

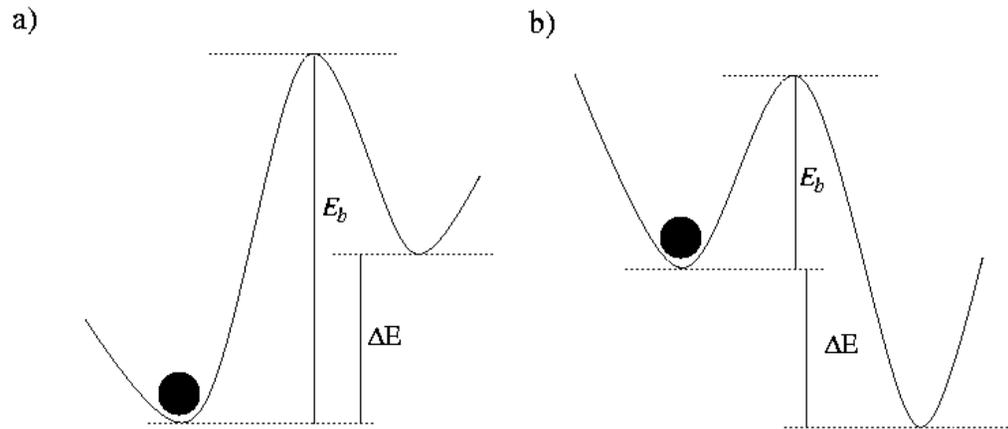
# 8. Kinetic Monte Carlo

[Duane Johnsons notes in web; Per Stoltze: Simulation methods in atomic-scale physics; Fichthorn, Weinberg: J. Chem. Phys. 95 (1991) 1090; Bortz, Kalos, Lebowitz, J. Computational Physics 17 (1975) 10]

# 8.1. Introduction

Above, we saw how simple random walks can be used to simulate movement processes. They work fine *per se*, but if we want to obtain a physical time scale for the simulated processes, we need to know the average jump time.

Let us now think about how realistic it is to expect we could know it in a microscopic process. Consider e.g. any kind of defect in a solid, the emission of a photon in a crystal, or a change in the geometry of a polymer. In many, probably most, cases these are activated processes, i.e. they start when the internal energy exceeds some barrier. Schematically:



Part a) shows a barrier which leads to a higher-energy state, part b) one which leads to a lower. For

barrier jumps, the relevant energy is in both cases  $E_b$ ;  $\Delta E$  does not play any role on the probability of the jump.

Typically the jump over the barrier occurs by thermal activation. In that case, and if we can work in the classical limit, the probability of exceeding the barrier most often simply follows a Boltzmann distribution:

$$P \propto e^{-E_b/k_B T}$$

The activated events do not necessarily need to be jumps, but could be other process as well which follow this equation (such as a geometry change in a large molecule).

By introducing a proportionality constant we can write the event frequency as

$$\text{event rate}(T) = w = w_0 e^{-E_b/k_B T} \quad (1)$$

where  $w_0$  can be interpreted as an “attempt frequency” telling how often an attempt is made to exceed the barrier. In case  $E_b = 0$ , or  $T = \infty$ , we see that every attempt would be successful.

In solids it is easy to understand the attempt frequency: it is simply the vibration frequency of the atom. It can often be predicted to good accuracy when the atom vibration (elastic and sound) properties of the lattice are well known. Typically it is of the order of  $1/(100 \text{ fs})$ .

As a good approximation,  $w_0$  is independent of  $T$ , at least in solids, basically because the elastic constants are almost independent of  $T$ .

In section we show that the probability density for a transition to occur is

$$f(t) = r e^{-rt}$$

Hence the use of an average transition time in the random walk is a quite crude approximation. If there is only one transition rate, the approximation may not be too bad. But if we want to simulate processes which involve many different kinds of transitions occurring at different rates, it is rather clear it is not justifiable to ignore the real, exponential time dependence.

Moreover, if we use Eq. 1 to derive the event probability in our simulations, we get the added advantage that we can do simulations at any temperature realistically, even if the temperature keeps changing during the modeling.

We can now think of 3 basic approaches to simulate a system with multiple activation energies:

1. Use a short  $\Delta t$ . For every step, go through all particles  $i$ , and use  $w_i$  to randomly choose whether it will move at this particular time interval. This approach has the advantage that it is intuitively clear, and that it is perfectly clear what the real time is. The disadvantage is that to preserve the ratios between different rates, one has to have  $\Delta t \ll 1/w_{\max}$ , where  $w_{\max}$  is the fastest event rate in the system. This makes this approach very slow and inefficient, as many time steps will be spent when nothing or only a few particles move, even though all particles have to be gone through at every step.
2. Pick a particle  $i$  randomly. Then let it jump according to a probability  $e^{-E_b/k_B T}$ . This works fine, and in fact is a special case of the Metropolis algorithm discussed later on during the course. The downside for this is that it is often not clear how to derive the real time scale from the number of Monte Carlo steps.
3. Pick a particle at random, but with a probability proportional to its jump rate. This clearly makes the routine efficient, as every step produces a jump. But the decisive advantage for this method came in 1975 when Bortz, Kalos and Lebowitz showed how the real time scale can be calculated for this approach. Since the method combines efficiency and real time, it is close to perfect for simulation of activated processes.

Approach 3 is the essence of the kinetic Monte Carlo method.

## 8.2. The kinetic Monte Carlo algorithm

For the kinetic Monte Carlo simulations, we consider a system with a set of transitions  $W_i$  from a state  $x_a$  into other possible states  $x_b$

$$W_i(x_a \rightarrow x_b)$$

For each  $W_i$  there is a transition probability per unit time, i. e. rate  $r_i$ .  $i$  loops over all possible transitions. The rate is typically given by Eq. 1.

