

Molecular dynamics with coupling to an external bath

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In molecular dynamics (MD) simulations the need often arises to maintain such parameters as temperature or pressure rather than energy and volume, or to impose gradients for studying transport properties in nonequilibrium MD. A method is described to realize coupling to an external bath with constant temperature or pressure with adjustable time constants for the coupling. The method is easily extendable to other variables and to gradients, and can be applied also to polyatomic molecules involving internal constraints. The influence of coupling time constants on dynamical variables is evaluated. A leap-frog algorithm is presented for the general case involving constraints with coupling to both a constant temperature and a constant pressure bath.

I. INTRODUCTION

The computer simulation method of molecular dynamics (MD) has become an important tool in the study of dynamical properties of liquids, molecular solutions, and macromolecules. The usual isochoric and adiabatic simulations solving Newton's equations of motion at constant volume cannot be used if dissipative nonequilibrium systems are studied (e.g., to obtain transport properties). Also in equilibrium simulations, especially if long range interactions are involved and a potential truncated at a cutoff radius is used, unavoidable slow drifts occur that need corrections. The interest to study properties as a function of temperature and pressure is much more extensive than the interest to use volume and energy as the independent variables. Therefore, either as a matter of necessity or convenience, the availability of methods for constant temperature and/or pressure dynamics is of great practical significance.

Various methods to impose external constraints on MD have been proposed and applied. Velocity scaling to correct for thermal drift has been common practice, usually rescaling as infrequently as possible to minimize influence on the trajectories. Velocity rescaling per step in order to exactly maintain a reference temperature was employed by Woodcock,¹ Evans,² and Schneider and Stoll.³ The latter tested this procedure on an exactly solvable system of 3200 coupled harmonic oscillators and found the influence on dynamical properties (frequencies and damping constants) to be negligible. Andersen⁴ proposed a Maxwellian rethermalization procedure by stochastic collisions. This method has been applied by Tanaka *et al.*⁵ Ciccotti and Tenenbaum⁶ imposed a thermal gradient by Maxwellian thermalization at two boundaries. Finally, Schneider and Stoll⁷ and Hiwatari *et al.*⁸ applied stochastic coupling to a heat bath using a Langevin equation. This procedure mimics frequent collisions with much lighter particles that have a Maxwellian velocity distribution at a given reference temperature.

For constraining pressure, Andersen⁴ proposed a Lagrangian in which the volume V acts as an additional variable, introducing pV as an additional potential term into the

Lagrangian. The equations of motion lead to a coordinate and concomitant volume scaling, the new variable V acting as the coordinate of a "piston" subject to an external constant reference pressure. The "mass" of the piston is an adjustable parameter. The method was implemented by Haile and Graben⁹ and used to evaluate the influence of the piston mass, simulating a Lennard-Jones fluid. Static properties appear to correspond closely to (N, V, E) simulations, but dynamic properties were not tested. Brown¹⁰ reformulated the algorithm to keep Cartesian coordinates, suitable for polyatomic molecules, while Ryckaert and Ciccotti¹¹ adapted the method to polyatomic molecules including holonomic constraints. Parinello and Rahman^{12,13} extended the method to include the full pressure tensor and allowing both shape and volume of the periodic cell to respond to the pressure tensor. Applications to nitrogen and carbon tetrafluoride were reported by Nosé and Klein.¹⁴ Recently Andersen's method was extended to include long range interactions.¹⁵

Other constraints or driving fields have been used as well, in particular those concerning velocities or strain rates in relation to the determination of viscoelastic properties.¹⁶⁻¹⁸

The effect of *ad hoc* rescaling of velocities and coordinates at regular intervals, driven by averages of temperature or pressure over the preceding interval, was evaluated by Broughton *et al.*¹⁹ The procedure gives reliable averages but contains discontinuous changes at the scaling intervals.

A method to incorporate constraints of pressure, temperature, or other properties in nonequilibrium dynamics into the Hamiltonian by the use of the Doll's tensor has been introduced both by Hoover *et al.*^{20,21} and Evans²² (the HMLE method). An application of this method to isothermal-isobaric MD was described by Evans and Morriss²³: Two variables α and ϵ are added to the modified equations of motion for position and momenta, which are themselves functions of positions and momenta. The result is that pressure and total kinetic energy are constants of the motion. This method has two disadvantages: First, inaccuracy of the algorithm can produce drift in p or T that is not stabilized; the reference pressure or temperature does not appear in the equations. Secondly, the Hamiltonian does not represent a physical system and the extent of the error introduced is not

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easily evaluated. If it is intended to obtain realistic simulations of physical systems, the use of a nonphysical Hamiltonian is questionable, even though mathematically consistent equations of motion are obtained. It is interesting, however, that the equations of motion are consistent with Gauss' principle of least constraint,²³ which is an expression of least squares local disturbance consistent with a given overall constraint. A principle of this kind seems a good general guiding principle for any kind of modified dynamics.

