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Principles of atomistic classical molecular dynamics computer simulations for non-metallic condensed matter

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Set of 3 talks

- Introduction to Molecular Dynamics for radiation effects in non-metallic systems
- Introduction to long time scale techniques with particular reference to non-metallic systems
- Applications..mainly oxides (MgO, ZnO, TiO₂) and spinels MgAl₂O₄, and inverse and partially inverse spinels

Landmarks in MD computer simulation

- I782 A. L. Lavoisier postulated that classical theory could be used to model chemical phenomena
- 1957 First MD simulations using hard spheres by Alder and Wainwright
- I960 MD simulations of radiation damage by Vineyard's group at Brookhaven
- I960 MD simulations of sputtering by Don Harrison
- 2012 Standard packages such as DLPOLY and LAMMPS are available for use.

The Classical Molecular Dynamics Method

Given a system of N interacting particles, the *i*th of which has mass m_i and position vector r_i , the system evolves by Newton's equations of motion

$$m_i rac{d^2 r_i}{dt^2} = F_i$$

where for non-dissipative systems

$$F_i = -
abla_{r_i} V(\mathbf{r}_1, \mathbf{r}_2, \mathbf{r}_{\mathrm{N}}).$$

and $V(r_1, r_2, ..., r_N)$ is a classical potential energy function. When there is no dissipation then the system is said to be a Hamiltonian system and can be formulated in another way.

The same method can also be used in Quantum MD. In this case the forces are determined from solving Schrödinger's equation.

The Verlet algorithm

$$\mathbf{r}(t+\delta t) = \mathbf{r}(t) + \mathbf{v}(t)\delta t + rac{1}{2}\mathbf{a}(t)\delta t^2 +$$
 $\mathbf{v}(t+\delta t) = \mathbf{v}(t) + \mathbf{a}(t)\delta t + rac{1}{2}\mathbf{a}'(t)\delta t^2 +$

$$\mathbf{a}'(t) = rac{\mathbf{a}(t+\delta t) - \mathbf{a}(t)}{\delta t} + O(\delta t)$$

giving

$$\mathrm{v}(t+\delta t) = \mathrm{v}(t) + rac{1}{2}(\mathrm{a}(t+\delta t)+\mathrm{a}(t))\delta t + O(\delta t^3)$$

The algorithm updates the position vectors, calculates the new accelerations from

$$\mathbf{a}(t+\delta t) = -\nabla V(\mathbf{r}[t+\delta t])/m,$$

then updates the velocities.

Thusonly 1 force evaluation per timestep and a local truncation error of $O(\delta t^3)$.

Hamiltonian Systems

Hamilton's principle : 'The motion of a system from time t_1 to t_2 is such that the line integral of the Lagrangian \mathcal{L} is an extremum i.e.

$$\delta\int_{t_1}^{t_2} \mathcal{L} dt = 0.$$

The Lagrangian \mathcal{L} is the difference between the KE and PE of the system. The Hamiltonian \mathcal{H} is given by

$$\mathcal{H} = \sum_{i=1}^{3N} \dot{q}^i p^i - \mathcal{L},$$

 $(r_1,...,r_N)=(q^1,...,q^{3N}), \ (m_1v_1...m_nv_N)=(p^1,...p^{3N}).$

With generalised co-ordinated (p,q,t),

$$\dot{q}^i = rac{\partial \mathcal{H}}{\partial p^i}, \quad -\dot{p}^i = rac{\partial \mathcal{H}}{\partial q^i}.$$

For modelling particle dynamics our Hamiltonians are of the form $\mathcal{H} \approx rac{1}{2}p^2 + V(q).$

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Some properties of Hamiltonian Systems

(1) In principle, if we integrate forward in time, we should be able to recover the initial state by integrating backwards in time.

(2) Defining $x = (q, p)^T$, $x(t) = T_M(t)x(0)$ where T_M is called the transfer matrix. A map of this kind is called sympletic iff the Jacobian M of the transformation T_M satisfies

 $M^T J M = J$ where $J = \begin{pmatrix} 0 & -I \\ -I & 0 \end{pmatrix}$.

Such maps preserve the area of phase space (Liouville's theorem). This is important because it means that trajectories that start off close remain close after the Hamiltonian system has evolved.