The Kinetic Monte Carlo method can be used to simulate these processes provided:

- 1° The transitions are Poisson processes
- 2° The different processes are independent, i.e. not correlated
- 3° The time increments between successful steps are calculated properly

Point 1° is explained below in section . There we will also prove the equation which calculates the time increments needed for step 3° . Requirement 2° has been discussed above, but to restate this: we require that one event is only dependent on the previous state of the system, but is not dependent on how any previous event occurred.



In addition to these, some theorists add a requirement

4° The transition probabilities follow a so-called “dynamical hierarchy” which obeys “detailed balance”

This requirement may be necessary when one uses the simulations to examine the static and dynamic properties of the Hamiltonian describing the system. However, it is perfectly possible to use KMC to model systems which are constantly out of equilibrium and do not satisfy criterion 4° . An example of such systems is so called “driven systems” where some external factor (irradiation, high pressure) keeps the system out of reaching thermodynamic equilibrium. Since criterion 4° is not necessary to fulfill to use KMC, we will not discuss it in detail.

Without any further ado, I will present the algorithm, known as the **residence-time** algorithm or the **n-fold way** or the **Bortz-Kalos-Liebowitz (BKL)** algorithm or the **kinetic Monte Carlo (KMC)** algorithm. A dear child certainly has many names. I would recommend using “residence-time algorithm”, since this is nowadays in quite common use, and “kinetic MC” can easily be misunderstood.

- 0° Set the time  $t = 0$
- 1° Form a list of all the rates  $r_i$  of all possible transitions  $W_i$  in the system
- 2° Calculate the cumulative function  $R_i = \sum_{j=1}^i r_j$  for  $i = 1, \dots, N$  where  $N$  is the total number of transitions. Denote  $R = R_N$
- 3° Get a uniform random number  $u \in [0, 1]$
- 4° Find the event to carry out  $i$  by finding the  $i$  for which

$$R_{i-1} < uR \leq R_i$$

- 5° Carry out event  $i$
- 6° Find all  $W_i$  and recalculate all  $r_i$  which may have changed due to the transition
- 7° Get a new uniform random number  $u \in [0, 1]$
- 8° Update the time with  $t = t + \Delta t$  where:

$$\Delta t = -\frac{\log u}{R} \tag{2}$$

- 9° Return to step 1

This algorithm is clearly  $O(N)$ , since at least step 2° has a sum over  $N$  elements. This sounds good, but remember that this means that we need  $N$  operations for every event, and probably want to simulate millions or billions of events. In case this is the bottleneck in terms of efficiency, it is possible to remake the algorithm to achieve below- $N$  scaling for every event, even down to  $O(\log_2 N)$ , using so called *binning* methods and recursive tree searches. We will not present these in detail here, since they belong more to the realm of computer science than physics, but if you start doing KMC on large scales, it is best to look into it.

We will now first look at what the central idea behind the selection scheme is (steps 2° – 5° ), then motivate and partly derive the time advancing equation in step 8° .

## 8.2.1. Motivation for the basic approach

Say we have a system with 3 objects

$$A_1, A_2, A_3$$

The system state  $x_a$  is then the list of objects  $\{A_1, A_2, A_3\}$ . The possible transitions are that each object may change into another object, i.e.

$$\begin{array}{ccc} A_1 & & A_2 & & A_3 \\ \downarrow & \text{or} & \downarrow & \text{or} & \downarrow \\ B_1 & & B_2 & & B_3 \end{array}$$

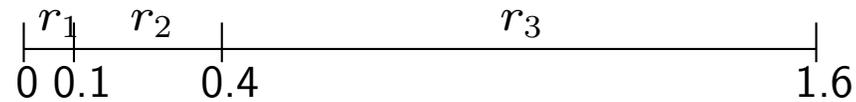
Then we have three transition rates. Let us arbitrarily say that they are

$$r_1 = 0.1, r_2 = 0.3, r_3 = 1.2$$

which would give the cumulative function  $R_i$  as

$$R_1 = 0.1, R_2 = 0.4, R_3 = 1.6$$

We can now plot the  $r_i$  as regions and  $R_i$  as points on a line as follows:



If we now generate a random number  $u$  between 0 and 1, and multiply it by  $R = 1.6$ , this number  $uR$  will correspond to some point on the line. It is clear from the figure that the probability of e.g. obtaining point 2 is

$$0.1 < uR < 0.4$$

i.e. proportional to  $r_2/R$ . So we will get the different events with a probability which corresponds to their rate. This is exactly what we wanted from the beginning.

## 8.2.2. Motivation of equation for time

To motivate eq. 2, we consider the activated processes discussed above, for which the jump frequency is

$$\text{jump rate}(T) = w(T) = w_0 e^{-E^b/k_B T}$$

Now consider a fixed  $T$ . We then have jumps occurring at a rate  $r = w(T)$ .

If further the probability of a jump to occur is independent of the previous history, and the same at all times (both quite reasonable assumptions), the transition probability is a uniform function of time. Then the process is a so called **Poisson process**, which are quite well known in the theory of stochastic processes [Fichthorn, J. Chem. Phys. 95, 1090, and references therein].

To derive the functional form of the time dependence, consider a single object with a uniform transition probability  $r$ . Call  $f$  the transition probability density, which gives the probability rate that the transition occurs at time  $t$ . The change of  $f(t)$  over some short time interval  $dt$  is proportional to  $r$ ,  $dt$  and  $f$  because  $f$  gives the probability density that particles still remain at time  $t$ . I.e.

$$df(t) = -r f(t) dt \implies \frac{df}{dt} = -r f$$

and the solution is

$$f(t) = A e^{-rt}$$

By using the boundary condition  $f(0) = r$  we get

$$f(t) = re^{-rt}$$

A useful feature of Poisson processes is that a large number  $N$  of Poisson processes, with rates  $r_i$ , will behave as another large Poisson process with the same properties of a single process. Hence for this process one can write the probability density as

$$F(t) = Re^{-Rt} \tag{3}$$

with

$$R = \sum_{i=1}^N r_i. \tag{4}$$

$F(t)$  now gives directly the transition probability density for the whole system. We know from section 4 how to generate random numbers in any distribution; the integral function is now  $e^{-Rt}$  and we get the inverse from

$$e^{-Rt} = u \implies t = -\frac{\ln u}{R} \tag{5}$$

where  $u$  is a uniform random number. This is exactly Eq. 2 above!

