

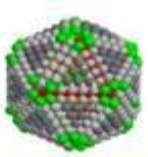
Introduction to classical Molecular Dynamics Simulations

Dr. Ali Kerrache

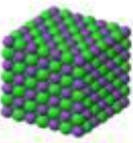
*Faculty of Science, Univ. of Manitoba, Winnipeg
WestGrid / Compute Canada*

E-mail: ali.kerrache@umanitoba.ca

Home Page: <https://ali-kerrache.000webhostapp.com/>



Introduction to MD simulations



Who am I?

❑ High Performance Computing Specialist

- WestGrid and Compute Canada.
- Software and User Support.
- National teams:
 - ✓ **BST**: Bio-molecular Simulation Team.
 - ✓ **RSNT**: Research Support National Team.



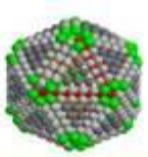
❑ Computational Physicist

- 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, ...

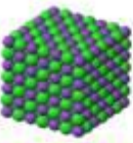


UNIVERSITY
OF MANITOBA





Introduction to MD simulations



Outline:

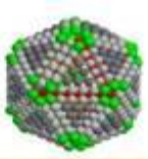
□ Introduction

- Basic concepts of Molecular Dynamics Simulations.
- **Examples** of Simulations using Molecular Dynamics.

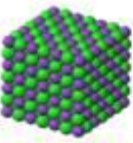
□ Setting and Running MD simulations (LAMMPS)

- **LAMMPS**: Molecular Dynamics Simulator.
- Building LAMMPS step by step.
- Running LAMMPS (Input, Output, ...).

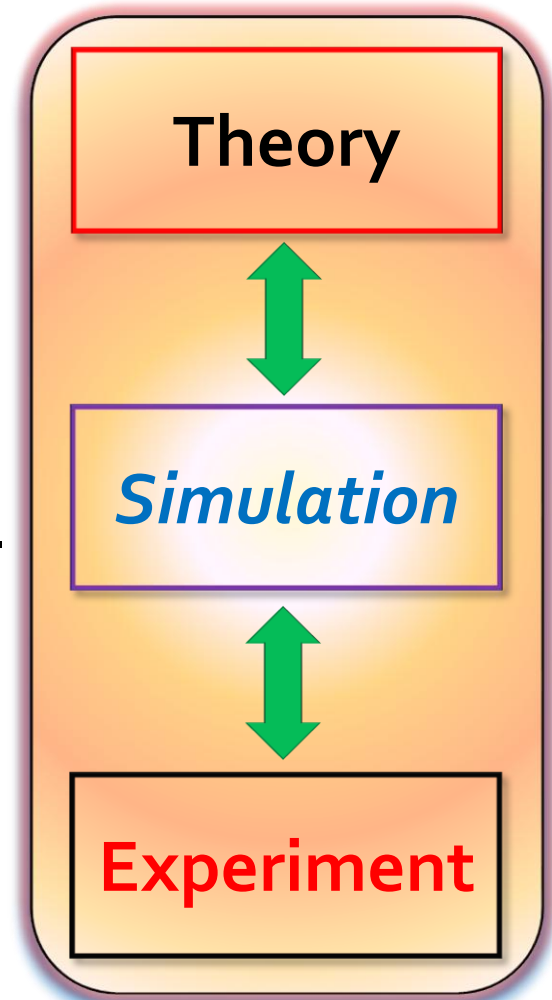
□ Readings and References

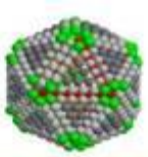


Why do we need simulations?

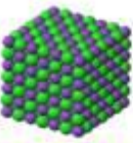


- ❑ **Except simple cases,** no analytical solutions for most of the problems.
- ❑ **In most cases, experiments are:**
 - Difficult or impossible to perform.
 - Too dangerous to ...
 - Expensive and time consuming.
 - Blind and too many parameters to control.
- ❑ **Simulation is a powerful tool:**
 -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





Atomistic / Molecular Simulations

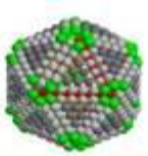


□ What are the atomistic/molecular Simulation?

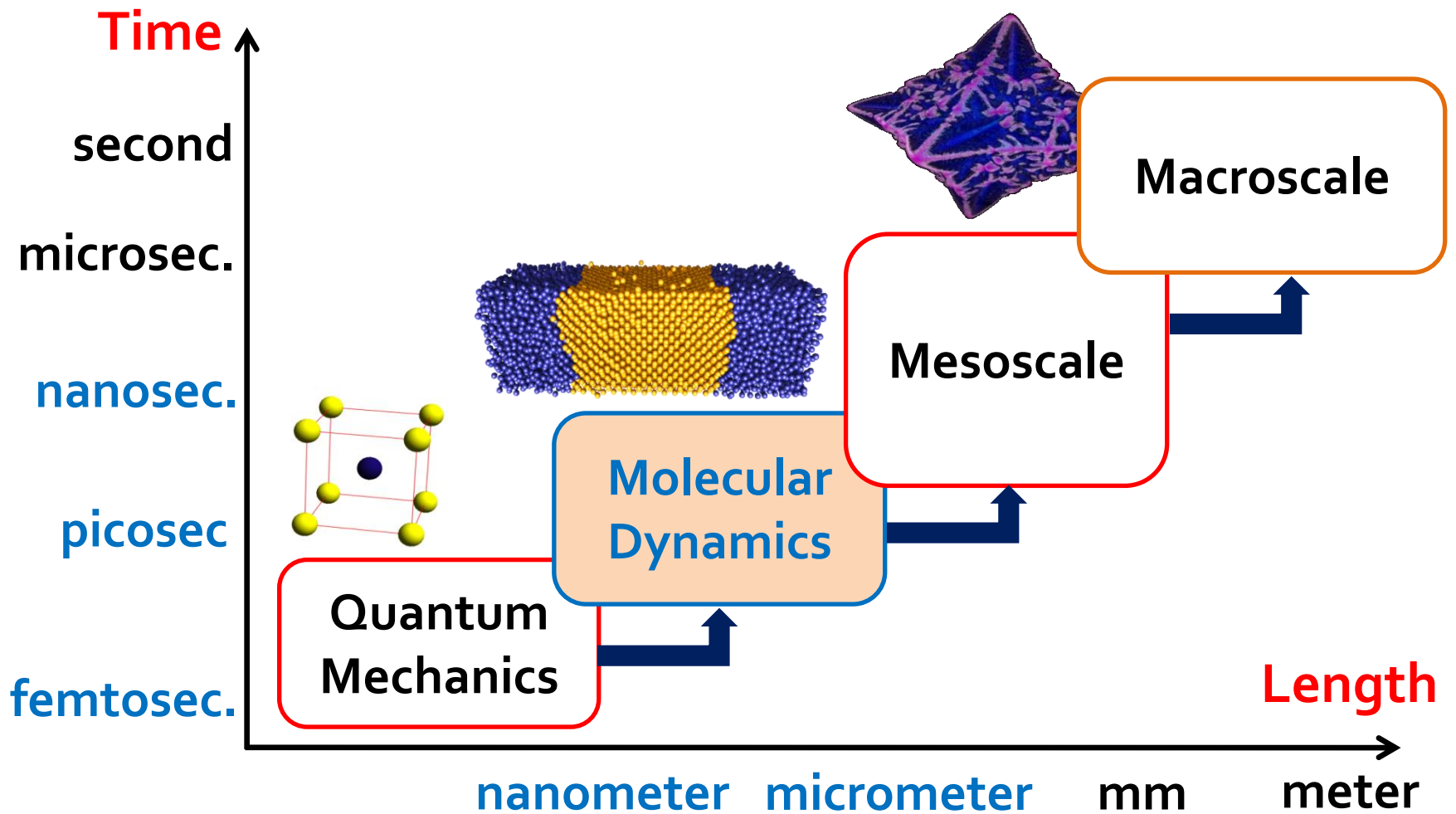
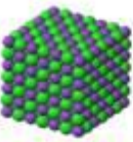
- a tool to get **insights** about the **properties of materials** at **atomic** or **molecular** level.
- used to predict and / or verify experiments.
- considered as a bridge between theory and experiment.
- provide a numerical solution when analytical ones are impossible.
- used to resolve the behavior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

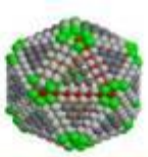
□ **Applications**, simulations can be applied in, but not limited to:

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

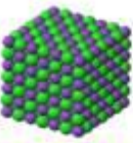


Length and Time Scales





Classical MD Simulation



□ Solution of Newton equations:

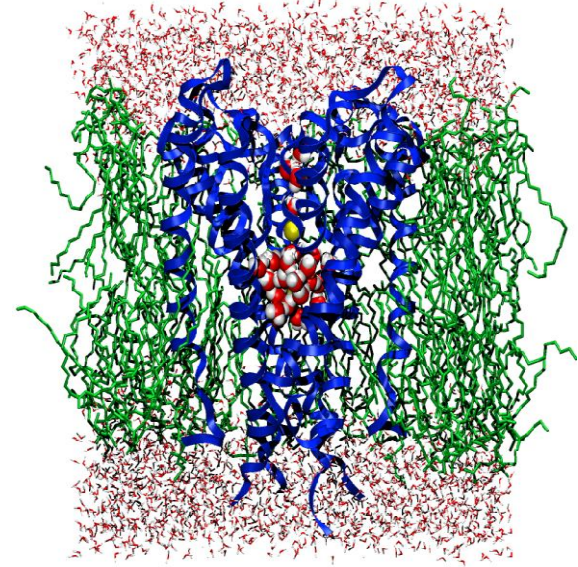
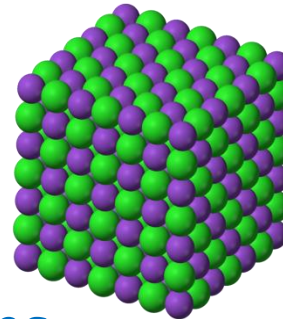
➤ MD is the **solution of the classical equations of motion** for a system of N atoms or molecules in order to obtain the time evolution of the system.

➤ Uses algorithms to integrate the equations of motion.

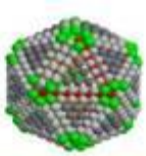
➤ **Applied to many-particle systems.**

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

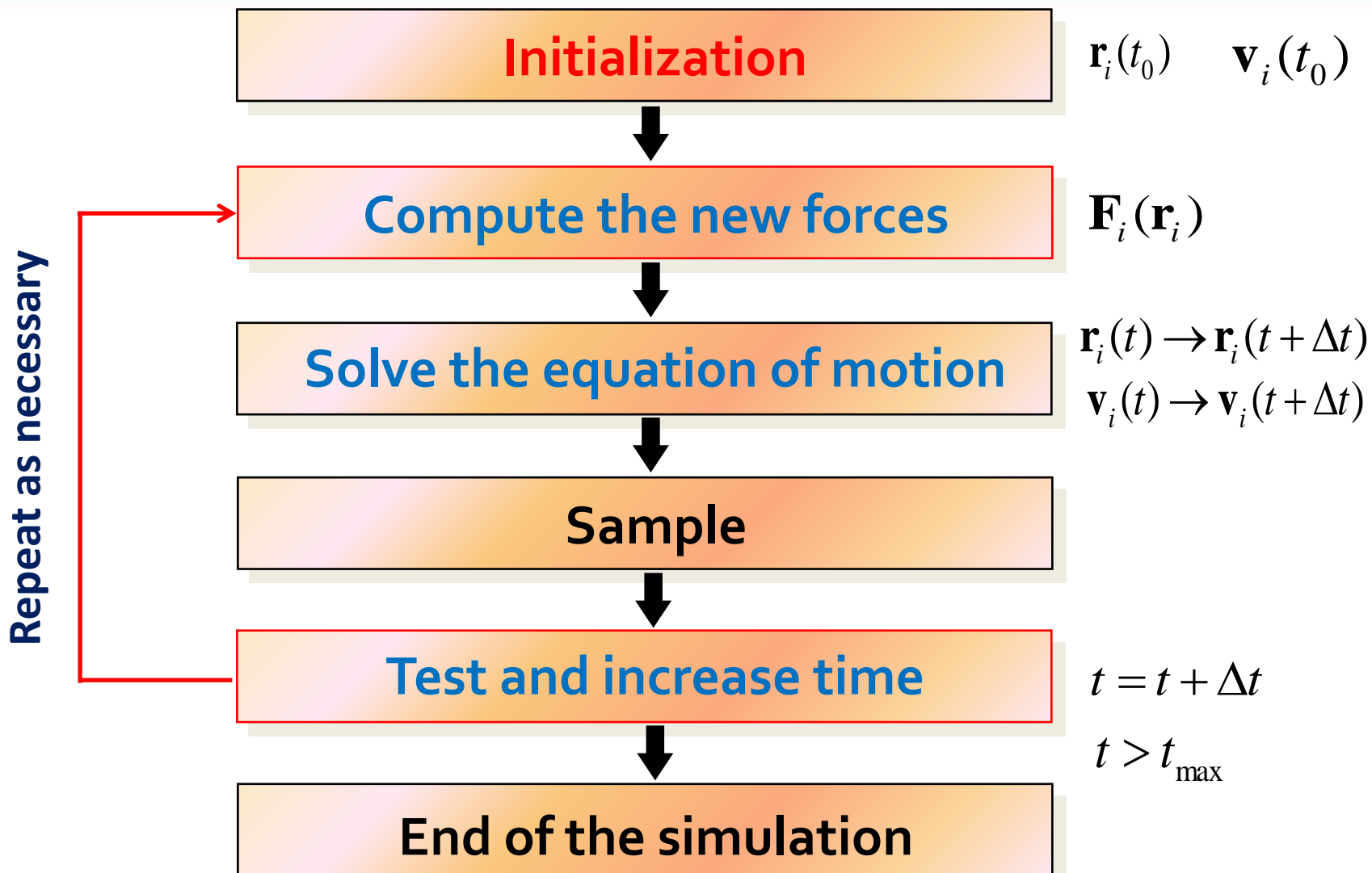
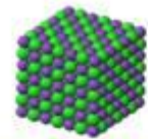
$$m_i \vec{a}_i = \vec{F}_i$$
$$\vec{F}_i = \sum_{j \neq i}^N \vec{f}_{ij}$$

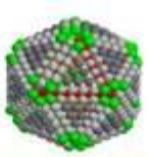


$$\vec{f}_{ij} = -\vec{\nabla}_i V(r_{ij})$$

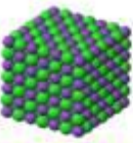


Structure of MD program





Forces: Newton's Equation



□ Potential function:

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

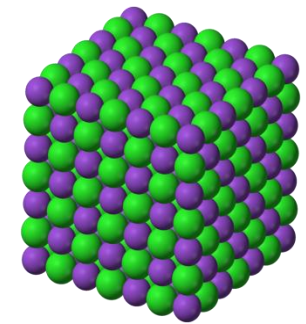
□ Evaluate the forces acting on each particle:

❖ The force on an atom is determined by: $\mathbf{F}_i = -\nabla U(\mathbf{r})$

■ $U(\mathbf{r})$: potential function

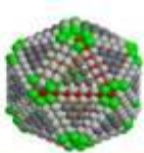
■ N : number of atoms in the system

■ \mathbf{r}_{ij} : vector distance between atoms i and j

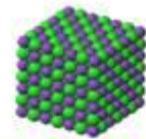


□ Newton equation:

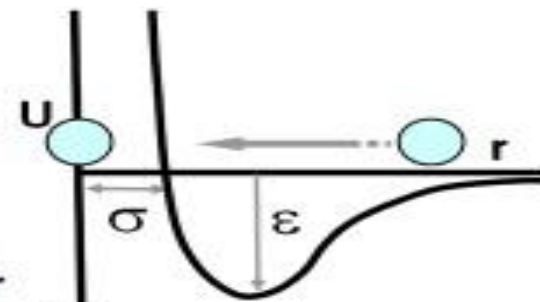
$$m_i \frac{d^2}{dt^2} \vec{x}_i = \vec{F}_i(\vec{x}_1, \dots, \vec{x}_N) \quad i = 1 \dots N$$



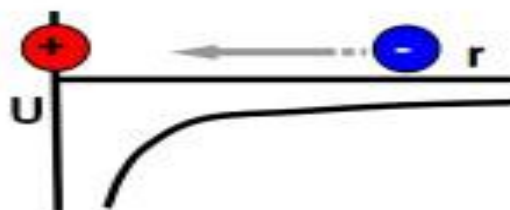
Force Fields used in MD Simulations



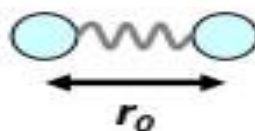
$$U = \sum_{i < j} \sum 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right]$$



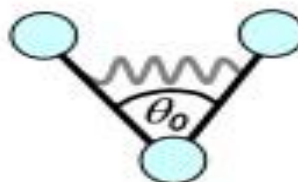
$$+ \sum_{i < j} \sum \frac{q_i q_j}{4\pi\epsilon_0 r_{ij}}$$