Radiation event MD simulations are inherently chaotic. Different computers can give different results for the trajectories after the initial stages of a simulation

Why symplectic integrators ?







Figure 2: Phase space plot (p_2, q_2) when $q_1 = 0$ for the system $H(q, p) = \frac{1}{2}(q_1^2 + q_2^2 + p_1^2 + p_2^2) + q_1^2 q_2 - \frac{1}{3}q_2^3$

Energy drift is a common problem in MD simulations that do not use the Verlet algorithm

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Units for use in the MD simulation

The time step δt typically ranges from 0.1 to 1.5 fs. (1 fs = 10^{-15} s)

A typical length scale is 1Å

The mass of an atom $m pprox Z imes 1.627 imes 10^{-27}$ kg

The potential function V has units of eV. Suitable units of force are eV/Å.

 $1 \text{ eV/Å} = 1.602 \text{ nN} (1.602 \times 10^{-19} \text{ eV} = 1 \text{ Joule})$

Thus we can use units of Å, fs and eV/Å in

$$m_i rac{d^2 \mathrm{r_i}}{\mathrm{dt}^2} = \mathrm{F_i}$$

if we scale the mass by replacing m_i with $rac{Z imes 1.627 imes 10^2}{1.602}$

Note a 1 fs time step means 10¹⁵ steps to simulate 1s of real time so MD simulations usually are restricted to ~ nanoseconds

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Initial and boundary conditions

- Bulk Radiation Event initiated by a neutron : Impart a given energy usually a few keV to an atom in a crystal and follow the evolution of the trajectory. Average over many such trajectories
- External Impact event (keV energies) : Impart energy to an atom above the surface of a crystal, directed towards the surface and follow the evolution (sputtering, crystal growth)
- Swift Heavy ion impact (GeV energies) : Set in motion atoms along an ion track and follow the evolution of the resulting cascade.
- Boundary Conditions : Periodic, Fixed or Free. Usually the simulation region is taken as a rectangular box.

Time step Control

$$\delta t = rac{lpha}{\sqrt{(lpha + eta * \gamma)}} ext{ fs.}$$

The time step depends on the parameter γ which is given by:

$$\gamma = E_{KE}^{max} + |E_{PE}^{max}|, \qquad (0.1)$$

where E_{KE}^{max} and E_{PE}^{max} is the maximum kinetic energy and potential energy of an atoms at time t. Typical values for α and β are 1.5 and 0.1 respectively.

Temperature control

(non-Hamiltonian)

1. Berendsen thermostat

The method of temperature control relies on the scaling of the velocity vectors at every time step with a factor λ

$$\lambda = \left[1 + \frac{\delta t}{\tau_T} \left(\frac{T_0}{T} - 1\right)\right]^{\frac{1}{2}}, \qquad (0.2)$$

in which T and T_0 are the actual and desired temperatures, δt is the time step of the integration algorithm and τ_T is a coupling parameter between the heat bath and the system. The system is brought towards the desired temperature at a rate determined by τ_T .

Temperature T is defined by $\sum m_i v_i^2 = 3 N k_B T$

Temperature control

2. Nosé-Hoover thermostat

The Nosé-Hoover method uses a modified equation of motion:

$$m_i \frac{d^2 \mathbf{r}_i}{dt^2} = \mathbf{F} - \zeta \frac{d \mathbf{r}_i}{dt}.$$
 (0.3)

The rate of change of the coefficient ζ is given by

$$rac{d\zeta}{dt} = rac{1}{Q} \left(\sum_{i}^{N} v_i^2 - 3Nk_B T_0
ight) \quad (-\zeta rac{d\zeta_1}{dt}), \quad (0.4)$$

where Q describes the strength of the coupling between the system and the heat bath.

There is a modified Hamiltonian from which the equations of motion can be derived.