We can now also do a consistency check by calculating the average time between jumps  $\langle t \rangle$  in

the composite system in two different ways. First we obtain  $\langle t \rangle$  by integrating equation 3

$$\langle t \rangle = \int_0^{\infty} Rte^{-Rt} dt = Rt \frac{-1}{R} e^{-Rt} \Big|_0^{\infty} - \int_0^{\infty} R \frac{-1}{R} e^{-Rt} dt = -R \frac{-1}{R} \frac{-1}{R} e^{-Rt} \Big|_0^{\infty} = \frac{1}{R}$$



But we can also obtain the average assuming Eq. 5 is valid, by obtaining the average of  $\ln u$  over all random numbers between 0 and 1, i.e.

$$\int_0^1 \ln u du = -1$$

Hence  $\langle t \rangle$  from Eq. 5 is also  $1/R$ , so everything is really consistent here.

## 8.2.3. Some analysis of the algorithm

### 8.2.3.1. Advantages

With some thought, we can see several interesting features in the KMC algorithm. One is that there is nothing in the algorithm which requires thermodynamic equilibrium; we can start with any set of transitions, and as long as they fulfill the basic criteria given above, we can use this method.

Moreover, because the  $r_i$  and  $W_i$  and the list of them are recalculated on every iteration (steps 1° , 2° and 6° ), the objects simulated can change character at every step. They can for instance react with each other to form reaction products, which can be entirely new objects, vanish from the system by some form of recombination, or an object may split up into several new objects.

If this kind of non-preservation of objects occurs, the method has another major advantage. Since  $R$  is recalculated every step depending on which objects are present, the time scale  $\Delta t$  of the steps will follow the system evolution automatically. So, if we initially for instance have a set of very fast-moving objects, which after some time have reacted so that there are only slow-moving objects left, the time scale will automatically get longer after the fast objects are gone. And this also works the other way: if a slow object breaks up and emits a fast-moving object, the method will immediately switch to shorter time scales.

Thanks to this feature, KMC can be used to model systems where the initial time scale is of the order of fs, and the final one of the order of minutes, hours or sometimes even years.

### 8.2.3.2. Disadvantages

The major physical disadvantage with KMC is that all possible rates  $r_i$  and reactions have to be known in advance. The method itself can do nothing about predicting them. Instead, they have to be obtained from experimental data, or derived from other simulation methods, typically electronic structure calculations or MD simulations.

This is a clear and strong contrast to MD simulations. These can, based on (hopefully) well motivated interatomic force models, predict transition rates, and sometimes even find entirely new kinds of transitions and reactions. But they are limited to short timescales, at most  $\mu\text{s}$ :s.

Another minor disadvantage from a computational efficiency point of view is forming all the lists and recalculating the  $r_i$  (steps 1<sup>o</sup>, 2<sup>o</sup> and 7<sup>o</sup>). Especially recalculating all  $r_i$  may be quite slow. But since every step only carries out one event  $i_e$ , and thus usually only affects a small subset of all objects, it is probably in most applications possible to deduce and update those  $r_i$  which may have been affected by the  $i_e$  event.

In fact, in complex systems with many different kinds of objects and events possible, the major effort in writing a KMC program tends to be in constructing the binning method, and finding and

implementing data structures and bookkeeping algorithms which allow for efficient updating, rather than on the physics side.

## 8.3. Applications

The presentation above was intentionally kept on an as abstract and general level as possible, to emphasize the fairly general character of the method. Now we will, to hopefully give a better idea of how this can work in practice, first list a few examples of where KMC has been used, then go through one real-life example of considerable practical importance in detail.

## 8.3.1. Examples

[Duane Johnsons article]

KMC has been at least used in simulations of the following physical systems:

1. Surface diffusion
2. Molecular beam epitaxy (MBE) growth
3. Chemical vapor deposition (CVD) growth
4. Vacancy diffusion in alloys
5. Compositional patterning in alloys driven by irradiation
6. Polymers: topological constraints vs. entanglements
7. Coarsening of domain evolution
8. Dislocation motion
9. Defect mobility and clustering in irradiated solids

In the following, we will discuss the last example, especially for the case of Si.

## 8.3.2. Point defects in Si

[Own knowledge, but see e.g. Mayer-Lau, *Electronic Materials Science For Integrated Circuits in Si and GaAs*, MacMillan 1990, and Chason *et al.*, *J. Appl. Phys* 81 (1997) 6513]

When a solid material is irradiated with ions, neutrons or electrons of sufficiently high energy ( $\sim 100$  eV for ions or neutrons, more than 100 keV for electrons), they produce damage in the material. If the material is crystalline, this damage can as a first approximation be described as consisting of empty lattice sites (=vacancies), and extra atoms between lattice sites (=interstitials).

The reason to this is simply that when the energetic particle collides with a lattice atom, it can kick it out from its own site, after which the atom most probably ends up in an interstitial site.

In reality, there is often also significant defect clustering going on, and in metals the clusters often in fact dominate the behaviour. But in Si it turns out that the simple vacancy-interstitial picture can be used as the starting point for studying defect migration with good results.

So we now consider Si only. During the manufacturing of Si computer chips (the very ones which are inside every present-day computer) ion irradiation is routinely used to introduce dopant atoms into silicon. In present-day chips the irradiation goes a few hundred nm deep in the Si. The depth

is of the same order of magnitude as the linewidth of the central components in the chip, which today (2004) is 130 nm in top-of-the-line Intel and AMD processors.

