

A Resource Letter CSSMD-1 Computer Simulation Studies by the Method of Molecular Dynamics

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In this letter we present a comprehensive bibliography on computer simulation studies by the method of Molecular Dynamics. The bibliography includes references to relevant literature published up to mid 1973, starting from the first paper of Alder and Wainwright, published in 1957. The procedure of the method of Molecular Dynamics, the main fields of study in which it has been used, its limitations and how these have been overcome in some cases are also discussed. We hope this resource letter would be of help to research workers, particularly to students and others who might wish to start computer simulation studies by using the Molecular Dynamics method.

Apresentamos, neste trabalho, extensa bibliografia sobre estudos de simulação em computador pelo método da Dinâmica Molecular. A bibliografia inclui referências a literatura relevante publicada até meados de 1973, começando pelo primeiro trabalho de Adler e Wainwright, publicado em 1957. O desenvolvimento do método da Dinâmica Molecular, os principais campos de trabalho em que tem sido empregado, as suas limitações e como têm elas sido superadas, são aqui discutidos. Esperamos que este trabalho seja de valia aos pesquisadores e, particularmente, aos estudantes e outros que pretendam trabalhar em estudos de simulação em computador, empregando o método da Dinâmica Molecular.

The Molecular Dynamics Method

The first paper on the Molecular Dynamics method was written by Alder and Wainwright¹. The method was designed to study molecular dynamic motion (hence the name Molecular Dynamics (MD)) by solving exactly the simultaneous classical equations of motion of several hundred particles by means of fast electronic computers. The method has been used to study non-equilibrium as well as equilibrium properties of a system. It may be mentioned that the Monte Carlo method of computer simulation studies provides information only on equilibrium properties.

The MD method owes its origin to the advent of electronic computers which could be used to study the many-body which cannot be solved

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analytically. To follow in detail the motion of a limited number of molecules, one must equate the instantaneous force on a molecule, due to all the others located at known positions, to its mass times its acceleration, and then solve all the simultaneous equations so obtained to find the trajectories of the molecules. However, it is a formidable task to obtain an analytic solution even for a three body system. Since all real physical systems are many body systems consisting of a very large number of particles, one has to study the mutual interactions of a large number of molecules, in order to obtain information on the thermodynamic, transport and structural behaviour of the system. An exception might be extremely rarified gases which could, perhaps, be treated as ideal gases whose molecules may be regarded as non-interacting with one another. It is in this context that the relevance and utility of the MD method should be evaluated. Given a law of intermolecular force, it is possible to trace out, with the aid of a computer, the molecular trajectories for a limited number of molecules and thus by-pass the insurmountable difficulties of finding an analytical solution.

The main features of MD computer simulation studies (or 'experiments') are:

(a) The systems are finite, the numbers of particles (N) usually being ≤ 1000 :

(b) The interaction potential is assumed to be known and treated pairwise additive, i.e.

$$\phi(1, \dots, N) = \sum_{i>j=1}^N \phi(r_{ij}); \quad (1)$$

(c) The range r , of the pair potential $\phi(r)$ is assumed to be finite. i.e. $r > r_c$, $\phi(r) = 0$;

(d) The classical equations of motion,

$$m a_i = m \frac{dV_i}{dt} = - \sum_{\substack{j=1 \\ i \neq j}}^N \frac{\partial}{\partial r_i} \phi(r_{ij}), \quad (2)$$

with

$$V_i = \frac{dx_i}{dt}, \quad (3)$$

are solved by finite difference techniques with time steps Δt between 10^{-14} and 10^{-15} secs. This means that knowing the force on the i 'th molecule

at a given instant of time. the new position of this molecule after a time increment Δt is computed. Several different algorithms have been used. The simplest which is in common use is

$$\mathbf{r}_i(t + \Delta t) = -\mathbf{r}_i(t - \Delta t) + 2\mathbf{r}_i(t) + \mathbf{a}_i(t)\Delta t^2. \quad (4)$$

The method in which the force summation on the right hand side of equation (2) is evaluated directly – requiring $(N - 1)$ additions – will be called the original MD method, since a new method has recently been proposed (Ref. 388) which avoids this summation for the long range forces.

(e) From the new positions and velocities of molecules, the potential acceleration and force experienced by each molecule, in the new configuration, are again found and the entire process repeated, timestep by timestep, to study the evolution of the system in time as well as space;

(f) The positions, velocities, accelerations and other relevant informations are stored on tapes for subsequent analysis of the results.

The Main Fields of Study

The literature on MD computer simulation studies, already very large, is increasing rapidly and the trend is bound to continue in view of the availability of bigger and faster computers and techniques to overcome the limitations (to be discussed later) from which the MD method suffers. Some of the major fields of studies investigated by this method are*:

(I) Structural and thermodynamic properties of mostly simple monatomic liquids which obey the Lennard-Jones (LJ) potential

$$\phi(r_{ij}) = \epsilon \left[\left(\frac{\sigma}{r_{ij}} \right)^{12} - \left(\frac{\sigma}{r_{ij}} \right)^6 \right], \quad (5)$$

where σ has dimensions of distance and ϵ those of energy (Refs. 36, 88, 121, 123, 159, 193, 197, 198, 202, 207, 238, 239, 243, 246, 249, 253, 254, 259, 262, 301, 303 and 364).