Force Field Models

The Lennard-Jones potential acts pairwise

$$V(r) = 4\epsilon igg((rac{\pmb{\sigma}}{r})^{12} - (rac{\pmb{\sigma}}{r})^6 igg)$$

The force is zero when $r = 2^{\frac{1}{6}}\sigma$ and then $V = -\epsilon$. The quantities σ and ϵ are fitting parameters chosen to match the lattice constant a and cohesive energy uof the material. The bulk modulus *B* can also be found in terms of σ and ϵ . For an fcc lattice $u = -8.5\epsilon$, $a = 1.541\sigma$ and $B = \frac{75\epsilon}{\sigma^3}$. $V/4\epsilon$



element	Ne	Ar	Kr	Xe
ϵ (eV)	0.0031	0.0104	0.0140	0.0200
$\sigma(\AA^3)$	2.74	3.40	3.65	3.98
$r_0({ m extsf{A}})$ expt.	3.13	3.75	3.99	4.33
$r_0({ m extsf{A}})$ theory	2.99	3.71	3.98	4.34
$u_0(eV)$ expt.	-0.02	-0.08	-0.11	-0.17
$u_0(eV)$ theory	-0.027	-0.089	-0.12	-0.172
$B(10^9$ pascals) expt.	1.1	2.7	3.5	3.6
$B(10^9$ pascals) theory	1.81	3.18	3.46	3.81

Table 1: Values of the fitting constants for the rare gases

The Lennard-Jones Pair-potential



$$V=Z_AZ_Be^2rac{\exp(-r/a)}{4\pi\epsilon_0 r}$$

was used to determine the penetration depth of ions in solids. Here a is called the screening length. This is related to the Bohr radius a_0 . The origin of the ZBL potential

 $V = V_{nn} + V_{en} + V_{ee} + V_k + V_a$

 V_{nn} — electrostatic PE between nuclei

 V_{ee} — electrostatic PE between electron distributions V_{en} — electrostatic PE between each nucleus and the other electron distribution

 V_k — increase in the KE of the electrons in the overlap region due to Pauli exclusion (free electron gas model) V_a — increase in the exchange energy of these electrons

V(r) calculated for 522 representative ion pairs and the resulting data fit to a formula.

 $\chi_M(x) = 0.18175 \exp(-3.1998x) + 0.50986 \exp(-0.94229x)$

 $+0.28022 \exp(-0.4029x)+0.028171 \exp(-0.20162x)$



Fixed charge pairwise ionic potentials
- Used for MgO, spinels and bixbyite simulations

$$\begin{aligned}
& \left\{ \begin{array}{ll} ZBL & r_{ij} < r_{a}; \\ g(r_{ij}) = e^{(f_{1} + f_{2}r_{ij} + f_{3}r_{ij}^{2} + f_{4}r_{ij}^{3} + f_{5}r_{ij}^{4} + f_{6}r_{ij}^{5})} & r_{a} \leq r_{ij} < r_{b}; \\ g(r_{ij}) = e^{(f_{1} + f_{2}r_{ij} + f_{3}r_{ij}^{2} + f_{4}r_{ij}^{3} + f_{5}r_{ij}^{4} + f_{6}r_{ij}^{5})} & r_{b} \leq r_{ij} < r_{b}; \\ A_{ij} \exp(-\frac{r_{ij}}{p_{ij}}) - \frac{Cij}{r_{ij}^{6}} + V_{coul}(r_{ij}) & r_{b} \leq r_{ij} < r_{c}; \\ h(r_{ij}) \times (A_{ij} \exp(-\frac{r_{ij}}{p_{ij}}) - \frac{Cij}{r_{ij}^{6}}) + V_{coul}(r_{ij}) & r_{c} \leq r_{ij} < r_{0}; \\ V_{coul}(r_{ij}) & r_{ij} \geq r_{0}, \\ h(r_{ij}) = \begin{cases} 1 & r_{ij} < r_{c}; \\ \frac{1}{2}(1 + \cos \pi \frac{r_{ij} - r_{c}}{d}) & r_{c} \leq r_{ij} < r_{0}; \\ 0 & r_{ij} \geq r_{0}, \end{cases} \\ \text{Interpotential are remarkable good compared to DFT results for bulk materials} \end{cases}$$

Variable charge ionic potentials Pioneered for MD simulations by Rappé and Goddard and van Duin (ReaXFF) and Streitz and Mintmire data (Ref. 23) Ref. 15 and this work 12 Minimise Total QEq at each step 10 Ref 7 Energy (eV) 8-6-Oxygen $E_{QEq} = \sum_{i} E_i + \sum_{i} \sum_{j \neq i} E_{ij}^{elec}$ Charge (e) (a)-1 100 data (Ref. 23) Ref. 15 and this work lon self-energy: Ref. 13 Energy (eV) 09 05 05 Ref. 8 $E_i = E_i(0) + \chi_i^0 q_i + \frac{1}{2} J_i^0 q_i^2$ Ref. 12 Titanium 0 (b) -2 3 4 -1 0 2 1 (b) Charge (e) Electronegativity Hardness FIG. 2. Atomic self-energy of ion (a) O, (b) Ti as a function of charge Fixed charge : Ti^{qt} ; O^{qo} ; qt = +4; qo = -2; Variable charge : gt and go depend on the local environment.