During this irradiation the doses are so large that a very high defect concentration forms in the Si, and usually it in fact amorphizes. Since the chip only works for crystalline Si, the Si wafer is raised to a very high temperature,  $\sim 1000$  K for furnace anneals,  $\sim 1300$  K for light-induced so called “rapid thermal” anneals, to recrystallize the amorphized region.

When the amorphized region recrystallizes, it will initially have a very high concentration of vacancies and interstitials. These will start migrating, many of the vacancies and interstitials will recombine, some will reach the surface where they essentially vanish, some will escape into the bulk of the Si, and some cluster with other defects of the same type to form vacancy and interstitial clusters. The clusters can also break up and emit new point defects. Understanding this process is crucial for further miniaturization of the chip components, and KMC can be the crucial tool for this, as it can simulate all of the processes described above.

For instance, a few years ago a major problem appeared when it turned out that there was an anomalous, so called “transient-enhanced” diffusion (TED) process driving boron dopant atoms much deeper in than they should be for the chip to work properly. Understanding of what was going

on was achieved by a combination of KMC simulations and experiments, which eventually revealed that Si interstitials were enhancing the mobility of the boron atoms.

Right now an additional, related problem is that there is no known easy way in which the B doping can be carried out shallower than 20 nm from the surface, since the required B concentrations will be so high that a boronization-enhanced diffusion will always drive the B in to at least this depth. If this problem is not solved, the further miniaturization of Si chips (as predicted by Moore's law with a time constant of 18 months) may stop completely sometime around 2010. Whatever the solution may be, it is likely KMC simulations will be somehow involved in obtaining it.

### 8.3.3. KMC simulation of point defects in Si

For educational purposes, and to make the rather abstract algorithm given above more concrete, I will now describe in detail how to simulate a stripped model of defect migration in Si. I will only consider the two basic defect types, the interstitial and vacancy, and ignore clustering completely. But I will include the most basic defect reaction: recombination. It is self-evident that if a vacancy and interstitial come sufficiently close to each other, the extra interstitial atom will fill in the vacant lattice site, and only perfect Si lattice will remain. So this is a true case of the simulated objects vanishing.



To simulate this process, the defect migration coefficients need to be known. They are actually not known to any good accuracy, and at low temperatures subject to controversy even in the order of magnitude. For high temperatures some sort of agreement on the values does exist. We will use the values reported in 1996 by Tang *et al.* [Phys. Rev. B. 55 (1997) 14279], giving the migration properties as

$$\text{jump rate}(T) = w = w_d e^{-E^m/k_B T}$$

where  $w_d$  is the defect jump rate prefactor and  $E^m$  the migration activation energy. The values given are:

$$w_i = 1.717 \text{ 1/fs}$$



$$E_i^m = 1.37 \text{ eV}$$

$$w_v = 0.001282 \text{ 1/fs}$$

$$E_v^m = 0.1 \text{ eV}$$

This means that at infinite  $T$  we would have an average time between jumps of

$$\tau_i = 1/w_i = 0.58 \text{ fs}$$

$$\tau_v = 1/w_v = 780 \text{ fs}$$

But at the melting point of Si, 1685 K,

$$w_i = 0.000137134 \implies \tau_i = 1/w_i = 7292 \text{ fs}$$

$$w_v = 0.000643859 \implies \tau_v = 1/w_v = 1553 \text{ fs}$$

so at all realistic temperatures the vacancy in this model moves faster than the interstitial because of the lower activation energy.

■ The jump length is set to the nearest-neighbour atom distance in Si, 2.35 Å, since this corresponds to the known migration mechanisms. Moreover, the KMC simulations in Si are usually performed as if the defect motion in it would occur in a random medium (so you can ignore the lattice structure).

Recombination is described simply by assuming that if an interstitial and vacancy are within 4 Å from each other, they will immediately recombine. This is a quite realistic assumption, except that the exact value of the recombination distance may vary.

■ So in our model system, there are 3 possible processes:

1. A vacancy jumps by 2.35 Å in a random direction
2. An interstitial jumps by 2.35 Å in a random direction
3. If a vacancy and interstitial are within 4 Å from each other, they will immediately recombine and vanish from the system.

So now the possible transitions  $W_i$  are just the defect jumps 1 and 2, and there is only one possible transition per defect. So the array of events will simply coincide with the array of defects.

Process 3 is not activated, so it is treated as a step which is not part of the actual residence-time algorithm.



Assuming we only simulate at constant temperature, here is description of how we can simulate this problem with KMC:

- 0 a°** Set the time  $t = 0$ . Set initial positions of all  $N$  defects  $\mathbf{x}_j$  for  $j = 1, \dots, N$  and their types  $t_j$ . Set the temperature  $T$  and recombination radius  $r_{\text{rec}} = 4.0 \text{ \AA}$ . Set  $N_{\text{iter}} = 0$  and select  $N_{\text{itermax}}$
- 0 b°** Go through all defects and for each defect find whether any defect of the opposite type is closer than  $r_{\text{rec}}$  to it. If so, remove both from the tables  $\mathbf{x}_j$  and  $t_j$ , set  $N = N - 2$

**0 c°** Calculate the jump rate for interstitials from  $T$ :  $w_i = w_i e^{-E_i^m/k_B T}$  and same for vacancies  $v$

**1°** Set  $r_j = w_d$  where  $d = i$  or  $d = v$ , depending on the defect type  $t_j$  for all  $j = 1, \dots, N$

**2°** Calculate the cumulative function  $R_j = \sum_{k=1}^j r_k$  for  $j = 1, \dots, N$ . Denote  $R = R_N$

**3°** Get a uniform random number  $u \in [0, 1]$

**4°** Find the defect to move  $j$  out by finding the  $j$  for which

$$R_{j-1} < uR \leq R_j$$

**5°** Carry out jump  $j$  by displacing defect  $j$  in a random direction in 3D by  $2.35 \text{ \AA}$

**6°** For defect  $j$ , find whether any defect of the opposite type is closer than  $r_{\text{rec}}$  to it. If so, remove both from the tables  $\mathbf{x}_j$ ,  $t_j$  and  $r_j$ , set  $N = N - 2$ .