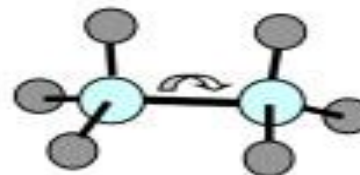
$$+ \sum_{bonds} \frac{1}{2} k_b (r - r_0)^2$$



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

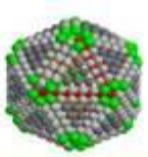


$$+ \sum_{torsions} k_\phi [1 + \cos(n\phi - \delta)]$$

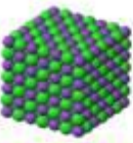


Interactions:

- Lennard-Jones
- Electrostatic
- Bonds
- Orientation
- Rotational



Derivation of Verlet Algorithm



Taylor's expansions :

position

acceleration

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

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

Add (I) and (II):

velocity

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

or :

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

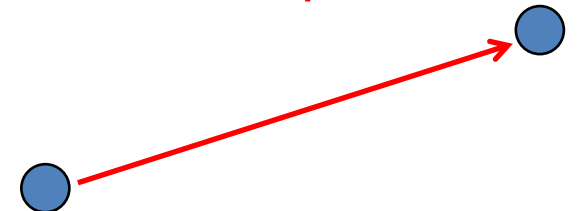
Subtract (III) from (I):

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

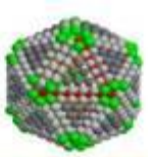
or :

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

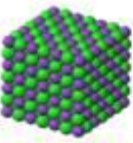
$\{r(t+\Delta t), v(t+\Delta t)\}$



$\{r(t), v(t)\}$ (IV)



Verlet and Leap-Frog Algorithms



From the initial positions and velocities:

$\mathbf{r}_i(t)$ $\mathbf{v}_i(t)$

$$\mathbf{a}(\mathbf{r}) = \frac{1}{m} \mathbf{F}(\mathbf{r}(t))$$

Obtain the positions and velocities at: $t + \Delta t$

- Velocity calculated explicitly
- Possible to control the temperature
- Stable in long simulation
- Most used algorithm

$$\mathbf{r}(t + \Delta t) = \mathbf{r}(t) + \mathbf{v}(t)\Delta t + \frac{1}{2} \mathbf{a}(\mathbf{r})\Delta t^2$$

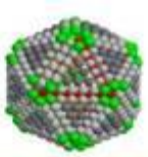
$$\mathbf{a}(t + \Delta t) = \frac{1}{m} \mathbf{F}(\mathbf{r}(t + \Delta t))$$

$$\mathbf{v}(t + \Delta t/2) = \mathbf{v}(t)\Delta t + \frac{1}{2} \mathbf{a}(\mathbf{r})\Delta t$$

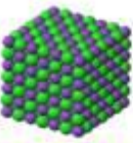
$$\mathbf{v}(t + \Delta t) = \mathbf{v}(t + \Delta t/2) + \frac{1}{2} \mathbf{a}(t + \Delta t)\Delta t$$

Leap-Frog algorithm

$$\begin{aligned} \mathbf{v}(t + \frac{\Delta t}{2}) &= \mathbf{v}(t - \frac{\Delta t}{2}) + \frac{\mathbf{F}(t)}{m} \Delta t \\ \mathbf{r}(t + \Delta t) &= \mathbf{r}(t) + \mathbf{v}(t + \frac{\Delta t}{2}) \Delta t \end{aligned}$$



Predictor Corrector Algorithm



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

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

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

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

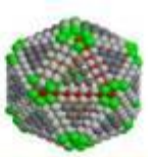
- **Corrector step:**
- get corrected acceleration: $\mathbf{a}^C(\mathbf{r}) = \frac{\mathbf{F}(\mathbf{r}^P(t + \Delta t))}{m}$

- using error in acceleration: $\Delta \mathbf{a}(t + \Delta t) \cong \mathbf{a}^C(t + \Delta t) - \mathbf{a}^P(t + \Delta t)$

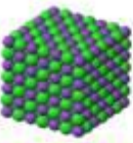
- correct the positions: $\mathbf{r}(t + \Delta t) \cong \mathbf{r}^P(t + \Delta t) + C_0 \frac{\Delta t^2}{2} \Delta \mathbf{a}(t + \Delta t)$

- correct the velocities: $\mathbf{v}(t + \Delta t) \cong \mathbf{v}^P(t + \Delta t) + C_1 \Delta t \Delta \mathbf{a}(t + \Delta t)$

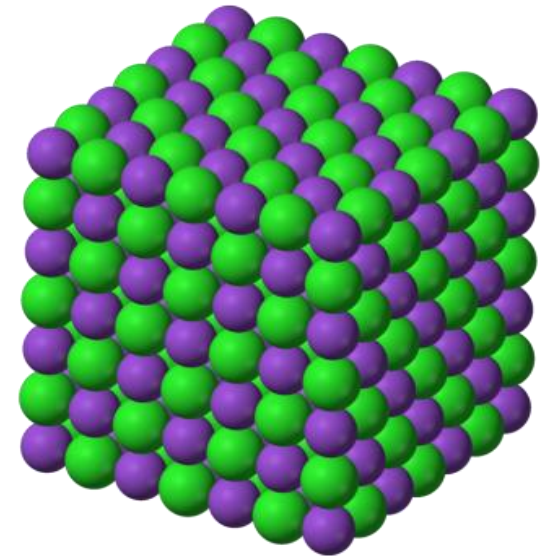
C_n : constants depending accuracy

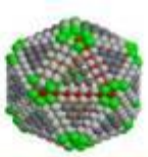


MD Simulation settings

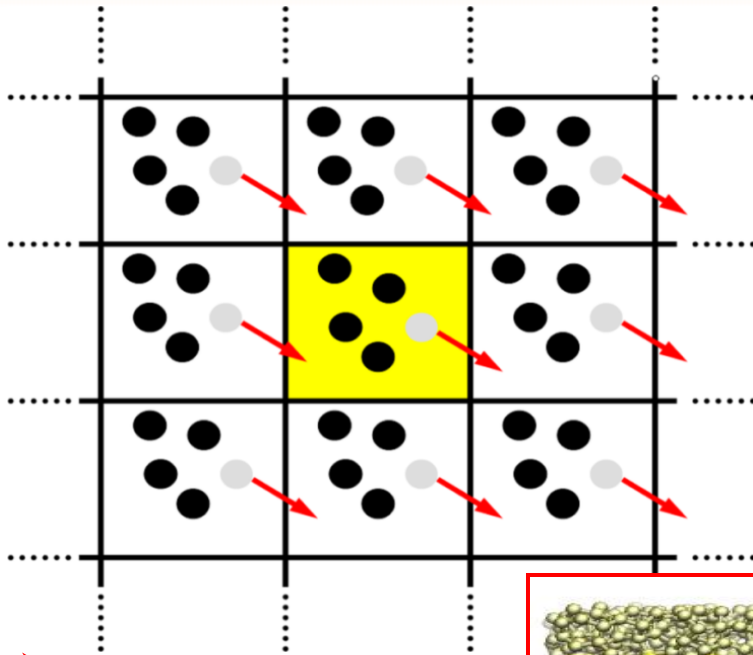
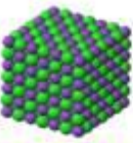


- Starting configuration:
 - Atomic positions (x, y, z)
 - density ...
 - mass, charge,
- Initial velocities: depend on **temperature**
- periodic boundary conditions (PBC):
 - required to simulate bulk properties.
- set the **appropriate potential**:
 - Depend on the system to simulate (**literature search**).
- set the appropriate **time step**: should be short (order of **1fs**).
- set the **temperature control**:
 - define the thermodynamic ensemble (NVT, NPT, NVE, ...).



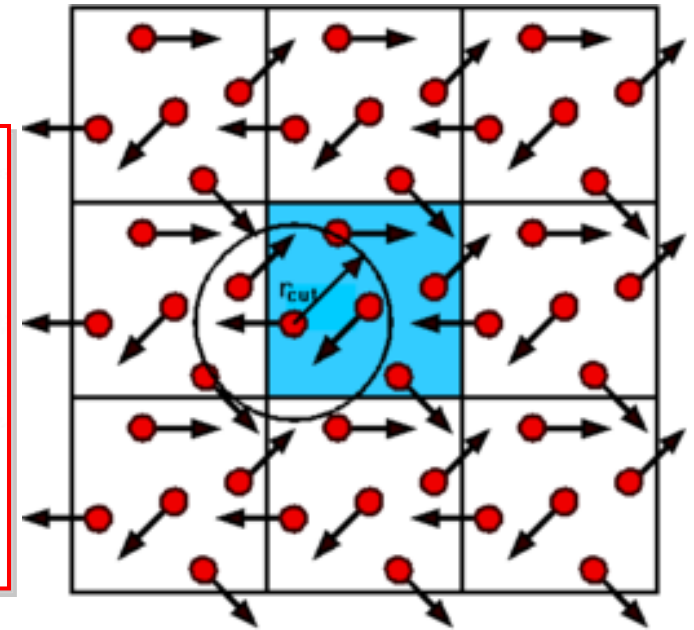
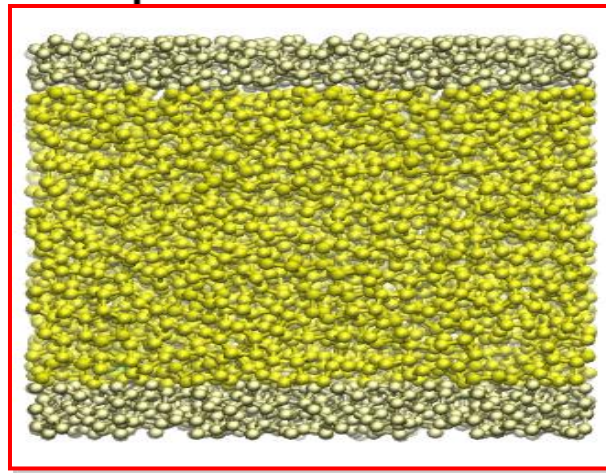


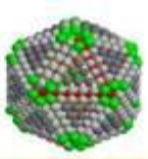
Periodic Boundary Conditions



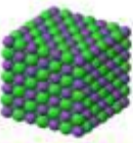
- Create **images** of the simulation box: **duplication** in all directions (x, y and z)
- An atom moving out of boundary comes from the other side.

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





Neighbour Lists

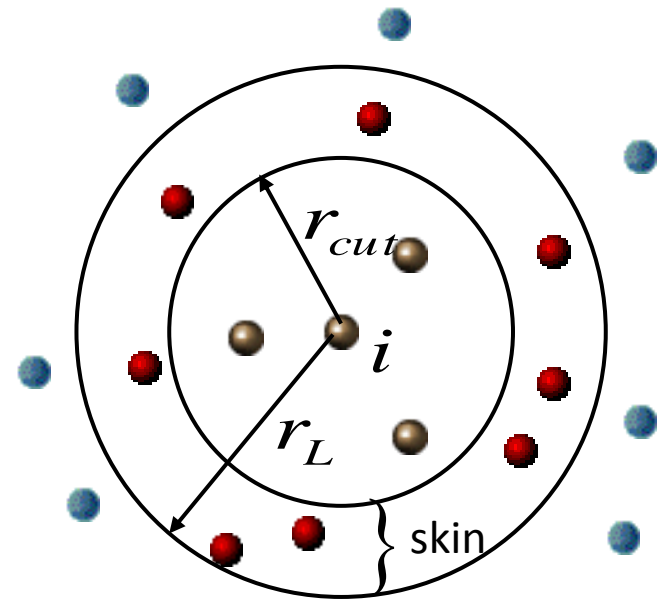


- Evaluate forces is **time consuming**:
- Pair potential calculation: $\propto O(N^2)$
- Atom moves $< 0.2 \text{ \AA}$ per time step
- Not necessary to include all the possible pairs.

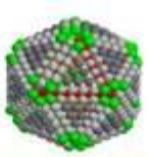
❑ **Solution: Verlet neighbor list**

- Containing all neighbors of each atom within: r_L
- Update every N_L steps

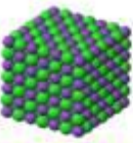
For each particle: $N-1$
For N particles: $N(N-1)$



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



Thermodynamic Ensembles



□ Ensembles:

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

Each ensemble is used for a specific simulation:

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

□ Temperature control:

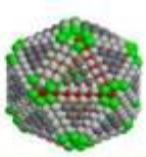
- **Berendsen thermostat (velocity rescaling)**
- **Andersen thermostat**
- **Nose-Hoover chain**

✓ Choose the ensemble that best fits your system and the properties you want to simulate

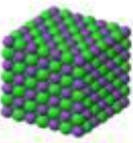
□ Pressure control:

- **Berendsen volume rescaling**
- **Andersen piston**

✓ start the simulation.
✓ Check the thermodynamic properties as a function of time.



Statistical Mechanics



□ 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. radial distribution function (RDF, $S(Q)$, Van-Hove, ...).

□ Dynamical Properties:

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

Thermodynamic Properties

❖ Kinetic Energy

$$\langle K.E. \rangle = \left\langle \frac{1}{2} \sum_i^N m_i v_i^2 \right\rangle$$

❖ Temperature

$$T = \frac{2}{3Nk_B} \langle K.E. \rangle$$

❖ Configuration Energy

$$U_c = \left\langle \sum_i^N \sum_{j>i}^N V(r_{ij}) \right\rangle$$

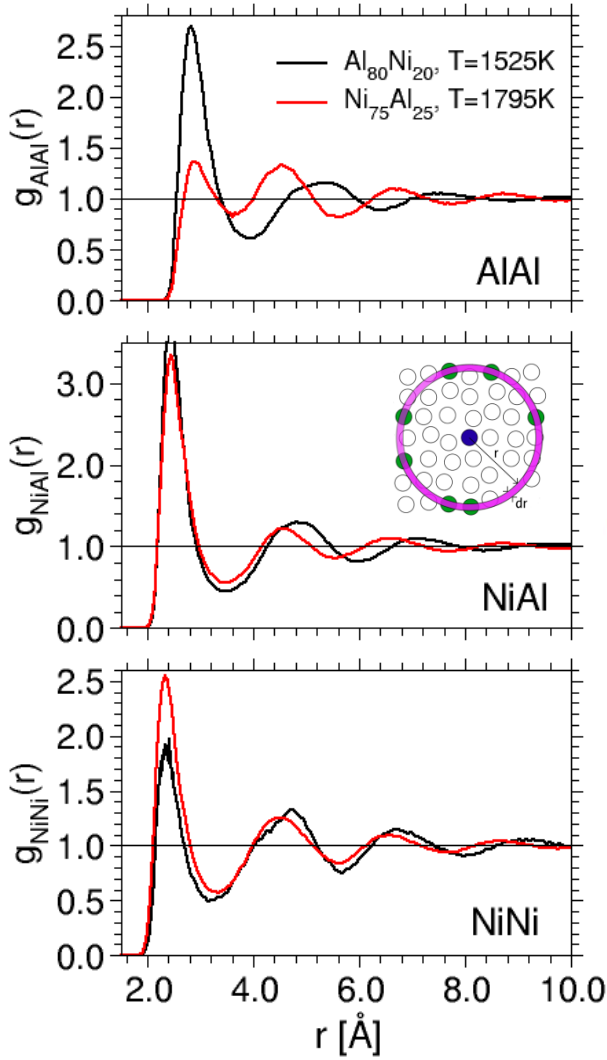
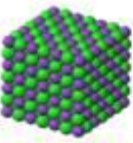
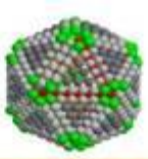
❖ Pressure

$$PV = Nk_B T - \frac{1}{3} \left\langle \sum_{i=1}^{N-1} \sum_{j>i}^N \vec{r}_{ij} \cdot \vec{f}_{ij} \right\rangle$$

❖ Specific Heat

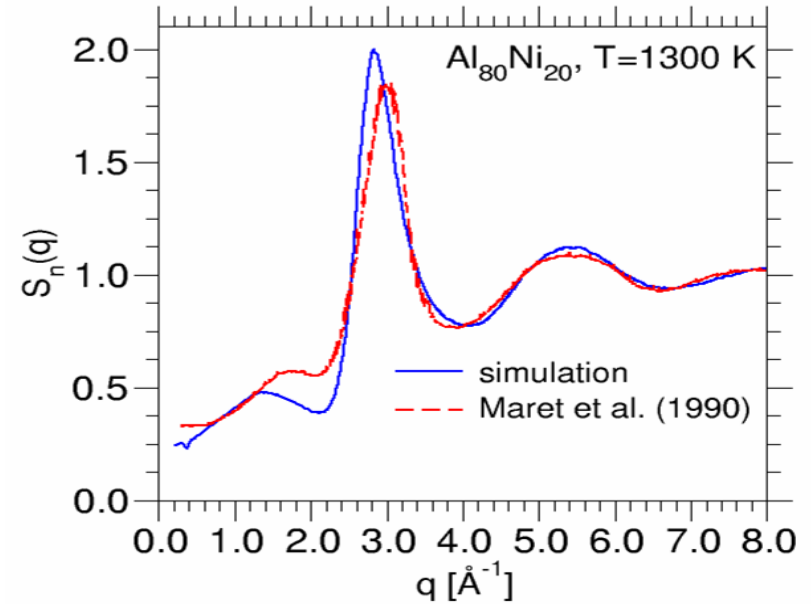
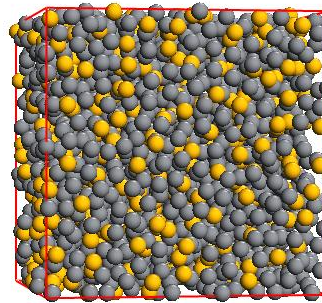
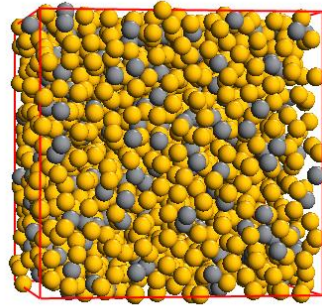
$$\langle \delta(U_c)^2 \rangle_{NVE} = \frac{3}{2} Nk_B^2 T^2 \left(1 - \frac{3Nk_B}{2C_v} \right)$$