Recently, Haile and Gupta²⁴ have reformulated constant temperature algorithms in terms of a generalized potential or generalized force introduced into modified Lagrangian equations of motion. The generalized potential formalism turns out to be equivalent to velocity scaling, while the generalized force formalism appears to be identical to the HLME method. Application of both methods to a Lennard-Jones fluid showed no deviations from microcanonical results within the expected statistical and systematic errors.

Finally we note that Brown and Clarke²⁵ have listed practical algorithms for several constant temperature and pressure molecular dynamic methods.

Instead of modifying the Hamiltonian we propose a different approach: *weak coupling to an external bath*, using the principle of least local perturbation consistent with the required global coupling. This approximates the perturbation that would occur in an ideal physical nonequilibrium experiment. Moreover, since the coupling strength can be varied, the effect of the coupling can be easily evaluated and controlled.

In Sec. II the principles of the coupling method are discussed, while in Sec. III explicit algorithms are given, including the use of intramolecular holonomic constraints. In Sec. IV we evaluate the influence of p, T coupling strength on static and dynamic properties of liquid water. Finally, Sec. V discusses the results and applicability of the method.

II. COUPLING TO AN EXTERNAL BATH

We first consider coupling of a system to a heat bath with fixed reference temperature T_0 . Such a coupling can be accomplished by inserting stochastic and friction terms in the equations of motion,⁷ yielding a Langevin equation

$$m_i \dot{v}_i = F_i - m_i \gamma_i v_i + R_i(t), \quad (1)$$

where F_i is the systematic force and R_i is a Gaussian stochastic variable with zero mean and with intensity

$$\langle R_i(t) R_j(t + \tau) \rangle = 2m_i \gamma_i k T_0 \delta(\tau) \delta_{ij}. \quad (2)$$

The damping constants γ_i determine the strength of the coupling to the bath. This equation corresponds physically to frequent collisions with light particles that form an ideal gas at temperature T_0 .

Through the Langevin equation the system couples not only globally to a heat bath, but is also locally subjected to random noise. If we are interested in imposing the global coupling with minimal local disturbance, we should modify Eq. (1) such that only the global coupling remains. Let us therefore consider how the temperature T of the system behaves under the influence of stochastic coupling. For convenience we choose the friction constants to be equal for all

particles: $\gamma_i = \gamma$. This is a matter of choice; different classes of degrees of freedom can in principle be coupled to the bath with different friction constants.

The time dependence of T can be derived from the derivative of the total kinetic energy E_k :

$$\frac{dE_k}{dt} = \lim_{\Delta t \rightarrow 0} \left[\left\{ \sum_{i=1}^{3N} \frac{1}{2} m_i v_i^2(t + \Delta t) - \sum_{i=1}^{3N} \frac{1}{2} m_i v_i^2(t) \right\} / \Delta t \right], \quad (3)$$

where N is the number of particles, and

$$\begin{aligned} \Delta v_i &= v_i(t + \Delta t) - v_i(t) \\ &= \frac{1}{m_i} \int_t^{t+\Delta t} [F_i(t') - m_i \gamma v_i(t') + R_i(t')] dt. \end{aligned} \quad (4)$$

Using the fact that $R_i(t')$ is uncorrelated with $v_i(t)$ and $R_i(t)$ for $t' > t$ and using the relation [from Eq. (2)]

$$\sum_{i=1}^{3N} \int_t^{t+\Delta t} dt' \int_t^{t'+\Delta t} dt'' R_i(t') R_i(t'') = 6Nm\gamma k T_0 \Delta t, \quad (5)$$

we obtain

$$\frac{dE_k}{dt} = \sum_{i=1}^{3N} v_i F_i + 2\gamma \left(\frac{3N}{2} k T_0 - E_k \right). \quad (6)$$

The first term on the right-hand side equals minus the time derivative of the potential energy; the second term is an additional term describing the global coupling to the heat bath. In terms of temperature this extra term reads

$$\left(\frac{dT}{dt} \right)_{\text{bath}} = 2\gamma(T_0 - T). \quad (7)$$

We note that the time constant τ_T of this coupling is equal to $(2\gamma)^{-1}$.

