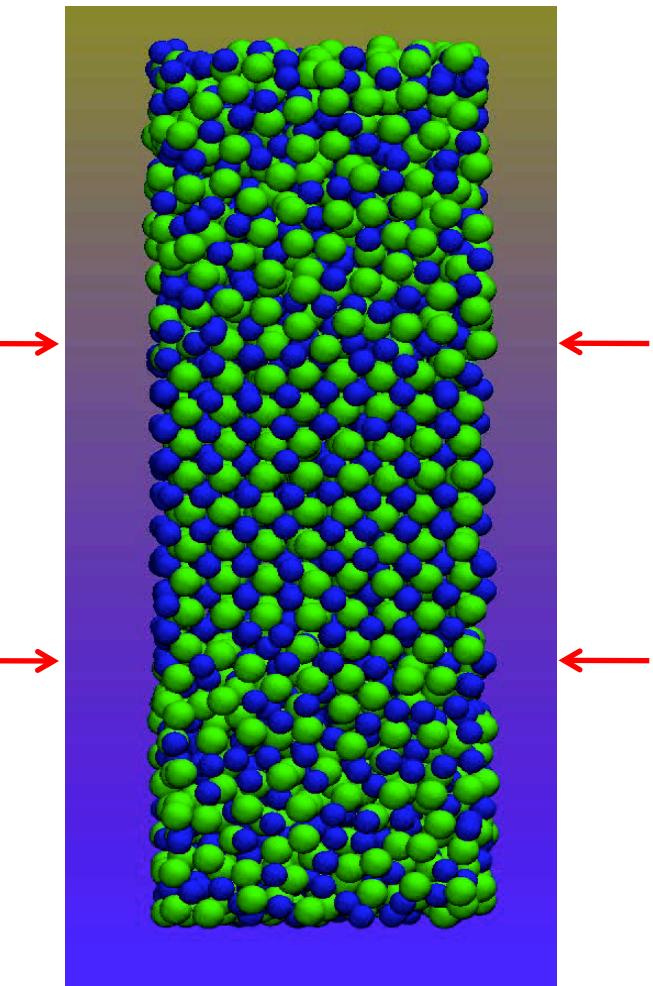
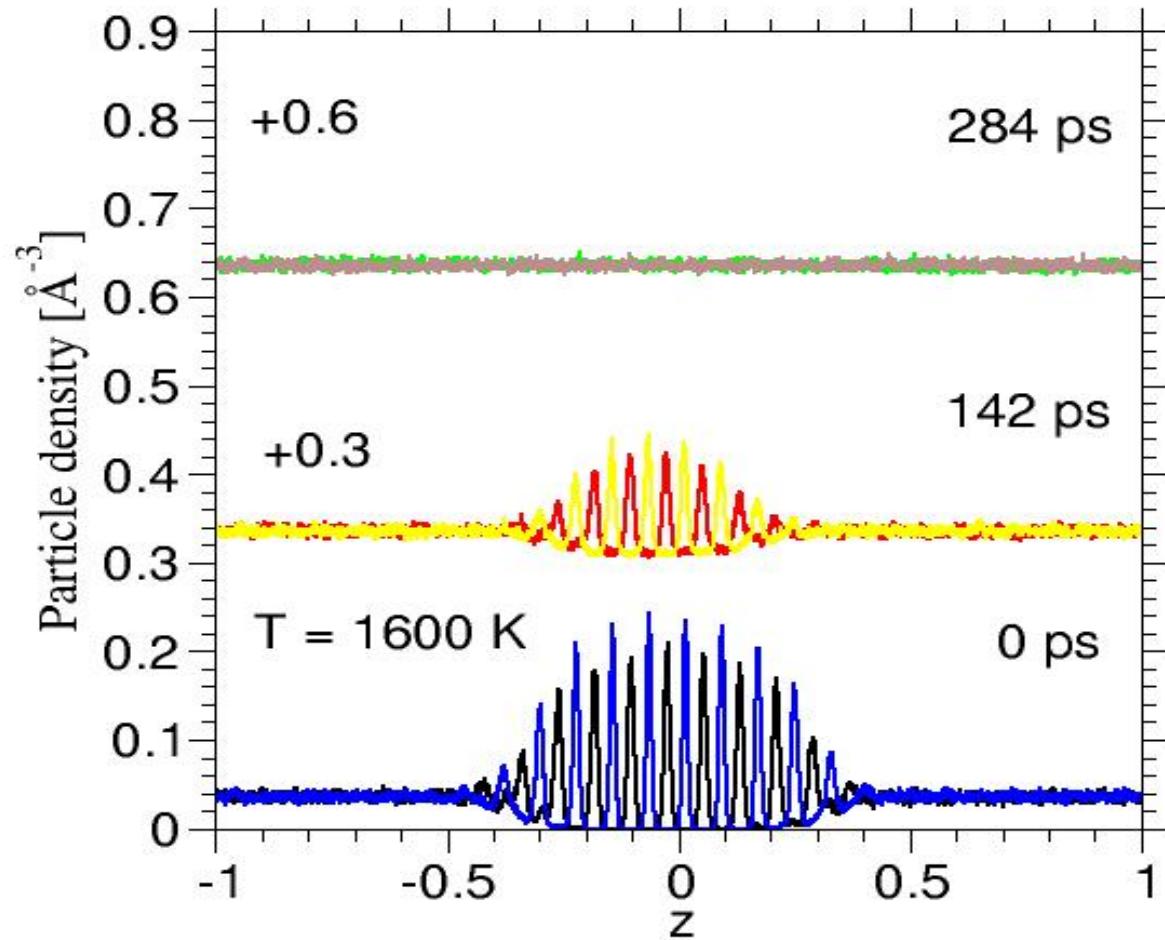
i, j and k: indices for nearest neighbors, $\theta(i,j,k)$: bond angle formed by **i, j** and **k** atoms.

Partial particle density profile



- ❖ constant density in the liquid region.
- ❖ solid-liquid interface over several layers.
- ❖ pronounced chemical ordering in the solid region.
- ❖ mass transport required for crystal growth.

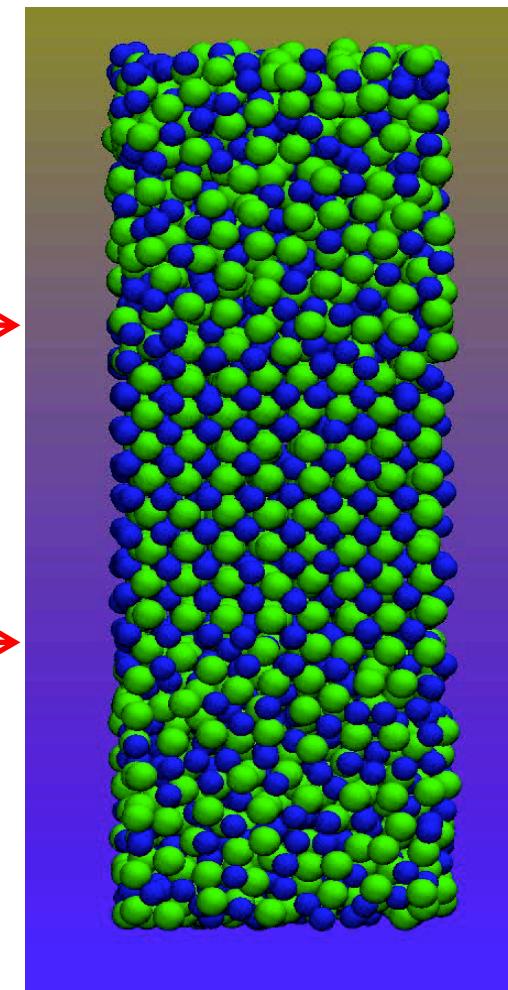
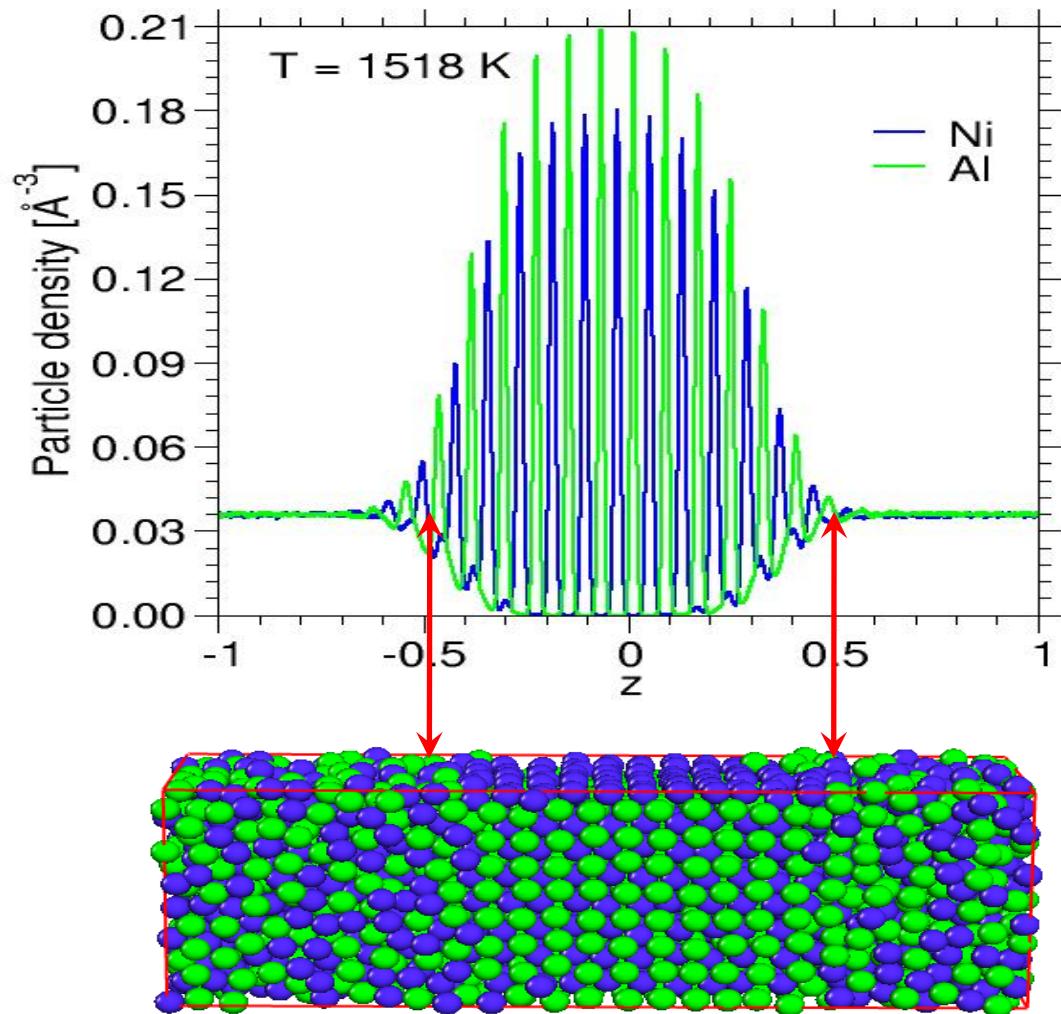
Melting of AlNi at 1600 K