Structural properties: AlNi



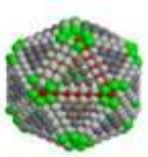
Radial Distribution Function (simulation)

$$g(r) = \frac{\langle n(r) \rangle}{4\pi\rho r^2 \Delta r} = \frac{V}{N^2} \left\langle \sum_i \sum_{j \neq i}^N \delta(r - r_{ij}) \right\rangle$$

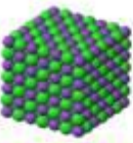


$$S(k) = 1 + 4\pi\rho \int_0^\infty \frac{\sin(kr)}{kr} (g(r) - 1) r^2 dr$$

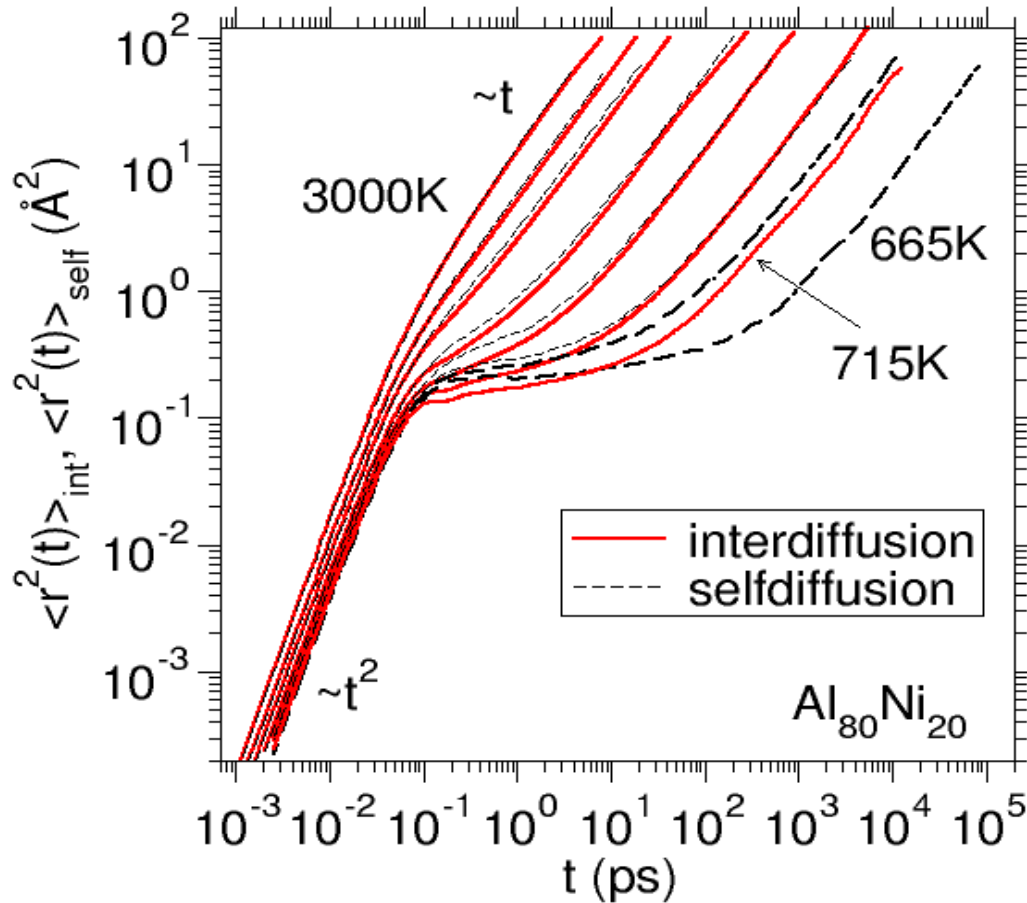
Structure Factor (experiments)



Dynamical Properties: AlNi



Mean Square Displacement (Einstein relation)

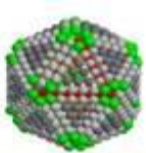


$$2Dt = \frac{1}{3} \langle |\mathbf{r}_i(t) - \mathbf{r}_i(0)|^2 \rangle$$

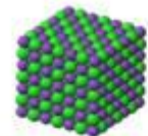
$$\text{MSD} = c_{\text{Al}} \langle (\vec{r}_{s,\text{Ni}}(t) - \vec{r}_{s,\text{Ni}}(0))^2 \rangle + c_{\text{Ni}} \langle (\vec{r}_{s,\text{Al}}(t) - \vec{r}_{s,\text{Al}}(0))^2 \rangle$$

Diffusion constants

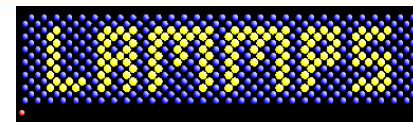
$$D = \lim_{t \rightarrow \infty} \frac{1}{N} \sum_{i=1}^N \frac{\langle (r(t) - r(0))^2 \rangle}{6t}$$



Available MD Programs



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:** <http://ambermd.org/>

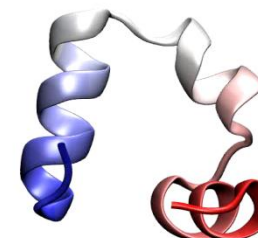


Home made codes:

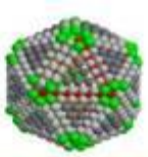
- ✓ **C, C++**
- ✓ **Fortran, ... etc**

Visualization:

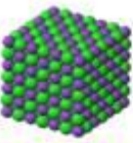
- **VMD**
- **OVITO, ...**



Analysis?



Molecular Dynamics: some Results



□ Binary Metallic alloys:

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

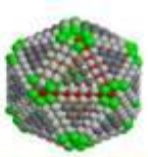
JOHANNES
GUTENBERG
UNIVERSITÄT
MAINZ



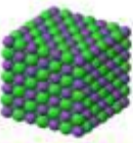
□ Glasses:

- How to prepare a glass using MD simulation?
- Glass Indentation using MD.



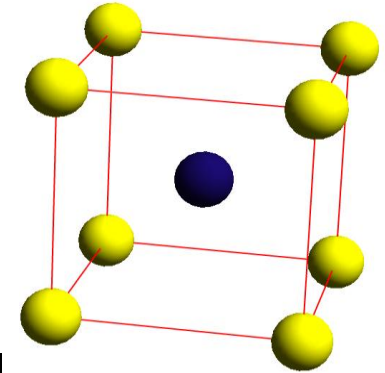


Solid-Liquid interface velocities



Why B2-Al₅₀Ni₅₀?

- ✓ B2-Al₅₀Ni₅₀: 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

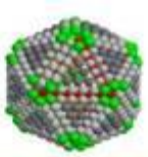


Questions:

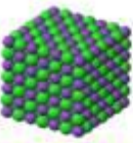
- crystal **growth** & accurate estimation of T_m ?
- solid-liquid interface velocity from **interface motion**?
- kinetic coefficients and their **anisotropy**?
- **solid-liquid interface** motion controlled by **mass diffusion**?
- solid-liquid **coexistence**, interface **structure**?
- how to distinguish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

➤ Wilson H.A., Philos. Mag. , **50** (1900) 238.

➤ Frenkel J., Phys. Z. Sowjetunion, **1** (1932) 498.



Solid-Liquid Interfaces: AlNi

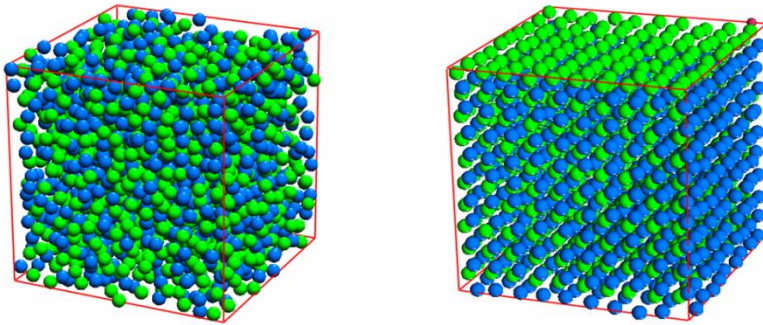


□ solve Newton's equation of motion for system of N particles:

- 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

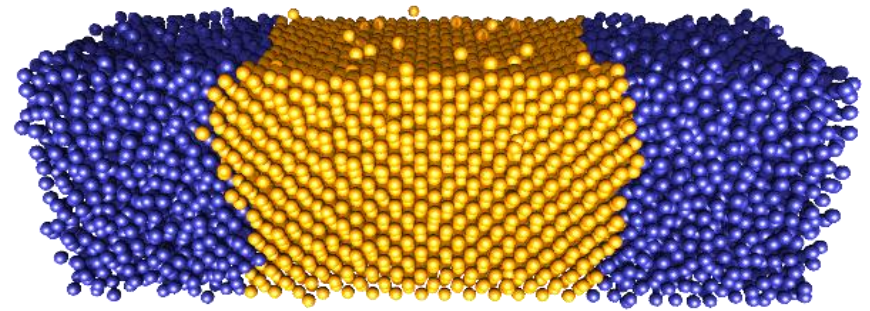
Allen M.P. and Tildesley D.J.,
Computer simulation of liquids, 1987
Anderson H.C., JCP **72** (1980) 2384

MD of pure systems

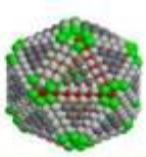


- lattice properties
- T dependence of density
- Structural quantities
- Self-diffusion constant

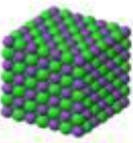
MD of inhomogeneous systems



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



Simulation Parameters



❑ 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. Y. Mishin *et al.*, PRB **65**, (2002) 224114.

J. Horbach *et al.*, PRB **75**, (2007) 174304.

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

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

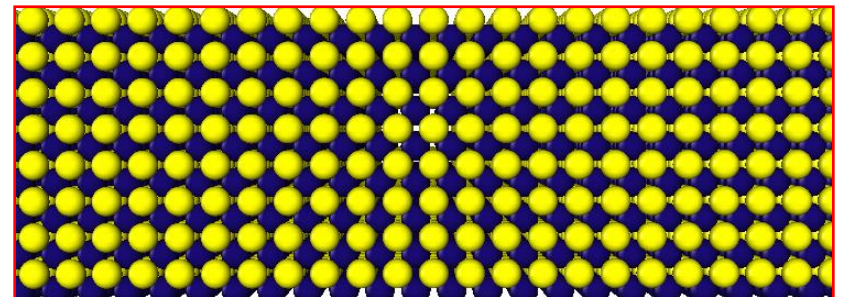
➤ **Solid** and **liquid** properties:

2000 particles ($L_x = L_y = L_z = 24.6 \text{ \AA}$)

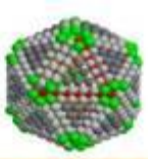
➤ **Solid-liquid** interfaces (N particles):

$N_{\text{Al}} = N_{\text{ni}} \Rightarrow D = L_z \approx 3 \times L_x \approx 3 \times L_y$

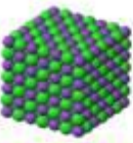
10386 and 12672 particles



← $D \approx 3 \times L_x$ →

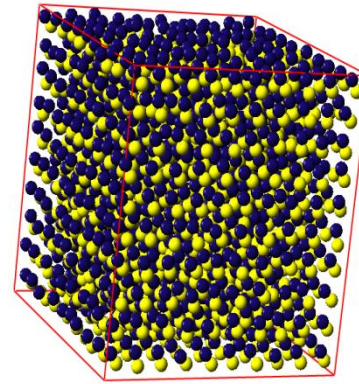
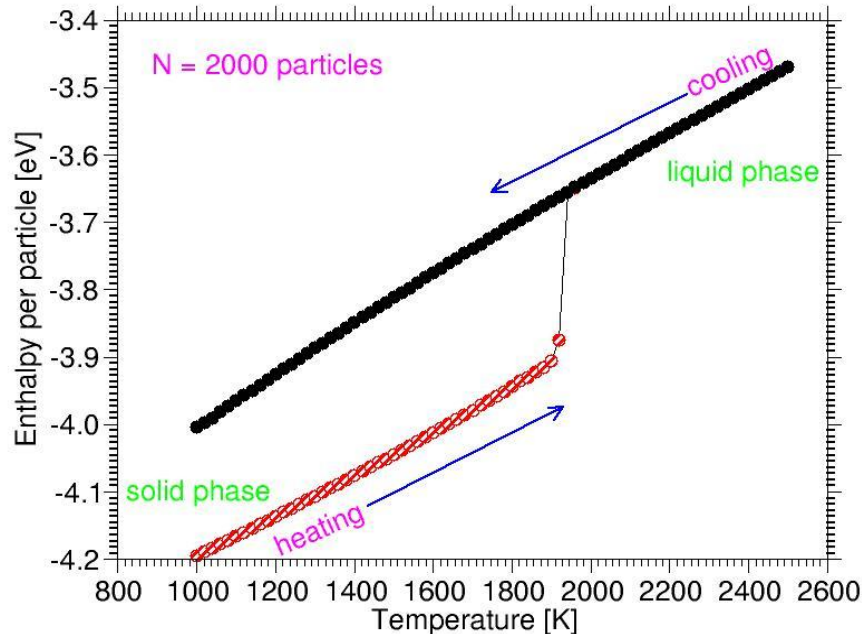
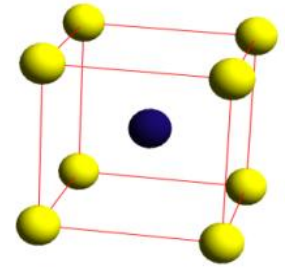


Pure Phases: crystal, liquid

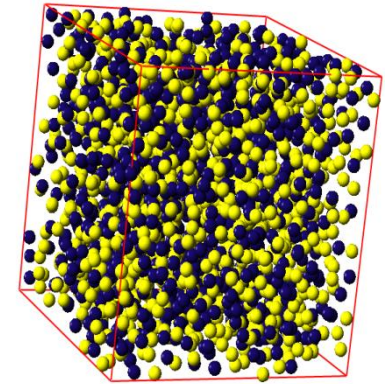


❑ How to go from **crystal to melt** & from **melt to crystal**?

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

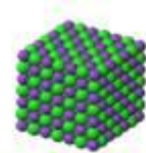
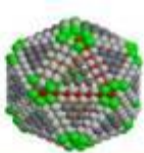


$T_m = ?$



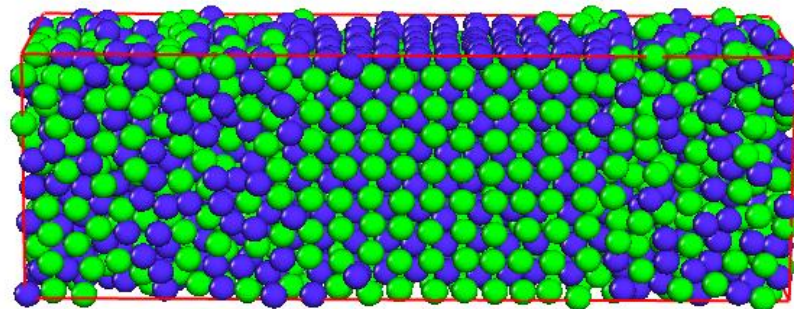
- binary alloys: **glass formers**.
- **crystallization**: process too slow
- brute force method: **not appropriate** to estimate T_M

❑ How to study crystallization?