Returning to Eq. (1), it is clear that the global additional temperature coupling [Eq. (7)] is accomplished by the equations

$$m_i \dot{v}_i = F_i + m_i \gamma \left(\frac{T_0}{T} - 1 \right) v_i, \quad (8)$$

without adding local stochastic terms, since from Eq. (8) it follows that

$$\frac{dE_k}{dt} = \sum m_i v_i \dot{v}_i = \sum_{i=1}^{3N} v_i F_i + 3N\gamma k (T_0 - T), \quad (9)$$

which is equivalent to Eq. (6)

Thus we have arrived at Eq. (8) as our modified equation of motion. It represents a proportional scaling of the velocities per time step in the algorithm from v to λv with (to first order)

$$\lambda = 1 + \frac{\Delta t}{2\tau_T} \left(\frac{T_0}{T} - 1 \right). \quad (10)$$

The change in temperature per step can also be made exactly equal to $(T_0 - T)\Delta t / \tau_T$, yielding

$$\lambda = \left[1 + \frac{\Delta t}{\tau_T} \left(\frac{T_0}{T} - 1 \right) \right]^{1/2}. \quad (11)$$

It is interesting to note that proportional scaling minimizes $\sum m_i (\Delta v_i)^2$, while $\sum \Delta (\frac{1}{2} m v^2)$ is constrained to a given value, as can be easily shown using a Lagrange multiplier. Thus proportional scaling gives a least squares local disturbance satisfying a global constraint. The principle of least

squares local disturbance has originally been introduced by Gauss in the context of imposing constraints while minimizing $\Sigma(\dot{v}_i - F_i/m_i)^2$. However, it seems a matter of choice which local deviation is minimized: Our choice of $\Sigma m_i(\Delta v_i)^2$ is the geometric mean of force $\Sigma m_i^2(\Delta v_i)^2$ and velocity $\Sigma(\Delta v_i)^2$ and has the advantage that the Maxwellian shape of the velocity distribution is conserved.

Coupling to a constant pressure bath can be accomplished according to the same principle. An extra term is added to the equations of motion that effects a pressure change

$$\left(\frac{dP}{dt}\right)_{\text{bath}} = \frac{P_0 - P}{\tau_P} \quad (12)$$

The pressure is given by

$$P = \frac{2}{3V}(E_k - \Xi), \quad (13)$$

where Ξ is the internal virial for pair-additive potentials:

$$\Xi = -\frac{1}{2} \sum_{i < j} \mathbf{r}_{ij} \cdot \mathbf{F}_{ij}, \quad (14)$$

and \mathbf{F}_{ij} is the force on particle i due to particle j . Since intramolecular contributions to the pressure vanish, in molecular systems Eqs. (13) and (14) can be evaluated using only the center of mass coordinates and velocities and forces acting on the centers of mass. A pressure change can be accomplished by changing the virial through scaling of interparticle distances. This is similar to the scaling that occurs in the constant pressure algorithm of Andersen.⁴ A simple proportional coordinate scaling, concomitant with volume scaling, minimizes local disturbances. So an extra term in the equation of $\dot{x} = v$ is added, proportional to x :

$$\dot{x} = v + \alpha x, \quad (15)$$

while the volume changes accordingly:

$$\dot{V} = 3\alpha V. \quad (16)$$

The pressure change is related to the isothermal compressibility β :

$$\frac{dP}{dt} = -\frac{1}{\beta V} \frac{dV}{dt} = -\frac{3\alpha}{\beta}. \quad (17)$$

With Eq. (12) this determines α :

$$\alpha = -\beta(P_0 - P)/3\tau_P. \quad (18)$$

Thus the modified equation of motion is

$$\dot{x} = v - \frac{\beta(P_0 - P)}{3\tau_P} x. \quad (19)$$

It represents a proportional scaling of coordinates and box length l (assuming an isotropic system in a cubic box) per time step from x to μx and l to μl with, to first order in Δt ,

$$\mu = 1 - \frac{\beta \Delta t}{3\tau_P}(P_0 - P). \quad (20)$$

An equivalent expression to the same order is

$$\mu = \left[1 - \frac{\Delta t}{\tau_P}(P_0 - P)\right]^{1/3}. \quad (21)$$

The compressibility, that may not be accurately known, oc-

curs in the expression for the scaling factor μ . Since an inaccuracy in β only influence the accuracy of the noncritical time constant τ_P , the imprecision of β is of no consequence for the dynamics. If β is not known for the potential model that is used in the simulation, it is sufficient to use an experimental value for the physical system that is approximated by the simulation.

