Dynamic and Stochastic Properties of Molecular Systems: From Simple Liquids to Enzymes

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Abstract. Molecular dynamics method (MDM) supplies to the solution of fundamental contradiction between macroscopic irreversibility and microscopic reversibility with data which help to reveal the origin of stochastization in many-particle systems. The relation between dynamic memory time t_m , fluctuation of energy dE and K -entropy (Lyapunov exponent) is treated. MDM is a method which retains Newtonian dynamics only at the times less than t_m and carries out a statistical averaging over initial conditions along the trajectory run. Meaning of t_m for real systems is related to the quantum uncertainty, which is always finite for any classical system and influence upon particle trajectories in a coarse-graining manner. Relaxation of kinetic energy to equilibrium state was studied by MDM for non-equilibrium strongly coupled plasmas. Two stages of relaxation were observed: initial fast non-Boltzmann oscillatory stage and further relatively slow Boltzmann relaxation. Violation of the microscopic reversibility principle in some enzymatic reactions is discussed.

Monte Carlo method is referred to stochastic methods of molecular simulation whereas molecular dynamics method (MDM) is usually called a dynamic method. The objective of the present paper is to show that MDM possesses both dynamic and stochastic features. Moreover if MDM had no hidden stochastic features MDM would not probably be able to achieve well-known successive results. Another objective is to present examples of MDM simulation of non-equilibrium relaxation when stochastic features influence the dynamics.

The topic is related to the occurrence of the irreversibility in the case of the classical molecular systems which has been discussing since Boltzmann-Zermelo debate. The present state was given at the round table "Microscopic origin of macroscopic irreversibility" at the XX International conference on statistical physics (Paris, 1998) [1, 2], see also [3].

1 Molecular Dynamics Method

The idea of MDM is very simple: all possible classical systems and media are simulated by a set of N moving atoms and/or molecules, which interact with each other (e.g., see [4–11]). The numerical integration of the corresponding system of Newton equations

$$m_i \frac{d\mathbf{v}_i(t)}{dt} = \mathbf{F}_i[\mathbf{r}(t)], \quad \frac{d\mathbf{r}_i(t)}{dt} = \mathbf{v}_i(t) \quad (1)$$

results in determination of the trajectories of all particles $\{\mathbf{r}, \mathbf{v}\}$. Here, m_i , $\mathbf{v}_i$, $\mathbf{r}_i$, and $\mathbf{F}_i$ are the mass, velocity, and coordinate of the i th particle and the force acting on this particle, respectively ($i = 1, \dots, N$); the $\mathbf{v}_i$ and $\mathbf{r}_i$ values explicitly depend only on time t ; $\mathbf{F}_i$ depends only on the coordinates of particles; $\mathbf{r}(t)$ is the set of the coordinates of all particles, $\mathbf{r}(t) = \{\mathbf{r}_1(t), \mathbf{r}_2(t), \dots, \mathbf{r}_N(t)\}$; $\mathbf{v}(t)$ is defined similarly; and

$$\mathbf{F}_i = -\frac{\partial}{\partial \mathbf{r}_i(t)} U(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N), \quad (2)$$

where U is the potential energy. Function U (forces $\mathbf{F}$) is assumed to be given in MDM. The total energy E of the system is the sum of the kinetic T and potential U energies,

$$E = T + U, \quad T = \sum_{i=1}^N \frac{mv_i^2}{2} \quad (3)$$

Set (1) is exponentially unstable for a system of more than two particles (e.g., see [3–15]). The parameter that determines the degree of instability, that is, the rate of divergence of initially close phase trajectories, is Lyapunov exponent or K -entropy K . It can be determined by several ways. As example for a given U function and particles of the same mass m and for identical initial conditions corresponding to the k th point on an equilibrium molecular-dynamical trajectory, solutions $\{\mathbf{r}(t), \mathbf{v}(t)\}$ to system (1) are found in steps Δt and trajectories $\{\mathbf{r}'(t), \mathbf{v}'(t)\}$ are calculated in steps $\Delta t'$. Averaged differences of the coordinates (velocities) of the first and second trajectories are determined at coinciding time moments,

$$\langle \Delta v^2(t) \rangle = \frac{1}{NI} \sum_{j,k}^{N,I} (v_{jk}(t) - v'_{jk}(t))^2, \quad (4)$$

$$\langle \Delta r^2(t) \rangle = \frac{1}{NI} \sum_{j,k}^{N,I} (r_{jk}(t) - r'_{jk}(t))^2, \quad (5)$$

