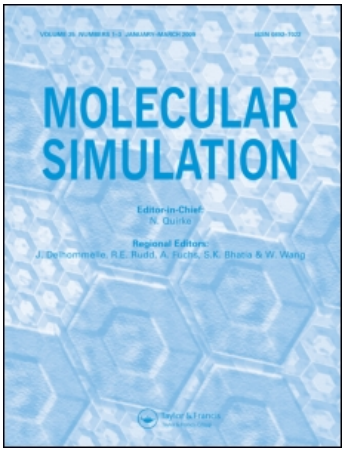

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Molecular Dynamics Simulations With First Order Coupling to a Bath of Constant Chemical Potential

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MOLECULAR DYNAMICS SIMULATIONS WITH FIRST ORDER COUPLING TO A BATH OF CONSTANT CHEMICAL POTENTIAL

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In molecular dynamics simulations the temperature or pressure can be controlled by applying a weak first-order coupling to a bath of constant temperature or pressure. This weak coupling technique to control system properties using a first-order relaxation equation is analyzed from a statistical mechanics point of view. It is shown, how the weak coupling scheme can be generalized and applied to a bath of contstant chemical potential. The presented method, to which in the following will be referred to as chemical potential weak coupling, is applied and tested on a Lennard-Jones fluid. The thermodynamic quantities known from the literature are accuratly reproduced.

The temperature and chemical potential weak coupling methods aim to sample the canonical and grand canonical ensembles respectively. By analyzing the fluctuations in energy and number of particles, the tight relation between the ensembles and the distributions obtained from the weak coupling simulations is demonstrated. The influence of the choice of the coupling parameters on the quality of the approximation of the ensemble distribution is discussed.

KEY WORDS: Computer simulation, molecular dynamics, chemical potential, temperature coupling, chemical potential coupling, grand canonical ensemble

1 INTRODUCTION

Grand canonical ensemble (GCE) simulations are of interest in different kinds of problems. Firstly, they are useful in simulations where the GCE system directly represents physical reality. This is the case in small pores that allow particle exchange with their environment [1]. Minimization of finite size effects are another motivation for GCE simulations [2]. Those can be important if either the concentration of a component in the system is very low or the system is close to a phase transition where the correlation length of the fluctuations diverges. Simulations of inhomogeneous systems are also well suited to a GCE approach [3]. Furthermore, if the chemical potential of a component, instead of its concentration, is known, the GCE, having the chemical potential as natural variable, allows direct simulation without knowing the concentration as function of the chemical potential. The increasing demands for precision of simulations and closeness to experiments make GCE simulations more and more important.

Several methods for sampling the GCE in simulations have been proposed, based either on Monte Carlo (MC) criteria [2, 3, 4, 5] or on an extended system approach [6] and they have been applied to various systems. In grand cononical MC methods, particles are moved or deleted and new particles are inserted according to a random procedure. A Markov chain is constructed by accepting new configurations only with a given probability. In the extended system approach, the Lagrangian obtains an additional term representing the potential energy due to the number of particles present in the system. The number of particles is made continuous and is considered as a further degree of freedom that appears in the equations of motion. However, these methods suffer from some limitations. On the one hand, pure MC approaches do not yield dynamic information, making these methods not attractive in many cases. On the other hand, pure molecular dynamics (MD) methods using the extended system approach are based on a second-order coupling to a particle bath [7], and so cause spurious fluctuations in the particle number. Furthermore, the influence of the constantly present fractional particles can, at least in small systems, not easily be judged. A combination of MD with MC can give some relief [3, 5]. In these methods MD is performed between MC particle insertion and deletion trials. However, these methods are either not applicable to systems with too slow diffusion or they still severely disturb the dynamics since they are based on acceptance of configurations created after insertion or deletion of whole particles according to a MC criterion.

In this paper, a novel method for constant chemical potential MD will be presented. The method is intended for systems in which dynamic quantities are of interest, but where a low diffusion constant hampers the equilibration. Such systems are of particular interest in biomolecular simulations.