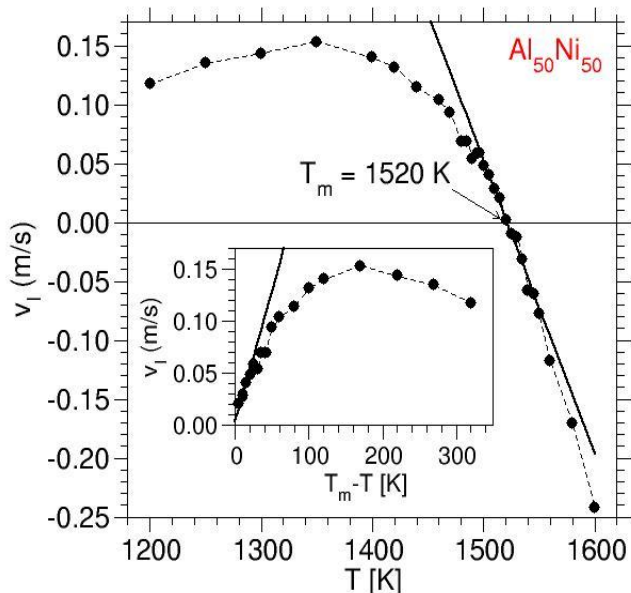


Estimation of Melting Temperature

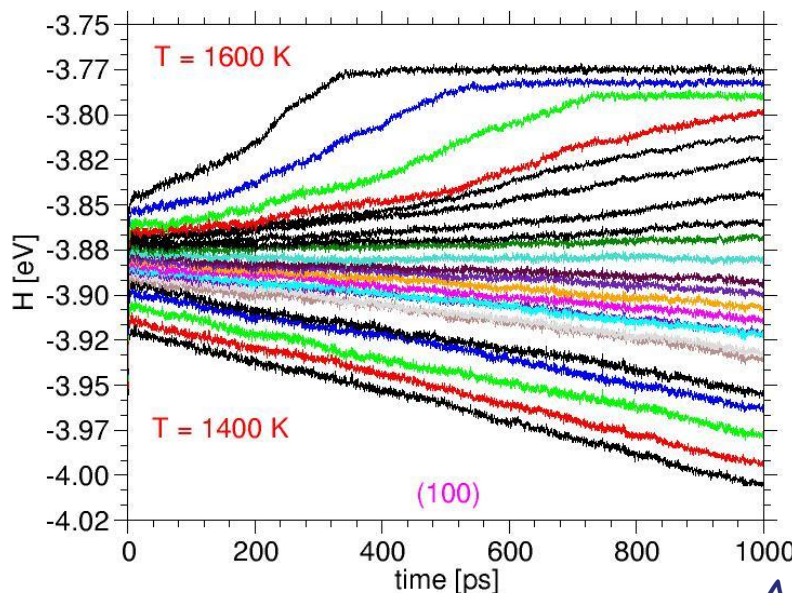
- Equilibrate a crystal (NPT, $p=0$)
- Fix the particles in the middle of the box
- Heat away the two other regions
- Quench at the target temperature



The Melting temperature T_M from *solid-liquid* interface motion:



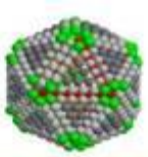
Interface velocity



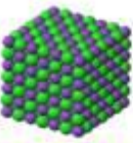
Enthalpy as a function of time

$T > T_M$:
melting
 $T = T_M$:
coexistence
 $T < T_M$:
crystallization

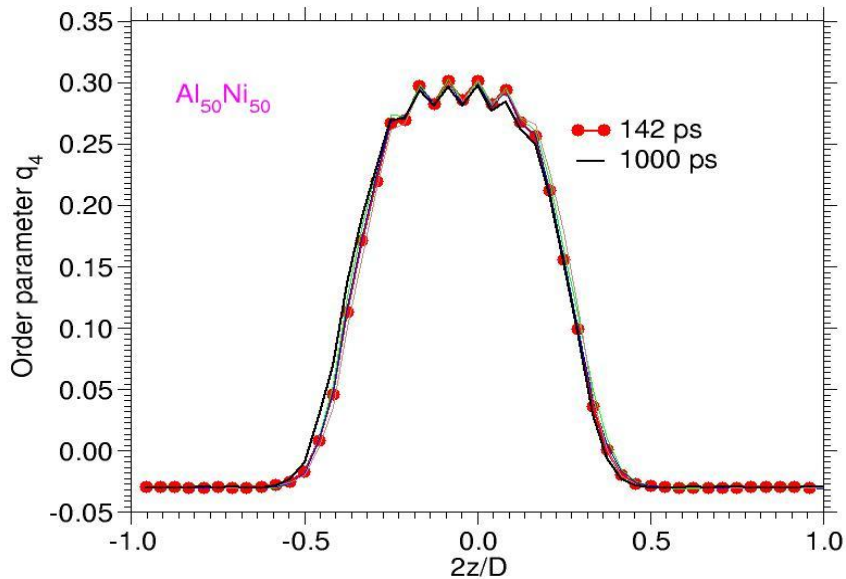
A. Kerrache et al.,
EPL 2008.



Characterization of S-L Interfaces



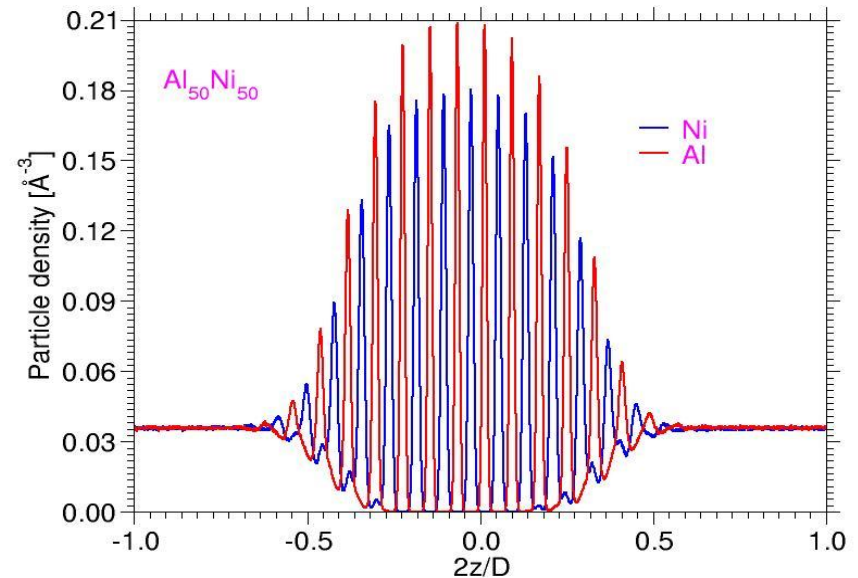
Bond order parameter profile
For different times



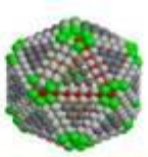
$$q_n = \left\langle \frac{1}{N} \sum_{i,j,k} \cos(n\theta_{xy}(i,j,k)) \right\rangle$$
$$n = 1, 2, \dots, 6$$

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

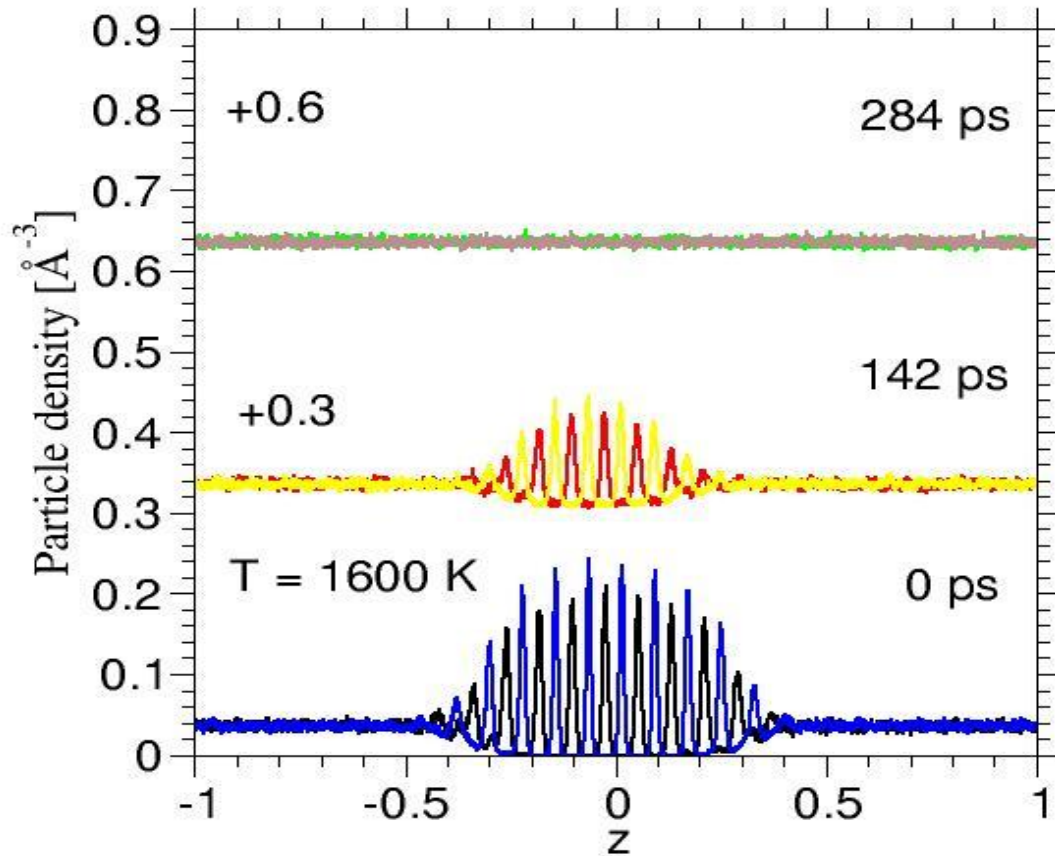
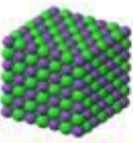
Partial particle density profile



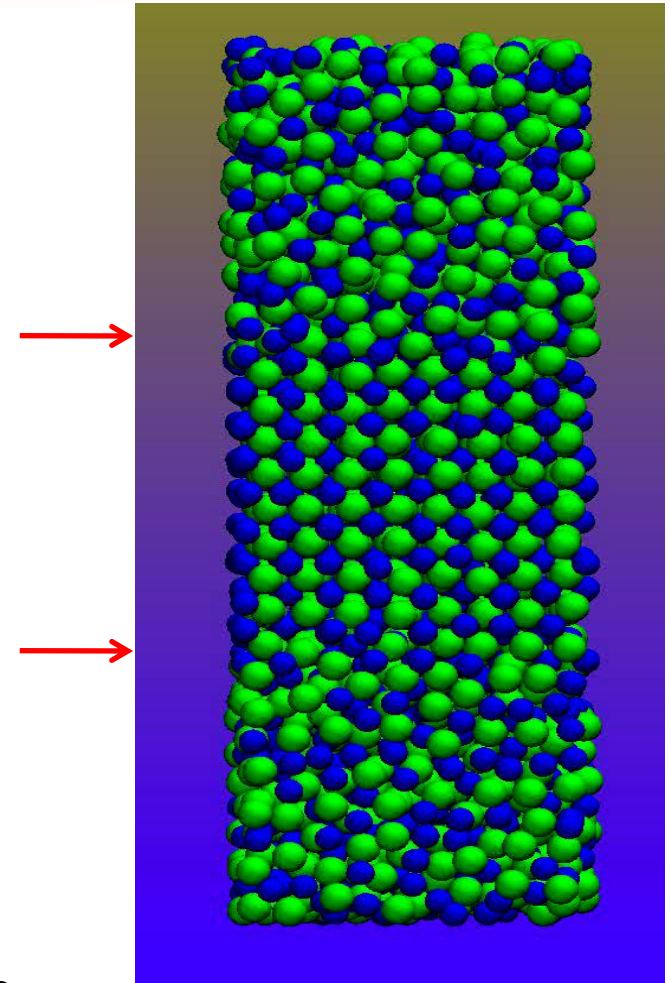
Constant density in the liquid region.
Solid-liquid interface over several layers.
Pronounced chemical ordering in the
solid region: **Mass transport required for
crystal growth.**



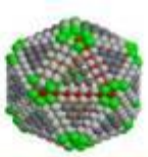
Melting of AlNi: 1600 K



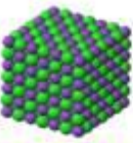
Particle density along the solid-liquid interface



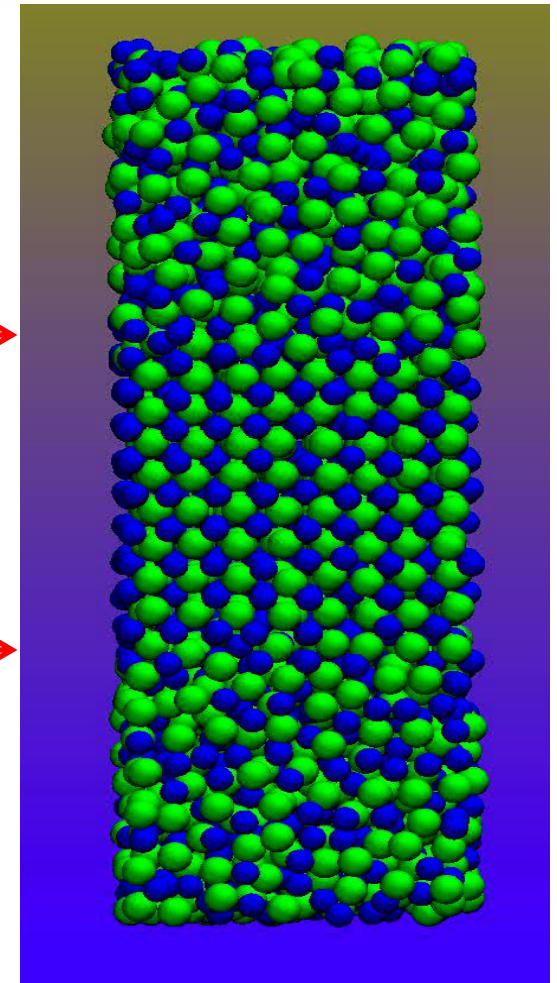
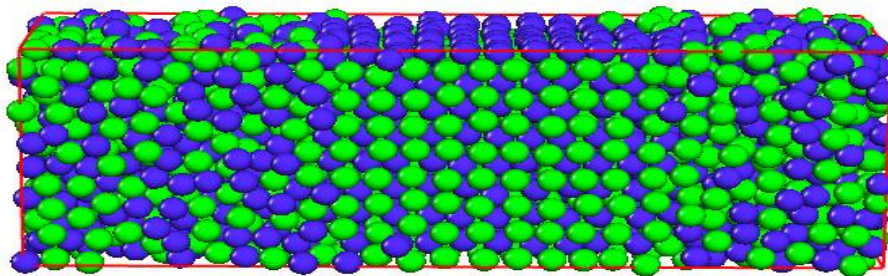
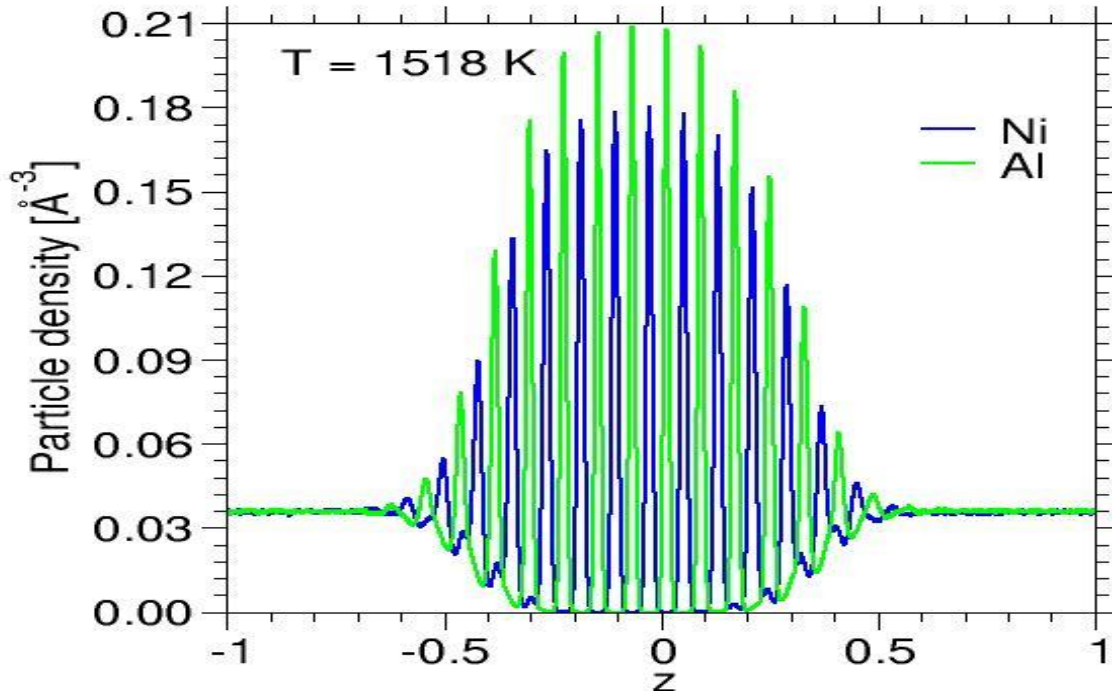
Melting



