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Molecular dynamics method for materials simulations

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Contents

- Group presentation
- Multiscale modelling framework for materials science
- The molecular dynamics method
 - In fairly big detail
- Nonequilibrium effects to MD
 - Briefly
- Interatomic potentials and their development
- Special case for CLIC simulations: HELMOD
- Examples of uses of regular MD
- How reliable is MD?
- Does it have predictive power?
- The long time scale limit and ways past it
- Kinetic Monte Carlo
 - Briefly

Group presentation



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Doc. Antti Kuronen Principal investigator



Doc. Krister Henriksson Nuclear Materials



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Irradiation of GaN

Dr.Harriet Åhlgren Nanoclusters



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Nanomechanics Carbon nanostructures



M Sc Fredric Granberg Dislocations



M Sc Morten Nagel Nuclear materials



M Sc Aleksi Leino Nanostructures in silica M Sc Kostya Avchachov Irradiation of metals Nanoclusters



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M Sc Anders Korsbäck Particle physics mat/ls (CERN)



M Sc Elnaz Safi Fusion reactor mat/ls



M Sc Alvaro Lopez Surface ripples



M Sc Shuo Zhang Mr Jesper Byggmästar Ion range calculations Nanowires



M Sc Ekaterina Baibuz Particle physics mat'ls



















MD = Molecular dynamics

- MD is solving the Newton's (or Lagrange or Hamilton) equations of motion to find the motion of a group of atoms
- Originally developed by Alder and Wainwright in 1957 to simulate atom vibrations in molecules
 - Hence the name "molecular"
 - Name unfortunate, as much of MD done nowadays does not include molecules at all
- First dynamic process simulations: 1960, Gibson simulated radiation effects in solids [Phys. Rev. 120 (1960) 1229)]
 - A few hundred atoms, very primitive pair potentials
 - But atom dynamics clearly visible





Simple (trivial) example of atom motion by MD: thermal motion in Cu at 600 K, cross section of 2 atom layers





Less trivial example: small atom collision event

- 500 eV kinetic energy Au impacting on Cu
 - Again cross section of 3D cell





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3D view of another bombardment





How is this actually achvieved? The MD algorithm, roughly







MD – atom representations

- MD naturally needs atom coordinates (and velocities)
- Atom coordinates can simply be read in from an ASCII text file

Simple but for atoms good enough format: .XYZ

	500			
FC	C cell	made by	makeFCC with a=	3.52 n= 5 5 5
Cu		-7.92	-7.92	-7.92 1
Cu		-6.16	-6.16	-7.92 1
Cu		-7.92	-6.16	-6.16 1
Cu		-6.16	-7.92	-6.16 1
C.J.		array (proof) (array (array))	unana ta	and the state of t
		- 6 . 1 C		
Λ	• • • • •			

Arrays in an MD code, e.g.:

double precision :: x(MAXATOMS), y(MAXATOMS), z(MAXATOMS)



MD – Solving equations of motion

- The solution step $\mathbf{r}^{(i+1)} = \mathbf{r}^{(i)} + \mathbf{v}^{(i)}\Delta t + \frac{1}{2}\mathbf{a} \Delta t^2$ + correction terms is crucial
- What are the "correction steps"?
- There is any number of them, but the most used ones are predictor-corrector type way to solve differential equations numerically:





MD – Solving equations of motion

Simplest possible somewhat decent algorithm: velocity Verlet

$$\mathbf{r}(t + \Delta t) = \mathbf{r}(t) + \Delta t \mathbf{v}(t) + \frac{1}{2} \Delta t^2 \mathbf{a}(t)$$
$$\mathbf{v}^{\mathrm{p}} \left(t + \frac{1}{2} \Delta t \right) = \mathbf{v}(t) + \frac{1}{2} \Delta t \mathbf{a}(t)$$
$$\mathbf{v}^{\mathrm{c}} \left(t + \Delta t \right) = \mathbf{v}^{\mathrm{p}} \left(t + \frac{1}{2} \Delta t \right) + \frac{1}{2} \Delta t \mathbf{a}(t + \Delta t).$$

[L. Verlet, Phys. Rev. 159 (1967) 98]