To improve accuracy, averaging over $k = 1, \dots, I$ is also performed. In some transient time t_l the differences become exponentially increasing with the same

value of K ,

$$\begin{aligned}\langle \Delta v^2(t) \rangle &= A \exp(Kt), \\ \langle \Delta r^2(t) \rangle &= B \exp(Kt) \\ \text{at } t_l < t < t_m.\end{aligned}\tag{6}$$

The values of A and B are determined by the difference of Δt and $\Delta t'$. An example for the three-dimensional Lennard-Jones system is given in Fig. 1. We use reduced units in which $m = \epsilon = \sigma = 1$, and time is measured in $(m\sigma^2/\epsilon)^{1/2}$ units.

Fig. 1. Normalized averaged differences of velocities Δv^2 and coordinates Δr^2 at coinciding time moments along two trajectories calculated for identical initial conditions in steps $\Delta t = 0.001$ and $\Delta t' = 0.0001$; L is the calculation cell edge length, $N = 64$, $r = 0.5$, and $T = 0.44$.

The exponential increase of $\langle \Delta v^2(t) \rangle$ is limited by the finite value of the thermal velocity of particles. Thus after the time t'_m

$$t'_m \approx K^{-1} \ln(6kT/Am), \tag{7}$$

where T is the temperature, saturation is reached. t'_m is a dynamic memory time [14–17]. For $t > t'_m$

$$\langle \Delta v^2(t) \rangle = 2 \langle v^2 \rangle = 6kT/m, \tag{8}$$

$$\langle \Delta r^2(t) \rangle = 6D(t - t'_m) + \langle \Delta r^2(t'_m) \rangle, \tag{9}$$

where $3kT/m$ is the square of thermal velocity v_T and D is the diffusion coefficient. Estimates show that $\langle \Delta r^2(t_m) \rangle = r_{av}$, where $r_{av} = (\sqrt{2}n\sigma)^{-1}$ is the mean path of particles between collisions.

The dynamic memory times are determined by calculating at the same Δt value and different $\Delta t'$ values of $\Delta t/2$, $\Delta t/5$, $\Delta t/10$, etc. The limiting value when $\Delta t'/\Delta t \rightarrow 0$ is the dynamic memory time t_m for a given system and the selected numerical integration step Δt [14, 15]. During numerical integration, the system completely “forgets” its initial conditions in time t_m , and the calculated molecular-dynamical trajectory completely ceases to correlate with the initial hypothetical Newtonian trajectory. In other words it determines the time interval during which the behavior of a dynamic system can be predicted from initial conditions and deterministic equations of motion [16, 18].

The calculated dependencies of Kt_m on the numerical integration step Δt can be presented in the form

$$Kt_m = -n \ln(\Delta t) + \text{const}, \quad (10)$$

where n is determined by the order of accuracy of the numerical integration scheme, or, in another form,

$$K(t_{m1} - t_{m2}) = n \ln(\Delta t_2/\Delta t_1), \quad (11)$$

where t_{m1} and t_{m2} are the dynamic memory times for the steps Δt_1 and Δt_2 , respectively. This result does not depend on either temperature, density, or the special features of the system under study [14, 15].

Because of the approximate character of numerical integration, energy E [Eq. (3)] is constant only in average. The E value fluctuates about the average value from step to step, and the trajectory obtained in molecular dynamics calculations does not lie on the $E = \text{const}$ surface, in contrast to exact solutions to Newton Eqs. (1). This trajectory is situated in some layer of thickness $\Delta E > 0$ near the $E = \text{const}$ surface [7, 8]. The value $\langle \Delta E^2 \rangle \sim \Delta t^n$ depends on the accuracy and the scheme of numerical integration [7, 8, 22–25]. Therefore

$$Kt_m = -\ln(\langle \Delta E^2 \rangle) + \text{const} \quad (12)$$

Equation (12) relates the K -entropy and the dynamic memory time to the noise level in the dynamic system. This equation corresponds to the concepts developed in [16, 18].

It follows from (10)–(12) that t_m grows no faster than logarithmically as the accuracy of numerical integration increases. The available computation facilities allow ΔE to be decreased by 5 orders of magnitude even with the use of refined numerical schemes [23–25]. This would only increase t_m two times. Estimates of dynamic memory times showed that, in real systems, t_m lies in the picosecond range. It means that t_m is much less than MDM run. So MDM is a method which retains Newtonian dynamics only at the times less than t_m and carries out a statistical averaging over initial conditions along the trajectory run.