Rappe, A.; Goddard, W. A. J. Phys. Chem. 1991, 95, 3358-3363 F.H Streitz and J. Mintmire Phys. Rev. B 50, 11996–12003 (1994) Halil et al PRB 73 165406 (2006) D. Raymand , A van Duin et al Surface Science 602 (2008) 1020–1031

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Other potentials...covalent materials

Tersoff type bond order potentials..Si, Ge, C, GaN, multicomponent Si-C-H (Brenner, Beardmore)

$$V(r_i) = \sum (f_R(r_{ij}) + b_{ij} f_A(r_{ij}))$$

Stillinger-Weber type 3-body potentials..Si, CdTe

$$V(\mathbf{r}_{i}) = \sum (V_{ij}(\mathbf{r}_{ij}) + \sum V_{ijk}(\mathbf{r}_{ij}, \mathbf{r}_{ik}, \mathbf{r}_{jk}))$$

If each atom were to interact with every other atom in the system the force evaluations would scale as N^2 for pair potentials. This is unacceptably slow.



neighbours (usually a small number relative to N),

i.e. force evaluations scale linearly with the number of atoms.

Parallelisation : Spatial decomposition and multiscale modelling

Length scales can be extended through the use of more and more processors



Here the force evaluations on atoms in each box are evaluated on separate processors. An atom in box 13 needs information from the 26 surrounding boxes. Data exchange is required so the communication time between processors needs to be small compared to the time of the force evaluations. Typically ~50,000 atoms per processor is optimal. So a one million atom simulation requires >~20 processors.

Coulomb sum evaluation

Coulomb sums lead to *conditionally* convergent series and are *long-ranged* e.g. ln(2.0) = 1 - 1/2 + 1/3 - 1/4 + 1/5 - 1/6 + 1/7 - 1/8 = 0.6931....

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we need to take ~20,000 terms to get 4 figure accuracy
Two methods commonly used:
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(1) Ewald summation for periodic systems (scales as N.log N)
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(2) Fast multipole method for non-periodic systems (Greengard and Rhoklin) (scales linearly with N)

You can also truncate the ionic potential. This is a relatively good approximation for systems that are charge neutral in the cut-off region ;