Another, much more accurate: Gear5, Martyna I recommend Gear5, Martyna-Tuckerman or other methods more accurate than Verlet,

[C. W. Gear, Numerical initial value problems in ordinary differential equations, Prentice-Hall 1971; Martyna and Tuckerman J. Chem Phys. 102 (1995) 8071]



MD – time step selection

- Time step selection is a crucial part of MD
 - Choice of algorithm for solving equations of motion and time step are related
- Way too long time step: system completely unstable, "explodes"
- Too short time step: waste of computer time
- Too long time step: total energy in system not conserved
 - Pretty good rule of thumb: the fastest-moving atom in a system should not be able to move more than 1/20 of the smallest

interatomic distance per time step – about 0.1 Å typically





MD – Periodic boundary conditions

- A real lattice can be extremely big
 - E.g. 1 cm^3 of Cu: 2.1e22 atoms => too much even for present-day computers
 - Hence desirable to have MD cell as segment of bigger real system

Standard solution: periodic boundary conditions

This approach involves "copying" the simulation cell to each of the periodic directions (1–3) so that our initial system "sees" another system, exactly like itself, in each direction around it. So, we've created a virtual crystal.





MD: periodics continued

- This has to also be accounted for in calculating distances for interactions
- Minimum image condition": select the nearest neighbour of an atom considering all possible 27 nearest cells
- Sounds tedious, but can in practice be implemented with a simple comparison:

```
if (rijx > box(1)/2.0) rijx=rijx-box(1)
if (rijy > box(2)/2.0) rijy=rijy-box(2)
if (rijz > box(3)/2.0) rijz=rijz-box(3)

if (rijx < -box(1)/2.0) rijx=rijx+box(1)
if (rijy < -box(2)/2.0) rijy=rijy+box(2)
if (rijz < -box(3)/2.0) rijz=rijz+box(3)</pre>
```





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MD method

MD – Boundary conditions

There are alternatives, though:

Open boundaries = no boundary condition, atoms can flee freely to vacuum

- Obviously for surfaces
- Fixed boundaries: atoms fixed at boundary
 - Unphysical, but sometimes needed for preventing a cell from moving or making sure pressure waves are not reflected over a periodic boundary
- Reflective boundaries: atoms reflected off boundary, "wall"
- Combinations of these for different purposes





MD – Temperature and pressure control

- Controlling temperature and pressure is often a crucial part of MD
- "Plain MD" without any T or P control is same as simulating NVE thermodynamic ensemble
 - In irradiation simulations NVE only correct approach to deal with the collisional phase !!

NVT ensemble simulation: temperature is controlled

- Many algorithms exist, Nosé, Berendsen, …
- Berendsen does not strictly speaking simulate thermodynamic
 NVT ensemble but is often good enough
- NPT ensemble simulation: both temperature and pressure is controlled
 - Many algorithms exist: Andersen, Nosé-Hoover, Berendsen, Berendsen does not strictly speaking simulate thermodynamic
 NPT ensemble – but is often good enough



Note on pressure control

- Never use pressure control if there is an open boundary in the system!!
- Why??
- Think about it...
- Hint: surface tension and Young's modulus

MD method

MD – cellular method and neighbour lists

- To speed up MD for large (> 100 or so) numbers of atoms, a combination of neighbour list and a cellular method to find the neighbours is usually crucial
- If one has N atoms, and want to find the neighbours for a finite-range potential, a direct search requires N² operations killing for large N
- Solution: if potential cutoff = r_{cut}, divide atoms into boxes of size >= r_{cut}, search for neighbours only among the neighbouring cells
- Neighbour list: form a list of neighbours within r_{cut}+ r_{skin} and update this only when needed

21	22	23	24	25
16	17	18	19	20
11	12	13	14	15
6	7	8	9	10
1	2	3	4	5



Nonequilibrium extensions

- The basic MD algorithm is not suitable for many nonequilibrium simulations
- But over the last ~30 years augmentations of MD for nonequilibrium simulations have been developed
 - Our group has specialized in irradiation effects
 - Slides on these are left at the end for interested readers, here just a few aspects described