**7°** Get a new uniform random number  $u \in [0, 1]$

**8°** Update the time with  $t = t + \Delta t$  where:

$$\Delta t = -\frac{\log u}{R}$$

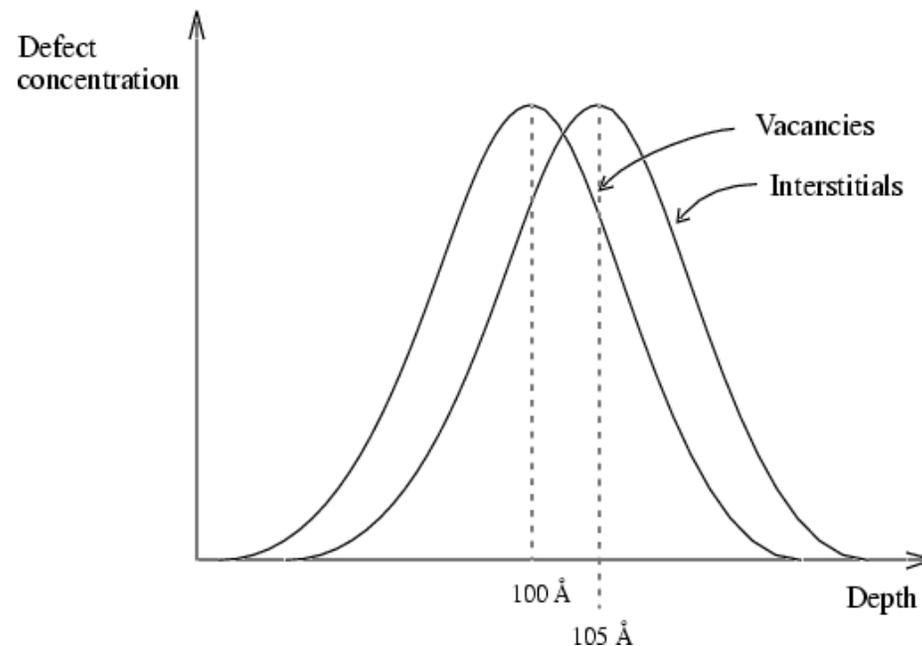
**9°** Set  $N_{\text{iter}} = N_{\text{iter}} + 1$ . If  $N_{\text{iter}} < N_{\text{itermax}}$  return to step 1.

**10°** Analyze for desired properties and print results

In the exercises you get to code this for yourself to get a good feeling for it.

### 8.3.3.1. Sample application

We now use this method to study the following question. During ion irradiation, the defects induced by a single incoming ion are as a rough first approximation produced in Gaussian distributions. The average depth of the interstitials is slightly deeper than the vacancies (simply because the ions tend to kick the atoms deeper in on average). Let us say the defect profiles would be two Gaussians with means of  $100 \text{ \AA}$  and  $105 \text{ \AA}$  and the same standard deviations of  $30 \text{ \AA}$ :



We want to simulate what happens in this system at different temperatures, especially what fraction of the defects recombine and where the rest end up (the surface or the bulk).



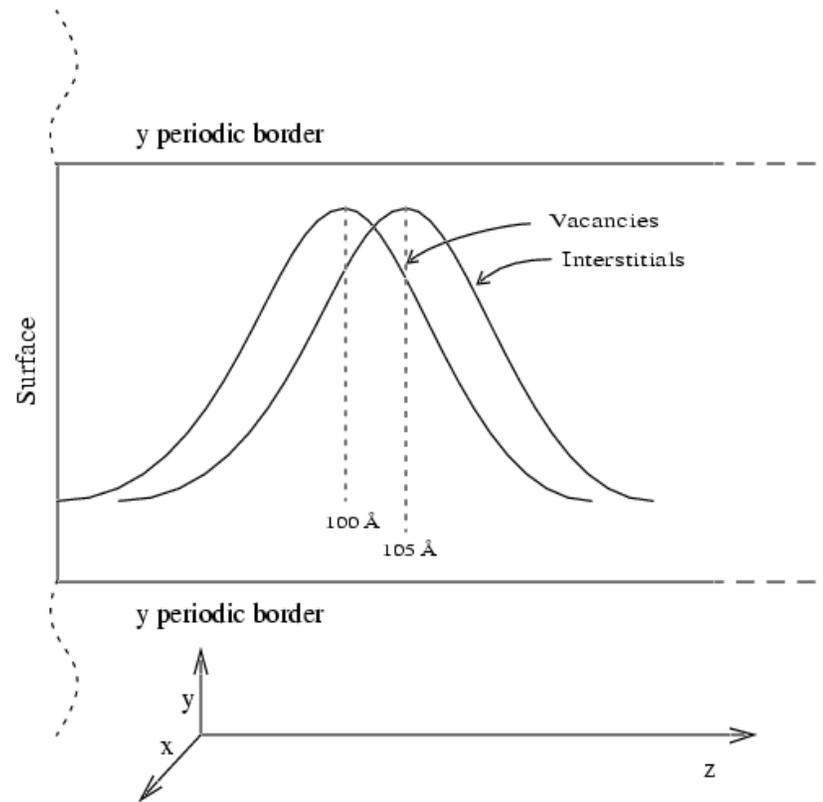
The irradiation is carried out on a very wide area (mm's or cm's), which we can not possibly simulate. But when we are interested in a section in the middle of the irradiation region, we can simply pick a small section of the Si, and apply periodic boundaries on the sides in  $x$  and  $y$  (i.e. let the defects move and interact over the boundary to the other side of the simulation cell). The size has to be clearly larger than the jump length or recombination radius, and large enough to contain a substantial amount of defects.