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e.g. ReaXFF truncates at 1 nm
The Fennel approximation does this smoothly
```

Length and time scales to be bridged in atomistic molecular dynamics (MD) simulations

Time scales to be bridged Integration time step ~ 1×10^{-15} s in an MD simulation On a modern computer with say 2000 atoms we can advance time by around 10 fs in 1 real second of computing time. 1 second would take 10^9 years.

Length scales to be bridged: 2000 atoms ~ 3nm x 3nm x 3nm 2m atoms ~ 30nm x 30nm x 30nm (Parallel computing)

Radiation damage phenomena

Dose rates maybe 1000's of dpa over a reactor lifetime so impossible using MD alone

Thin Film Growth

Rates are monolayers per second ~ time bridging a long way off with MD

Bridging Length Scales in atomistic simulations

 Use DFT calculations, system sizes ~ 100's of atoms to parameterise classical potentials for MD simulations (DFT-MD)

• Parallel Computing

- Solve Newton's laws of motion numerically with forces derived from the parameterised potentials
- Assuming 10²⁷ atoms per cubic metre, i.e. 10⁹ per cubic micron. With 10⁵ atoms per processor in a typical MD simulation you need 10⁴ processors to simulate atomistically 1 cubic micron of material.
- Embed an atomistic region in a continuum (MD-FE)

Atomistics to finite elements



- This extends the system size without the same increase in computational cost.
- The MD region is embedded in a FE mesh.
- Imaginary atoms (green and blue) make up the neighbours of real atoms.
- The first layer of elements overlaps with the imaginary atoms.

E. Mcgee, S.D. Kenny and R. Smith Int. J. Mater. Res. 98 430 (2007)

Communication FE to MD

- Linear interpolation is used to position imaginary atoms according to nodal displacements.
- An atom p with fractional coordinates (ξ_p, η_p, ζ_p) has displacements (u_p, v_p, w_p) .
- coordinates constant.
- This provides feedback from the FE

Communication MD to FE

0

0

- - I/3I/31/3
- Forces are present on imaginary atoms due to real atoms.
- The forces are assigned to nodes according to shape function values.
- The nodal force is then used in the dynamical FE update.
- FE calculations on one processor; spatial decomposition for the atomic system

$$F_{nde} = \sum_{i=1}^{n_a} N_{nde} \mid_i F_i$$

1/2

I/2

0

2

3

Simplest models due to Lindhard, Scharff and Shiott, also Firsov.

Implemented in MD easily by rescaling the positions and velocities at each time step or by the introduction of a damping coefficient (-gamma x velocity) extracted from the models.

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Analysis Tools

Defect Identification in crystallographic systems:

<u>Interstitials</u> : An atom that is greater than a distance r_{int} from a lattice site. Typically r_{int} is chosen as ~ one third of the nearest neighbour distance.

<u>Vacancy</u> : A lattice site that has no atom within a distance r_{int} .

q4 Parameter : A parameter based on evaluating the spherical harmonics $Y_{Im}(r_{ij})$ for each neighbouring atom j of i. Lechner and Dellago J. Chem Phys. 129 114707 (2008)

$$q_{lm}(i) = \frac{1}{N_b(i)} \sum_{j=1}^{N_b(i)} Y_{lm}(\mathbf{r}_{ij}).$$

$$q_{l}(i) = \sqrt{\frac{4\pi}{2l+1} \sum_{m=-l}^{l} |q_{lm}(i)|^{2}}.$$

Visualisation Tools

Lots of free software

Pov-Ray : <u>http://www.povray.org</u>/

PDB visualisers : <u>http://www.bernstein-plus-sons.com/</u> <u>software/rasmol/</u>

Write your own with vtk.

pdb file

HEAD	DER pKc =2.4	pKn =9.8	13-JUL-93					
	COMPND	glycine GLY N	1W = 57					
ATOM	I N GLY	i -1.476 0.2	32 0.252 1.00 0.00					
ATOM	2 CA GLY	I -0.012 0.2	96 0.348 1.00 0.00					
ATOM	3 C GLY	I 0.596 -0.6	52 -0.648 1.00 0.00					
ATOM	4 O GLY	I -0.124 -1.3	20 -1.368 1.00 0.00					
ATOM	5 OXT GLY	I I.916 -0.	760 -0.740 1.00 0.00					
ATOM	6 H3 GLY	I -1.736 -0.2	52 -0.592 1.00 0.00					
ATOM	7 HA2 GLY	I 0.292 0.0	20 1.364 1.00 0.00					
ATOM	8 HAI GLY	I 0.320 I.3	20 0.132 1.00 0.00					
ATOM	9 H9 GLY	I -1.636 -0.2	36 1.132 1.00 0.00					
ATOM	I0 HI GLY	-1.9 6 .	36 0.272 1.00 0.00					
	TER	II GLY	I					
END								

xyz file