The K -values were calculated by MDM for systems of neutral particles [3, 7–11, ?, 20], two-component [15] and one-component [17] plasmas and primitive polymer model [21]. The values of K turn out to be the same for both velocities and coordinates deviations. It is also seen that the K values for electrons and

ions are close to each other at the initial stage of divergence. At $t = t_{me}$ the quantity $\langle \Delta v^2(t) \rangle$ for electrons reaches its saturation value and, therefore, at $t > t_{me}$ only ion trajectories continue to diverge exponentially with another value of K -entropy depending on M/m as $K_i \sim (M/m)^{-1/2}$. The ratio t_{me}/t_{mi} is a fixed value. The dependence of t_{mi} on the electron-ion mass ratio also fits the square root law.

System of 10 polymer molecules with atom-atom interaction potential and periodic boundary conditions was studied in [21]. Each model molecule consisted of 6 atoms with constant interatomic distances and variable angles ϕ between links. Divergence of velocities $\Delta v^2(t)$ and coordinates $\Delta r^2(t)$ for both atoms and molecule center-of-masses as well as angles $\Delta \phi^2(t)$ were calculated. All the five dependencies follow the exponential law before saturation. All the five exponents turned out to be equal to each other, as for electrons and ions in plasmas. One can expect that it is a general conclusion for systems with different degrees of freedom.

2 Stochasticity of dynamic systems

Kravtsov et al. [16, 18] considered the measuring noise, fluctuation forces and uncertainty in knowledge of differential deterministic equations of the system as the reasons why t_m has a finite value. It is a characteristic of a simulation model in [7, 14, 15, 17]. The time t_m was related to the concept of quasi-classical trajectory, which takes into account small but finite quantum effects in classical systems: broadening of particle wave packets and diffraction effects at scattering [14, 15, 26, 27], to weak inelastic processes [18]. Quasi-classical trajectories themselves are irreversible. The intrinsic irreversibility in quantum mechanics originates from the measurement procedure which is probabilistic by definition.

Our premise coincide with the Karl Popper's conviction foundation stone that "nontrivial probabilistic conclusions can only be derived (and thus explained) with the help of probabilistic premises" [28]. The probabilistic premise we use is the quantum nature of any motion which is used to be considered as a deterministic classical one. The idea was inspired by an old remark of John von Neumann [29] and Landau [30] that any irreversibility might be related to the probabilistic character of measurement procedure in quantum mechanics.

Estimates of dynamic memory times were obtained for molecular dynamics numerical schemes. Since t_m values very weakly (logarithmically) depend on the noise level, it allowed us to extend qualitative conclusions to real systems of atoms, in which the finiteness of the dynamic memory time is caused by quantum uncertainty.

Though the primary source of the stochastic noise is probabilistic character of measurement procedure there are other factors which remarkably increase the noise value and permit to forget about quantum uncertainty at simulation. For example it is water molecule background that creates the stochastic noise in electrolytes. One is able to add Langevin forces into (1) and apply MDM to study their influence on dynamic properties of Coulomb system [31]. The dependence

of the dynamic memory time on the value of Langevin force is presented in Fig. 2. It is seen that collisions of ions with water molecules does not change essentially the value of t_m .

Fig. 2. Dynamic memory time for different values of Langevin force. The dashed line corresponds the level of the Langevin force which acts on the ions in the water solution.

3 Boltzmann and Non-Boltzmann Relaxation

Boltzmann equation is a fundamental equation of kinetic theory of gases; there are numerous attempts to modify the equation and extend it to dense media as well [32, 33]. Kinetic theory of gases deals only with probabilities of collision results. It is an initial assumption at the derivation of Boltzmann equation. Another fundamental assumption is Stosszahlansatz, which means that molecules are statistically independent. Molecular chaos hypothesis is a base of the kinetic theory, i.e. it is implied that molecule motion is stochastized. However it is apparent that dynamic motion precedes to stochastic processes [13, 32, 33]. It is supposed that dynamic motion governed by intermolecular interactions defines the values of collision cross-sections but does not influence time dependence of kinetic processes. One can expect that Boltzmann description of kinetic processes is valid only for the times greater than t_m .

MDM can be a powerful tool for studying non-Boltzmann relaxation phenomena in more or less dense media. Some non-equilibrium processes have been already studied with MDM for example in [14, 19, 34–38].