Expressions (20) or (21) apply to an isotropic system. The equations can be modified to anisotropic triclinic systems. Now the pressure P becomes a tensor

$$P = \frac{1}{V} \left\{ \sum_i m_i \mathbf{v}_i \mathbf{v}_i^T + \sum_{i < j} \mathbf{r}_{ij} \mathbf{F}_{ij}^T \right\}, \quad (22)$$

where a row vector is denoted as transpose of a column vector. The volume V is the determinant of the matrix h formed by the column vectors \mathbf{a} , \mathbf{b} , \mathbf{c} that represent the edges of the unit cell in a space-fixed Cartesian coordinate system:

$$V = \det h = \mathbf{a} \cdot (\mathbf{b} \times \mathbf{c}). \quad (23)$$

Assuming β to be a scalar, Eq. (20) now becomes a tensorial equation:

$$\boldsymbol{\mu} = \mathbf{1} - \frac{\beta \Delta t}{3\tau_P}(P_0 - P). \quad (24)$$

Particle coordinates \mathbf{r}_i are scaled as

$$\mathbf{r}'_i = \boldsymbol{\mu} \mathbf{r}_i, \quad (25)$$

while the unit cell is scaled as

$$h' = \boldsymbol{\mu} h. \quad (26)$$

This implies that

$$V' = (\det \boldsymbol{\mu}) V. \quad (27)$$

Equations (24)–(27) reduce to the isotropic case if $\boldsymbol{\mu} = \mu \mathbf{1}$. It is possible to use a tensorial β , but this has only consequences for the time constants with which the various component of P relax to the reference value P_0 . The case of orthorhombic symmetry is particularly simple because all tensors remain diagonal. We note that the equations are much more simple if one adheres to Cartesian coordinates, instead of using contravariant relative coordinates that imply a metric tensor in the equations of motion.

III. ALGORITHM FOR P, T COUPLING

The scaling terms for velocities and coordinates can most easily be incorporated into a leap-frog algorithm²⁶ for solving the equations of motion. The following scheme applies to a general algorithm involving temperature coupling (T), pressure coupling (P), and internal constraints (C). A step denoted by T or P applies only if temperature coupling or pressure coupling is used. Steps denoted by C apply only in the presence of constraints. Through the procedure SHAKE^{27–29} distance constraints are satisfied in a way consistent with the Verlet algorithm, which is equivalent to the leap-frog scheme. SHAKE changes an unconstrained configuration \mathbf{x} into a constrained configuration \mathbf{y} with displacement vectors in a direction given by a reference configuration \mathbf{x}_{ref} ; this is denoted by

$$\text{SHAKE}(\mathbf{x} \rightarrow \mathbf{y}; \mathbf{x}_{\text{ref}}).$$

For cases without P or T scaling or without constraints, the steps denoted by P , T , or C can be omitted.

A. P , T coupling algorithm

(Isotropic case, suitable for polyatomic molecules including internal constraints.)

Given: configuration $\mathbf{x}(t)$ and velocities $\mathbf{v}(t - \frac{1}{2}\Delta t)$ for all atoms, box length $l(t)$, volume $V(t)$.

(1) Evaluate (unconstrained) forces $\mathbf{F}(t)$ on all atoms:

$$\mathbf{a}_i(t) = \mathbf{F}_i(t)/m_i.$$

Note: Forces of periodic images within the cutoff range (if applicable) are to be included.

(2P) Evaluate the pressure from the virial Ξ and kinetic energy based on centers of mass:

$$\Xi(t) = \frac{1}{2} \sum_{\alpha < \beta} \mathbf{R}_{\alpha\beta}(t) \mathbf{F}_{\alpha\beta}(t), \quad (28)$$

where $\mathbf{R}_{\alpha\beta} = \mathbf{R}_\alpha - \mathbf{R}_\beta$ is the relative position vector of the centers of mass of molecules α and β and $F_{\alpha\beta} = \sum_{i\alpha, j\beta} F_{i\alpha j\beta}^{\text{pair}}$ is the sum of all pair interactions of atoms $i\alpha$ of molecule α with atoms $j\beta$ of molecule β . Nonpair interactions (angles, dihedrals) are omitted from the sum.