Particle density along the solid-liquid interface

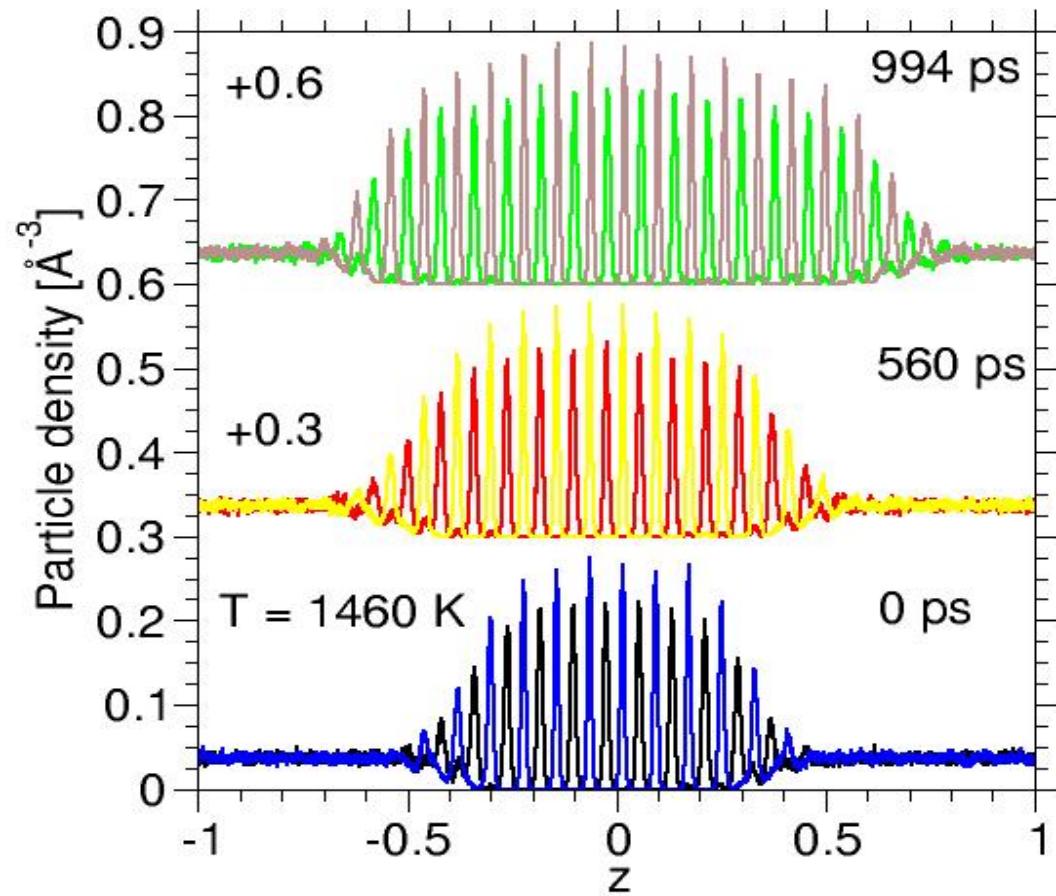
Melting

Particle density along the solid-liquid interface

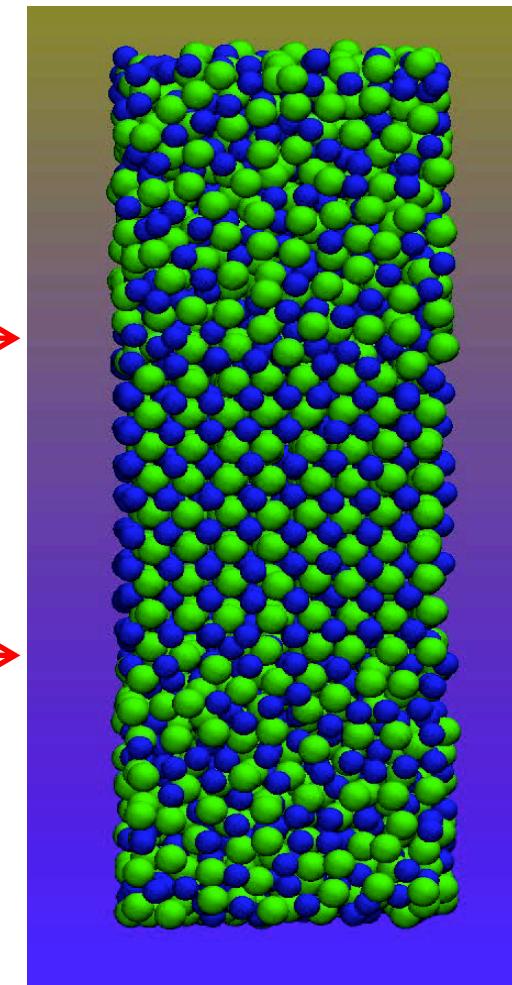


□ Coexistence

Crystallization of AlNi at 1400 K

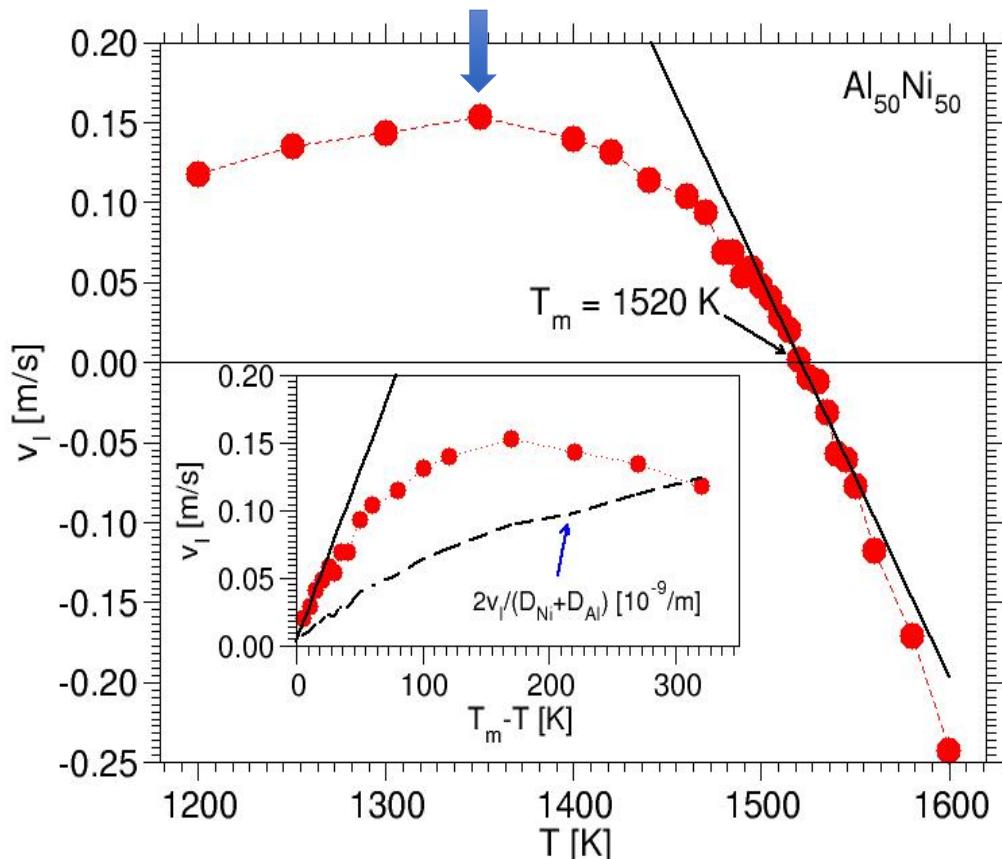


Particle density along the solid-liquid interface



Crystallization

Crystal growth: diffusion limited



Solid-liquid interface velocity as a function of temperature

Inset: as a function of under-cooling

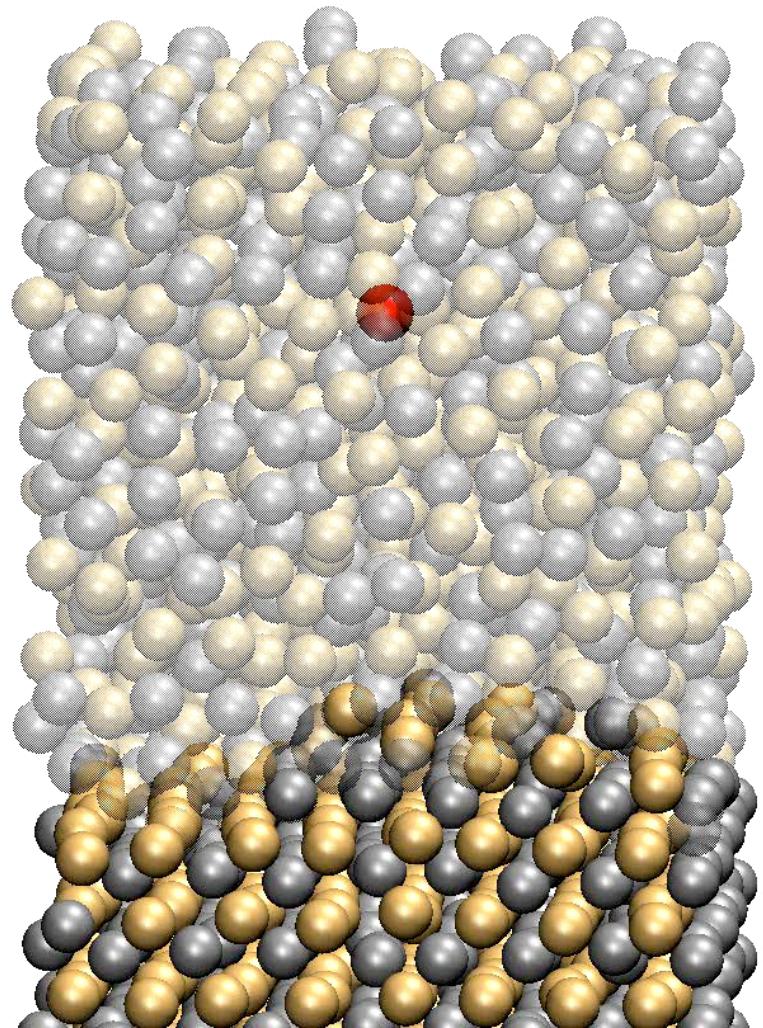
- Why the solid-liquid interface velocity presents a maximum?

- ✓ Maximum of 0.15 m/s at 180 K
- Interface velocity divided by the average self diffusion constant.
- ✓ Maximum due to decreasing of diffusion constant.
- ✓ Linear regime only up to 30 K of under-cooling.

What about the mass transport across the solid-liquid interface?

Mass transport across the interface

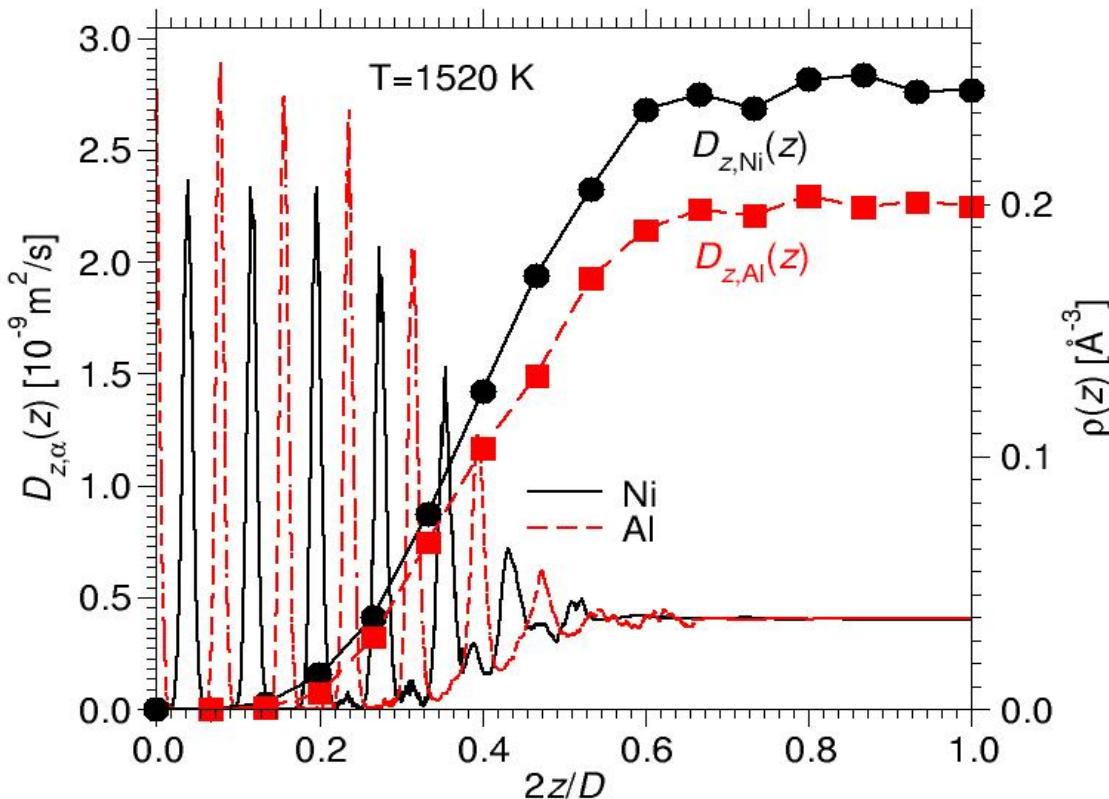
- Role of the mass transport on the crystal growth:
 - order parameter to distinguish solid and liquid particles locally.
 - compute the particle density and mass density profiles.
 - order parameter profile.
 - number of solid-like particles.
 - solid-liquid interface velocities from the number of solid-like particles.
 - diffusion across the interface.



Mass transport on the liquid phase and across the interface



Mass transport across the interface



Mass transport and particle density across the solid-liquid interface

Crystal growth: controlled by mass transport in the liquid phase and solid-liquid interface

$$D_{z_s, \alpha}(z_s) = \lim_{t \rightarrow \infty} \frac{1}{N_s} \sum_{i_s=1}^{N_s} \frac{\langle (z_{i_s}(t) - z_{i_s}(0))^2 \rangle}{2t}$$

The diffusion constants decrease when we cross the solid-liquid interface.

Wilson-Frenkel theory:
activated process controlled by mass diffusion in the liquid phase

Wilson H.A. *Philos. Mag.*, **50** (1900) 238.
Frenkel J., *Phys. Z. Sowjetunion*, **1** (1932) 498.
A. Kerrache et al. *EPL*, 2008.

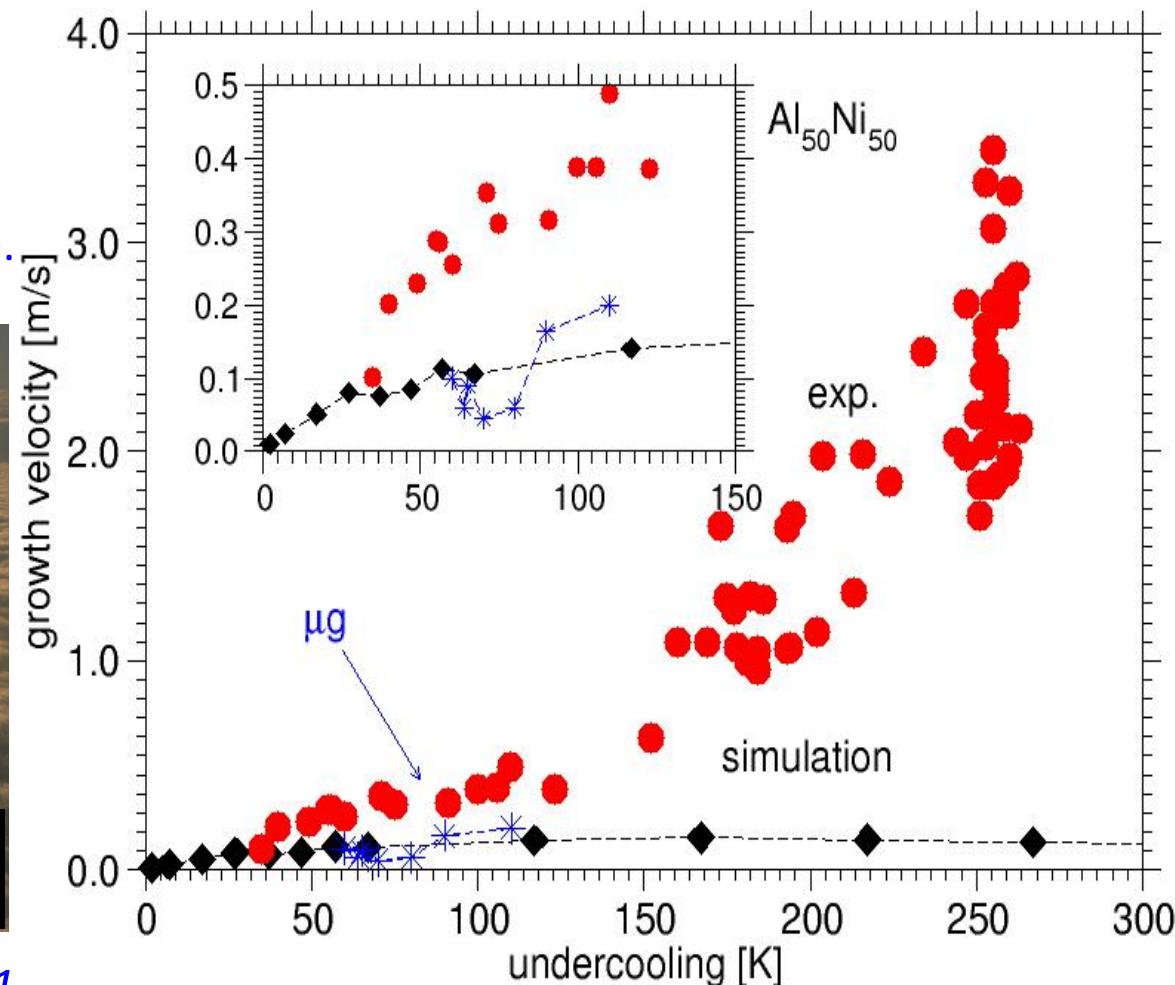
Experimental data?

Comparison to experimental data

Interface velocities: simulation, lab. exp., micro-gravity experiments

- ✓ terrestrial data (Assadi *et al.*)
- ✓ μg data (parabolic flight) , H. Hartmann (PhD thesis)

H. Assadi, *et al.*, Acta Mat. 54, 2793 (2006).



A. Kerrache *et al.*, EPL 81 (2008) 58001.

□ Binary Metallic alloys:

- Melting and crystallization.
- Solid-Liquid interfaces.
- Crystal growth from melt.
- Crystal growth is diffusion limited process.