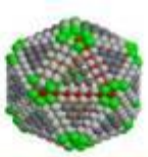
Solid-Liquid coexistence: 1518 K



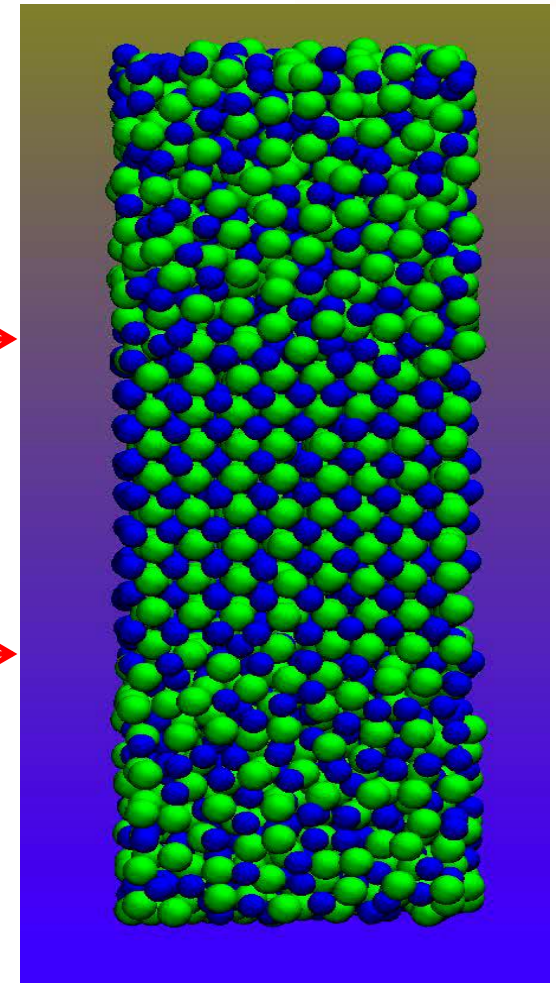
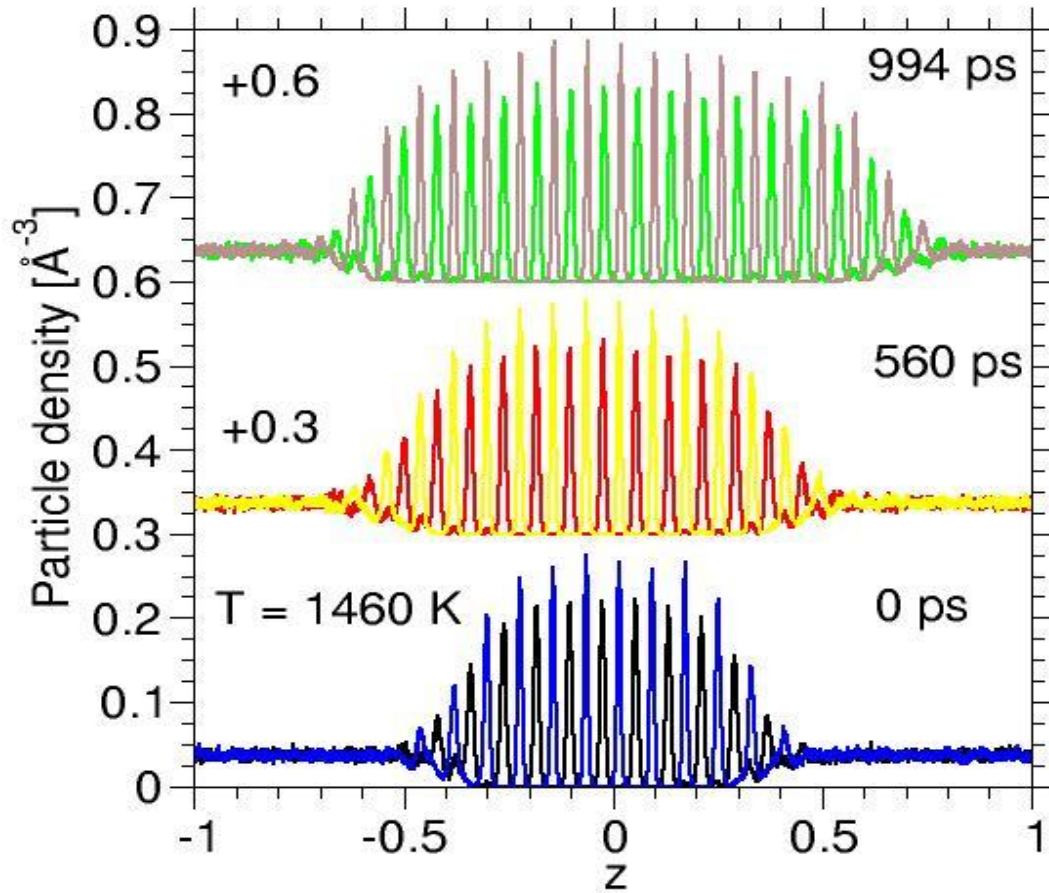
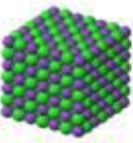
Particle density along the solid-liquid interface



Coexistence

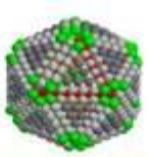


Crystallization of AlNi: 1460 K

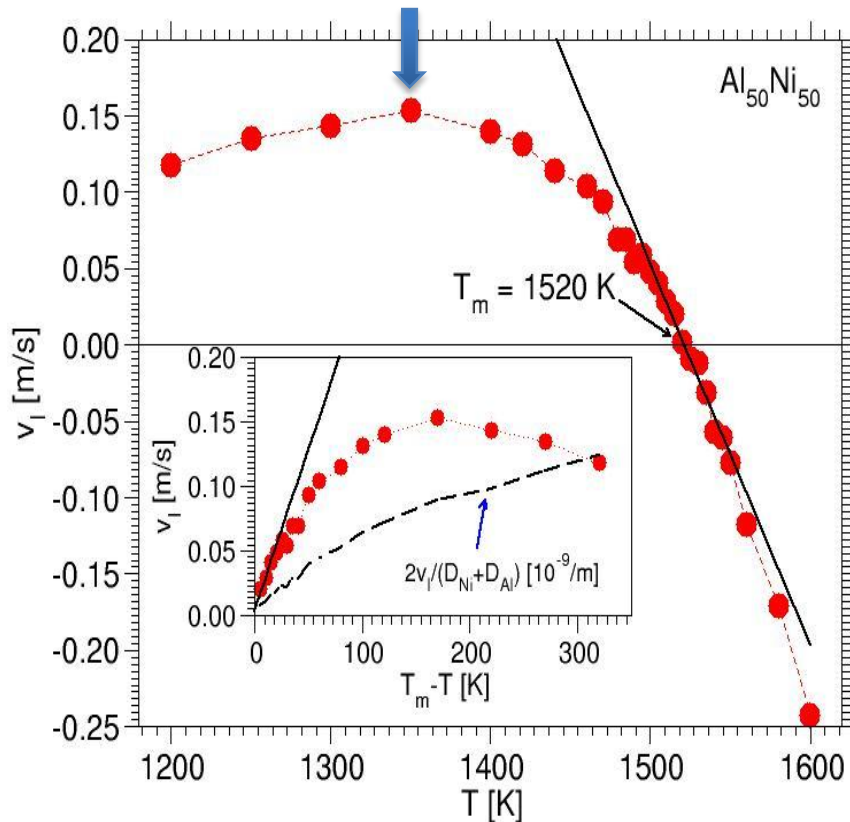
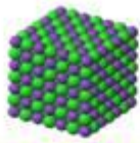


Particle density along the solid-liquid interface

Crystallization



Crystal Growth: Diffusion Limited

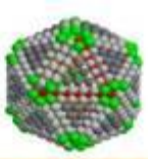


Solid-liquid interface velocity as a function of temperature
Inset: as a function of under-cooling

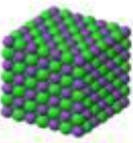
□ Why the solid-liquid interface velocity presents a maximum?

- ✓ 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.

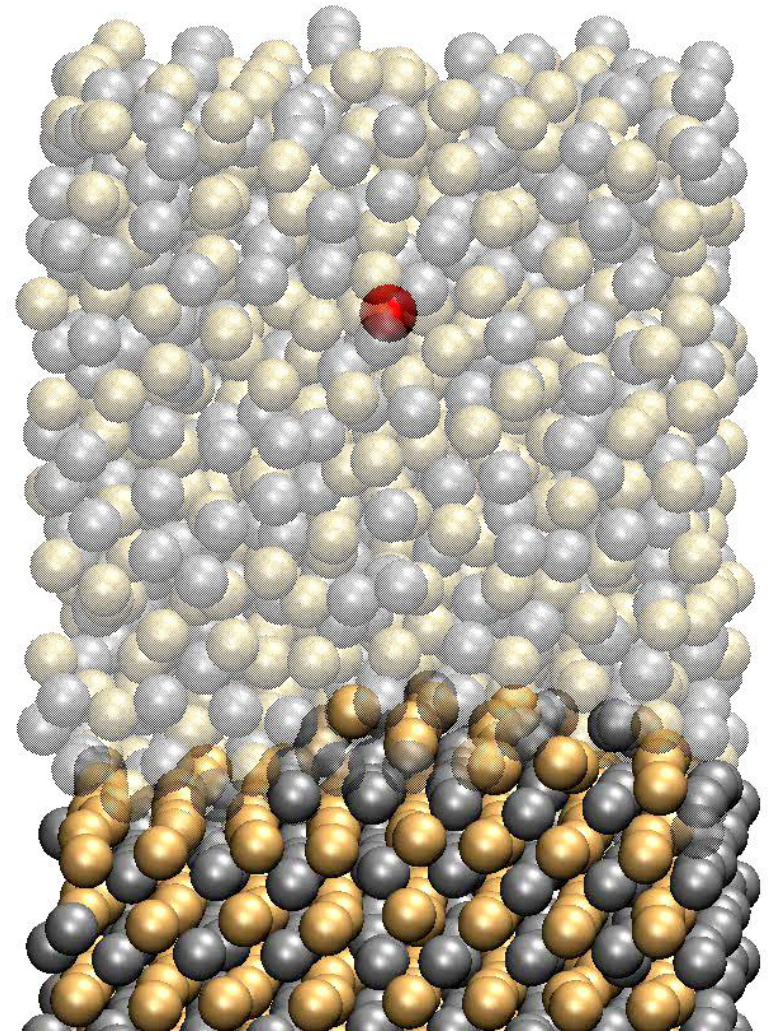
What about the mass transport across the solid-liquid interface?

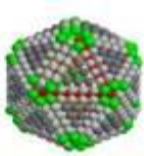


Mass Transport across the interface

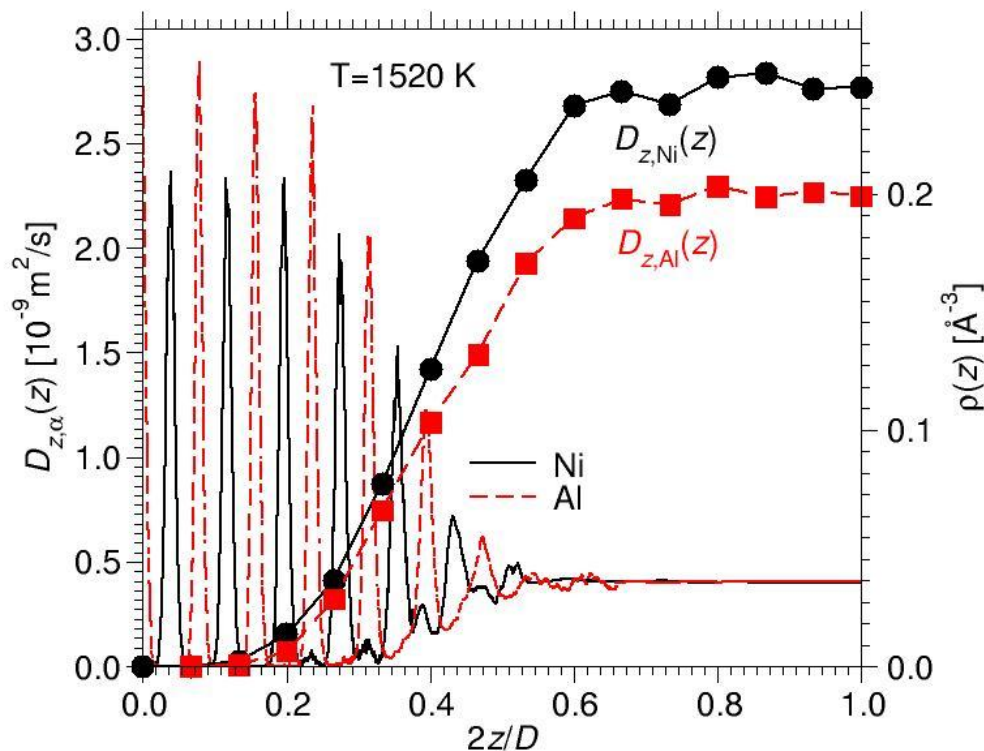
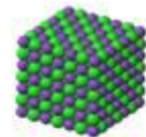


- Order parameter to distinguish solid and liquid particles locally
- compute the particle density and mass density profiles
- Order parameter profile
- Number of solid-like particles
- Solid-liquid interface velocities from the number of solid-like particles
- Diffusion along the interface





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

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

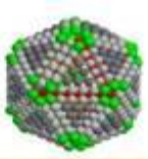
The diffusion constants decrease when we cross the solid-liquid interface.

Wilson-Frenkel theory:

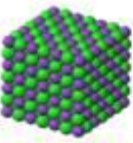
activated process controlled by mass diffusion in the liquid phase

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

Experimental data?

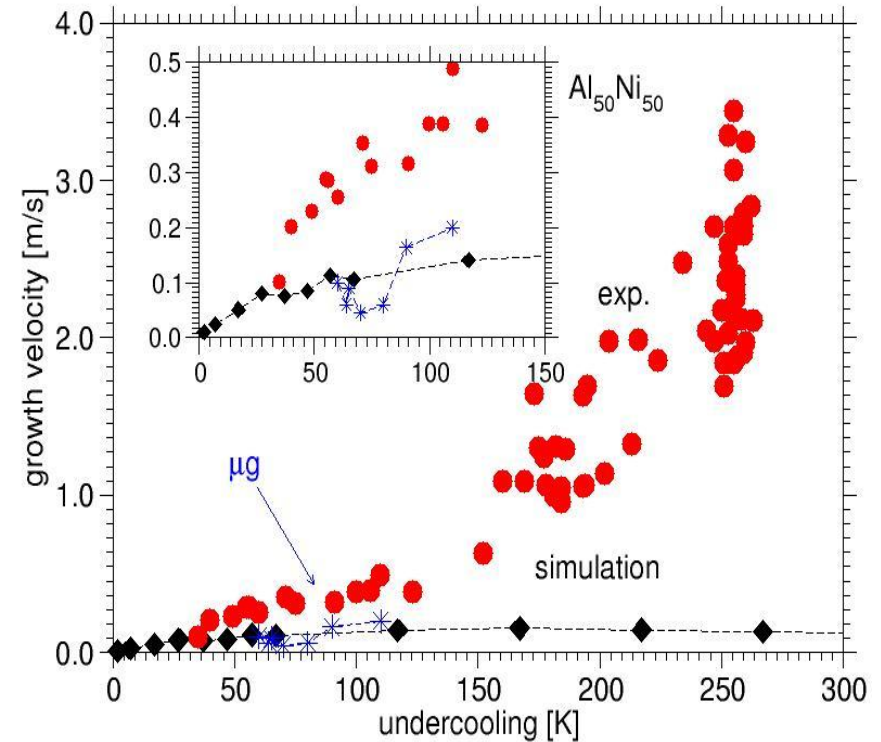


Comparison to Experimental Data

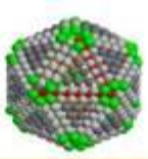


- ✓ **terrestrial** data (Assadi *et al.*)
- ✓ **μg** data (parabolic flight), H. Hartmann (PhD thesis)

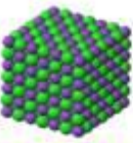
H. Assadi, *et al.*, *Acta Mat.* 54, 2793 (2006).



A. Kerrache *et al.*, *EPL* 81 (2008) 58001. good agreement with experimental data



Glasses



□ Binary Metallic alloys:

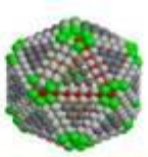
- Melting and crystallization.
- Solid-Liquid interfaces.
- Crystal growth from melt.
- Crystal growth is diffusion limited process.



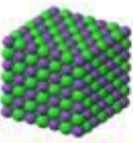
□ Glasses:

- How to prepare a glass using MD simulation?
- Glass Indentation using MD.

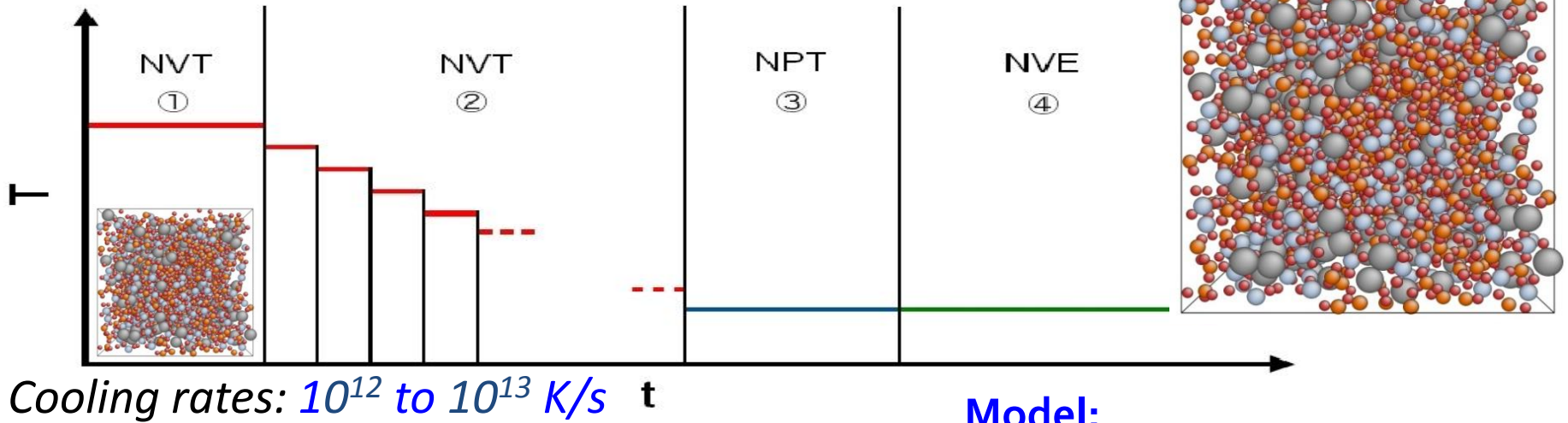




How to prepare a glass?