Nonequilibrium extensions to MD Variable time step schemes

In case the velocities of atoms are varying during the simulation, it is worth using a variable time step
 Example for irradiation simulations

$$\Delta t_{n+1} = \min\left(\frac{\Delta x_{\max}}{v_{\max}}, \frac{\Delta E_{\max}}{F_{\max}v_{\max}}, c_{\Delta t}\Delta t_n, \Delta t_{\max}\right)$$

Here ∆x_{max} is the maximum allowed distance moved during any t (e.g. 0.1 Å), ∆ E_{max} is the maximum allowed change in energy (e.g. 300 eV), v_{max} and F_{max} are the highest speed and maximum force acting on any particle at t, respectively, c_{∆t} prevents sudden large changes (e.g. 1.1), and t_{max} is the time step for the equilibrated system.
This relatively simple algorithm has been demonstrated to be able to handle collisions with energies up to 1 GeV

[K. Nordlund, Comput. Mater. Sci. 3, 448 (1995)].



Nonequilibrium extensions to MD Special boundary conditions

- In a zone which is far from thermodynamic equilibrium, one cannot and should not use any thermodynamic ensemble simulation method!
- Only use NVE = direct solution of Newton's equation of motion, "Free MD"
- Example for various irradiation cases:





Interatomic potentials and their development Interatomic potentials

- The key (and often only) physics input to the MD algorithm are the interatomic forces
 - Either from classical interatomic potentials or quantum mechanical methods (typically DFT)
 - Reliability of results depends entirely on this!
- Efficiency of MD for practical purposes:
 - Classical (analytical) potentials: 100 million atoms
 - DFT: 100 atoms
- Classical interatomic potentials are hence very desirable to have, and their development is a long-going iterative process
- By now, good potentials exist for almost all pure elements and most binary alloys of practical interest



iik

r_{ik}

Interatomic potentials and their development

Interatomic potentials

In general, total energy of a system of N atoms can be written:

$$V_{TOT} = \sum_{i}^{N} V_1(\vec{r}_i) + \sum_{i,j}^{N} V_2(\vec{r}_i, \vec{r}_j) + \sum_{i,j,k}^{N} V_3(\vec{r}_i, \vec{r}_j, \vec{r}_k) + \cdots$$

Because the energy of a bond should not depend on the explicit atom coordinates, and if there are no external forces V1, this can be simplified to:

$$V_{TOT} = \sum_{i,j}^{N} V_2(r_{ij}) + \sum_{i,j,k}^{N} V_3(r_{ij}, r_{ik}, \theta_{ijk}) + \cdots$$

From these the forces can be obtained in principle simply using $ec{F}_i =
abla_{ec{r_i}} V_{TOT}$

In reality, doing and coding this derivative for already a 3-body potentials is incredibly tedious: it has to be **perfect** for energy conservation in the MD simulation



Interatomic potentials and their development Interatomic potentials

Interatomic potentials can in general be divided in 2 classes:

Molecular mechanics force fields

- Used in chemistry and biophysics and biology, with a few exceptions non-reactive, i.e. covalent chemical bonds cannot break
 - Also same element can have different interactions
 depending on place in molecular: Carbon-1, Carbon-2, …
- Useless in most materials science applications, since these typically involve phase changes, bond breaking etc.

(Reactive) Interatomic potentials

- Chemical bonds can break and reform
- Only one atom type per element



Interatomic potentials and their development **Equilibrium potentials**

- In modern materials science potentials used are almost always many-body in nature (i.e. beyond pair potentials)
 - 3-body potentials, and sometimes more
- Tersoff-like:

$$V_{i} = \sum_{\text{neighbours}} \left[V_{\text{repulsive}}(r_{ij}) + b_{ijk}(r_{ij}, r_{ik}, \theta_{ijk}) V_{\text{attractive}}(r_{ij}) \right]; b_{ijk} \propto \frac{1}{\sqrt{\text{coordination of } i}}$$

Embedded-atom method-like (EAM)

$$V_{i} = \sum_{\text{neighbours}} V_{\text{repulsive}}(r_{ij}) + F_{i}\left(\sum_{j} \rho(r_{ij})\right)$$

- Both can be motivated in the second momentum approximation of tight binding (extended Hückel approximation)
 - Related to Pauling's theory of chemical binding
 - [K. Albe, K. Nordlund, and R. S. Averback, Phys. Rev. B 65, 195124 (2002)]