$$E_{\text{kin}}^{\text{cm}}\left(t - \frac{1}{2}\Delta t\right) = \sum_{\alpha} \frac{1}{2} M_{\alpha} \mathbf{V}_{\alpha}^2\left(t - \frac{1}{2}\Delta t\right), \quad (29)$$

where M_{α} is the total mass of molecule α and $\mathbf{V}_{\alpha} = M_{\alpha}^{-1} \sum_i m_{i\alpha} \mathbf{v}_{i\alpha}$ the center of mass velocity of molecule α ;

$$P(t) = \frac{1}{3V(t)} \left[E_{\text{kin}}^{\text{cm}}\left(t - \frac{1}{2}\Delta t\right) - \Xi(t) \right]. \quad (30)$$

The pressure scaling factor becomes

$$\mu = \left\{ 1 + \frac{\Delta t}{\tau_P} \beta [P(t) - P_0] \right\}^{1/3}. \quad (31)$$

Note 1: The kinetic energy is not available at time t , but the use of E_{kin} at $t - \frac{1}{2}\Delta t$ does not introduce a significant error because the coupling time constant is long compared to Δt .

Note 2: The pressure evaluation must be based on the centers of mass in the case that forces on atoms involve internal non-pair-additive contributions.¹¹ The virial expression (14) is only valid for pair-additive forces. Internal contributions to the virial are cancelled (on the average) by the internal kinetic energy. If all interactions are pair additive, the pressure calculation may be based on atomic interactions, but this introduces additional fluctuations in the pressure.

(3T) Evaluate

$$T\left(t - \frac{1}{2}\Delta t\right) = \frac{2k}{3N - M - 3} E_{\text{kin}}\left(t - \frac{1}{2}\Delta t\right), \quad (32)$$

where N is the number of atoms, M the number of constraints, and

$$E_{\text{kin}}\left(t - \frac{1}{2}\Delta t\right) = \sum \frac{1}{2} m_i v_i^2\left(t - \frac{1}{2}\Delta t\right). \quad (33)$$

The temperature scaling factor becomes

$$\lambda = \left[1 + \frac{\Delta t}{\tau_T} \left\{ \frac{T_0}{T(t - \frac{1}{2}\Delta t)} - 1 \right\} \right]^{1/2}. \quad (34)$$

(4) Compute velocities

$$\mathbf{v}(t + \frac{1}{2}\Delta t) = \mathbf{v}(t - \frac{1}{2}\Delta t) + \mathbf{a}(t)\Delta t. \quad (35)$$

(5T) Scale \mathbf{v} : $\mathbf{v}(t + \frac{1}{2}\Delta t) \leftarrow \lambda \mathbf{v}(t + \frac{1}{2}\Delta t)$. (36)

Note. Although λ is based on the temperature at $t - \frac{1}{2}\Delta t$, its value can be used to scale the velocity at $t + \frac{1}{2}\Delta t$ because of the slow variation of λ .

(6) Compute new (unconstrained) positions:

$$\mathbf{x}(t + \Delta t) = \mathbf{x}(t) + \mathbf{v}(t + \frac{1}{2}\Delta t)\Delta t.$$

(7C) Apply constraints to coordinates:

$$\text{SHAKE } [\mathbf{x}(t + \Delta t) \rightarrow \mathbf{x}(t + \Delta t); \mathbf{x}(t)].$$

(8C) Compute constrained velocities:

$$\mathbf{v}(t + \frac{1}{2}\Delta t) = [\mathbf{x}(t + \Delta t) - \mathbf{x}(t)]/\Delta t.$$

(9P) Perform pressure scaling on coordinates and box size:

$$\begin{aligned} \mathbf{x}(t + \Delta t) &\leftarrow \mu \mathbf{x}(t + \Delta t), \\ l(t + \Delta t) &= \mu l(t), \\ V(t + \Delta t) &= \mu^3 V(t). \end{aligned}$$

Note 1. Whether scaling is performed on atomic coordinates or on centers of mass is a matter of choice. If scaling is performed on the centers of mass, each particle has to be reconstructed after the scaling by applying a translation equal to the translation of the center of mass. Center of mass scaling is to be preferred for small molecules with internal constraints, for large molecules with internal flexibility atomic scaling yields a smoother response to pressure changes. Atomic scaling slightly affects the constraints, but this is of no consequence for the stability of the algorithm because the application of SHAKE in the next step prevents the propagation of constraint errors.