MDM was applied in [39] to the study of electron and ion kinetic energy relaxation in strongly coupled plasmas. Two-component fully ionized system of $2N$ single-charged particles with masses m (electrons) and M (ions) was

considered. It is assumed that the particles of the same charge interact via the Coulomb potential, whereas the interaction between particles with different charges was described by the effective pair potential (“pseudo-potential”). The nonideality was characterized by a parameter $\gamma = e^2 n^{-1/3} / kT$, where $n = n_e + n_i$ is the total density of charged particles. The values of γ were taken in the interval from 0.2 to 3. The details of the plasma model and numerical integration scheme are presented in [15].

The following procedure was used to prepare the ensemble of nonequilibrium plasma states. Equilibrium trajectory was generated by MD for a given value of γ . Then a set of $I = 50 - 200$ statistically independent configurations were taken from this run with the velocities of electrons and ions dropped to zero. Thus the ensemble of initial states of nonequilibrium plasma was obtained. MD simulations were carried out for every of these initial states and the results were averaged over the ensemble.

An example of relaxation of average kinetic energy $T(t) = \frac{1}{NI} \sum_{j,k}^{N,I} v_{jk}^2(t)$ is presented in Fig. 3a for the total relaxation period. The values of T for both electrons and ions are normalized by the final equilibrium value. The nonideality parameter γ_f in final equilibrium state differs from initial γ value. The time is measured in periods of plasma oscillations $\tau_e = 2\pi/\Omega_e$. Fig. 3a reveals Boltzmann character for time $t > 5\tau_e$. It is evident from the insertion where the difference between the electron and ion kinetic energies is presented in the semi-logarithmic scale. The character of this long time relaxation agrees with earlier results [34, 36].

Fig. 3. The kinetic energy for electrons (1), ions (2) and average value (3): a) at Boltzmann relaxation stage; b) for times less than the dynamic memory time. The equilibrium dynamic memory time is given by a vertical arrow. $\gamma = 1$, $\gamma_f = 3.3$, $M/m = 100$, $2N = 200$.

At the times less than $0.1\tau_e$ both electron and ion kinetic energies increase according to the quadratic fit (Fig. 3b). Then the electron kinetic energy passes through the maximum and undergoes several oscillations damping at $t \approx t_m$ while the ion kinetic energy increases monotonously. The possibility of two stages of relaxation was noted in [36].

The relative importance of non-Boltzmann relaxation stage for different non-ideality parameters can be derived from Fig. 3. It is seen (as an example from the velocity autocorrelation function decay time) that it decreases with decrease of plasma nonideality. The calculation shows as well that the oscillatory character of non-Boltzmann relaxation vanishes when the nonideality parameter becomes less than $\gamma = 0.5$.

Fig. 4. γ -dependencies of various electron relaxation times. Crosses are dynamic memory time t_m , asterisks — inverse Lyapunov exponent, open (filled) circles correspond the values of 0.1 (e^{-1}) of normalized electron velocity autocorrelation function, triangles (reverse triangles) are the inverse frequencies corresponding to the minimum (maximum) of dynamic structure factor. Curve and strait line are drawn in order to guide the eye. $M/m = 100$, $2N = 200$.

Another example of a particular relaxation process is related to arising of irreversibility in the case of enzyme catalysis. Microscopic reversibility principle is a fundamental principle of physical and chemical kinetics. In particular it means that all intermediate states coincide for forward and backward chemical reactions. However, Vinogradov [40] obtained experimental evidence for different pathways for direct and reverse enzymatic reactions in the case of hydrolysis and synthesis of ATP and some other mitochondrial molecular machines and supposed that "the one-way traffic" principle is realized at the level of a single enzyme.

Since microscopic reversibility principle follows from the time reversibility of fundamental dynamic equations, the occurrence of the irreversibility in the case of enzyme catalysis might be similar to the case of the classical molecular systems. The latter problem has been existing as intermediate between physics and philosophy. Hypothesis [40] switches it to experiment and applied science.

If there are two pathways along the hypersurface of potential energy between initial and final states there should be at least two bifurcation points. It is not Maxwell demon but Lyapunov instability, stochastic terms and asymmetry of complicated potential relief with developed system of relatively hard valence bonds that define the local choice of reaction pathway in the bifurcation point [41]. The physical sense of stochastic terms is related to thermal fluctuations of the relief and noise produced by collisions with water molecules while the main features of the relief do not depend on time essentially.

Molecular simulation example [42, 43] for a primitive model confirms this conclusion. The local choice is determined by the local parameters. The situation is equivalent to the statement that there is no thermodynamic equilibrium in the area around the bifurcation point and the theory of transient state is not valid here.

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