Interatomic potentials and their development Potential development aims

- First consider a potential for a pure element A.
- To be able to handle the effects described above, the potential should give:
 - The correct ground state: cohesive energy, crystal structure etc.
 - Describe all phases which may be relevant
 - Describe melting well
 - Describe defect energetics and structures well
- If we further consider irradiation of a compound AB:
- For high-dose irradiation the compound may segregate, so we need good models for elements A and B separately!
 - Fulfills all the requirements just given for a pure element
 - Describes well the heat of mixing of the compound
 - Describes defects involving atom types A and B well



Interatomic potentials and their development Potential development approach

Achieving all this starts to sound prohibitively difficult
 But there is one common factor for the main requirements:

- Melting, defects and different phases all involve unusual atom coordination states
- Hence if we use a framework to fit as many coordination states of the system as possible, we have some hope of getting many of the properties right

A Tersoff (Abell / Brenner)-like formalism can do this!



Interatomic potentials and their development Potential development approach

- We start by obtaining information on as many coordination states as possible:
 - Usually at least:

Z:	1	3	4	6	8	12
	dimer	graphite	diamond	SC	BCC	FCC

Data from experiments or DFT calculations

- Cohesive energy, lattice constant, bulk modulus for all Z
 Elastic constants for most important
- Fitting of these potentials in our group done in systematic approach introduced by Prof. Karsten Albe (TU Darmstadt)



Interatomic potentials and their development "Albe" fitting formalism

Use Tersoff potential in Brenner form (unique mathematical transformation)

$$E = \sum_{i>j} f_{ij}(r_{ij}) \left[V_R^{ij}(r_{ij}) - \underbrace{\frac{b_{ij} + b_{ji}}{2}}_{\overline{b_{ij}}} V_A^{ij}(r_{ij}) \right]$$
$$V_R(r) = \frac{D_o}{S - 1} \exp\left(-\beta\sqrt{2S(r - r_o)}\right)$$
$$V_A(r) = \frac{SD_o}{S - 1} \exp\left(-\beta\sqrt{2/S(r - r_o)}\right)$$

The 3 parameters r_0 , D_0 and β can be set directly from the experimental dimer interatomic distance, energy and vibration frequency!



Interatomic potentials and their development "Albe" fitting formalism

- Key idea:
 - In nn formulation,
 - if material follows

Pauling theory of

chemical bonding,

$$E_b = -D_o \exp\left(-\beta\sqrt{2S}(r_b - r_o)\right)$$

for all coordinations



Bonding distance

[Albe, Nordlund and Averback, Phys. Rev. B 65 (2002) 195124]



Interatomic potentials and their development "Albe" fitting formalism

Pair-specific A-B interaction

Three-body part:

Second-moment approximation exponential $b_{ij} = (1 + \chi_{ij})^{-1/2}$ $\chi_{ij} = \sum_{k(\neq i,j)} f_{ik}(r_{ik})g_{ik}(\theta_{ijk}) \exp[2\mu_{ik}(r_{ij} - r_{ik})]$ ik-dependent angular term modifying strength of ij bond This form for b_{ij} conforms to $b_{ijk} \propto \frac{1}{\sqrt{\text{coordination of }i}}$ consistent with Pauling's theory of chemical bond [Albe, Nordlund and Averback, Phys. Rev. B **65** (2002) 195124]



Interatomic potentials and their development

The "blood, sweat and tears" part

- There are all in all 11 parameters that must be specified
- Constructing a good potential means finding suitable values for these
 - This is done by fitting to different experimental or densityfunctional theory values of ground state and hypothetical phases





Interatomic potentials and their development

Potentials developed in our group

- We, and/or the Albe group, have so far developed potentials for:
 - BN, PtC, GaAs, GaN, SiC, ZnO, FePt, BeWCH, FeCrC
 - All these potentials include all the pure elements and combinations!
- Fitting code "pontifix" freely availably, contact Paul Erhart
- Just to give a flavour of complexity: prolonged irradiation of WC by H and He