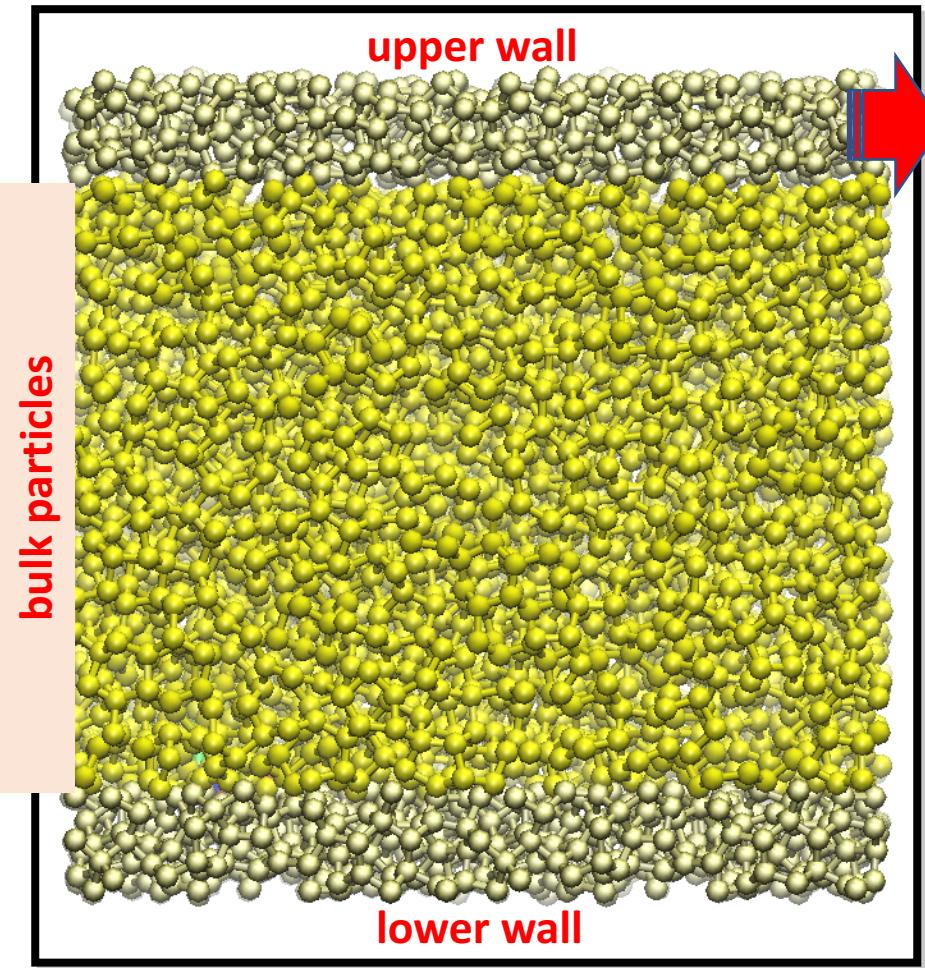
□ Glasses:

- Shear deformations in amorphous materials
- How to prepare a glass using MD simulation?
- Glass Indentation using MD.

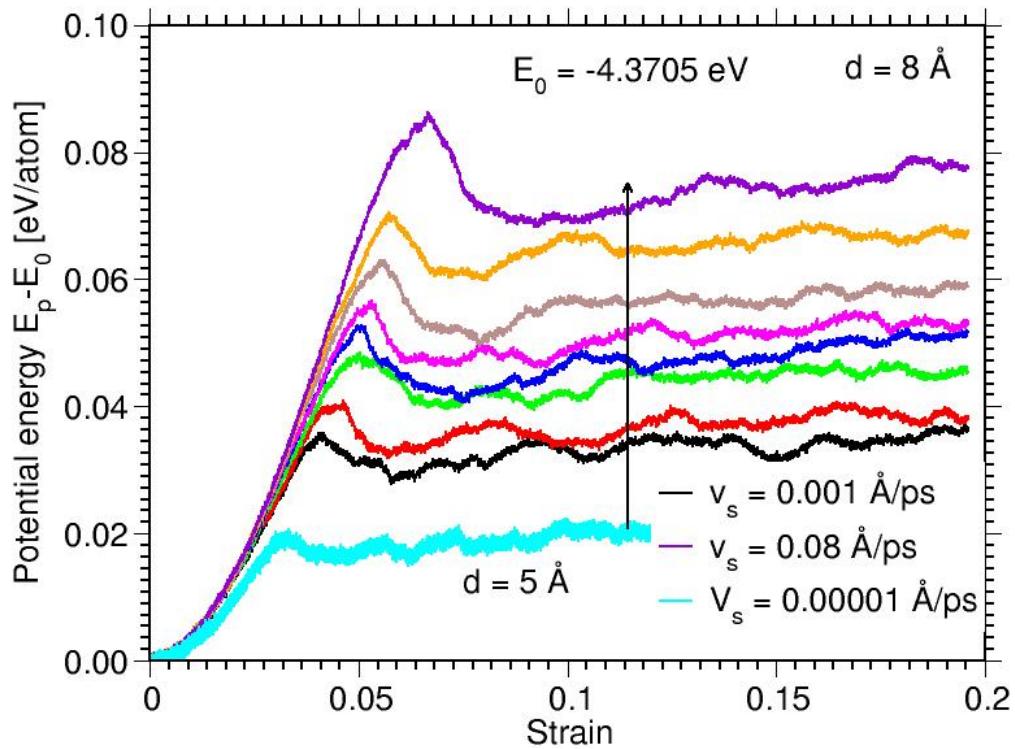


- equilibration of the sample at the desired temperature (Bulk simulation).
- define the lower & upper walls.
- move the particles of upper wall with a fixed shear velocity v_s
- integrate the equation of motion of the mobile particles.
- equilibration for 5 ns: **fixed walls**
- periodic boundary conditions fixed in y direction.

Temperature:
rescaling the velocities using the
y and z components

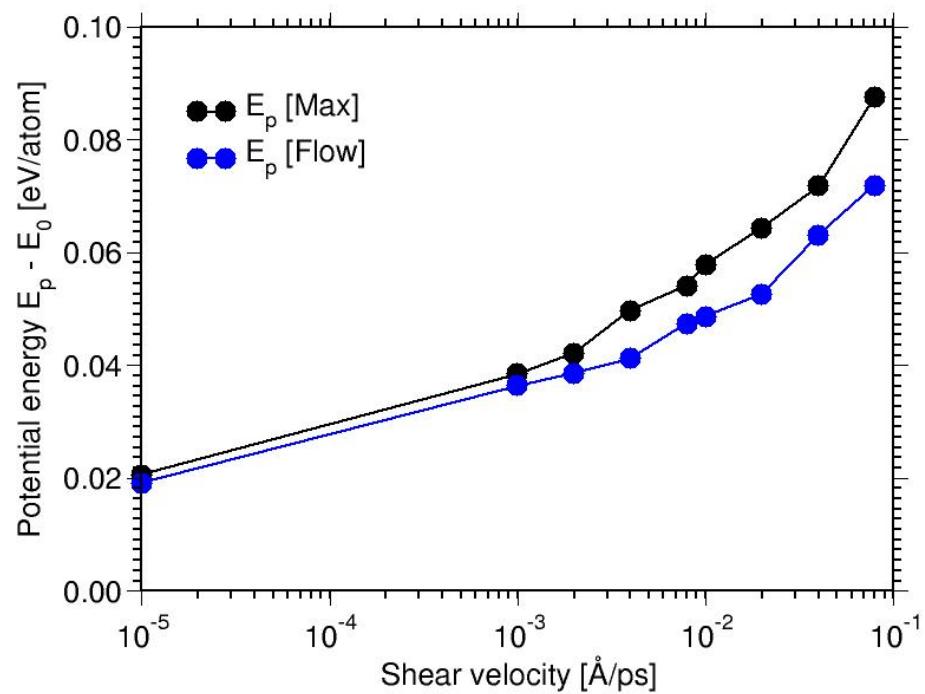


Typical starting configuration of s-Si



- ❖ Shear velocity: 10^{-5} to $8 \times 10^{-2} \text{ \AA/ps}$
- ❖ Quadratic increase of E_p and strain
- ❖ independent at small strain.
- ❖ E_{\max} increases with shear velocity.

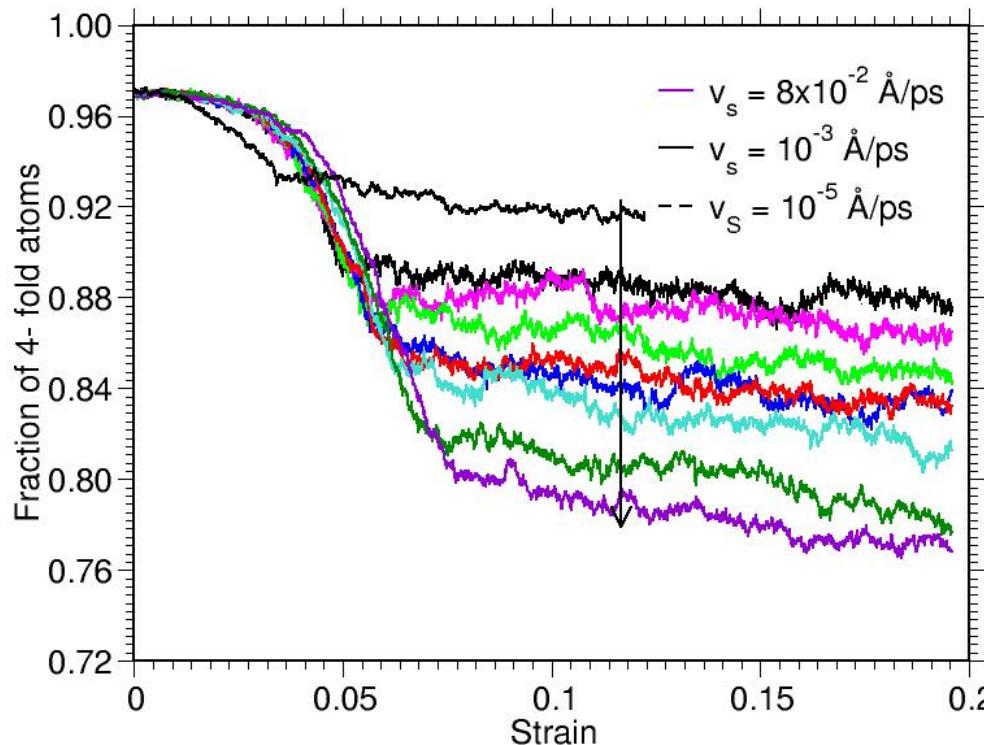
Potential energy difference ΔE as a function of imposed strain at 300 K



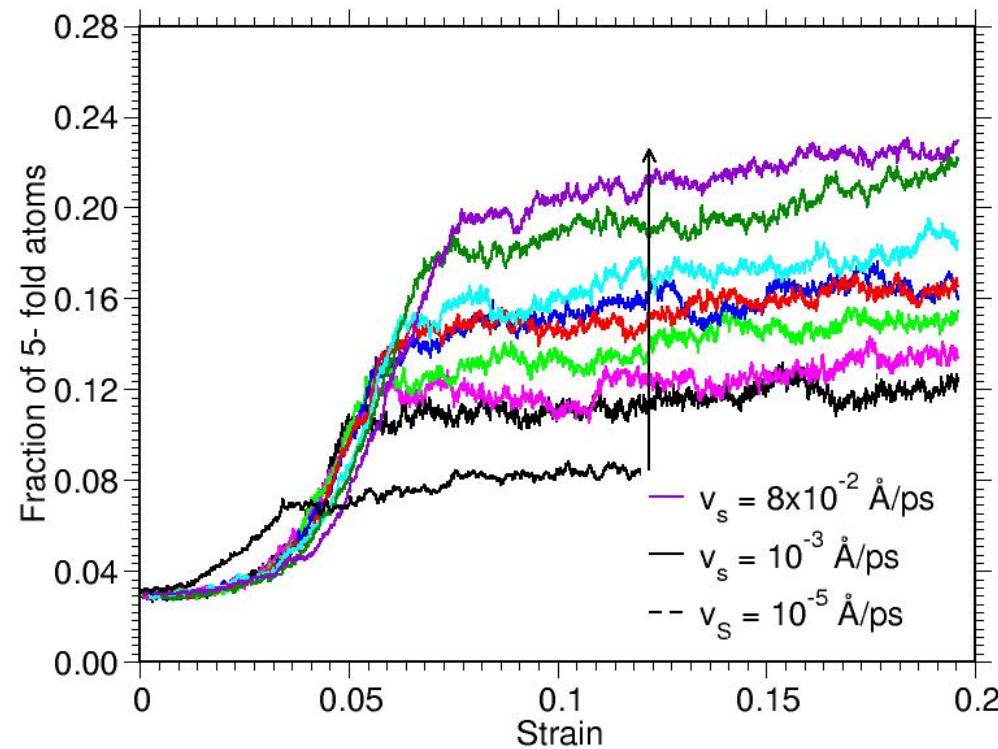
$10^{-3} \text{ \AA/ps} \rightarrow 8 \text{ ns}$
 $10^{-5} \text{ \AA/ps} \rightarrow 800 \text{ ns}$

A. Kerrache et al. PRB 83 (2011) 134122.

Fraction of perfect 4-fold atoms



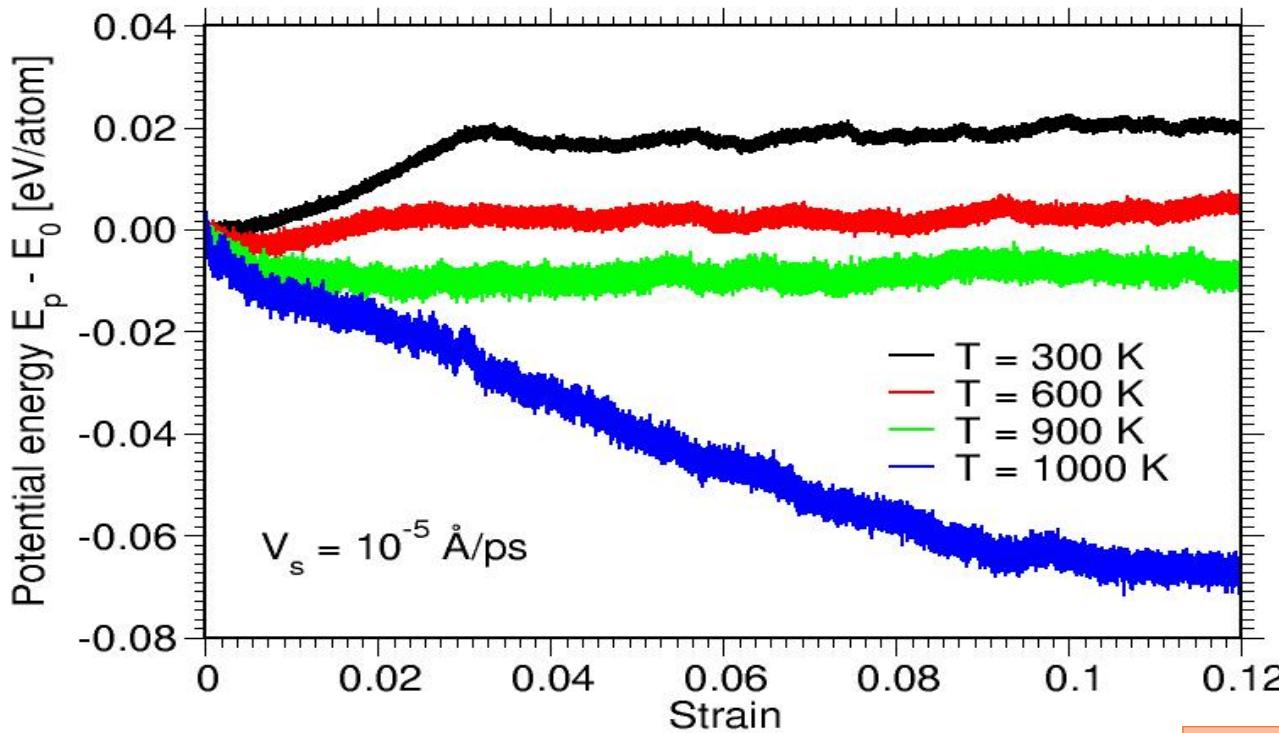
Fraction of 5-fold atoms



- ☐ Increasing shear velocity leads:
 - an increase of the fraction of 5-fold atoms
 - a decrease of the fraction of 4-fold atoms
 - ❖ Increases the disorder and the defects

- ☐ What will happen if the shear deformations were applied at high temperature?