(II) Diatomic liquids (Refs. 120, 368), ionic liquids (Refs. 245, 256, 305, 325), liquid metals (Refs. 67, 127, 165, 369), and water (Refs. 242, 309, 310, 353 – 361).

(III) Velocity autocorrelation function, diffusion coefficients and liquid structures (Refs. 36, 37, 93, 176, 195, 205, 249, 259, 261, 301, 302, 303, 370).

*Some references included in the bibliography are given here for each field of study.

- (IV) Time correlation functions (Refs. 199, 204, 221, 265).
- (V) Free-path distributions (Refs. 51, 122).
- (VI) Binary mixtures (Refs. 34, 210, 240, 253, 254, 291).
- (VII) Studies of gases (Refs. 130, 247, 304, 320, 363).
- (VIII) Liquid-solid phase transition (Refs. 161, 299, 312, 318).
- (IX) Solid-liquid phase transition (Refs. 95, 129, 206, 237, 241, 251, 298, 317, 367, 372, 390).
- (X) Surface properties of crystals (Ref. 164); lattice dynamics of solids (Ref. 167).
- (XI) Radiation damage in crystals (Refs. 12, 30, 371).
- (XII) Point defects and vacancy motion (Refs. 153, 196, 200, 263, 300).
- (XIII) Solids under shockwave compression (Refs. 78, 319, 365).
- (XIV) Neutron scattering (Ref. 6, 68); X-ray scattering (Ref. 124).
- (XV) Properties and phase transitions of elastic spheres (Refs. 1, 5, 11, 34, 35, 51, 128, 163, 195, 236, 260, 263, 264, 266), discs (Refs. 19, 26, 90, 128), squares (Refs. 308, 311, 314, 373).
- (XVI) Ground-state properties of quantum systems (Ref. 94).
- (XVII) Magnetic systems (Ref. 188).
- (XVIII) Electric dipoles (Refs. 91, 113, 160, 244).
- (XIX) Time behaviour of harmonic and anharmonic oscillators (Refs. 189, 190).
- (XX) Liquid structure and light scattering (Refs. 198, 366, 374).
- (XXI) Molecular dynamics as a test for intermolecular potentials (Ref. 316).

The Limitations

The core capacity and speed of computers inevitably limited the application of the MD method to finite systems usually consisting of, as already mentioned, $N \leq 1000$ molecules.

The bottleneck in the original MD method is the calculation of the forces on all the particles. To find the force on each particle requires the summation of contributions from each of the other $(N-1)$ particles in the system, thus a total of $\sim N^2$ computer operations is required to find the force on all N particles. This work may be reduced if the potential of interaction is only of short range by limiting the force contributions to nearby particles ($r < r_c$). Even so the largest system reported using the original MD method is that of Schofield (Ref. 370) on the study of the liquid state obtained with a system of 4,000 particles.

The finiteness of the system also influenced the choice of the substances and the problems which have been investigated by the MD method. The choice of the substances whose interaction can be described in terms of the LJ potential is made partly because the interaction of a molecule with other molecules beyond a certain region can be ignored and, therefore, in effect, a molecule interacts only with a limited number of molecules in a given region surrounding it. Thus, the finiteness of the system is not too restrictive in the study of such substances. However, the original MD method has been used to study ionic substances also, see e.g., Woodcock (Ref. 245), Woodcock et al. (Ref. 325) and Rahman et al. (Ref. 305). The number of particles included in the simulations of such substances is typically only 64 or 216. Since to study the phase transition and the coexistence of both the phase of a substance, a relatively large number of particles, $N \approx 10^4$ is considered desirable (Ref. 7), systems having $N \leq 10^3$ are obviously not suitable to study phase transitions in three dimensions. Thus, the finite size of the system in the MD method is restrictive of the choice of problems also.

The Modified Method

The MD method has recently been modified by Hockney *et al.* (Ref. 388) to make it applicable even to those systems in which long range interactions must be studied. In the modified method, the long range electrostatic potential in, e.g., an ionic system is found by solving Poisson's equation for the given charge configuration on a spatial finite-difference mesh.

Short range force contributions, from nearby particles only, are then added in the usual way. This new Particle-Particle/Particle-Mesh (PPPM) method avoids the need to sum force contributions from all other particles in the system. The number of computer operations required to calculate the long range forces is proportional to N (as compared with N^2 for the original method) and consequently large systems with 10,000 particles can be simulated. Although the initial work has been done in two-dimensions the method generalises to three dimensions and is potentially capable of handling larger systems with long range forces that are of arbitrary shape.

The Bibliography

The references in the bibliography are arranged in the chronological order to appreciate how the use of the MD method for computer simulation studies has been increasing during the last fifteen years or so. All relevant references that came to our notice have been included in the bibliography. However, it is possible that some references might have been omitted. We would very much appreciate if any such references are brought to our notice. To make the bibliography more useful, we have included in it some references whose results are akin to or have a bearing on those of the MD method. The MD references can be easily distinguished by the letters MD which generally accompany their serial numbers in the bibliography.

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