Special case for CLIC simulations: HELMOD



Hybrid ED&MD (HELMOD) by Djurabekova et al

- A new kind of molecular dynamics was developed by us to enable
- simulation of metal surfaces under electric field
- Atomic interactions obtained from EAM-like potentials as in usual metal MD

But in ED&MD hybrid code $\vec{F} = -\nabla V(\vec{r_i}) + \vec{F_q} + \vec{F_{Coul}}$ for surface atoms as due to the excess or depletion of electron density (atomic charge)

E_{loc} is obtained by solution of the Laplace equation $abla^2 arphi = 0$ in the vacuum above the metal surface

Gauss law implemented on a surface $\sigma = \mathcal{E}_0 E_{loc}$ is applied to calculate the charges q_i on surface atoms



Thus, the motion of surface atoms is corrected due to the pulling effect of the electric field as a 1-body force $F_q = E_{loc}q_i$



Special case for CLIC simulations: HELMOD Hybrid ED&MD (HELMOD) by Djurabekova *et al*





φ=const (conductive material)







Special case for CLIC simulations: HELMOD Example: Short tip on Cu (100) surface at the electric field 10 GV/m at 500 K



Kai Nordlund, Department of F

Examples of uses of regular MD



Example 1: MD of soft landing of Cu₃Ni nanocluster on Cu surface

0 ps







Examples of uses of regular MD

Example 2: Nanoindentation

- Nanoindentation can be very well simulated by MD
- Example: diamond indentation of a-Si





Examples of uses of regular MD Example 3: explosive welding

- Fe and Cu explosively welded together
 - Explosion front velocity 1.5 km/s can be exactly matched on MD timescale: 1.5 m/s = 1.5 nm/ps.
- We have simulated on the atomic scale explosive welding
- Results showed that local melting is a prerequisite for jet formation



[Saresoja, Nordlund, Kuronen, Adv. Engr. Mater 14 (2012) 265]

Examples of uses of regular MD



Animation



How reliable is MD?

Ion range calculations

After 3 PhD theses in 1995-2005, we reached the state where we can reproduce **all** experimentally measured ion implantation depth profiles

Also in demanding channeling geometries



[J. Sillanpää, K. Nordlund, and J. Keinonen, Phys. Rev. B 62, 3109 (2000); J. Sillanpää J. Peltola, K. Nordlund, J. Keinonen, and M. J. Puska, Phys. Rev. B 63, 134113 (2000); J. Peltola, K. Nordlund, and J. Keinonen, Nucl. Instr. Meth. Phys. Res. B 217, 25 (2003); J. Peltola, K. Nordlund, and J. Keinonen, Nucl. Instr. Meth. Phys. Res. B 212, 118 (2003)]



How reliable is MD?

Craters: simulation vs. experiment



- We have studied surface crater formation extensively
 Experimental and simulated crater sizes agree well with experiments
- Also mechanism fully understood



[Birtcher and Donnelly, PRB 1997]



How reliable is MD? Sputtering yields



- In another of our big topics, we have examined systematically how reliable our interatomic potentials really are
- We compared the so called EAM and MD/MC CEM potentials with experiments on Au irradiation of Au(111)
 - Qualitative results the same
 - Crater sizes about the same
 - But sputtering yields
 have large differences
 at some energies!
 - The CEM potential agrees almost perfectly



[Samela et al, Nucl. Instr. Meth. Phys. Res. B (2005)]



How reliable is MD?

Ion ripple wavelengths

First principles (= no empirical input) ripple wavelengths compared to experiments:



[Norris et al, Nature Communications 2 (2011) 276] Very good agreement considering no adjustable parameters



Does MD have predictive power? Case 1: Defects in carbon nanotubes

In 2000-2005 we predicted several features of irradiation defect production in carbon nanotubes:





The most abundant defects in irradiated SWNTs are vacancies. [Krasheninnikov et al, Phys. Rev. B 63 (2001) 245405] Carbon atoms absorbed on nanotube walls (adatoms) play the role of interstitials, and are highly mobile [Lehtinen et al, Phys. Rev. Lett. 91 (2003) 017202]

These findings were later verified experimentally by Sumio lijima et al.