Crystallization induced by shear



- Temperatures: 300, 600, 900 and 1000 K
- Shear velocity: $10^{-5} \text{ \AA}/\text{ps}$
- Total displacement: $\delta = 5 \text{ \AA}$

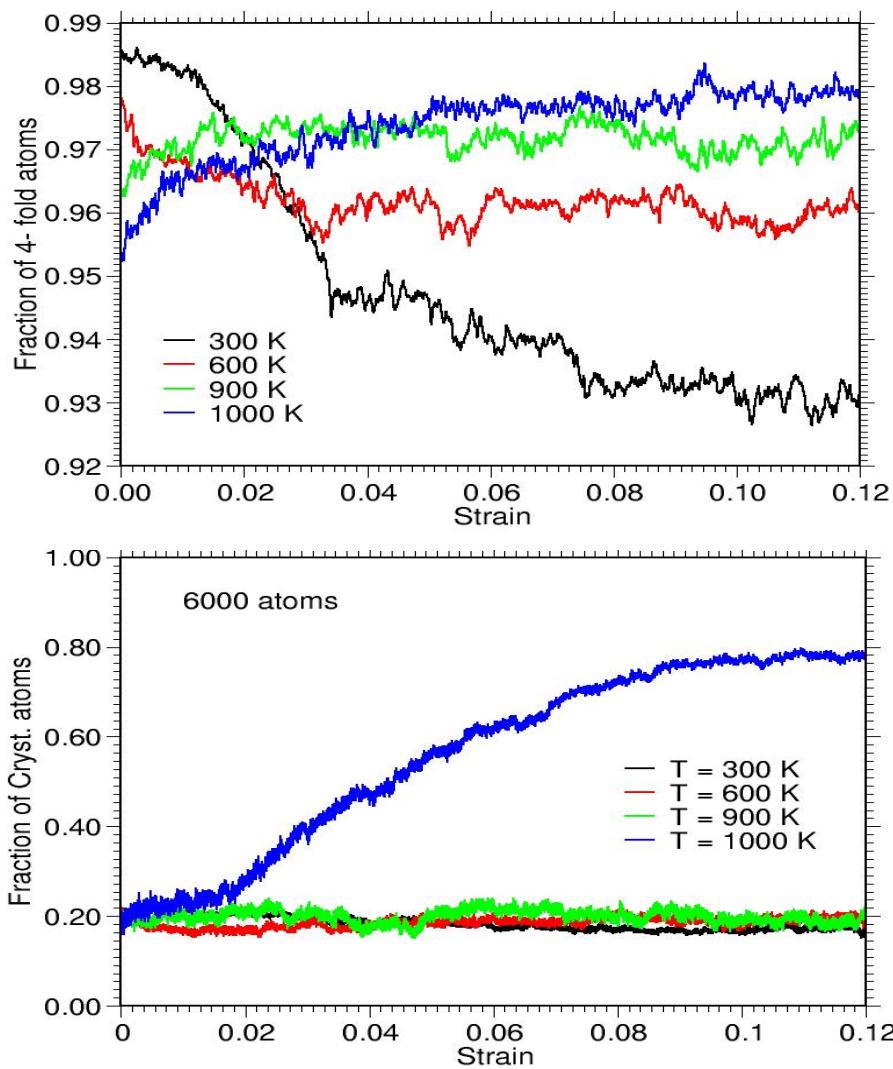
Potential energy ΔE_p as a function of imposed strain

- Increase of the disorder at 300 and 600 K.
- At 900 K: increase of the order without crystallization.
- At 1000 K: shear induce the **crystallization** of *a-Si*.

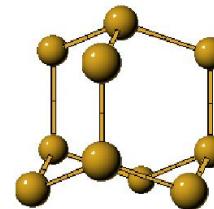
T	300	600	900	1000
ΔE_p	+0.02	+0.005	-0.01	-0.065

A. Kerrache et al.
PRB 84 (2011) 041110.

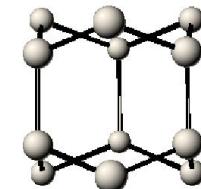
Crystallization induced by shear



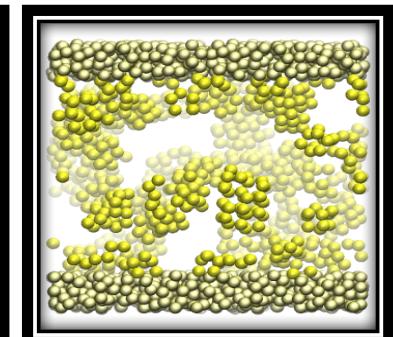
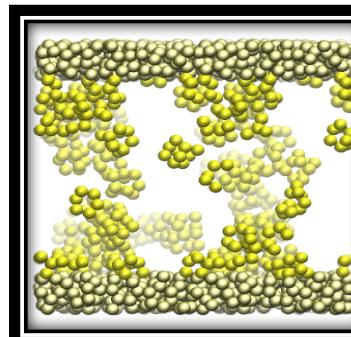
Coordination Number



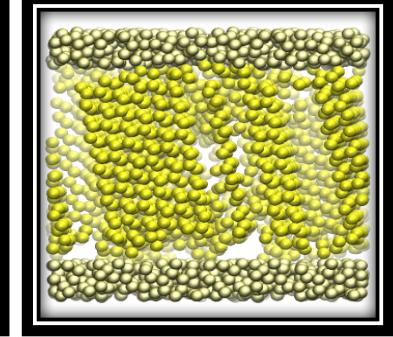
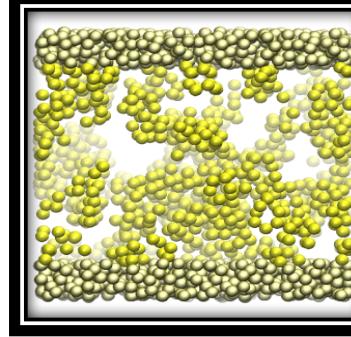
300 K



600 K



Number of
crystalline
particles



P. Beaucage et al. PRB (2005).

❑ Binary Metallic alloys:

- Melting and crystallization.
- Solid-Liquid interfaces.
- Crystal growth from melt.
- Crystal growth is diffusion limited process.



❑ Glasses:

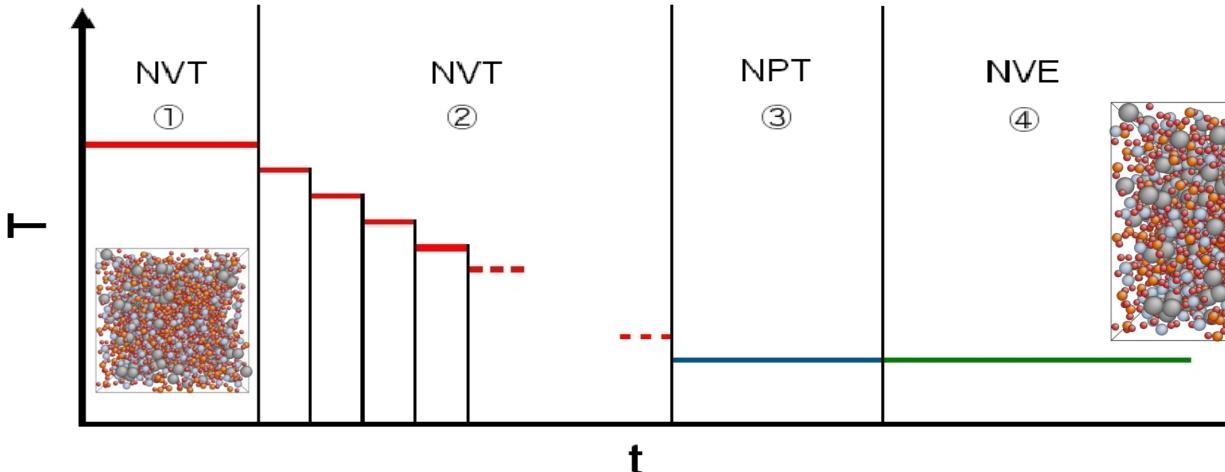
- Shear deformations in amorphous materials
- How to prepare a glass using MD simulation?
- Glass Indentation using MD.



How to prepare a glass? MD/experiment

Glass preparation diagram:

Cooling rates: 10^{12} to 10^{13} K/s



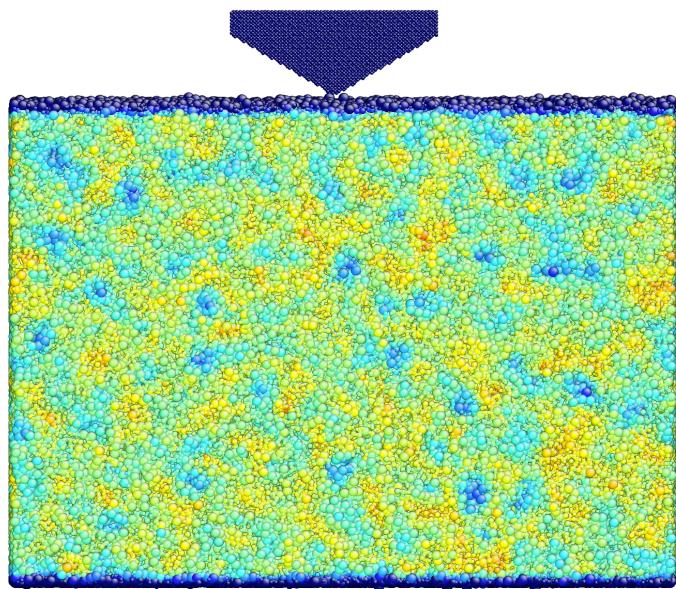
Glass preparation procedure:

- ✓ Random configuration (**N atoms**).
- ✓ Liquid equilibration du at 5000 K (**NVT**).
- ✓ Cooling per steps of 100 K– (**NVT**).
- ✓ Glass equilibration at 300 K (**NPT**).
- ✓ Trajectory simulation at 300 K (**NVE**).

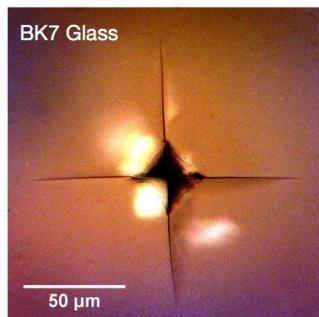
Model

- MD Simulations (**DL-POLY**).
- System of N particules.
- Time step: **1 fs**
- SBN glasses**
- $\text{SiO}_2\text{-B}_2\text{O}_3\text{-Na}_2\text{O}$
 - ✓ $R = [\text{Na}_2\text{O}] / [\text{B}_2\text{O}_3]$
 - ✓ $K = [\text{SiO}_2] / [\text{B}_2\text{O}_3]$

Movie provided by: **Dimitrios Kilymis**
Laboratoire Charles Coulomb (L2C), UMR
5221 CNRS-Univ. Montpellier, France.

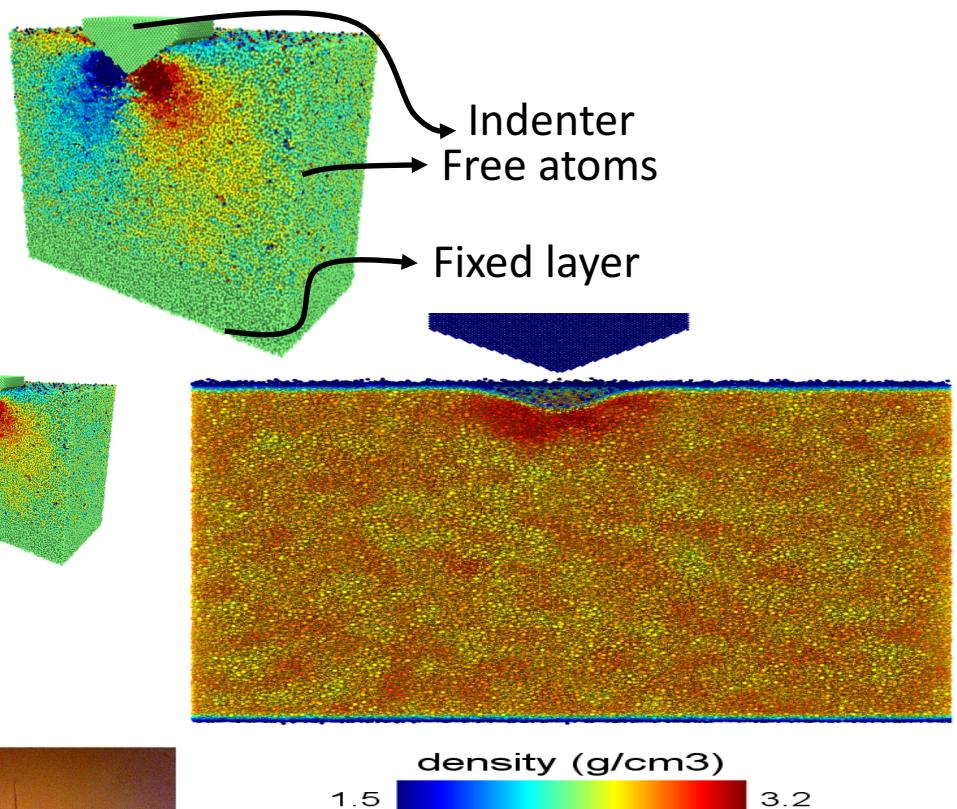


Glass indentation



50 μm

BK7 Glass



density (g/cm^3)
 1.5 3.2

- $N = 2.1 \times 10^6$ atoms
- Temperature : 300 K
- Speed: 10 m/s
- Depth: ~3.0 nm

Acknowledgments



Prof. Dr. Jürgen Horbach, Dusseldorf, Germany.
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Prof. Laurent J. Lewis, Qc, Canada.

Dr. Dimitrios Kilymis, Montpellier, France.
Prof. Jean-Marc Delaye, CEA, France.



Dr. Victor Teboul, Angers, France.
Prof. Hamid Bouzar, UMMTO, Tizi-Ouzou, Algeria.



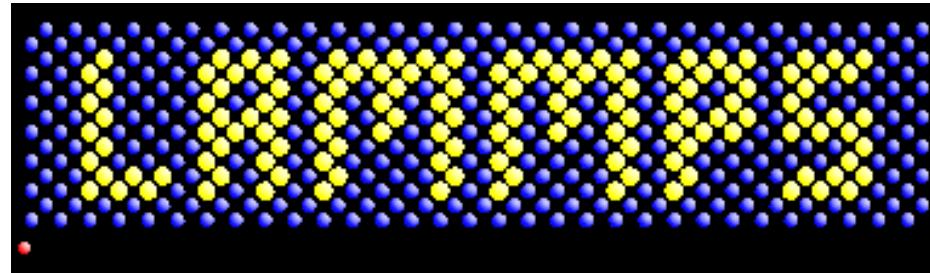
Setting and Running MD simulations

LAMMPS

- **LAMMPS**: Molecular Dynamics Simulator (introduction).
- Building LAMMPS step by step.
- Running LAMMPS (input, output, ...).
- Benchmark and performance tests.