The surface is a perfect sink for defects, i.e. any defect which goes above  $z = 0$  vanishes from the system. The size inside the cell is assumed to be infinite (in reality it typically is  $\sim 1$  mm, large enough that we will never reach it with  $2.35 \text{ \AA}$  jumps in our simulations).

So the simulation geometry is as follows, in a 2D projection:





I slightly modified the algorithm above to simulate this; the additions are just the periodic boundaries and sink at the surface (note that in the exercise you need neither of these!).

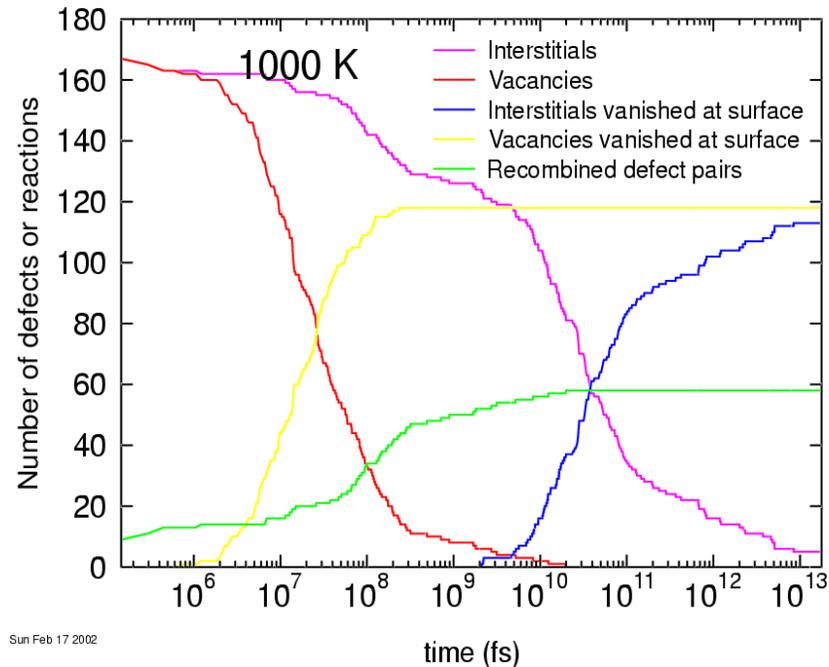
The atomic density in Si is  $0.050 \text{ atoms}/\text{\AA}^3$ . So if we choose the  $xy$  cell size as  $20 \text{ \AA}$ , and consider that 68 % of the defects will be within 1 standard deviation (now  $30 \text{ \AA}$ ) of the average, the relation between the simulated number of defects of each type  $N$  and the defect concentration  $\rho$  in the

central region will be

$$\rho = \frac{0.68N}{20^2 \times 30 \times 0.05} = 0.0000567N$$

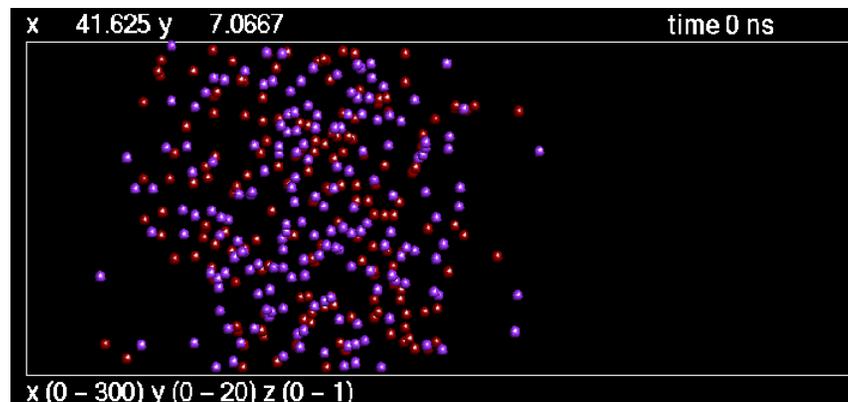
So to get a typical defect concentration of e.g. 1%, we need to have 176 defects of each type, i.e. 352 in total.

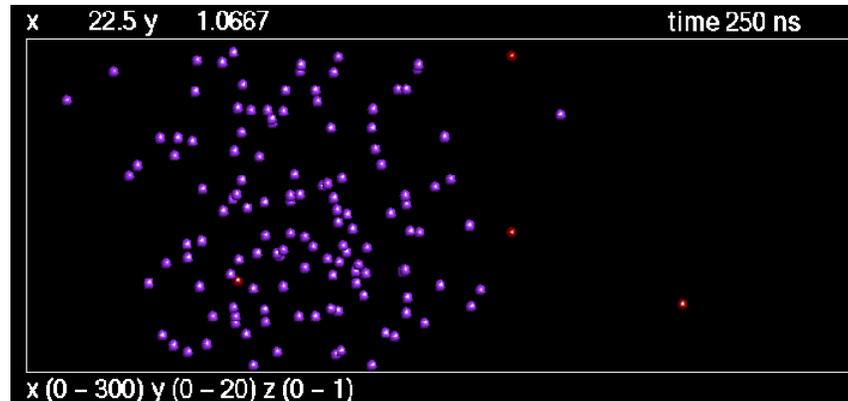
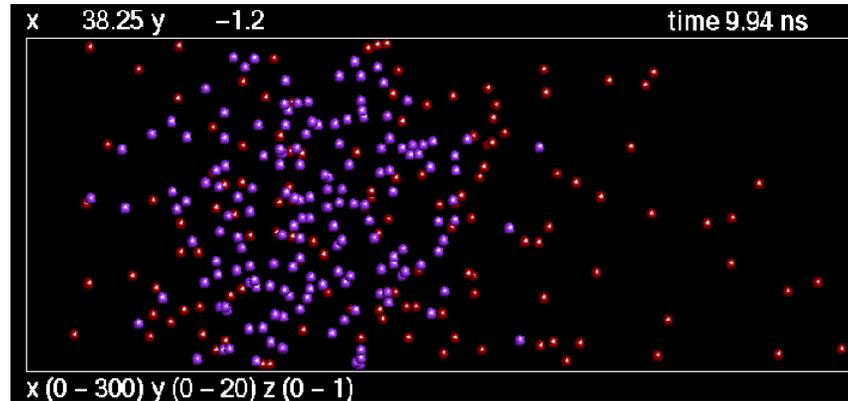
After running the simulation, we can plot the time dependence of the numbers of defects and reactions as follows. This is for 1000 K, a typical “furnace annealing” temperature:



So what happens is that there is almost immediately some recombination, as closeby vacancies and interstitials recombine. After that the more mobile vacancies tend to vanish at the surface, and keep on recombining. At about  $10^{10}$  fs the last vacancy is gone, the simulation speeds up significantly, and the interstitials start moving. In the very end, at about  $10^{13}$  fs (0.01 s), only a few interstitials remain.

Here is a sequence of picture illustrating what is going on initially: The red dots are vacancies, the purple ones interstitials. The plotting region is 0-20 Å in the  $x$  direction, 0-300 Å in the  $z$  direction (the labels in the figure are misleading). The surface  $z = 0$  is to the left.



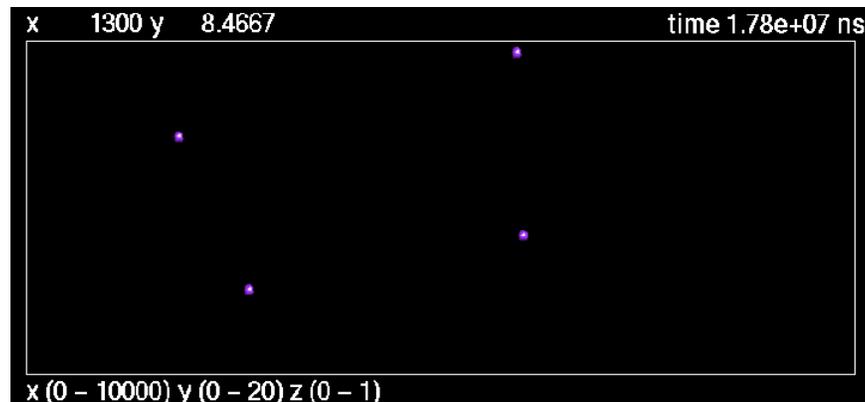


The interstitials do not move essentially at all in this phase, so what happens is just that the vacancies vanish by recombination and at the surface. But a few vacancies go deep into the bulk.

But on longer time scales, these vacancies have a chance to come back to the interstitial layer and recombine. This is what happens. Here is a plot of the state at  $1 \mu s$  (note that the  $z$  scale is now extended from 0 to 10000 Å):



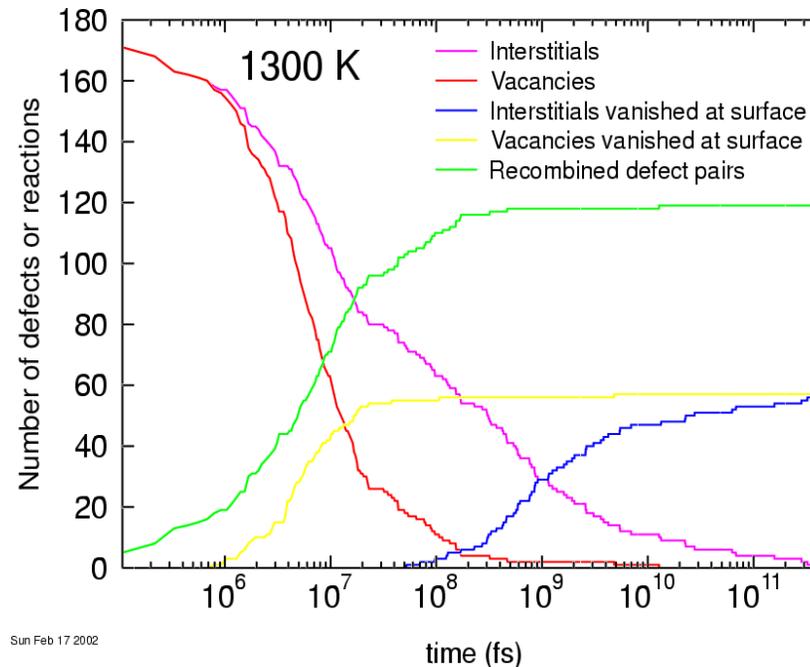
So the vacancies are indeed quite far from the interstitials, but from the time dependence plot we see that they do eventually recombine. Here is then the final state at almost  $2 \times 10^{13}$  fs = 0.02 s:



On even longer time scales, the interstitials would most probably eventually reach the surface. The total number of defect steps simulated in this run was about 56 million.