Glass preparation diagram



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).

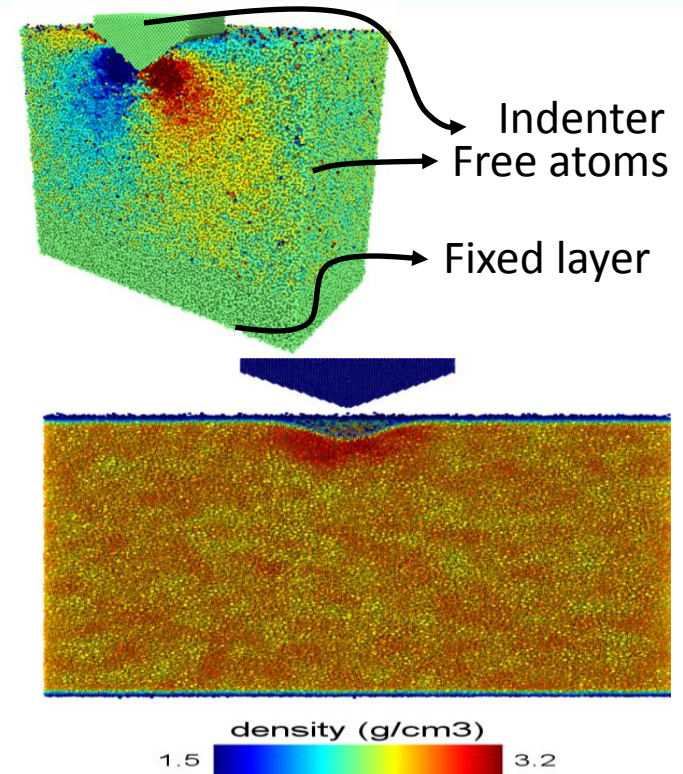
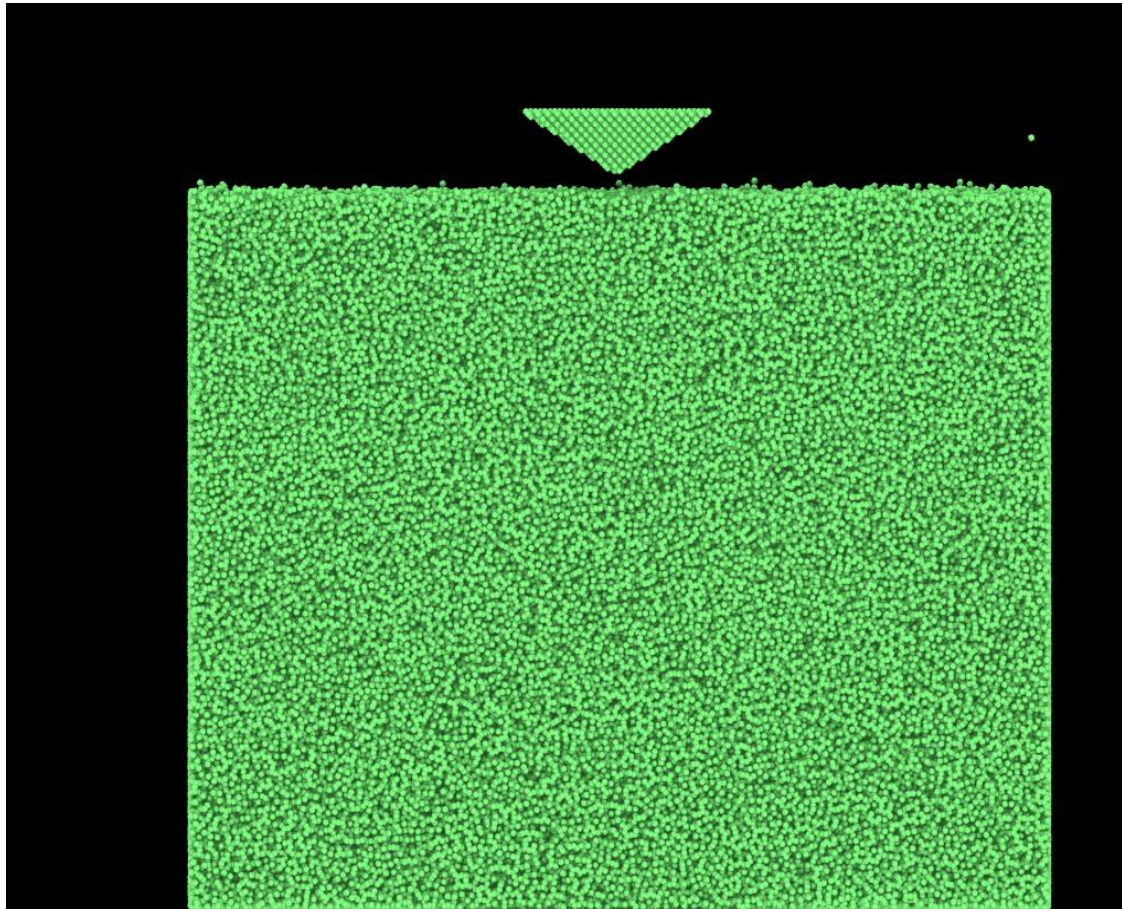
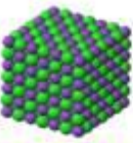
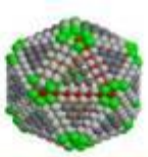
Model:

- MD Simulations (**DL-POLY**).
- Systems of N particules.
- Time step: 1 fs

SBN glasses:

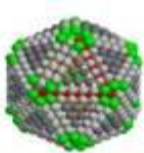
- $\text{SiO}_2\text{-B}_2\text{O}_3\text{-Na}_2\text{O}$
 - ✓ $R = [\text{Na}_2\text{O}] / [\text{B}_2\text{O}_3]$
 - ✓ $K = [\text{SiO}_2] / [\text{B}_2\text{O}_3]$

Glass Indentation

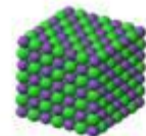


Movie provided by: Dimitrios Kilymis
UMR 5221 CNRS-Univ. Montpellier, France.

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



Acknowledgments



Prof. Dr. Jürgen Horbach, Dusseldorf, Germany.
Prof. Dr. Kurt Binder, Mainz, Germany.
Prof. A. Meyer and Prof. D. Herlach (DLR), Koln.



Prof. Normand Mousseau, Qc, Canada.
Prof. Laurent J. Lewis, Qc, Canada.

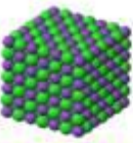
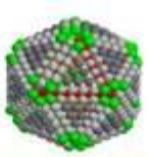


Dr. Dimitrios Kilymis, Montpellier, France.
Prof. Jean-Marc Delaye, CEA, France.



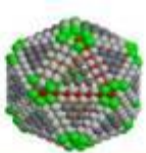
Dr. Victor Teboul, Angers, France.
Prof. Hamid Bouzar, UMMTO, Tizi-Ouzou, Algeria.



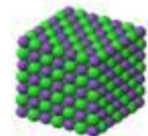


Setting and Running MD simulations (LAMMPS)

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

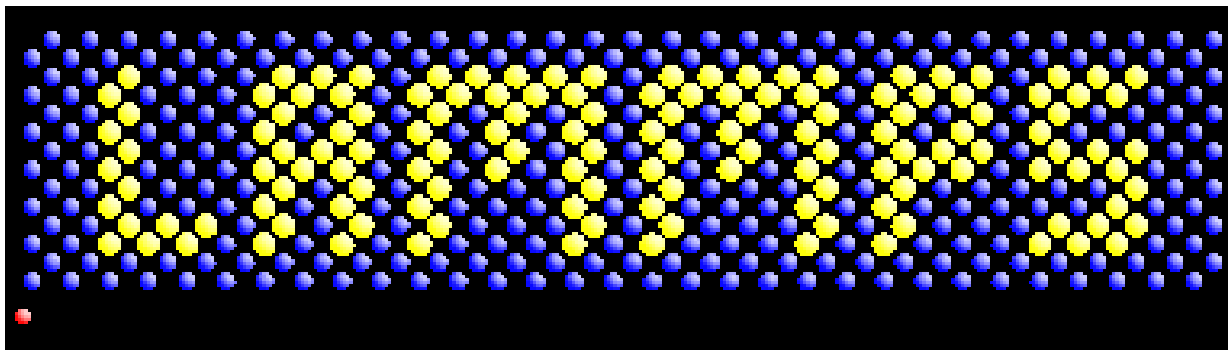


Intorducion to LAMMPS

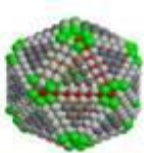


LAMMPS

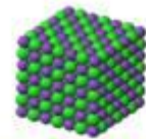
Large-scale Atomic / Molecular
Massively Parallel Simulator



Source: some material and images were adapted from [LAMMPS home page](#)



Start with LAMMPS



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>

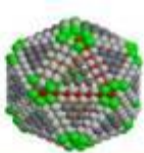
Resources:

➤ Online Manual: <http://lammps.sandia.gov/doc/Manual.html>

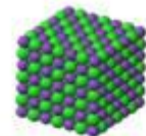
➤ Search the mailing list: <http://lammps.sandia.gov/mail.html>

➤ Subscribe to the Mailing List:

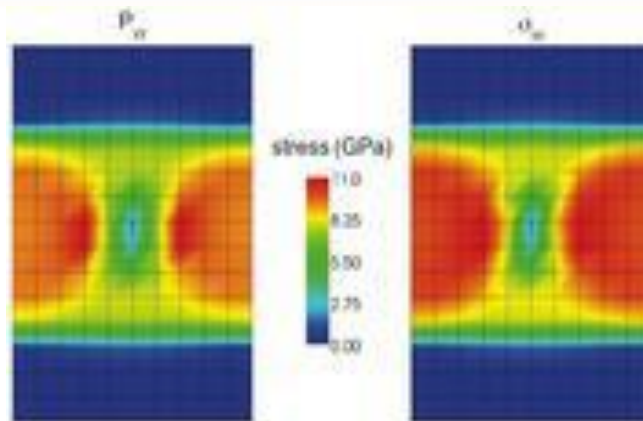
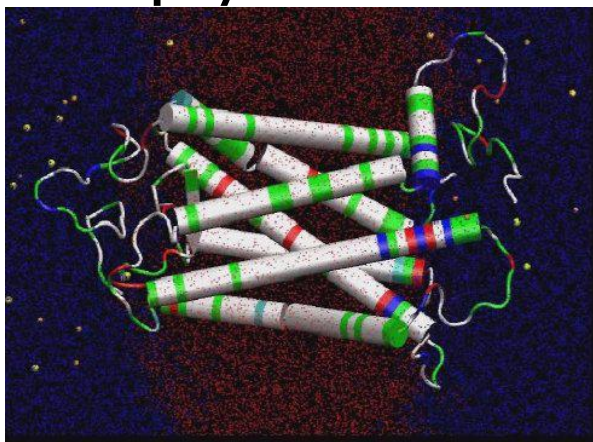
<https://sourceforge.net/p/lammps/mailman/lammps-users/>



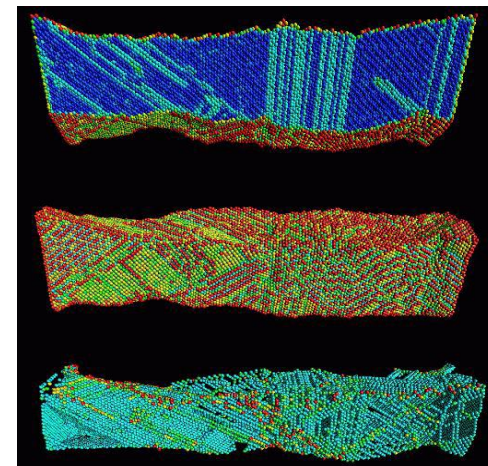
LAMMPS use cases



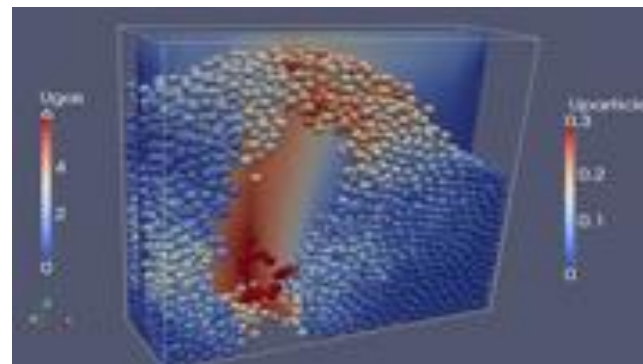
➤ Biophysics



➤ Solid Mechanics

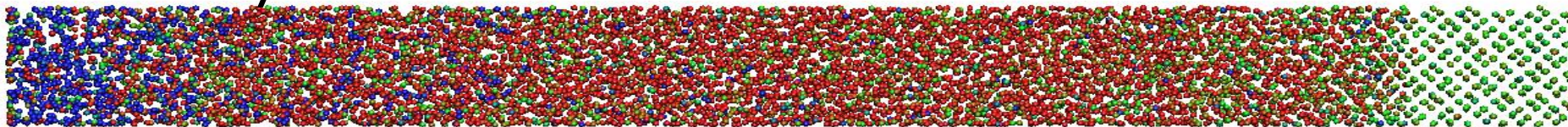


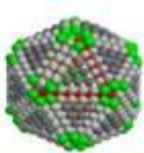
➤ Material Science



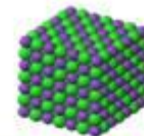
➤ Granular Flow

➤ Chemistry





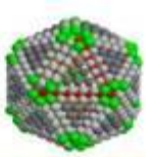
LAMMPS Home Page



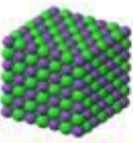
Big Picture	Code	Documentation	Results	Related Tools	Context	User Support
Features	Download	Manual	Publications	Pre/Post processing	Authors	Mail list
Non-features	SourceForge	Developer guide	Pictures	Pizza.py Toolkit	History	Workshops
FAQ	Latest features & bug fixes	Tutorials	Movies	Offsite LAMMPS packages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

Recent LAMMPS News

- **NEW** (9/17) Wrapper on the LATTE DFTB (density-functional tight-binding) quantum code via the [fix latte](#) command. See details [here](#).
- **NEW** (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](#).
- **NEW** (8/17) New stable release, 11Aug17 version.
- **NEW** Biennial [LAMMPS Workshop and Symposium](#) in ABQ, NM. PDFs of talks and posters and the tutorial sessions are available at the workshop link.
- **NEW** (3/17) New stable release, 31Mar17 version.
- **NEW** (1/17) Added a [fix mscc](#) command to enable building of multi-scale coarse-graining (MSCG) models via the Voth group's (U Chicago) [MS-CG library](#).
- **NEW** (12/16) Significant features added to LAMMPS in the fourth quarter of 2016 include these new commands: [compute global/atom](#) global_atom.html, [temper/grem](#) and [fix grem](#), [pair tersoff/mod/c](#), [pair agni](#), [pair born/coul/dsf](#) and [pair_style born/coul/dsf/cs](#), [dump nc](#) and [dump nc/mpio](#), [fix halt](#), [fix dpd/energy](#), [dump modify thresh LAST](#) option, and [fix wall/gran/region](#). See authors [here](#) and details [here](#).



Design of LAMMPS code

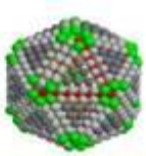


❖ License

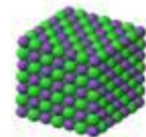
- LAMMPS is provided through **GNU Public License**
<https://www.gnu.org/licenses/licenses.en.html#GPL>
- Free to Use, **Modify**, and Distribute.
- **Contribute** to LAMMPS:
<http://lammps.sandia.gov/contribute.html>

❖ 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, ...).



How to obtain LAMMPS?