LAMMPS

Large-scale Atomic / Molecular Massively Parallel Simulator



Source: some material and images were adapted from LAMMPS home page



Large-scale Atomic / Molecular Massively Parallel Simulator

S. Plimpton, A. Thompson, R. Shan, S. Moore, A. Kohlmeyer, ...

Sandia National Labs: <http://www.sandia.gov/index.html>

➤ Home Page: <http://lammps.sandia.gov/>

Results:

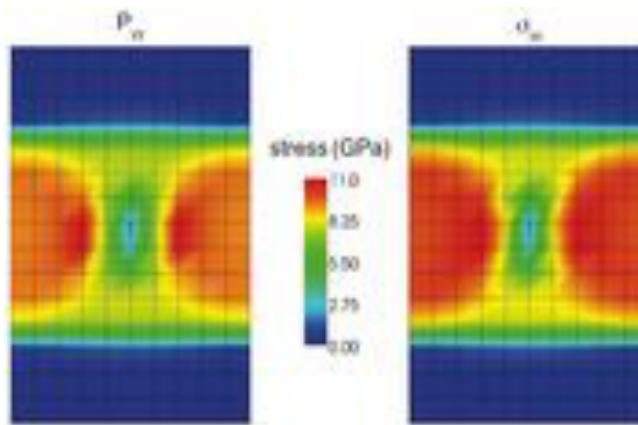
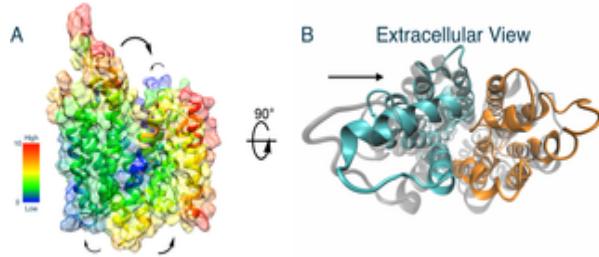
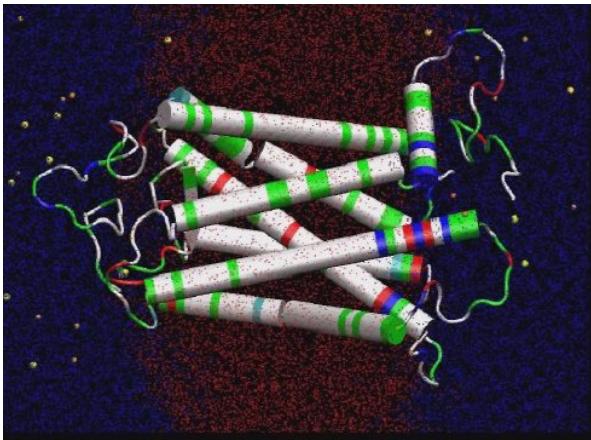
- Papers: <http://lammps.sandia.gov/papers.html>
- Pictures: <http://lammps.sandia.gov/pictures.html>
- Movies: <http://lammps.sandia.gov/movies.html>

Resources:

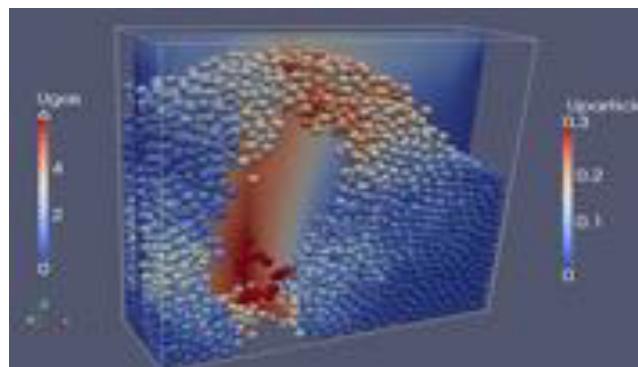
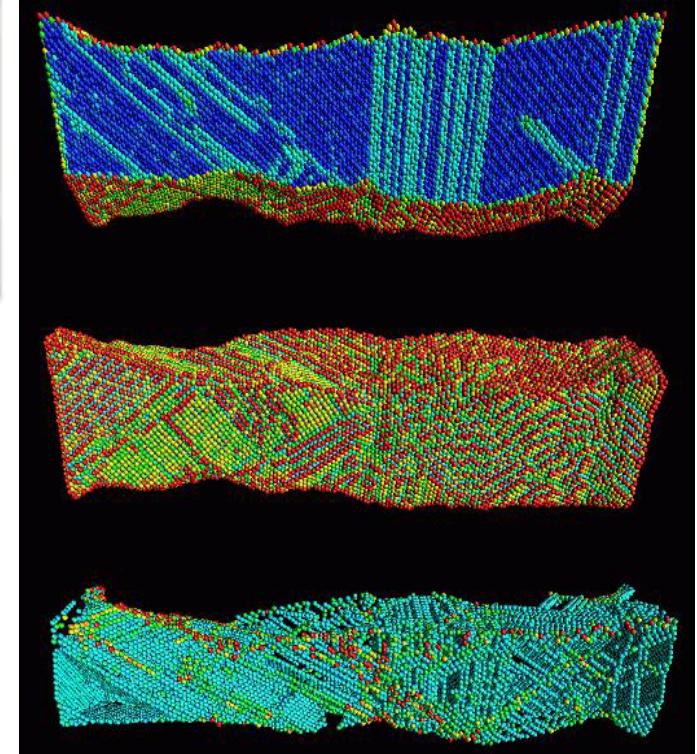
- Online manual: <http://lammps.sandia.gov/doc/Manual.html>
- Search the mailing list: <http://lammps.sandia.gov/mail.html>
- Subscribe to the Mailing List:
<https://sourceforge.net/p/lammps/mailman/lammps-users/>

Where LAMMPS has been used?

► Biophysics



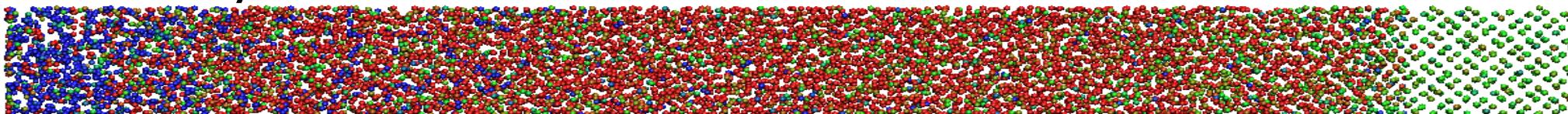
► Solid Mechanics



► Granular Flow

► Material Science

► Chemistry



Big Picture	Code	Documentation	Results	Related Tools	Context	User Support
Features	Download	Manual	Publications	Pre/Post processing	Authors	Mail list
Non-features	SourceForge	Developer guide	Pictures	Pizza.py Toolkit	History	Workshops
FAQ	Latest features & bug fixes	Tutorials	Movies	Offsite LAMMPS packages & tools	Funding	User scripts and HowTos
Wish list	Unfixed bugs	MD to LAMMPS glossary	Benchmarks	Visualization	Open source	Contribute to LAMMPS

Recent LAMMPS News

- (5/18) **New fix bond/react** command to enable simulation of one or more complex heuristic reactions that rearrange molecular topology. See details [here](#).
- (3/18) **New stable release**, 16Mar18 version.
- (9/17) Wrapper on the **LATTE DFTB** (density-functional tight-binding) quantum code via the [fix latte](#) command. See details [here](#).
- (9/17) **USER-MESO** package from the Karniadakis group at Brown University, with various dissipative particle dynamics (DPD) models, including eDPD, mDPD, tDPD. See details [here](#).
- (8/17) **New stable release**, 11Aug17 version.

❖ License

- LAMMPS is provided through **GNU Public License**
<https://www.gnu.org/licenses/licenses.en.html#GPL>
- Free to Use, **Modify**, and Distribute.
- Contribute to LAMMPS: <http://lammmps.sandia.gov/contribute.html>

□ Code Layout

- C++ and Object-Oriented approach
- Parallelization via **MPI** and **OpenMP**; runs on **GPU**.
- is invoked by **commands** through **input scripts**.
- possibility to **customized output**.
- could be interfaced with other codes (python, ...): **library**.
- possibility to **contribute to LAMMPS**: potential, fixes, ...

❖ Download Page:

<http://lammmps.sandia.gov/download.html>

➤ Distributions:

- ✓ [Download a tarball](#)
- ✓ [Git checkout and update](#)
- ✓ [SVN checkout and update](#)
- ✓ [Pre-built Ubuntu executables](#)
- ✓ [Pre-built binary RPMs for Fedora/RedHat/CentOS/openSUSE](#)
- ✓ [Pre-built Gentoo executable](#)
- ✓ [OS X with Homebrew](#)
- ✓ [Windows installer package](#)
- ✓ [Applying patches](#)

Build LAMMPS
from source

➤ Build from RPMs

- ✓ Pre-built Ubuntu executables
- ✓ Pre-built binary RPMs for Fedora/RedHat/CentOS/openSUSE
- ✓ Pre-built Gentoo executable

➤ Mac

- ✓ OS X with Homebrew

➤ Install under windows

- ✓ Windows installer package

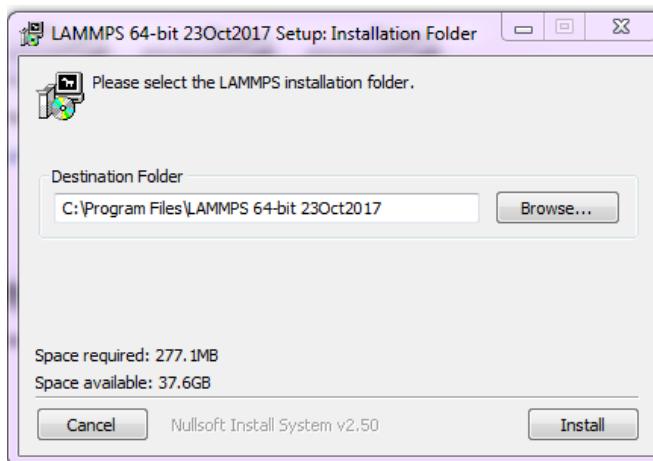
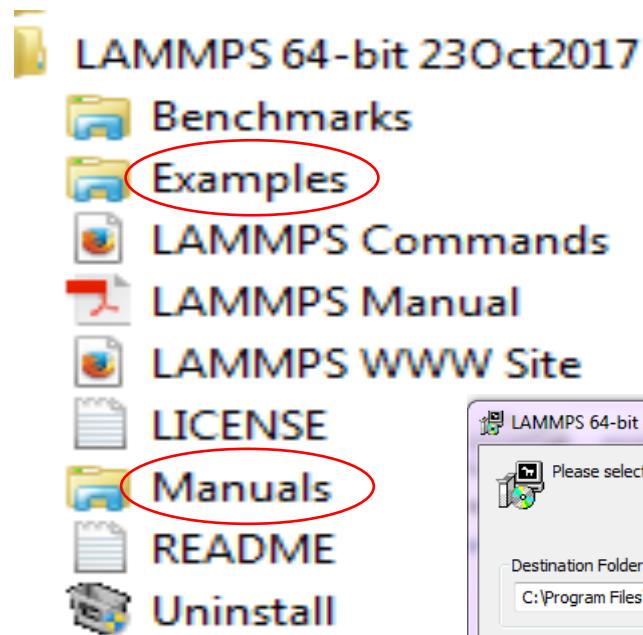
➤ Build from source code

- ✓ Download a tarball
- ✓ Git checkout and update
- ✓ SVN checkout and update
- ✓ Applying patches

does not include all packages
super-user access

For a customized installation: build from source files
Different versions

- Download Page: <http://rpm.lammps.org/windows.html>
- Installer: **lammps-64bit-latest.exe**



Directory:

Program Files\LAMMPS 64-bit 20171023

Binaries under bin: abf_integrate.exe ffmpeg.exe

Imp_mpi.exe restart2data.exe binary2txt.exe chain.exe

Imp_serial.exe msi2Imp.exe createatoms.exe

```
C:\Windows\system32\CMD.exe
C:\Test_Lammps>Imp_serial.exe < in.melt
LAMMPS (26 Jan 2017-ICMS)
OMP_NUM_THREADS environment is not set. Defaulting to 1 thread. (.../comm.cpp:90)

using 1 OpenMP thread(s) per MPI task
Lattice spacing in x,y,z = 1.6796 1.6796 1.6796
Created orthogonal box = (0 0 0) to (16.796 16.796 16.796)
1 by 1 by 1 MPI processor grid
Created 4000 atoms
Neighbor list info ...
  update every 20 steps, delay 0 steps, check no
  max neighbors/atom: 2000, page size: 100000
  master list distance cutoff = 2.8
  ghost atom cutoff = 2.8
  binsize = 1.4, bins = 12 12 12
  1 neighbor lists, perpetual/occasional/extral = 1 0 0
  (1) pair lj/cut, half, perpetual
    pair build: half/bin/newton
    stencil: half/bin/3d/newton
    bin: standard
Setting up Verlet run ...
  Unit style   : lj
  Current step : 0
  Time step   : 0.005
Memory usage per processor = 3.18356 Mbytes
Step Temp E_pair E_mol TotEng Press
  0      -2.2744931   -3.7033504
  50     -2.2823355   5.6700642
  100    -2.2811312   5.6891042
  150    -2.280608    5.9589514
  200    -2.2811136   5.7364886
  250    -2.281821   5.9567365
```

- Execute: **Imp_serial.exe < in.lammps**

Download the source files:

<http://lammps.sandia.gov/download.html#tar>

Download a tarball

Select the code you want, click the "Download Now" button, and your browser should download a gzipped tar file. Unpack it with the following commands, and look for a README to get you started.

```
tar -xzvf file.tar.gz
```

There have been ~256,700 downloads of LAMMPS from Sept 2004 thru Dec 2016.

Old version

Current version is: **13 Mar 2018**

LAMMPS molecular dynamics package:

- [LAMMPS](#) --- Stable version (11 Aug 2017) - Recent C++ version source tarball, GPL license, ~121 Mb. Includes all bug fixes and new features described on [this page](#), up to the date of the most recent stable release.
- [LAMMPS](#) --- Development version - Most current C++ version source tarball, GPL license, ~121 Mb. Includes all bug fixes and new features described on [this page](#).
- [LAMMPS 2001](#) --- older f90 version source tarball, GPL license, 1.1 Mb, last updated 17 Jan 2005
- [LAMMPS 99](#) --- older f77 version source tarball, GPL license, 840 Kb
- No package

[Download Now](#)

Archive: lammps-stable.tar.gz

Alternatively, use wget from your terminal:

- `wget http://lammps.sandia.gov/tars/lammps-stable.tar.gz`
- `wget http://lammps.sandia.gov/tars/lammps-11May18.tar.gz`



- Download and unpack the source code: `lammmps-stable.tar.gz`
- LAMMPS directory: `lammmps-11May18` (lammmps-version)
 - ✓ **bench**: benchmark tests (potential, input and output files).
 - ✓ **doc**: documentation (PDF and HTML)
 - ✓ **examples**: input and output files for some simulations
 - ✓ **lib**: libraries to build before building LAMMPS
 - ✓ **LICENSE** and **README** files.
 - ✓ **potentials**: some of the force fields supported by LAMMPS
 - ✓ **python**: to invoke LAMMPS library from Python
 - ✓ **src**: source files (*.cpp, **PACKAGES**, **USER-PACKAGES**, ...)
 - ✓ **tools**: some tools like `xmovie` (similar to VMD but only 2D).