Note 2. It is not correct to interchange steps (8C) and (9P) because according to Eq. (19) the pressure scaling should not influence the velocities. Interchanging steps (8C) and (9P) leads to instability of the algorithm. Hence it is also not possible to apply SHAKE [step (7C)] after the pressure scaling, because step (8C) must follow step (7C).

(10) Replace coordinates of particles that have moved out of the box limits by the coordinates of their images within the box. Depending on how forces are evaluated, this resetting may be done on the basis of centers of mass, molecular centers, or atomic group centers.

We note that the addition of coupling to an external bath does not perceptibly increase the required computer time, because only a minor calculation proportional to the number of particles is added. The algorithm remains general: inserting values for τ_T and τ_P much larger than the length of the dynamic run reduces the simulation to a micro-canonical and isochoric one. The algorithm can be easily modified to introduce temperature, pressure, or velocity gradients and thus is suitable for general nonequilibrium molecular dynamics (NEMD).

IV. EVALUATION

We have applied coupling to a temperature and pressure bath to simulations of 216 molecules of liquid water using the SPC model³⁰ in order to test the effect of the coupling constants. Simulations of water with its long range di-

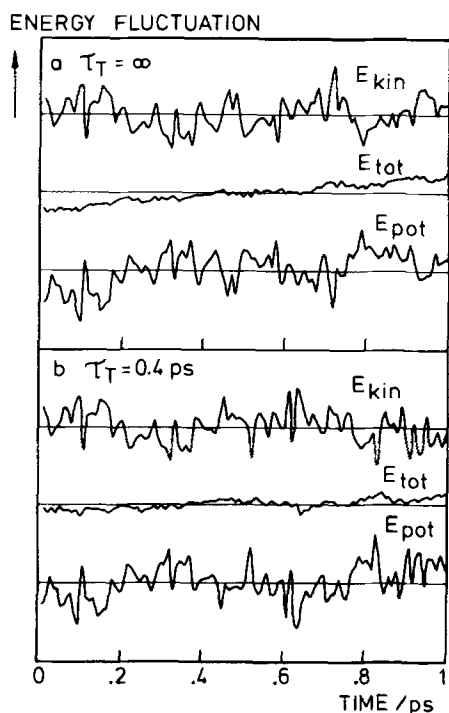


FIG. 1. Fluctuations of kinetic, total, and potential energy in two 1 ps molecular dynamics runs of 216 water molecules, starting from the same initial conditions ($T = 300$ K). a isochoric, microcanonical simulation ($\tau_T = \infty$), b isochoric simulation with weak coupling to constant temperature bath ($\tau_T = 0.4$ ps). The vertical scale represents 1 kJ/mol per division. Horizontal lines represent averages for each curve.

polar interaction normally produce a cutoff noise and drift [Fig. 1(a)]. Using T coupling the drift is removed but the average temperature is slightly larger than the reference temperature of the bath. In Fig. 1(b) a τ_T of 0.4 ps was used: With this time constant the opposing fluctuations in kinetic and potential energy remain similar to those of the uncoupled simulation. Even the details of the fluctuations reproduce for times up to 0.4 ps. When τ_T is reduced below 0.1 ps,

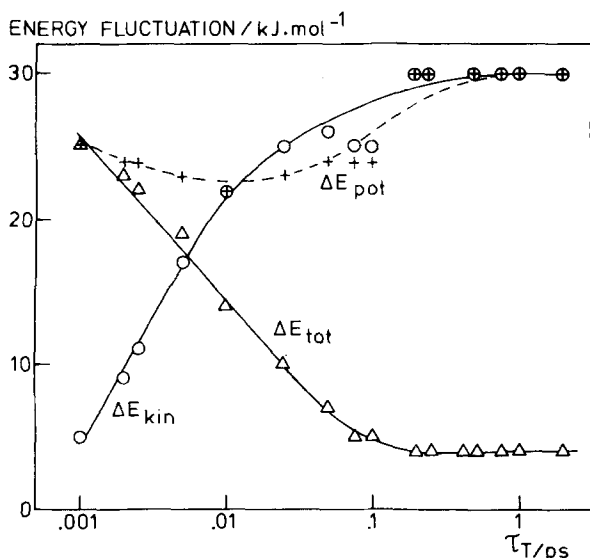


FIG. 2. Root means square fluctuations in kinetic, total, and potential energies, measured over several 0.1 ps simulations of liquid water.

the fluctuations in the kinetic energy are reduced at the expense of increasing fluctuation in the total energy (Fig. 2). The fluctuations in potential energy are not sensitive to the value of the coupling time constant.