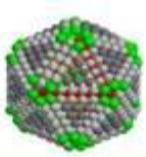


❖ Download Page:

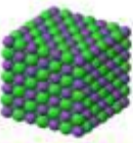
<http://lammps.sandia.gov/download.html>

➤ Distributions:

- ✓ Download a tarball ← **Source Code**
 - ✓ Git checkout and update
 - ✓ SVN checkout and update
 - ✓ Pre-built Ubuntu executables ← **Executable Ubuntu**
 - ✓ Pre-built binary RPMs for Fedora/RedHat/CentOS/openSUSE
 - ✓ Pre-built Gentoo executable
 - ✓ OS X with Homebrew ← **Mac**
 - ✓ Windows installer package ← **Installation under Windows**
 - ✓ Applying patches
- RPMs - Linux** → Pre-built binary RPMs for Fedora/RedHat/CentOS/openSUSE



Building LAMMPS



➤ Build from RPMs

- ✓ [Pre-built Ubuntu executables](#)
- ✓ [Pre-built binary RPMs for Fedora/RedHat/CentOS/openSUSE](#)
- ✓ [Pre-built Gentoo executable](#)
- ✓ [OS X with Homebrew](#)

➤ Install under windows

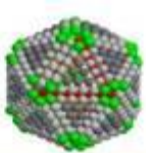
- ✓ [Windows installer package](#)

➤ Build from source code

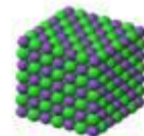
- ✓ [Download a tarball](#)
- ✓ [Git checkout and update](#)
- ✓ [SVN checkout and update](#)
- ✓ [Applying patches](#)

does not include
all packages

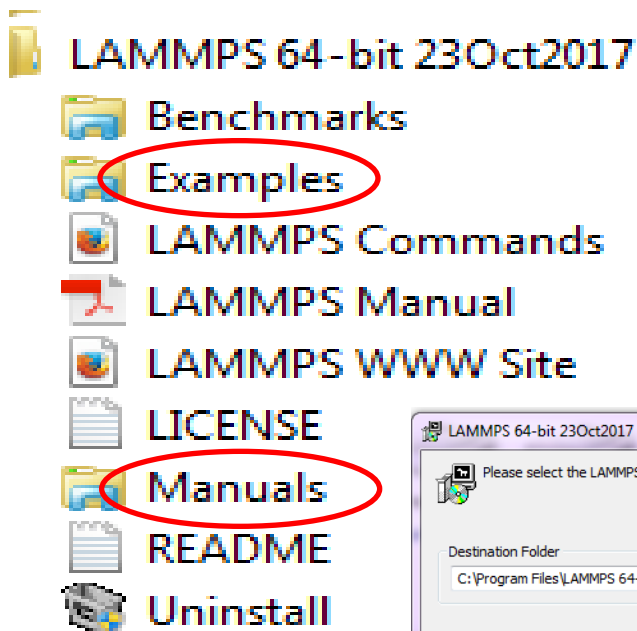
for a customized
installation, build
from source files:
modules



LAMMPS under Windows



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

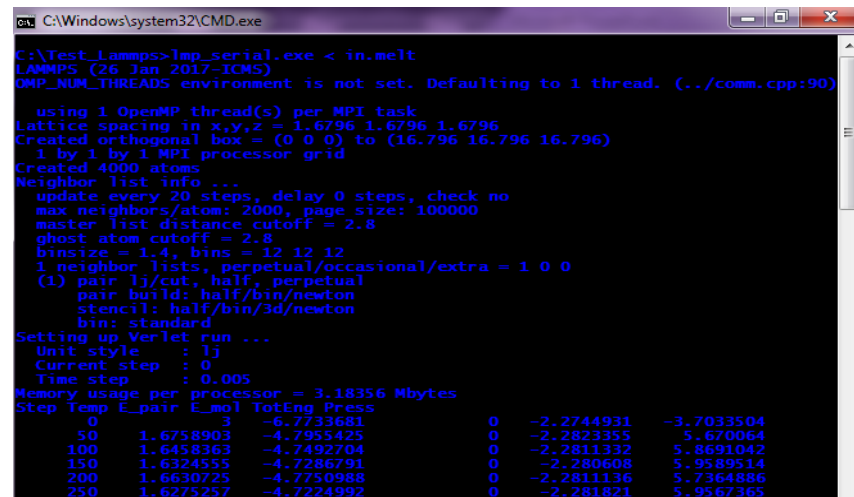
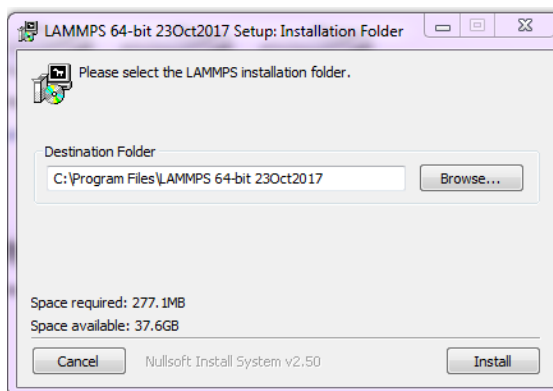


Directory:

Program Files\LAMMPS 64-bit 20171023

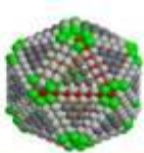
Executable under bin:

abf_integrate.exe **ffmpeg.exe** **Imp_mpi.exe**
restart2data.exe **binary2txt.exe** **Imp_serial.exe**
chain.exe **msi2Imp.exe** **createatoms.exe**

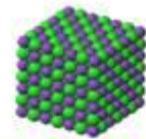


➤ Execute:

Imp_serial.exe < in.lammps



Building LAMMPS from source



<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
```

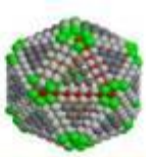
There have been ~256,700 downloads of LAMMPS from Sept 2004 thru Dec 2016.

[LAMMPS](#) molecular dynamics package:

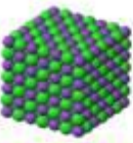
- [LAMMPS](#) --- Stable version (11 Aug 2017) - Recent C++ version source tarball, GPL license, ~121 Mb. Includes all bug fixes and new features described on [this page](#), up to the date of the most recent stable release.
- [LAMMPS](#) --- Development version - Most current C++ version source tarball, 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

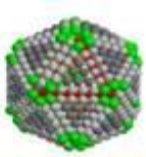
Archive: [lammps-stable.tar.gz](#)



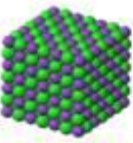
LAMMPS source overview



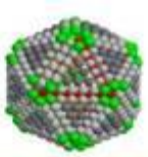
- **Download** the source code: lammps-stable.tar.gz
- LAMMPS directory: [lammps-11Aug17](#)
 - ✓ **bench**: Benchmark tests (potential, input and output files).
 - ✓ **doc**: documentation (PDF and HTML)
 - ✓ **examples**: input and output files for some simulations
 - ✓ **lib**: libraries to build 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).



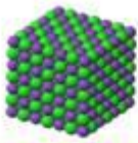
Building LAMMPS



- First: **Build libraries if required.**
- Choose a Makefile compatible with your system
- **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



Use GNU Make to build LAMMPS

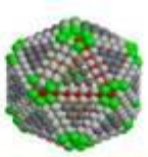


- ❑ machine is one of these from **src/MAKE**:
 - # **mpi** = MPI with its default compiler
 - # **serial** = GNU g++ compiler, no MPI

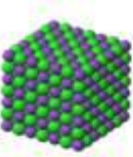
- ❑ ... or one of these from **src/MAKE/OPTIONS**:
 - # **icc_openmpi** = OpenMPI with compiler set to Intel icc
 - # **icc_openmpi_link** = Intel icc compiler, link to OpenMPI
 - # **icc_serial** = Intel icc compiler, no MPI

- ❑ ... 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

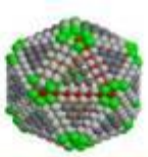
- ❑ ... or one of these from **src/MAKE/MINE**: (write your own Makefile)



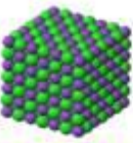
Building LAMMPS: demonstration



- Download the latest stable version from LAMMPS home page.
- Untar the archive: `tar -xvf lammeps-stable.tar.gz`
- Change the directory and list the files: `cd lammeps-11Aug17`
`bench bin 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, no-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.



Running LAMMPS



❑ Executable: **Imp_machine**

❑ Files:

➤ Input File: **in.Imp_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:

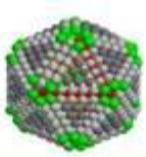
```
$ ./Imp_machine < in.Imp_file
```

```
$ ./Imp_machine -in in.Imp_file
```

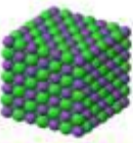
❑ Redirect output to a file:

```
$ ./Imp_machine < in.Imp_file > output_file
```

```
$ ./Imp_machine -in in.Imp_file -l output_file
```



Command line options



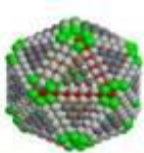
□ Command-line options:

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

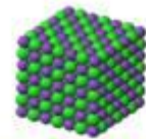
-e or **-echo**, **-h** or **-help**, **-i** or **-in**, **-k** or **-kokkos**, **-l** or **-log**,
-nc or **-nocite**, **-pk** or **-package**, **-p** or **-partition**, **-pl** or **-plog**,
-ps or **-pscreen**, **-r** or **-restart**, **-ro** or **-reorder**, **-sc** or **-screen**,
-sf or **-suffix**,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

□ For example:

```
mpirun -np 8 Imp_machine -l my.log -sc none -in in.alloy  
mpirun -np 8 Imp_machine < in.alloy > my.log
```

Overview of a simulation run



INPUT

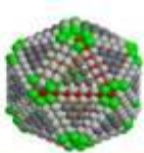
- Initial positions
- Initial velocities
- Time step
- Mass
- PBC
- Units
- Potential
- Ensemble
- etc.

RUNNING

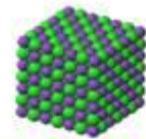
- Molecular Dynamics Simulation (NPT, NVT, NVE)
- Minimization
- Monte Carlo
 - Atomic to Continuum

OUTPUT

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



Overview of a Simulation Run



❑ Command Line:

➤ Every simulation is executed by supplying an input text script to the LAMMPS executable: `Imp < 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:**

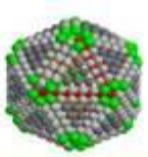
✓ Inter-atomic potential (pair_style, pair_coeff)

✓ Run time simulation parameters (e.g. time step)

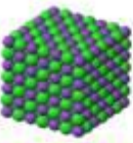
✓ **Fixes:** operations during dynamics (e.g. thermostat)

✓ **Computes:** calculation of properties during dynamics

❑ Run the simulation for N steps.



LAMMPS input 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

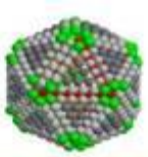
velocity all create 3.0 87287

Initialize the
velocities

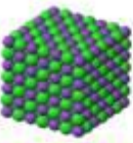
Potential

pair_style lj/cut 2.5
pair_coeff 1 1 1.0 1.0 2.5

Define the
potential



LAMMPS input 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

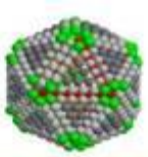
thermo 50

Log file:
customize output

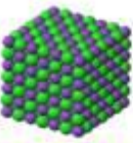
run 250

End of the simulation.

Run the simulation
for N steps

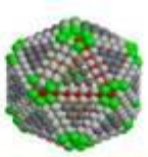


LAMMPS: **input commands**

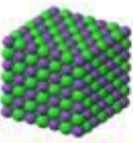


□ Initialization

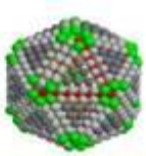
- **Parameters:** set parameters that need to be defined before atoms are created: [units](#), [dimension](#), [newton](#), [processors](#), [boundary](#), [atom style](#), [atom modify](#).
- If force-field parameters appear in the files that will be read: [pair style](#), [bond style](#), [angle style](#), [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.



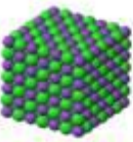
LAMMPS: settings



- ❑ 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.



Cutumize the output

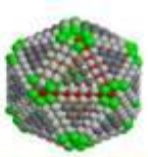


thermo freq_steps
thermo_style style args

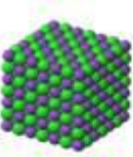
- **style** = *one* or *multi* or *custom*
- **args** = list of arguments for a particular style
 - one* args = none
 - multi* args = none *custom*
 - args = list of keywords possible

□ **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**, **pyy**, **pzz**, **pxy**, **pxz**, **pyz**

etc

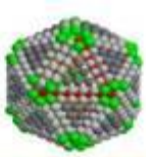


Running LAMMPS: demonstration

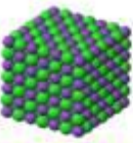


- ❑ After compiling LAMMPS, run some examples:

- ❑ Where to start to learn LAMMPS?
 - Make a copy of the directory examples in your working directory.
 - Choose an example to run.
 - Indicate the right path to the executable.
 - Edit the input file and check all the parameters.
 - Check the documentation for the commands and their arguments.
 - Run the test case: `mpicc -xopenmpi < in.melt` .
 - Check the output files (log files), plot the thermodynamic properties, ...



LAMMPS: output example



LAMMPS (30 Jul 2016)

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

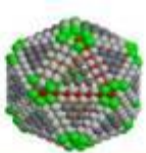
3d Lennard-Jones melt

```
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
```

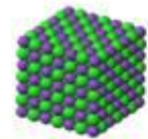
Created orthogonal box = (0 0 0) to (16.796 16.796 16.796) 2 by 2 by 3
MPI processor grid

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