❑ Common problems:

- command not found,
- undefined reference to fftw, boost, petsc, ...
- permission denied, ...

❑ Configuration:

- ✓ `./configure --prefix=/home/$USER/software ... options`
- ✓ `cmake .. --DCMAKE_INSTALL_PREFIX=/home/$USER/software`
- ✓ `./setup` or other provided scripts

❑ Compile or build the program:

- make or `make {options}`

❑ Installation:

- ✓ `make install`

- **First:** Build libraries if required (atc, meam, reax, ...).
- Choose a **Makefile**: compatible with your system (**Compiler**, ...)
- Choose and **install the packages** you need.

✓ make package	# list available packages
✓ make package-status (ps)	# status of all packages
✓ make yes-package	# install a single package in src
✓ make no-package	# remove a single package from src
✓ make yes-all	# install all packages in src
✓ make no-all	# remove all packages from src
✓ make yes-standard (yes-std)	# install all standard packages
✓ make no-standard (no-std)	# remove all standard packages
✓ make yes-user	# install all user packages
✓ make no-user	# remove all user packages
□ Build LAMMPS:	
➤ make machine	# build LAMMPS for machine

Choose an appropriate Makefile

- machine is one of these from **src/MAKE**:
 - # **mpi** = MPI with its default compiler
 - # **serial** = GNU g++ compiler, no MPI
- ... or one of these from **src/MAKE/OPTIONS**:
 - # **icc_openmpi** = OpenMPI with compiler set to Intel icc
 - # **icc_openmpi_link** = Intel icc compiler, link to OpenMPI
 - # **icc_serial** = Intel icc compiler, no MPI
- ... or one of these from **src/MAKE/MACHINES**:
 - # **cygwin** = Windows Cygwin, mpicxx, MPICH, FFTW
 - # **mac** = Apple PowerBook G4 laptop, c++, no MPI, FFTW 2.1.5
 - # **mac_mpi** = Apple laptop, MacPorts Open MPI 1.4.3, ...
 - # **ubuntu** = Ubuntu Linux box, g++, openmpi, FFTW3
- ... or one of these from **src/MAKE/MINE**: (write your own Makefile)

- Download the latest stable version from LAMMPS home page.
 - Untar the archive: `tar -xvf lammps-stable.tar.gz`
 - Change the directory and list the files: `cd lammps-11May2018`
 - `bench doc examples lib LICENSE potentials python README src tools`
 - Choose a Makefile (for example: `machine=icc_openmpi`)
 - `src/MAKE/OPTIONS/Makefile.icc_openmpi`
 - Load the required **modules** (Intel, OpenMPI, ...)
 - Check the **packages**: package, package-status, yes-package, ...
 - To build LAMMPS, run: `make icc_openmpi`
 - Add or remove a **package** (if necessary), then recompile.
 - If necessary, edit **Makefile** and fix the path to libraries.
-
- **Exercise:** use an interactive job asking for 4 cores
 - Compile LAMMPS without any package included.
 - Add a package and recompile.

□ Steps to follow:

1. Download and unpack the source files:
`wget http://lammps.sandia.gov/tars/lammps-stable.tar.gz`
`tar -xvf lammps-stable.tar.gz`
2. Submit an interactive job: 4 cores, 1 hour, mem-per-cpu=3500M
3. Load the required modules (eigen, voro++, hdf5, ...)
4. Choose and edit the appropriate Makefile: **Makefile.icc_openmpi**
5. Remove all the packages: **make no-all**
6. Compile LAMMPS: **make icc_openmpi**
7. Add one or two packages: **make yes-asphere**; **make yes-voro++**
8. Make the necessary changes: **paths**, **libraries**, ... etc.
9. Clean and recompile the code: **make clean-all && make icc_openmpi**
10. To add more packages: repeat 7 to 9 (**with different packages**).

1. wget <http://lammps.sandia.gov/tars/lammps-stable.tar.gz>
tar -xvf lammps-stable.tar.gz
2. cp -r lammps-16Mar18 build-lammps-16Mar18
3. cd build-lammps-16Mar18/src && make clean-all
4. source ../../get_lammps_dependencies.sh
5. make **icc_openmpi**
6. make clean-all
7. make yes-voro++
8. Change the Makefile: **Makefile.icc_openmpi**
9. Recompile: make **icc_openmpi**

- Executable: **lmp_machine**
- Files:
 - Input File: **in.lmp_file**
 - Potential: see examples and last slides for more details.
 - Initial configuration: can be generated by LAMMPS, or another program or home made program.
- Interactive Execution:

```
$ ./lmp_machine < in.lmp_file
$ ./lmp_machine -in in.lmp_file
```
- Redirect output to a file:

```
$ ./lmp_machine < in.lmp_file > output_file
$ ./lmp_machine -in in.lmp_file -I output_file
```

- ❖ To know more about the modules installed, use "**module spider**" .
- ❖ Search for modules with the name "lammmps"
module spider lammmps
- ❖ Search for all modules that have the character "lammmps" in their names:
module -r spider '.*lammmps.*'
- ❖ Search of a particular module of interest: **lammmps-omp/20170811**
module spider lammmps-omp/20170811
- ❖ Load the module of interest: **lammmps-omp/20170811**
module load nixpkgs/16.09 intel/2016.4 openmpi/2.1.1 lammmps-omp/20170811
- ❖ Check if the module is correctly loaded: **module list**
- ❖ For more information:
module show lammmps-omp/20170811

☐ Command-line options:

At run time, LAMMPS recognizes several optional command-line switches which may be used in any order.

-e or -echo, -h or -help, -i or -in, -k or -kokkos, -l or -log, -nc or -nocite, -pk or -package, -p or -partition, -pl or -plog, -ps or -pscreen, -r or -restart, -ro or -reorder, -sc or -screen, -sf or -suffix, -v or -var

☐ As an interactive job:

- **mpirun -np 16 Imp_machine -in in.alloy**
- **mpiexec -n 4 Imp_machine < in.alloy**

☐ As a submitted job (Torque, SLURM, ...):

- **mpiexec Imp_machine < in.alloy > my.log**
- **mpirun Imp_machine < in.alloy > my.log**
- **srun Imp_machine < in.alloy > my.log**

INPUT

- Initial positions
- Initial velocities
- Time step
- Mass
- Charges
- PBC (or fixed)
- Units
- Potential
- Ensemble
- etc.

RUNNING

- Molecular Dynamics Simulation (NPT, NVT, NVE)
- Minimization
- Monte Carlo
- Atomic to Continuum

OUTPUT

- Trajectories
- Velocities
- Forces
- Energy
- Temperature
- Pressure
- Density
- Snapshots
- Movies
- ... etc.



□ Command Line:

- Every simulation is executed by supplying an input text script to the LAMMPS executable: `lmp < lammps.in > log_lammps.txt`

□ Parts of an input script:

- **Initialize:** units, dimensions, PBC, etc.
- Atomic positions ([built in or read from a file](#)) and velocities.
- **Settings:**
 - ✓ Inter-atomic potential (`pair_style`, `pair_coeff`)
 - ✓ Run time simulation parameters (e.g. time step)
 - ✓ [Fixes](#): operations during dynamics (e.g. thermostat)
 - ✓ [Computes](#): calculation of properties during dynamics
 - ✓ Rendering: snapshots of MD trajectory, movie.

□ Run the simulation for N steps (time step = δt).

LAMMPS input file example: LJ melt

```
# 3d Lennard-Jones melt
```

Comment

```
units          lj  
atom_style    atomic
```

Define units

```
lattice       fcc 0.8442  
region        box block 0 10 0 10 0 10  
create_box    1 box  
create_atoms  1 box  
mass          1 1.0
```

Create the simulation box
Or read data from a file

```
velocity      all create 3.0 87287
```

Initialize the
velocities

```
# Potential
```

```
pair_style    lj/cut 2.5  
pair_coeff   1 1 1.0 1.0 2.5
```

Define the
potential



LAMMPS input file example: LJ melt

Neighbour list:

neighbor 0.3 bin

neigh_modify every 20 delay 0 check no

Monitor the
neighbour list

set the thermodynamic ensemble:

fix 1 all nve

Thermodynamic
Ensemble

dump id all atom 50 dump.melt

#dump_modify

Store the
trajectory

log log.melt

thermo_style custom step temp etotal

thermo 50

Log file:
customize output

run

250

Run the simulation
for N steps

End of the simulation.

❑ Initialization

- **Parameters:** set parameters that need to be defined before atoms are created: [units](#), [dimension](#), [newton](#), [processors](#), [boundary](#), [atom style](#), [atom modify](#).
- If force-field parameters appear in the files that will be read:
[pair style](#), [bond style](#), [angle style](#), [dihedral style](#), [improper style](#).
- **Atom definition:** there are 3 ways to define atoms in LAMMPS.
 - ✓ Read them in from a data or restart file via the [read data](#) or [read restart](#) commands.
 - ✓ Or create atoms on a lattice (with no molecular topology), using these commands: [lattice](#), [region](#), [create box](#), [create atoms](#).
 - ✓ Duplicate the box to make a larger one the [replicate](#) command.

- Once atoms are defined, a variety of settings need to be specified:
force field coefficients, simulation parameters, output options ...
- ❖ Force field coefficients:
[pair_coeff](#), [bond_coeff](#), [angle_coeff](#), [dihedral_coeff](#), [improper_coeff](#),
[kspace_style](#), [dielectric](#), [special_bonds](#).
- ❖ Various simulation parameters:
[neighbor](#), [neigh_modify](#), [group](#), [timestep](#), [reset timestep](#), [run style](#),
[min_style](#), [min_modify](#).
- ❖ Fixes: [nvt](#), [npt](#), [nve](#), ...
- ❖ Computations during a simulation:
[compute](#), [compute_modify](#), and [variable](#) commands.
- ❖ Output options: [thermo](#), [dump](#), and [restart](#) commands.

thermo **freq_steps**
thermo_style **style args**



Thermodynamic
properties

- **style** = *one* or *multi* or *custom*
- **args** = list of arguments for a particular style

one args = none

multi args = none *custom*

args = list of keywords possible

□ **keywords** = **step**, elapsed, elaplong, dt, **time**, cpu, tpcpu, spcpu, cpuremain, part, timeremain, atoms, **temp**, **press**, **pe**, **ke**, **etotal**, **enthalpy**, evdwl, ecoul, epair, ebond, eangle, edihed, eimp, emol, elong, etail, **vol**, **density**, **lx**, **ly**, **lz**, **xlo**, **xhi**, **ylo**, **yhi**, **zlo**, **zhi**, **xy**, **xz**, **yz**, **xlat**, **ylat**, **zlat**, **bonds**, **angles**, **dihedrals**, **impropers**, **pxx**, **ppy**, **pzz**, **pxy**, **pxz**, **pyz** Etc

□ **Example:**

thermo_style custom step temp press pe ke etotal density lx ly lz



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OF MANITOBA

Summer School, June 25-28, 2018



- ❖ **dump command:**
Options: **vtk, h5md, molfile, netcdf, image, movie**

- ❖ **Syntax:**
dump ID group-ID style N file args

- D = user-assigned name for the dump
- group-ID = ID of the group of atoms to be dumped
- style = *atom* or *atom/gz* or *atom/mpiio* or *cfg* or *cfg/gz* or *cfg/mpiio* or *custom* or *custom/gz* or *custom/mpiio* or *dcd* or *h5md* or *image* or *local* or *molfile* or *movie* or *netcdf* or *netcdf/mpiio* or *vtk* or *xtc* or *xyz* or *xyz/gz* or *xyz/mpiio*
- N = dump every this many time steps
- file = name of file to write dump info to
- args = list of arguments for a particular style

- ❖ **Example:**
➤ **dump myDump all atom 100 dump.atom**
➤ **dump 2 subgroup atom 50 dump.run.bin**

Trajectories
Snapshots Movie

- ❑ After compiling LAMMPS, run some examples:
- ❑ Where to start to learn LAMMPS?
 - Make a copy of the directory examples to your working directory.
 - Choose and example to run.
 - Indicate the right path to the executable or use modules available (if any).
 - Edit the input file and check all the parameters.
 - Check the documentation for the commands and their arguments.
 - Run the test case: `Imp_icc_openmpi < in.melt`
 - Check the output files (log files), plot the thermodynamic properties, ...
 - Use VMD (or any other software) for visualization.

- ❑ Connect to cedar and/or graham

ssh -Y [user@cedar.computecanada.ca](ssh -Y user@cedar.computecanada.ca)

ssh -Y [user@graham.computecanada.ca](ssh -Y user@graham.computecanada.ca)

- ❑ Go to the directory where you copied or download the exercises.
- ❑ To run LAMMPS interactively, submit an interactive job using salloc

salloc -ntasks=1 -mem-per-cpu=2500M -time=00-00:30

- ❑ Submit some jobs using sbatch: `sbatch your_script.sh`
- ❑ Edit the input files
- ❑ Run the jobs
- ❑ Check the output files.

LAMMPS (30 Jul 2016)

using **1 2** OpenMP thread(s) per MPI task

3d Lennard-Jones melt

```
units      ljatom_style    atomic
lattice    fcc 0.8442Lattice spacing in x,y,z = 1.6796 1.6796 1.6796
region     box block 0 10 0 10 0 10
create_box  1 box
```

Created orthogonal box = (0 0 0) to (16.796 16.796 16.796) 2 by 2 by 3 MPI processor grid

```
create_atoms 1 box
Created 4000 atoms
```

```
mass       1 1.0
```

thermo 100

run 25000

Neighbor list info ...