Does MD have predictive power? Case 2: power law damage distribution

In 2014 we predicted that damage cluster size distributions in W
 follow a power law
 [A. E. Sand, S. L. Dudarev, and
 K. Nordlund, EPL 103, 46003
 (2013)]

This was verified by us and our experimental collaborators in 2015



[X. Yi, A.E. Sand, D.R. Mason, M.A. Kirk, S.G. Roberts, K. Nordlund and S.L. Dudarev, EPL (2015)]



Long-time scale limit of MD

- Many real materials processes take microseconds, seconds, days or years
- This is clearly beyond the scope of molecular dynamics: the iteration time step is typically ~1 fs, and can normally not be much larger than this
 - => 1 million iterations of the MD loop only gives 1 ns time
- There are accelerated MD techniques such as "Hyperdynamics" and "Temperature-accelerated dynamics" that sometimes can get to ms or even s timescals – but limited in range of problems they can do
- Non-MD methods that can get to very long time scales:
- Kinetic Monte Carlo (KMC)
- **Rate equations** (numerical solution of differential equations)

[K. O. E. Henriksson, K. Nordlund, A. Krasheninnikov, and J. Keinonen, Appl. Phys. Lett. 87, 163113 (2005); K. O. E. Henriksson, K. Nordlund, A. Krasheninnikov, and J. Keinonen, Fusion Science & Technology 50, 43 (2006)]



Kinetic Monte Carlo

Kinetic Monte Carlo algorithm

Form a list of all N possible transitions i in the system with rates r_i Calculate the cumulative function $R_i = \sum_{i=0}^{i} r_i$ for all i=0,...,NFind a random number u_1 in the interval [0,1] Carry out the event for which $R_{i-1} < uR_N < R_i$ Move time forward: $t = t - \log u_2/R_N$ where u_2 random in [0,1] Figure out possible changes in r_i and N, then repeat



Kinetic Monte Carlo

Comments on KMC algorithm

- The KMC algorithm is actually exactly right for so called Poisson processes, i.e. processes occuring independent of each other at constant rates
 - Stochastic but exact
- Typical use: atom diffusion: rates are simply atom jumps
- But the big issue is how to know the input rates r_i ??
 - The algorithm itself can't do anything to predict them
 - I.e. they have to be known in advance somehow
- From experiments, DFT simulations, …
- Also knowing reactions may be difficult
- Many varieties of KMC exist: object KMC, lattice object KMC, lattice all-atom KMC, …
 - For more info, see wikipedia page on KMC (written by me ☺)



Kinetic Monte Carlo Principles of object KMC for defects

- Basic object is an impurity or intrinsic defect in lattice
- Non-defect lattice atoms are not described at all!
- Basic process is a diffusive jump, occurring at Arrhenius rate

$$r_i = r_0 e^{-E_A/k_B T}$$

But also reactions are important: for example formation of divacancy from two monovacancies, or a pair of impurities
 Reactions typically dealt with using a simple recombination radius: if species A and B are closer than some recombination radius *r*_{AB}, they instantly combine to form defect complex



Kinetic Monte Carlo Example animation

- Simple fusion-relevant example: He mobility and bubble formation in W
 - Inputs: experimental He migration rate, experimental flux, recombination radius of 3 Å, clusters assumed immobile



[K. O. E. Henriksson, **K. Nordlund**, A. Krasheninnikov, and J. Keinonen, Fusion Science & Technology **50**, 43 (2006).]



Further reading on methods

A full course on MD:

http://www.acclab.helsinki.fi/~knordlun/atomistiset/

A full course on MC, including KMC:

https://moodle.helsinki.fi/course/info.php?id=11740

- Books:
 - Allen, Tildesley: "Computer simulation of liquids", Oxford University Press 1989
 - An old classic, still fully relevant in theory parts
 - Frenkel, Smit: "Understanding molecular simulation: from algoritms to applications", Academic Press 2002
 - More modern, has e.g. Modern interatomic potentials described
- And of course all the references given in the slides



Reliable (according to me) wikipedia pages

- I can also for a quick introduction recommend the following wikipedia pages (I have written or checked and modified them myself ⁽ⁱ⁾):
 - Sputtering
 - Kinetic Monte Carlo
 - Molecular dynamics
 - Interatomic potential





Extra slides: irradiation effect special methods



1) keV and MeV-energy collisions between nuclei

- To handle the high-E collisions, one needs to know the high-energy repulsive part of the interatomic potential
 - We have developed DFT methods to obtain it to within ~1% accuracy for all energies above 10 eV
 - So called "Universal ZBL" potential accurate to ~5% and very easy to implement
- Simulating this gives the *nuclear stopping* explicitly!