The method is based on a first order relaxation equation. The technique, known as weak coupling (WC) or Berendsen thermostat [8], has been successfully applied in MD to simulate at constant temperature and constant pressure. It is widely used and is part of standard simulation packages like AMBER, CHARMM, and GROMOS [9, 10, 11]. The system is coupled to the bath by rescaling the kinetic energy respectively the volume by an amount proportional to the difference between the measured value and the imposed (bath) value. The popularity of the method is mostly due to its reliability and efficiency is stabilizing the system in the presence of heating or cooling caused by numerical noise and also its use in driving the systems to different values of temperature and pressure. Moreover, the method can easily be implemented and included in MD algorithms. It ensures that correct averages are obtained. However, if, as is usually done, the scaling is carried out at every time step and the coupling or relaxation time parameter is not properly chosen, the (energy) fluctuations will not be canonical. A further drawback of the method is, that under certain conditions an unphysical energy flow into the centre of mass motion can be observed [12].

Analogously, the chemical potential coupling (CPWC) method presented here allows a stable coupling to a bath with given chemical potential. The method ensures that correct averages of the thermodynamic quantities are obtained. Moreover, with an appropriate choice of the coupling parameter, the grand canonical (particle number) fluctuations can be reproduced. The method can easily be implemented and added to existing simulation packages.

2 THEORY

It is instructive to discuss first the weak coupling (WC) to a temperature bath and then to generalize it to CPWC. Originally WC was justified by dynamical arguments, stating its equivalence to the interaction with a hypothetical ideal gas [8]. More elaborate arguments supporting the view that the distribution obtained by the weak coupling scheme actually approximates the canonical distribution were recently given by Heiner [13]. In the following WC will be considered from a statistical mechanical point of view, allowing the generalization to chemical potential weak coupling.

When applying WC to a temperature bath with temperature T, the aim is to reproduce the canonical distribution. A simulation of an isolated system yields a microcanonical distribution. However, according to ensemble theory, the canonical ensemble can be obtained from the microcanonical ensemble through a Laplace transformation. Thus, the canonical partition function Z can be expressed as a weighted sum over microcanonical subensembles with energy E:

$$Z = \int w(E) e^{-(E/k_B T)} dE \tag{1}$$

where $\omega(E)$ is the density of states and k_B is the Boltzmann constant. If the system is sufficiently large, the integrand is strongly peaked and only subensembles with energies close to the most probable value are relevant. Thus the integrand can be approximated by a Gaussian [14]. Furthermore, if within the domain where the integrand is not vanishing, the specific heat can be considered as constant to a good approximation, finite size effects concerning energies and temperatures can be neglected in the transformation between the ensembles [15, 16]. In the following this condition is assumed to be fulfilled.

In MD, the kinetic energy E_{kin} serves as an instantaneous measure of the temperature:

$$T_i(t) = \frac{2}{3Nk_B} E_{\text{kin}}(t) \tag{2}$$

where N is the number of particles. The index i stands for instantaneous. In the microcanonical ensemble, the equipartition theorem together with the virial theorem ensures that the time average of $T_i(t)$ corresponds to the temperature of the system under investigation [17]. Since the canonical ensemble is only a weighted sum over microcanonical ensembles, the weighting of $T_i(t)$, while forming the average, will ensure that the expectation value of $T_i(t)$ in the canonical ensembles will reproduce the imposed temperature T.

The key to understanding WC from a statistical point of view is that fact that the probability distribution $P(T_i, E)$ to find the system with a total energy E at the instantaneous temperature T_i can be written as

$$P(T_i, E) = P_{T_i}(T_i, E) P_{E_{\text{tot}}}(E) \tag{3}$$

where $P_{E_{\text{tot}}}(E)$ is the probability distribution of the total energy and $P_{T_i}(T_i, E)$ is the conditional probability distribution of the instantaneous temperature at fixed total energy E. The most probable value of the total energy (E_o) is simplicitly given through

the choice of the strength of its conjugate field (T). E_o is the energy a microcanonical ensemble must contain, in order to have the imposed temperature T. Its knowledge would allow the set up of a corresponding microcanonical simulation. In subensembles having an energy close to E_o, the form of the instantaneous temperature distribution is conserved. The distributions are equal up to a shift which is due to the specific heat, C_v, of the system. Thus, the equation above can be approximated with:

$$P(T_i, E) = P_{T_i}\left(T_i - \frac{E - E_o}{C_v}, E_o\right) P_{E_{\text{tot}}}(E) \tag{4}$$

In MD it is straightforward to produce the probability distribution of the instantaneous kinetic energy at fixed total energy, P_{T_i}. However, the total energy distribution of the canonical ensemble, $P_{E_{\text{tot}}}(E)$, and especially E_o, being determined by the energy and the entropy, are not directly accessible to simulation. In WC, the distribution P_{T_i} is exploited to produce a biased random walk along E by changing the subensemble according to

$$E(t + \Delta t) = E(t) + \alpha_T(T - T_i(t)) \tag{5}$$

with the coupling constant $\alpha_T > 0$.