1 neighbor list requests

update every 20 steps, delay 0 steps, check no

max neighbors/atom: 2000, page size: 100000

master list distance cutoff = 2.8

ghost atom cutoff = 2.8

binsize = 1.4 -> bins = 12 12 12

Memory usage per processor = 2.05293 Mbytes

Step Temp E_pair E_mol TotEng Press

0	3	-6.7733681	0	-2.2744931	-3.7033504
100	1.6510577	-4.7567887	0	-2.2808214	5.8208747
200	1.6393075	-4.7404901	0	-2.2821436	5.9139187
300	1.6626896	-4.7751761	0	-2.2817652	5.756386

25000 1.552843 -4.7611011 0 -2.432419 5.7187477

Loop time of 15.4965 on 12 procs for 25000 steps with 4000 atoms

Performance: 696931.853 tau/day, 1613.268 timesteps/s

90.2% CPU use with 12 MPI tasks x 1 OpenMP threads

MPI task timing breakdown:

Section	min time	avg time	max time	%varavg	%total
---------	----------	----------	----------	---------	--------

Pair	6.6964	7.1974	7.9599	14.8	46.45
Neigh	0.94857	1.0047	1.0788	4.3	6.48
Comm	6.0595	6.8957	7.4611	17.1	44.50
Output	0.01517	0.01589	0.019863	1.0	0.10
Modify	0.14023	0.14968	0.16127	1.7	0.97
Other		0.2332			1.50

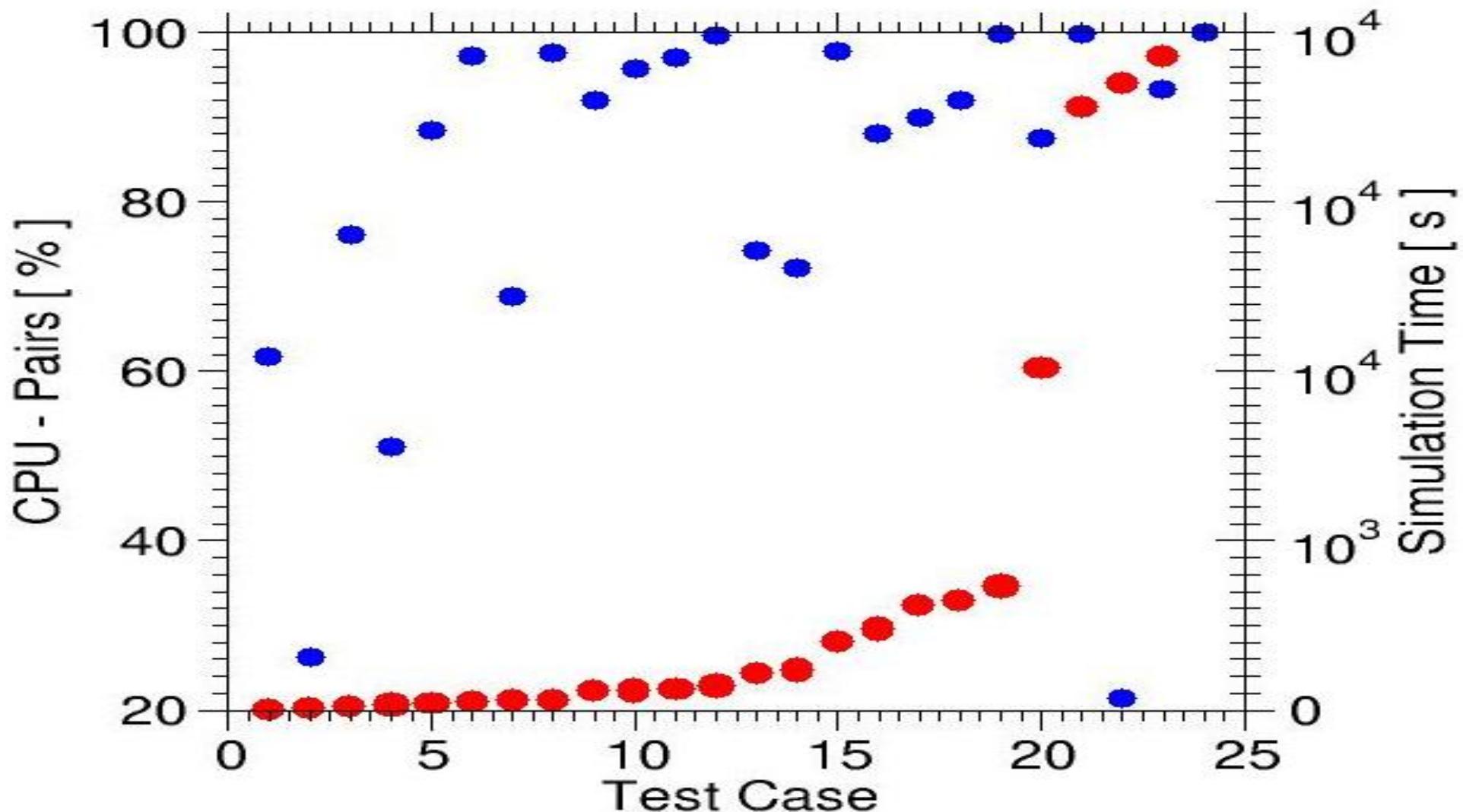
Total wall time: 0:00:15



- | | |
|-------------|--------------------------|
| 1. granular | 13. spce |
| 2. fene | 14. protein |
| 3. lj | 15. gb |
| 4. dpd | 16. reax_AB |
| 5. eam | 17. airebo |
| 6. sw | 18. reaxc_rdx |
| 7. rebo | 19. smtbq_Al |
| 8. tersoff | 20. vashishta_table_sio2 |
| 9. eim | 21. eff |
| 10. adp | 22. comb |
| 11. meam | 23. vashishta_sio2 |
| 12. peri | 24. smtbq_Al2O3 |

Parameters:

- 24 different cases.
- Number of particles: about 32000
- CPUs = 1
- MD steps = 1000
- Record the simulation time and the time used in computing the interactions between particles.

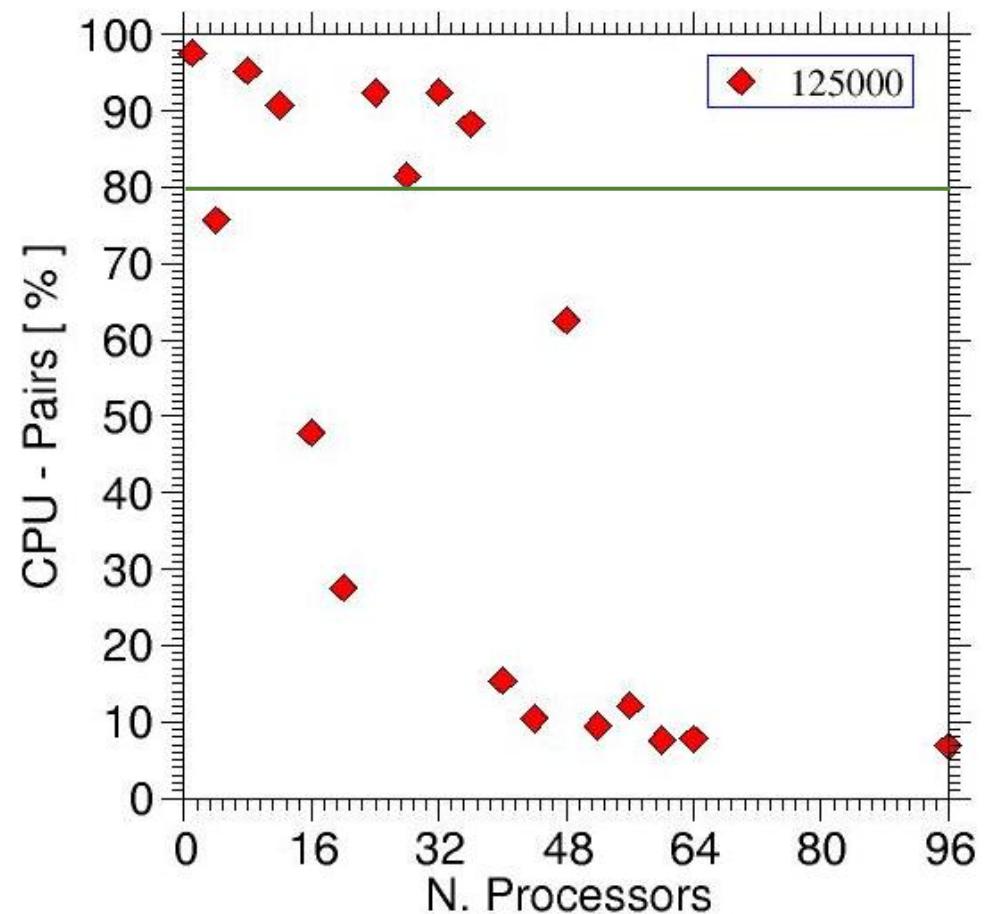
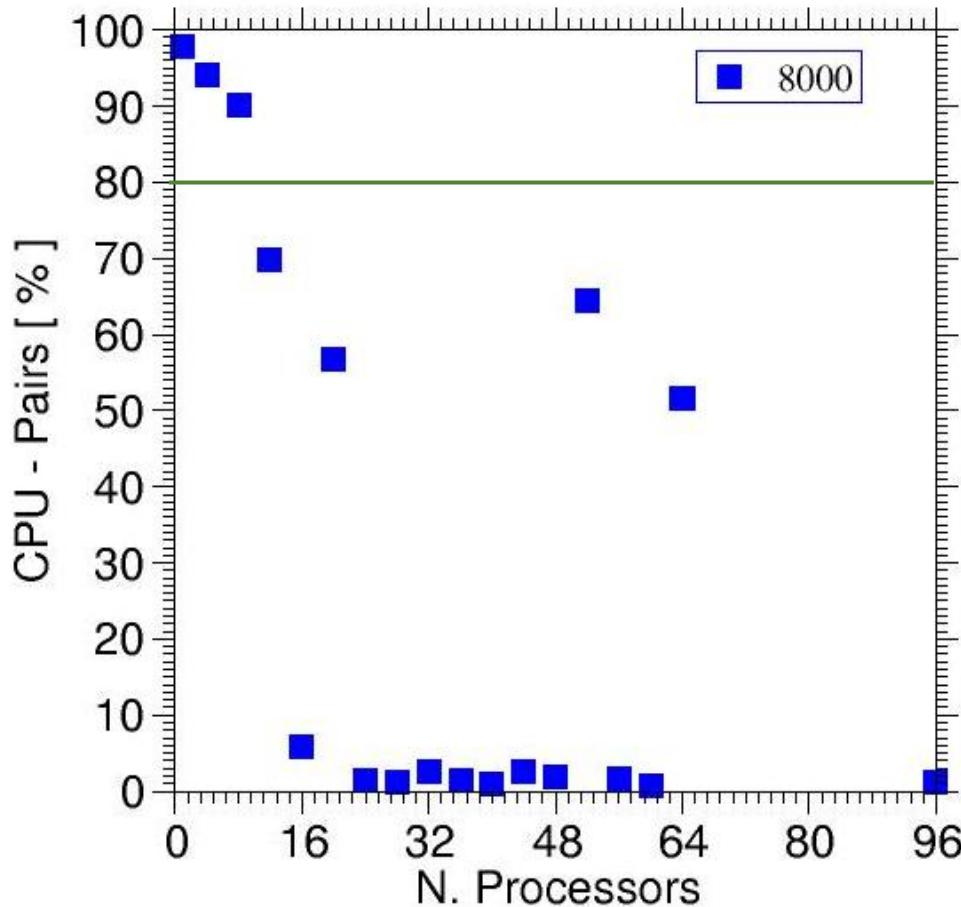


- ❑ Directory: Benchmark
- ❑ Simulation: LJ Melt
- ❑ Number of atoms: 2048, 4000, 6912, 13500
- ❑ Exercise:
 - Submit the jobs using different number of cores: 1, 2, 4, 8, 16
 - For each system: collect the data:
 - time used for pair interactions as a function of number of cores.
 - time used for communications as a function of number of cores.

Time spent for pair interactions computing and communications as a function of number of cores for different systems

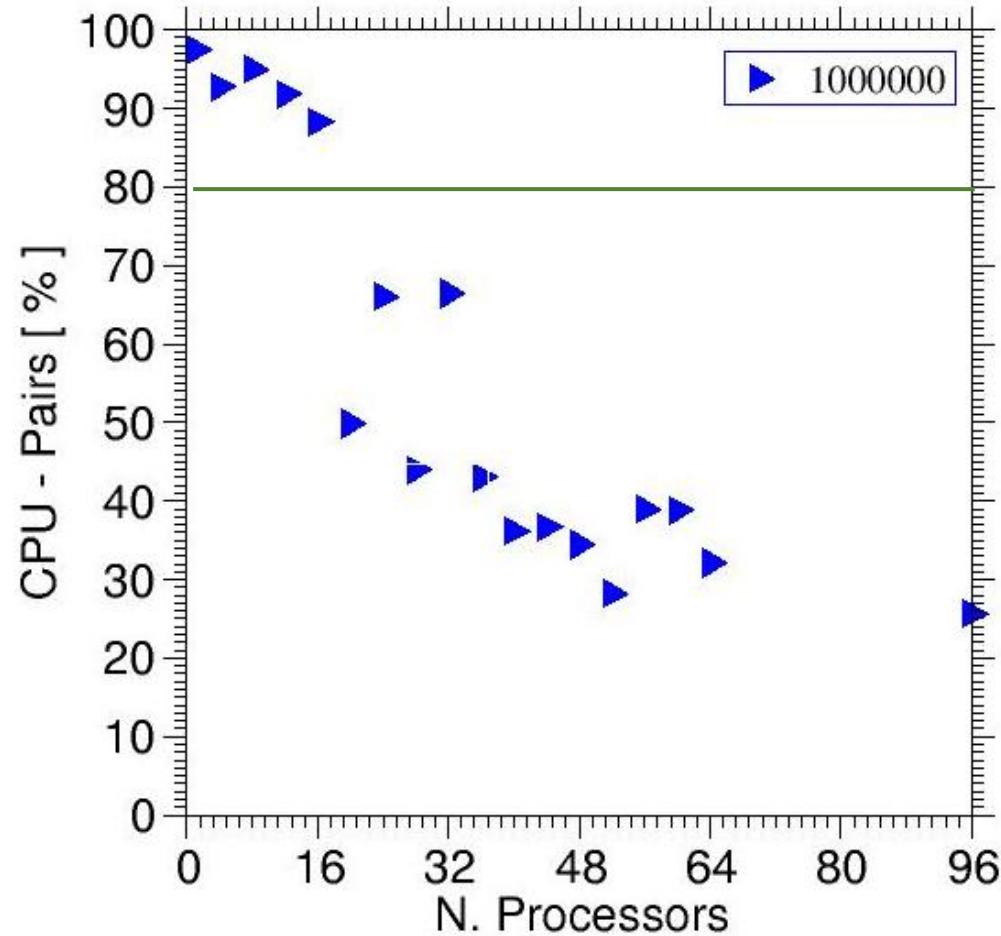
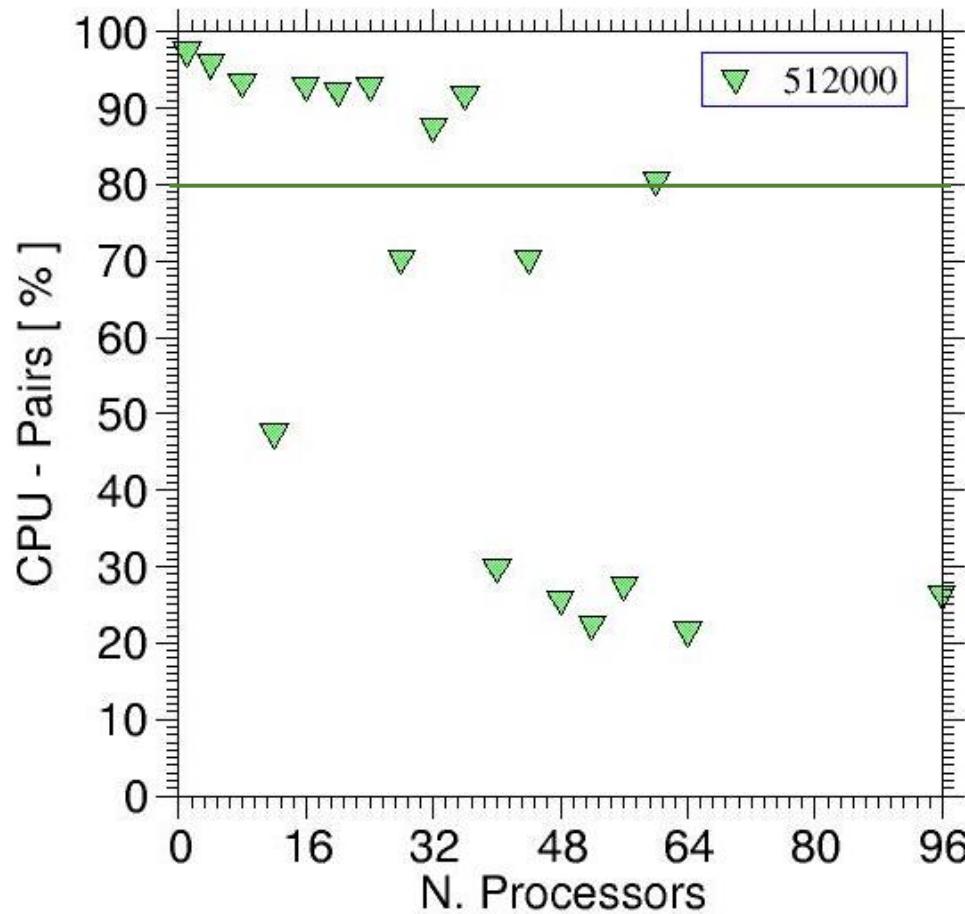
Cores	Pairs	Comm	Pairs	Comm	Pairs	Comm	Pairs	Comm
1	73.68	1.36	73.70	1.28	73.66	1.27	73.72	1.29
2	70.35	5.19	70.77	4.68	70.51	5.11	67.80	8.77
4	62.77	13.98	64.93	12.19	67.52	8.99	67.74	8.71
8	58.36	20.14	61.78	15.58	64.10	12.86	62.06	8.71
16	56.69	20.18	56.70	20.18	56.97	19.80	56.41	20.38
	2048		4000		6912		13500	