8							
Ι	7.17	4.42	3.45	0.0000	-4.2208	-0.6967	
2	7.01	4.38	4.38	0.0000	-4.2208	0.3204	
3	6.27	4.40	3.09	0.0000	-4.2208	0.3740	
4	9.51	4.30	1.69	0.0000	-4.2208	-0.6906	
5	9.61	5.23	1.47	0.0000	-4.2208	0.3181	
6	8.74	4.29	2.27	0.0000	-4.2208	0.3830	
7	2.87	1.04	2.93	0.0000	-4.2208	0.3233	
8	0.93	1.34	2.54	0.0000	-4.2208	0.2552	

0.4 keV cascade snapshots

Defects in amorphous systems e.g. glasses

Three possible approaches : but more work required

- Use Voronoi tesselation to study defects in amorphous structures
- Investigate by use of a short range ordering parameter $c_{ij} = p_{ij}/p_{ij}^0 I$, where p_{ij} is the probability of finding atoms i and j as neighbours and p_{ij}^0 is the unirradiated probability
- Can also monitor the cascades by visualising the displaced atoms.

Other considerations not mentioned

- Optimisation algorithms
 - Conjugate gradient, steepest descents, quasi-Newton
- Potential construction
 - Fitting methods e.g. neural networks
- Constant pressure MD and implementation of constraints
- ab initio methods
 - use hellman-Feynman theorem to determine forces

Some Examples

Structure of spinel

Unit cell: 8 formula units of MgX_2O_4 (X= Al, Ga, In) Spinels can exhibit appreciable **disordering** of cations within their structures - site exchange

Defects in normal spinel, MgAl₂O₄

Mg split interstitial

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Example : 10 keV PKA cascade in magnesium aluminate spinel (fixed charge ionic potential)

Example : 10 keV PKA cascade in magnesium aluminate spinel (fixed charge ionic potential)

Diebold, Ulrich "The surface science of titanium dioxide" Surface Science Reports 48 pp. 53-229

Example: The oxidation of the TiO₂ rutile {110} surface (variable charge potential)

O dimer added to the trench

MD deposition of C_{60} onto Si{100} (2 x 1) at 600K (Tersoff-Brenner potential)

Question : What is physically unrealistic about this movie ? Answer : Unrealistic deposition rates

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Example : Particle moving in a 2-D potential field

deep red -- maxima light red -- minima

The system gets trapped in the basin around a minimum and transits to the next basin over a saddle point

V(x,y) = sin(2x) cos(xy) x₀ = 3π/4 y₀ = 4.0

Conclusions

MD simulations can now be run routinely on systems containing millions of atoms

Potentials are now so refined that they can model both teh close interactions and the chemical bonding with reasonable accuracy

The length scale problem is almost solved by using parallel computing and embedding in a finite element region

The time scale problem is not yet solved but will be effectively solved within the next decade (see next lecture)

For a 2×2 system where

$$M=egin{pmatrix} a & b \ c & d \end{pmatrix}$$

The condition for sympecticity $M^T J M = J$ gives

$$\begin{pmatrix} a & c \\ b & d \end{pmatrix} \begin{pmatrix} 0 & 1 \\ -1 & 0 \end{pmatrix} \begin{pmatrix} a & b \\ c & d \end{pmatrix} = \begin{pmatrix} 0 & 1 \\ -1 & 0 \end{pmatrix}$$

i.e.

$$egin{pmatrix} 0 & ad-bc \ bc-ad & 0 \end{pmatrix} = egin{pmatrix} 0 & 1 \ -1 & 0 \end{pmatrix}$$

i.e. det M = 1.

What is special about the Verlet algorithm

Consider the problem of simple harmonic motion. In Hamiltonian form this can be written

$${\cal H}=rac{1}{2}(p^2+k^2q^2) \hspace{0.5cm} \dot{q}=p \hspace{0.5cm} \dot{p}=-k^2q^2$$

A second order Runge-Kutta method could be given by

$$egin{aligned} k_1 &= f(t_n, y_n), \; k_2 &= f(t_n + h, y_n + hk_1), \ y_{n+1} &= y_n + f(t_n + h, y_n + rac{1}{2}h(k_1 + k_2)) \end{aligned}$$

Applying this method to the SHM problem gives

$$egin{pmatrix} q_{n+1} \ p_{n+1} \end{pmatrix} = egin{pmatrix} 1 - rac{1}{2}(hk)^2 & -hk^2 \ -h & 1 - rac{1}{2}(hk)^2 \end{pmatrix} egin{pmatrix} q_n \ p_n \end{pmatrix}$$

whereas the Verlet algorithm gives

$$egin{pmatrix} q_{n+1} \ p_{n+1} \end{pmatrix} = egin{pmatrix} 1 - rac{1}{2}(hk)^2 & h \ -hk^2(1 + rac{1}{2}(hk)^2) & 1 - rac{1}{2}(hk)^2 \end{pmatrix} egin{pmatrix} q_n \ p_n \end{pmatrix}$$

For the R-K case det $M=1+rac{1}{4}(hk)^4$

For the Verlet case det M = 1