Coupling to a constant pressure bath introduces volume (density) fluctuations, while the low frequency components of the pressure fluctuation are reduced. Pressure fluctuations are not significantly reduced for $\tau_P > 0.1$ ps, while for $\tau_P = 0.01$ ps pressure fluctuations are reduced by an order of magnitude. Volume fluctuations increase by almost an order of magnitude when τ_P is decreased from 0.1 to 0.01 ps. We have observed that further reduction of τ_P to values approaching the time step (0.001 ps) leads to instability of the algorithm with increased pressure and volume fluctuations. It is recommended to use pressure coupling time constants of 0.1 ps or larger.

Although short coupling time constants greatly influence fluctuations, average thermodynamic quantities are not disturbed even for time constants as short as 0.01 ps. Table I shows the results for average potential energy and density for various values of τ_T and τ_P . Observed differences can be traced to differences in average values of temperature and pressure; the deviations from reference temperature and pressure depend on the coupling time constants. If E_{pot} and ρ are corrected to $T = 300$ K and $P = 1$ bar using values derived from simulations of the SPC water model for specific heat $c_v = 76$ J mol⁻¹ K⁻¹, $(\partial E_{tot}/\partial P)_T = 0.5$ J mol⁻¹ bar⁻¹, expansion coefficient $\alpha = 5.7 \times 10^{-4}$ K⁻¹, and isothermal compressibility $\beta = 4.9 \times 10^{-5}$ bar⁻¹, the potential energy and density are the same within experimental error for all simulations. Also radial distribution functions do not differ significantly, only the isochoric simulation at $\rho = 1$ (run 9 in Table I) is slightly less structured, but this is related to the density difference only.

We conclude that static average properties are not significantly influenced even for time constants as small as 0.01 ps. Fluctuations of global properties, however, are strongly influenced for time constants less than 0.1 ps; the intensity of such fluctuations cannot be used to derive thermodynamic properties.

Dynamic properties of individual particles are not significantly altered, although the velocity autocorrelation function shows some deviation for very short time constants. Figure 3 shows the velocity correlation functions and their spectral densities for $\tau_T = \tau_P = 0.1$ and 0.01 ps. For values above 0.1 ps these functions are the same as for 0.1 ps; small observed differences can be related to temperature differences. Diffusion constants are not significantly different from values expected when the temperature differences are taken into account. Correlation times τ_1 and τ_2 for the first and second order spherical harmonics of the dipole vector agree within experimental error for the various simulations ($\tau_1 = 3.3 \pm 0.3$ ps, $\tau_2 = 1.4 \pm 0.2$ ps), except for $\tau_T = \tau_P = 0.01$ ps, where values of 3.8 and 1.7 ps were found. Although these deviations may not be significant, they indicate the possibility of a deviation in dynamic properties for time constants as low as 0.01 ps. We conclude that reliable dynamic properties can be derived for coupling time constants above 0.1 ps.

TABLE I. Thermodynamic quantities for water using coupling to a P, T bath.^a

Run	τ_T	τ_P	T^c (K)	P^c (bar)	E_{pot}^b (kJ/mol)	$E_{\text{pot}}(T=300, P=1)$ (kJ/mol)	ρ^c	$\rho(T=300, P=1)$
1	0.5	∞	307(1)	420(200)	-41.6	-41.8	0.987(0)	0.970(10)
2	0.1	∞	300(1)	240(150)	-41.9	-41.8	0.987(0)	0.975(7)
3	0.01	∞	298(0.1)	40(100)	-42.0	-41.9	0.987(0)	0.984(5)
4	0.5	0.4	305(0.5)	20(20)	-41.7	-41.9	0.981(5)	0.983(7)
5	0.5	0.2	303(0.5)	9(20)	-41.8	-41.9	0.981(5)	0.983(5)
6	0.5	0.1	306(0.5)	-4(20)	-41.5	-41.8	0.971(10)	0.974(10)
7	0.1	0.1	300(1)	7(20)	-41.8	-41.8	0.971(10)	0.971(10)
8	0.01	0.01	198(0.1)	2(1)	-42.1	-42.0	0.977(12)	0.976(12)
9	Rescaling every 200 Δt ; $\Delta t = 0.5$ fs		300(0.5)	470(100)	-42.2	-42.0	1.000(0)	0.977(5)

^a216 molecules during 10 ps (25 ps for runs 4 and 5); $\Delta t = 1$ fs; cutoff range 0.9 nm; reference temperature 298 K, reference pressure 1 bar.