Performance test: Tersoff potential



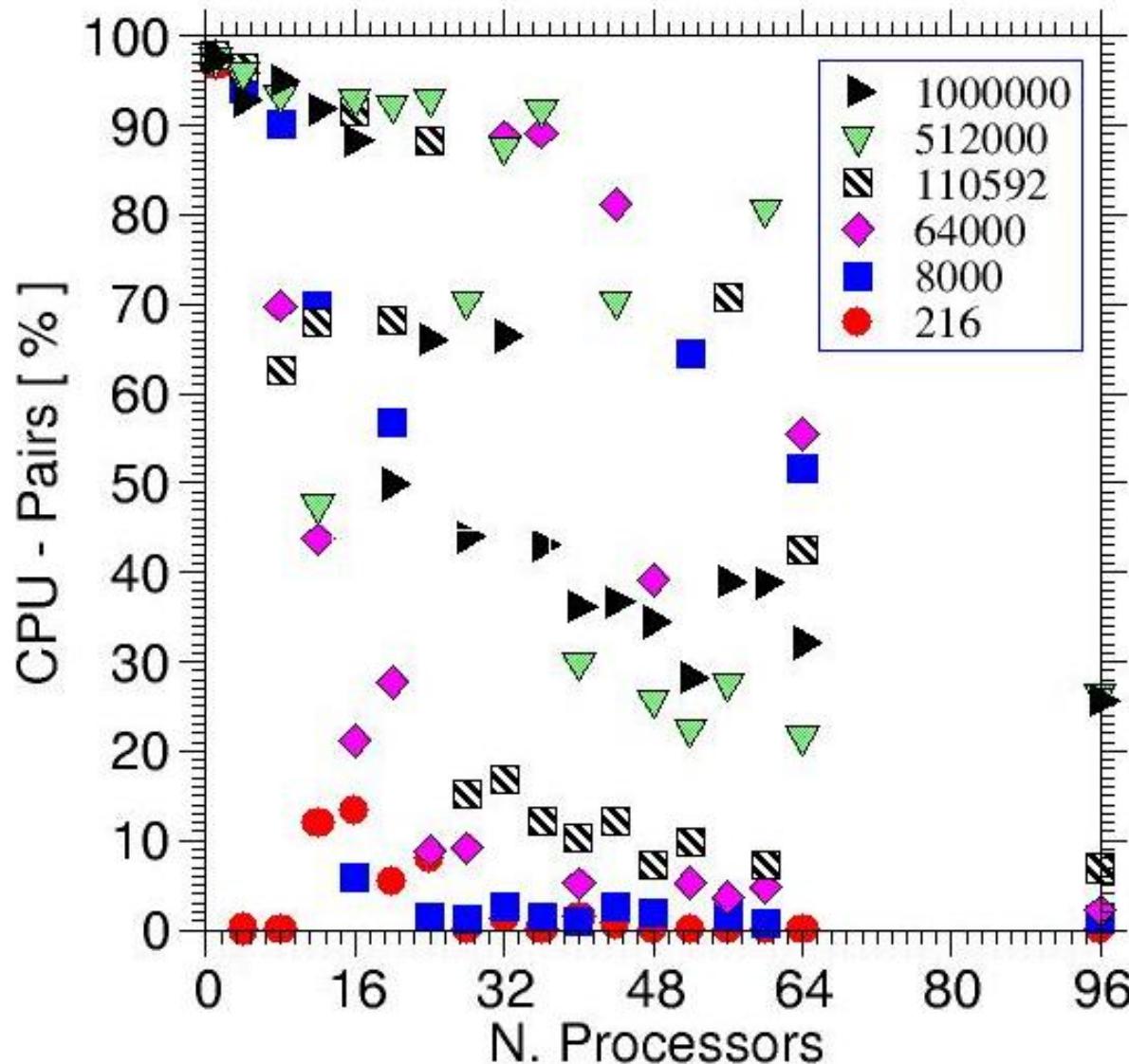
CPU time used for computing the interactions between particles as a function the number of processors for different system size.

Performance test: Tersoff potential

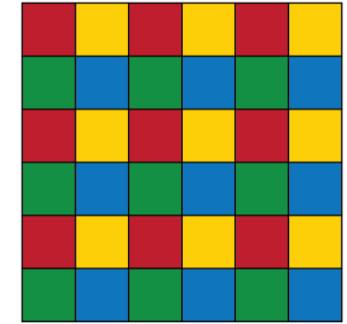
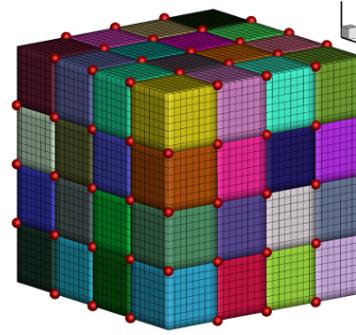


CPU time used for computing the interactions between particles as a function the number of processors for different system size.

Performance test: Tersoff potential



□ Domain decomposition



- Size, shape of the system.
- Number of processors.
- size of the small units.
- correlation between the communications and the number of small units.
- Reduce the number of cells to reduce communications.

- **Home Page:** <http://lammps.sandia.gov/>
- **Examples:** deposit, friction, micelle, obstacle, qeq, streitz, MC, body, dipole, hugoniostat, min, peptide, reax, tad, DIFFUSE, colloid, indent, msst, peri, rigid, vashishta, ELASTIC, USER, comb, eim, nb3b, pour, shear, voronoi, ELASTIC_T, VISCOSITY, coreshell, ellipse, meam, neb, prd, snap, HEAT, accelerate, crack, flow, melt, nemd
- **Results:**
 - Papers: <http://lammps.sandia.gov/papers.html>
 - Pictures: <http://lammps.sandia.gov/pictures.html>
 - Movies: <http://lammps.sandia.gov/movies.html>
- **Resources:**
 - **Online Manual:** <http://lammps.sandia.gov/doc/Manual.html>
 - **Search the mailing list:** <http://lammps.sandia.gov/mail.html>
 - **Mailing List:**
<https://sourceforge.net/p/lammps/mailman/lammps-users/>

- **Bio-molecules:** CHARMM, AMBER, OPLS, COMPASS (class 2), long-range Coulombic via PPPM, point dipoles, ...
- **Polymers:** all-atom, united-atom, coarse-grain (bead-spring FENE), bond-breaking, ...
- **Materials:** EAM and MEAM for metals, Buckingham, Morse, Yukawa, Stillinger-Weber, Tersoff, EDIP, COMB, SNAP, ...
- **Chemistry:** AI-REBO, REBO, ReaxFF, eFF
- **Meso-scale:** granular, DPD, Gay-Berne, colloidal, peri-dynamics, DSMC...
- **Hybrid:** combine potentials for hybrid systems: water on metal, polymers/semiconductor interface, colloids in solution, ...

- Pair-wise potentials: Lennard-Jones, Buckingham, ...
- Charged Pair-wise Potentials: Coulombic, point-dipole
- Many-body Potentials: EAM, Finnis/Sinclair, modified EAM (MEAM), embedded ion (EIM), Stillinger-Weber, Tersoff, AI-REBO, ReaxFF, COMB
- Coarse-Grained Potentials: DPD, GayBerne, ...
- Meso-scopic Potentials: granular, peri-dynamics
- Long-Range Electrostatics: Ewald, PPPM, MSM
- Implicit Solvent Potentials: hydrodynamic lubrication, Debye
- Force-Field Compatibility with common: CHARMM, AMBER, OPLS, GROMACS options

[pair style none](#) - turn off pairwise interactions

[pair style hybrid](#) - multiple styles of pairwise interactions

[pair style hybrid/overlay](#) - multiple styles of superposed pairwise interactions

[pair style zero](#) - neighbor list but no interactions

[pair style adp](#) - angular dependent potential (ADP) of Mishin

[pair style airebo](#) - AIREBO potential of Stuart

[pair style airebo/morse](#) - AIREBO with Morse instead of LJ

[pair style beck](#) - Beck potential

[pair style body](#) - interactions between body particles

[pair style bop](#) - BOP potential of Pettifor

[pair style born](#) - Born-Mayer-Huggins potential

[pair style born/coul/long](#) - Born-Mayer-Huggins with long-range Coulombics

[pair style born/coul/long/cs](#) - Born-Mayer-Huggins with long-range Coulombics

and core/shell

[pair style born/coul/msm](#) - Born-Mayer-Huggins with long-range MSM

Coulombics



[pair style born/coul/wolf](#) - Born-Mayer-Huggins with Coulombics via Wolf potential

[pair style brownian](#) - Brownian potential for Fast Lubrication Dynamics

[pair style brownian/poly](#) - Brownian potential for Fast Lubrication Dynamics with polydispersity

[pair style buck](#) - Buckingham potential

[pair style buck/coul/cut](#) - Buckingham with cutoff Coulomb

[pair style buck/coul/long](#) - Buckingham with long-range Coulombics

[pair style buck/coul/long/cs](#) - Buckingham with long-range Coulombics and core/shell

[pair style buck/coul/msm](#) - Buckingham long-range MSM Coulombics

[pair style buck/long/coul/long](#) - long-range Buckingham with long-range Coulombics

[pair style colloid](#) - integrated colloidal potential

[pair style comb](#) - charge-optimized many-body (COMB) potential

[pair style comb3](#) - charge-optimized many-body (COMB3) potential

[pair style coul/cut](#) - cutoff Coulombic potential

[pair style coul/debye](#) - cutoff Coulombic potential with Debye screening

[pair style coul/dsf](#) - Coulombics via damped shifted forces

[pair style coul/long](#) - long-range Coulombic potential

[pair style coul/long/cs](#) - long-range Coulombic potential and core/shell

[pair style coul/msm](#) - long-range MSM Coulombics

[pair style coul/streitz](#) - Coulombics via Streitz/Mintmire Slater orbitals

[pair style coul/wolf](#) - Coulombics via Wolf potential

[pair style dpd](#) - dissipative particle dynamics (DPD)

[pair style dpd/tstat](#) - DPD thermostatting

[pair style dsmc](#) - Direct Simulation Monte Carlo (DSMC)

[pair style eam](#) - embedded atom method (EAM)

[pair style eam/alloy](#) - alloy EAM

[pair style eam/fs](#) - Finnis-Sinclair EAM

[pair style eim](#) - embedded ion method (EIM)

[pair style gauss](#) - Gaussian potential

[pair style gayberne](#) - Gay-Berne ellipsoidal potential

[pair style gran/hertz/history](#) - granular potential with Hertzian interactions

[pair style gran/hooke](#) - granular potential with history effects

[pair style gran/hooke/history](#) - granular potential without history effects

[pair style hbond/dreiding/lj](#) - DREIDING hydrogen bonding LJ potential

[pair style hbond/dreiding/morse](#) - DREIDING hydrogen bonding Morse potential

[pair style kim](#) - interface to potentials provided by KIM project

[pair style lcbop](#) - long-range bond-order potential (LCBOP)

[pair style line/lj](#) - LJ potential between line segments

[pair style lj/charmm/coul/charmm](#) - CHARMM potential with cutoff Coulomb

[pair style lj/charmm/coul/charmm/implicit](#) - CHARMM for implicit solvent

[pair style lj/charmm/coul/long](#) - CHARMM with long-range Coulomb

[pair style lj/charmm/coul/msm](#) - CHARMM with long-range MSM Coulombics

[pair style lj/class2](#) - COMPASS (class 2) force field with no Coulomb

[pair style lj/class2/coul/cut](#) - COMPASS with cutoff Coulomb

[pair style lj/gromacs/coul/gromacs](#) - GROMACS-style LJ and Coulombic potential

[pair style lj/long/coul/long](#) - long-range LJ and long-range Coulombics

[pair style lj/long/dipole/long](#) - long-range LJ and long-range point dipoles

[pair style lj/long/tip4p/long](#) - long-range LJ and long-range Coulomb for TIP4P

water

[pair style lj/smooth](#) - smoothed Lennard-Jones potential

[pair style lj/smooth/linear](#) - linear smoothed Lennard-Jones potential

[pair style lj96/cut](#) - Lennard-Jones 9/6 potential

[pair style lubricate](#) - hydrodynamic lubrication forces

[pair style lubricate/poly](#) - hydrodynamic lubrication forces with polydispersity

[pair style lubricateU](#) - hydrodynamic lubrication forces for Fast Lubrication

Dynamics

[pair style lubricateU/poly](#) - hydrodynamic lubrication forces for Fast Lubrication
with polydispersity

[pair style meam](#) - modified embedded atom method (MEAM)

[pair style mie/cut](#) - Mie potential

[pair style morse](#) - Morse potential

[pair style nb3b/harmonic](#) - nonbonded 3-body harmonic potential

[pair style nm/cut](#) - N-M potential

[pair style nm/cut/coul/cut](#) - N-M potential with cutoff Coulomb

[pair style nm/cut/coul/long](#) - N-M potential with long-range Coulombics

[pair style peri/eps](#) - peridynamic EPS potential

[pair style peri/lps](#) - peridynamic LPS potential

[pair style peri/pmb](#) - peridynamic PMB potential

[pair style peri/ves](#) - peridynamic VES potential

[pair style polymorphic](#) - polymorphic 3-body potential

[pair style reax](#) - ReaxFF potential

[pair style rebo](#) - 2nd generation REBO potential of Brenner

[pair style resquared](#) - Everaers RE-Squared ellipsoidal potential

[pair style snap](#) - SNAP quantum-accurate potential

[pair style soft](#) - Soft (cosine) potential



[pair style sw](#) - Stillinger-Weber 3-body potential

[pair style table](#) - tabulated pair potential

[pair style tersoff](#) - Tersoff 3-body potential

[pair style tersoff/mod](#) - modified Tersoff 3-body potential

[pair style tersoff/zbl](#) - Tersoff/ZBL 3-body potential

[pair style tip4p/cut](#) - Coulomb for TIP4P water w/out LJ

[pair style tip4p/long](#) - long-range Coulombics for TIP4P water w/out LJ

[pair style tri/lj](#) - LJ potential between triangles

[pair style vashishta](#) - Vashishta 2-body and 3-body potential

[pair style yukawa](#) - Yukawa potential

[pair style yukawa/colloid](#) - screened Yukawa potential for finite-size particles

[pair style zbl](#) - Ziegler-Biersack-Littmark potential