[K. Nordlund, N. Runeberg, and D. Sundholm, Nucl. Instr. Meth. Phys. Res. B 132, 45 (1997)].



1) keV and MeV-energy collisions between nuclei

- During the keV and MeV collisional phase, the atoms move with very high velocities
 - Moreover, they collide strongly occasionally
- To handle this, a normal equilibrium time step is not suitable
- On the other hand, as ion slows down, time step can increase
- Solution: adaptive time step



1) keV and MeV-energy collisions between nuclei

Example:

$$\Delta t_{n+1} = \min\left(\frac{\Delta x_{\max}}{v_{\max}}, \frac{\Delta E_{\max}}{F_{\max}v_{\max}}, c_{\Delta t}\Delta t_n, \Delta t_{\max}\right)$$

Here ∆x_{max} is the maximum allowed distance moved during any t (e.g. 0.1 Å), ∆ E_{max} is the maximum allowed change in energy (e.g. 300 eV), v_{max} and F_{max} are the highest speed and maximum force acting on any particle at t, respectively, c_{∆t} prevents sudden large changes (e.g. 1.1), and t_{max} is the time step for the equilibrated system.
This relatively simple algorithm has been demonstrated to be able to handle collisions with energies up to 1 GeV

[K. Nordlund, Comput. Mater. Sci. 3, 448 (1995)].



2) Energy loss to electronic excitations

- The energy loss to electronic excitations = electronic stopping can be included as a frictional force in MD
- The nice thing about this is that it can be compared directly to experiments via BCA or MD range or ion transmission calculations
 Electronic stopping power



[J. Sillanpää, K. Nordlund, and J. Keinonen, Phys. Rev. B 62, 3109 (2000); J. Sillanpää J. Peltola, K. Nordlund, J. Keinonen, and M. J. Puska, Phys. Rev. B 63, 134113 (2000); J. Peltola, K. Nordlund, and J. Keinonen, Nucl. Instr. Meth. Phys. Res. B 217, 25 (2003); J. Peltola, K. Nordlund, and J. Keinonen, Nucl. Instr. Meth. Phys. Res. B 212, 118 (2003)]



- **3)** Transition to high-pressure and high-T thermodynamics
 - Requires realistic intermediate part in potential



 Can be adjusted to experimental high-pressure data and threshold displacement energies

[K. Nordlund, L. Wei, Y. Zhong, and R. S. Averback, Phys. Rev. B (Rapid Comm.) 57, 13965 (1998); K. Nordlund, J. Wallenius, and L. Malerba. Instr. Meth. Phys. Res. B 246, 322 (2005); C. Björkas and K. Nordlund, Nucl. Instr. Meth. Phys. Res. B 259, 853 (2007); C. Björkas, K. Nordlund, and S. Dudarev, Nucl. Instr. Meth. Phys. Res. B 267, 3204 (2008)]



3) Transition to high-pressure and high-T thermodynamics

- The transition to thermodynamics occurs natuarally in MD
- But boundary conditions a challenge due to heat and pressure wave emanating from a cascade





What is needed to model irradiation effects? MD irradiation temperature control

Central part has to be in NVE ensemble, but on the other hand extra energy/pressure wave introduced by the ion or recoil needs to be dissipated somehow

Exact approach to take depends on physical question:

a) surface, b) bulk recoil, c-d) swift heavy ion, e) nanocluster, f) nanowire



Kai Nordlund, Depa [A. V. Krasheninnikov and K. Nordlund, J. Appl. Phys. (Applied Physics Reviews) 107, 071301 (2010).



4) Realistic equilibrium interaction models

Finally one also needs the **normal equilibrium part** of the interaction model



- Since we start out with the extremely non-equilibrium collisional part, all chemical bonds in system can break and reform and atoms switch places
 - Conventional Molecular Mechanics force fields are no good at all!
 - More on potentials later