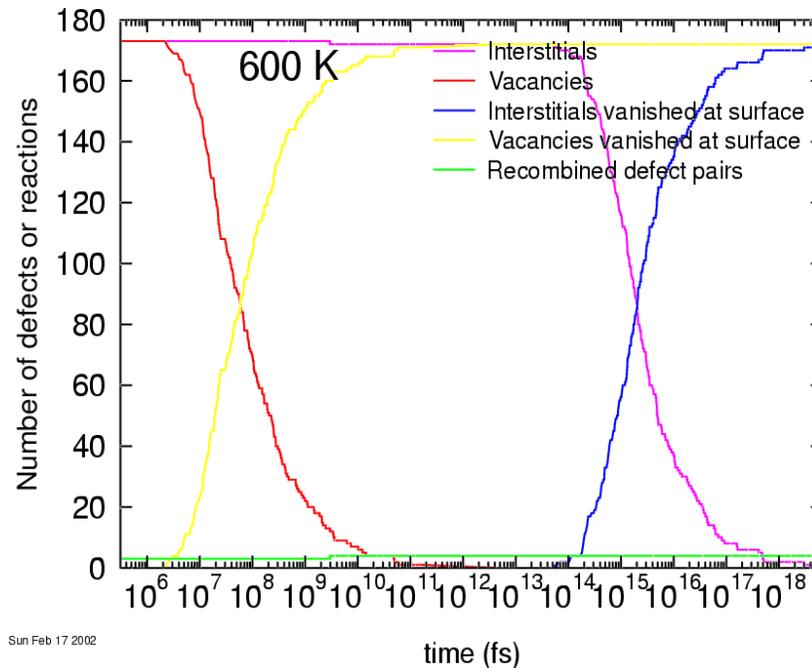


At higher temperatures, 1300 K (a typical rapid thermal anneal temperature), the picture changes somewhat because the interstitials and vacancies are mobile on comparable time scales. Hence the relative time scale difference on the number of i's and v's is considerably less:



The total time scale here is much less than at 1000 K, as expected for higher temperatures. In this case the simulation ended when all particles had vanished.

If we look at a clearly lower temperature, say 600 K, everything of course is slower still, and there is no interstitial mobility at all on the time scales when the vacancies move:



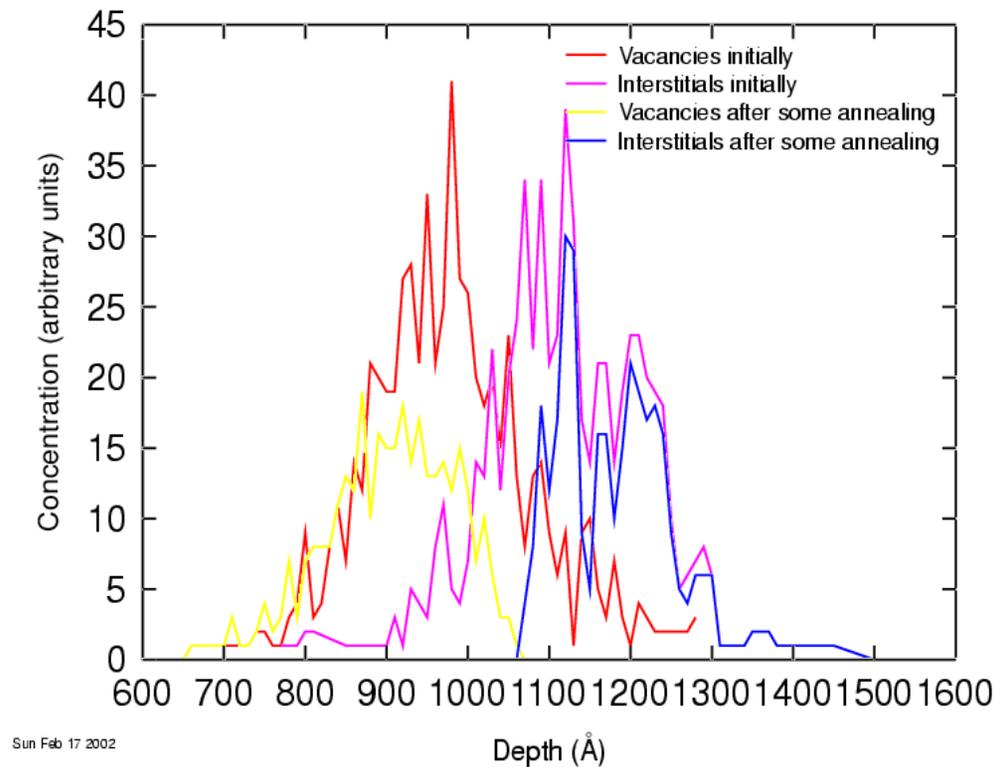
Sun Feb 17 2002

Note the huge difference in time scales here: the vacancies vanish completely in 0.16 ms, while the interstitials only start moving on time scales of seconds, and subsequently vanish on timescales of hours! This illustrates well the power of KMC to simulate widely disparate timescales.

There is also very little recombination now; apparently the recombination is significant primarily when the interstitials are mobile on time scales comparable to the vacancy. In additional tests as a function of temperature, I found that there was very little recombination even at 800 K, and only at temperatures close to 900 K and above did it become significant.

Now that we have seen the results, did it matter that the interstitials were 5 Å deeper in than the vacancies? Almost certainly not, since each step was 2.35 Å, and the number of steps taken very large, so the 5 Å difference probably got washed out completely.

But the difference could be of consequence if the difference was much larger than the step size and average number of steps before recombination. I tested this having mean ranges of 1000 Å for vacancies, and 1100 Å for interstitials, and standard deviations of 100 Å for both. The initial distributions still overlap significantly, but after some minor annealing, there is no overlap at all. So we have produced a defect zone with only vacancies, and another one with only interstitials:



This is the concept behind concept of a “vacancy implanter”, which actually has been built and may provide a solution to the TED problem mentioned above (not that this information belongs would belong to this course).

Note that in these examples, we still had a fairly small number of objects to study. If this were a serious study, one would of course have to repeat the simulations for different seed numbers

and larger system sizes to ensure that the non-physical simulation parameters do not affect the conclusions drawn.

And include the defect clustering reactions...

But still, the models used were not entirely unrealistic, and the qualitative results actually do correspond to reality.