```
mass          1 1.0
```



LAMMPS: output example



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

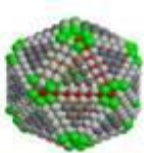
ghost atom cutoff = 2.8

binsize = 1.4 -> bins = 12 12 12

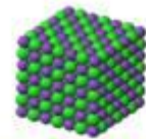
Memory usage per processor = 2.05293 Mbytes

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



LAMMPS: output example



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

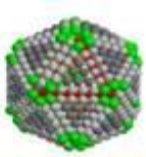
90.2% CPU use with 12 MPI tasks x 1 OpenMP threads

MPI task timing breakdown:

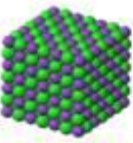
Section | min time | avg time | max time |%varavg| %total

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



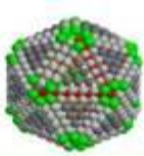
Potential Benchmark



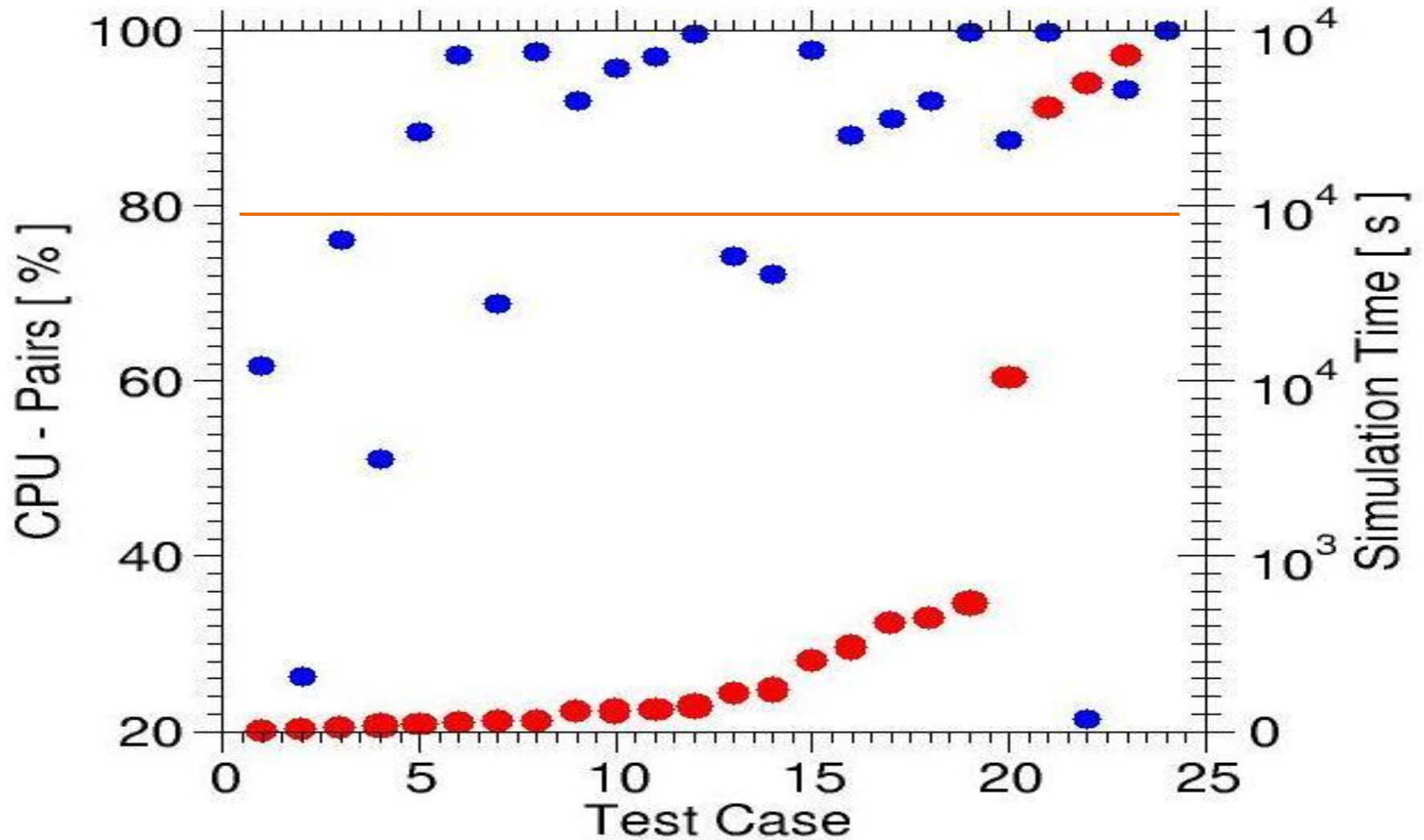
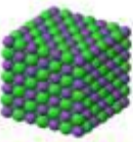
1. granular
2. fene
3. lj
4. dpd
5. eam
6. sw
7. rebo
8. tersoff
9. eim
10. adp
11. meam
12. peri
13. spce
14. protein
15. gb
16. reax_AB
17. airebo
18. reaxc_rdx
19. smtbq_Al
20. vashishta_table_sio2
21. eff
22. comb
23. vashishta_sio2
24. smtbq_Al2O3

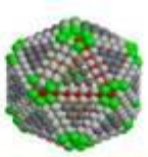
Parameters:

- 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.

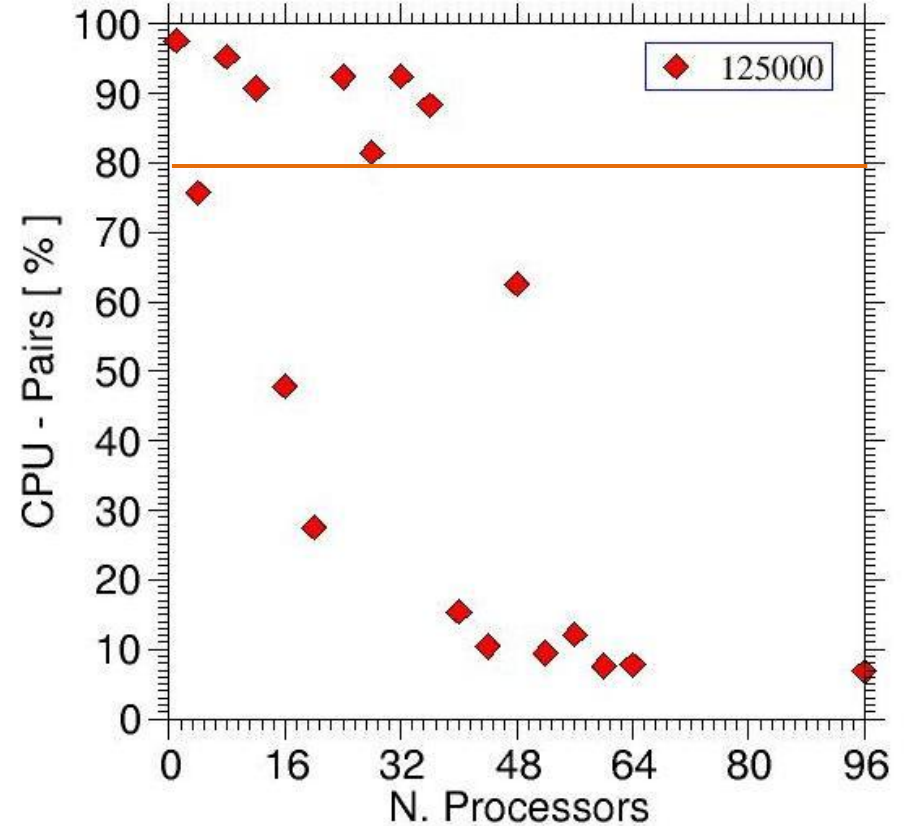
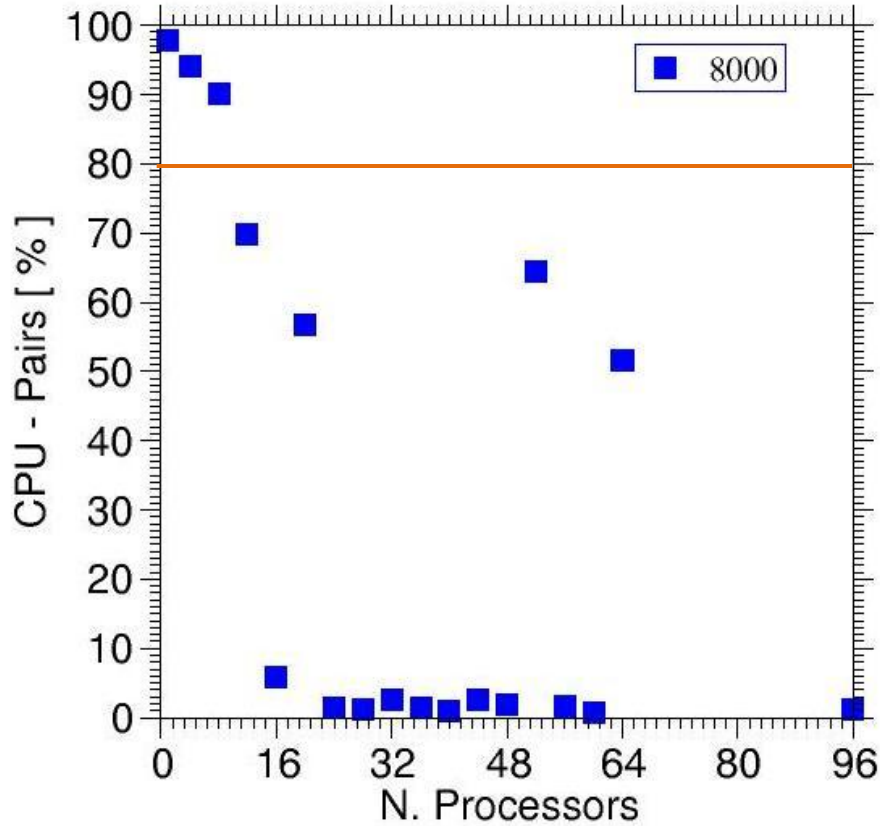
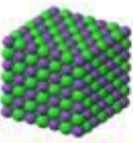


Potential Benchmark

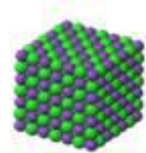
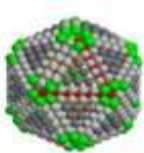




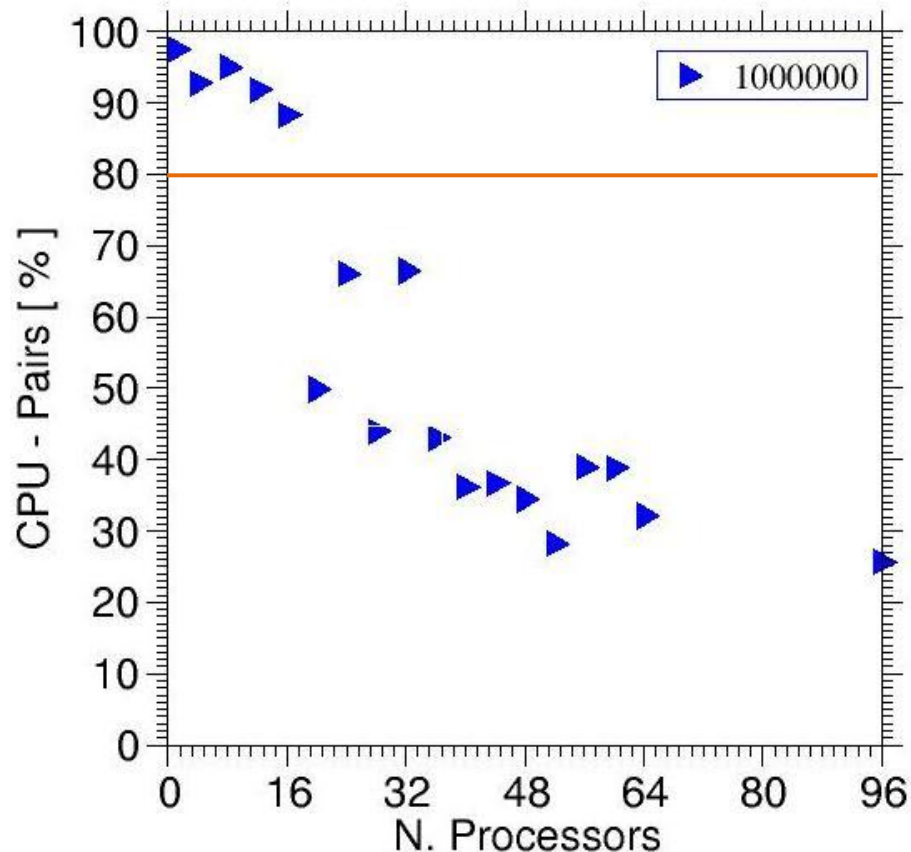
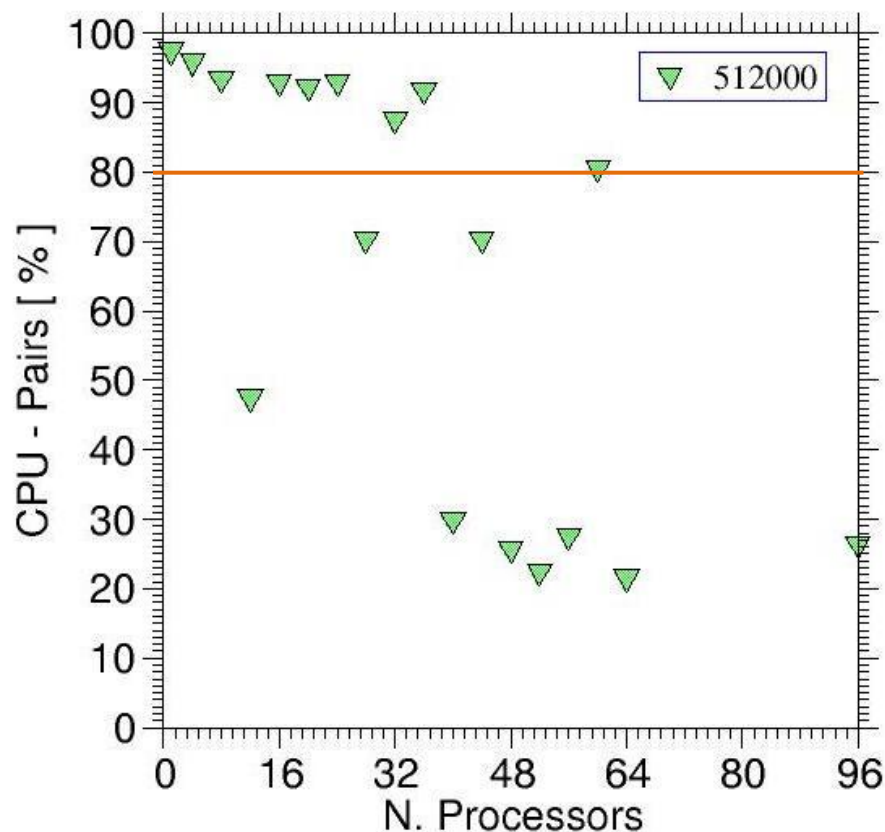
Performance Test: Tersoff potential



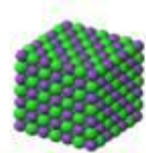
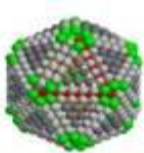
CPU time used for computing the interactions between particles as a function the number of processors for different system size.



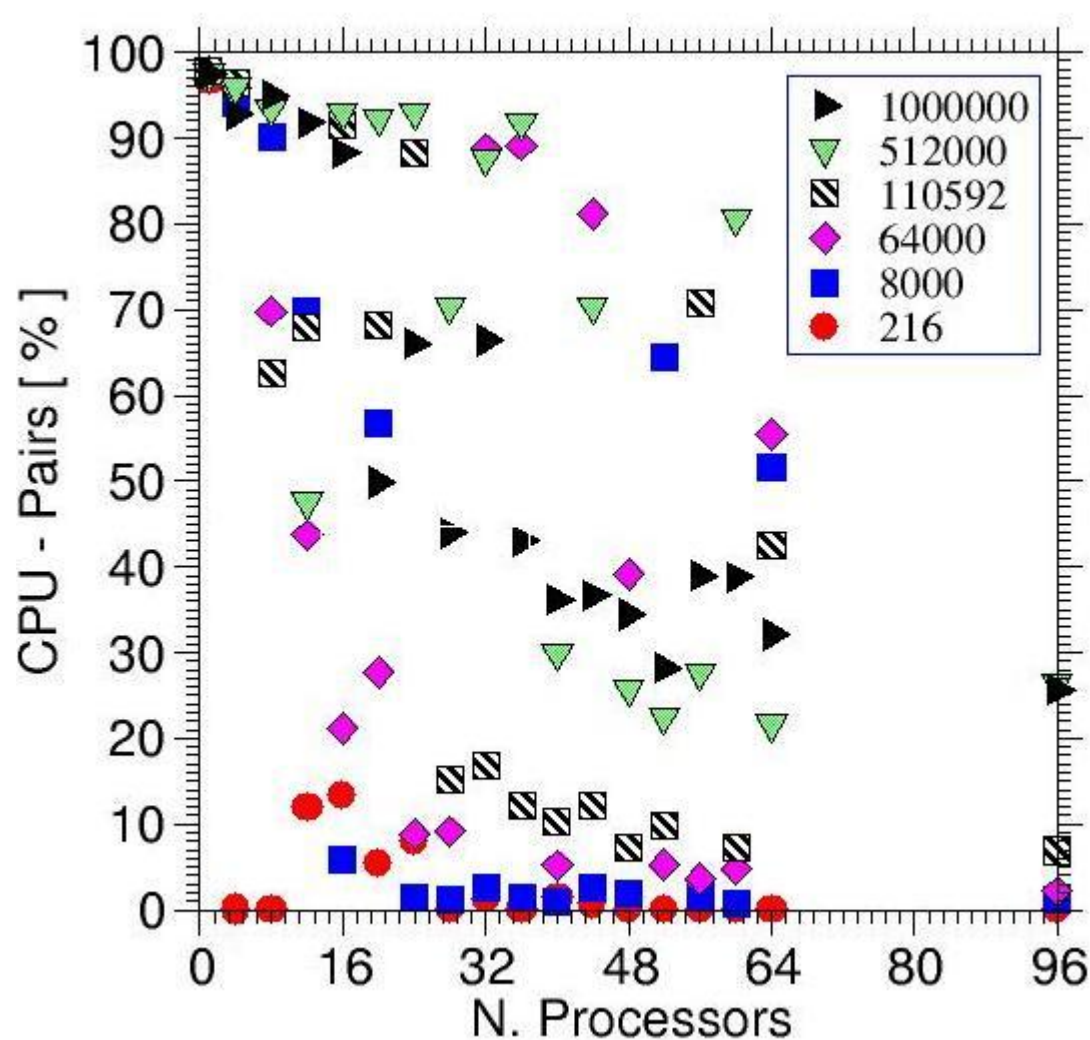
Performance Test: Tersoff potential



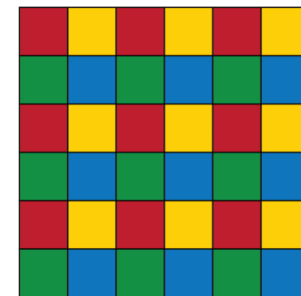
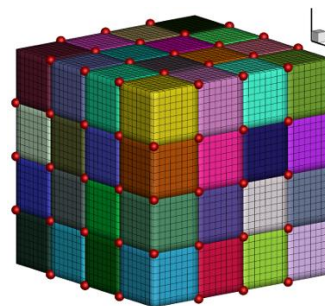
CPU time used for computing the interactions between particles as a function of the number of processors for different system sizes.



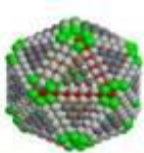
Performance Test: Tersoff potential



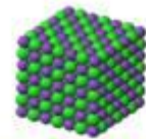
Domain decomposition



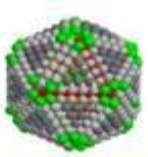
- Size, shape of the system.
- Number of processors.
- size of the small units.
- correlation between the communications and the number of small units.
- Reduce the number of cells to reduce communications.



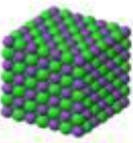
Learn more about LAMMPS



- ❑ **Home Page:** <http://lammps.sandia.gov/>
- ❑ **Examples:** deposit, friction, micelle, obstacle, qeq, streitz, MC, body, dipole, hugonostat, 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/>



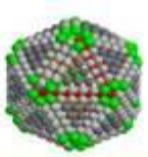
Introduction to MD Simulations



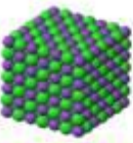
Thanks to LAMMPS developers

Thanks to LAMMPS contributors

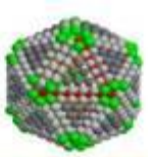
Thank you for your attention



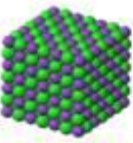
Potentials: **classified by materials**



- **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, peridynamics, DSMC...
- **Hybrid:** combine potentials for hybrid systems: water on metal, polymers/semiconductor interface, colloids in solution, ...



Potentials: classified by functional form



- **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