^bAccuracy is ± 0.1 kJ/mol in E_{pot} , ± 0.5 K in T .

^cAccuracy in last digit given between parentheses.

V. CONCLUSIONS

The method described here to couple a simulated system loosely to a constant temperature and/or pressure bath has proved to be reliable and easy to implement. It provides a stable algorithm that allows smooth changes to new values of pressure or temperature without the need for intermediate adjustments. The method was used by us^{31,32} to increase the temperature of a circular dodecapeptide in order to generate new conformations. The temperature of the bath was suddenly increased, first from 300 to 600 K and 10 ps later to 1200 K, with a coupling constant of 0.1 ps. The kinetic, potential and total energies reached new equilibrium values within 2 ps after the jumps, with smooth nonoscillatory transitions.

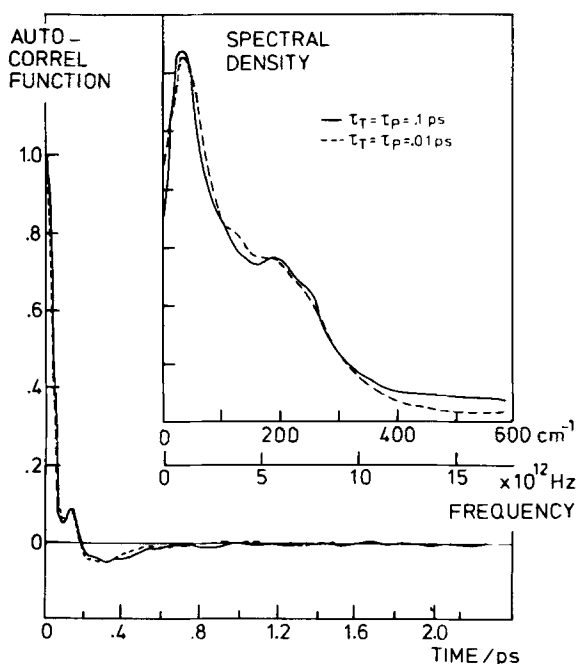


FIG. 3. Autocorrelation function and spectral density for center-of-mass velocity of water molecules for various values of coupling constants to temperature bath (τ_T) and pressure bath (τ_P). All curves coincide for $\tau_T > 0.1$ ps and $\tau_P > 0.1$ ps (drawn curves). Broken curves: $\tau_T = \tau_P = 0.01$ ps.

The coupling method has two distinct advantages above methods that are based on Lagrangians modified to include certain constraints. First, the coupling can be made as weak as desired to minimize the disturbance of the system, and the strength of the coupling can easily be varied to suit the needs of a given application. Traditional microcanonical or isothermal–isochoric conditions are just limiting cases, requiring no change in the algorithm. Second, the algorithm is numerically stable and truncation errors will not develop undesired deviations that need *ad hoc* corrections. This is of considerable practical value when conditions are adjusted to new values, as well as for long “unattended” runs.

The aperiodic coupling to a pressure bath through a first order process has the advantage above Andersen’s method⁴ that responses to pressure changes are nonoscillatory.

The method is ideally suited to NEMD (nonequilibrium molecular dynamics). Gradients of temperature, pressure, velocities, etc. are easily incorporated in such a way that the best compromise between disturbing the physical behavior of the system and maintaining the desired gradients is obtained. Coupling to unorthodox constraints is possible: In a simulation of protein dynamics in the crystalline state we have applied a weak coupling of the atomic positions to the positions known from x-ray diffraction: This allows local motional freedom while systematic deviations due to inaccurate potentials are corrected on a long time scale.

We have not been able to prove the exact nature of the ensemble generated by the coupling method, and hence no useful equations can be given that will allow the use of measured fluctuations in the ensemble. We do not consider this a disadvantage because in cases where coupling to an external bath is required, i.e., either in nonequilibrium conditions or in the presence of nonnegligible truncation errors, ensemble fluctuations are generally insufficiently accurate to be useful as a source for the derivation of macroscopic properties.

The method has been used in polypeptide and protein simulations,^{31–34} in the determination of free energy of cavity formation in water³⁵ and in the study of hydration of dioxane.³⁶ It has been incorporated as standard into the GROMOS program library.³⁷

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