The shift of P_{T_i} along T_i as function of the total energy E and the change of sign in the scheme (eq. 5) ensure a driving force towards E_o, which increases with the deviation of E from E_o. Thus, exploiting the kinetic energy fluctuations, WC introduces a coupling of the total energy fluctuations to the corresponding susceptibility, which is in this case C_v, as imposed by the fluctuation-dissipation theorem. In sufficiently large systems, symmetry guarantees that the average energy measured will correspond to E_o. In practice, this condition is very well fulfilled. Usually WC yields averages very close to the desired values. Moreover, the fluctuation of the energy, the size of which can be controlled by the coupling constant α_T, reproduces an important feature of canonical ensembles.

Chemical potential weak coupling can be understood in a similar way. Formally this similarity can be shown using generalized ensemble theory [15]. The GCE allows fluctuation of the particle number around the most probable value N_o, which is determined through the choice of the chemical potential. The size of the fluctuations is again related to a susceptibility, which is in this case the isothermal compressibility κ_T. The GCE can be thought of being constituted by canonical subensembles, thus ensembles with fixed N. The crucial point in implementing WC is to find a quantity analogous to the instantaneous measure of the temperature, namely an instantaneous measure for the chemical potential. By analogy with the constant temperature bath, this quantity can be used to drive the system to the correct number of particles if the strength of its conjugated field is known.

An estimation of the so-called mean Boltzmann factor,

$$MBF(N) = \langle e^{[-(U_{\text{test}}/k_B T)]} \rangle_N \tag{6}$$

known from the Windom particle insertion method [18, 19], is an adequate choice. In this expression U_{test} is the energy of a randomly inserted ghost particle, and the brackets indicate the ensemble average. In a canonical ensemble having N particles, the

mean Boltzmann factor is related to the excess chemical potential μ^{ex} by the following relation:

$$\mu^{ex} = -k_B T \ln(MBF(N)) \tag{7}$$

The excess chemical potential μ^{ex} together with the ideal gas contribution μ^{id} yield the chemical potential μ,

$$\mu = \mu^{id} + \mu^{ex} \tag{8}$$

If the mean Boltzmann factor is not totally converged, there remain well defined statistical fluctuations, which can be exploited to guide a biased random walk along the particle number (N) degree of freedom by WC. In the following, estimated mean Boltzmann factors will serve as instantaneous measures of the chemical potential. Instead of the chemical potential μ itself, the quantity serving as reference value for the coupling will be w_o, which is related to the excess chemical potential μ^{ex} by the inverse of the configurational part z^{ex} of the fugacity z,

$$w_0 = \frac{1}{z^{ex}} = e^{[-(\mu^{ex}/k_B T)]} \tag{9}$$

Using the following formula:

$$N(t + \Delta t) = N(t) + round(\alpha_N(w_o - MBF(N(t)))) \tag{10}$$

the fluctuations in the energy due to the test-particle-insertions are converted to fluctuations of the number of particles. Here, α_N denotes the coupling constant, and the function *round* delivers the integer nearest to its real argument. For sufficiently large systems, the number of particles (N) will be driven to the required number (N_o), since the function

$$(N - N_o)(w_o - MBF(N)) \tag{11}$$

has a minimum for $N = N_o$. The size condition must again be imposed in order to have an approximately linear relation between N and $MBF(N)$ within the size of the fluctuations.

However, there is one important difference between the standard WC to a temperature bath and WC to a bath of constant chemical potential as presented here. Since the introduction of a new particle disturbs the system heavily, the instantaneous thermodynamic quantities of the starting configuration in the new subensemble will be far off the average values. Thus, estensive relaxation followed by sampling in the subensemble before changing to the next subensemble is crucial. In WC to a temperature bath, where usually a very small coupling constant α_T is chosen, the system is only slightly disturbed, which allows to change the subensemble at every MD integration step. The consequences of this difference will be discussed later.

3 ALGORITHM

Based on the theoretical considerations given above the following CPWC algorithm is proposed:

1. *Sampling period.*
   During n_1 MD steps the $MBF(t)$ value is determined by performing n_w Widom particle insertions per MD time step. Then, the change in the number of particles is determined using the formula (10).
2. *Growing/shrinking period.*
   If particles have to be added, they are grown into the system during n_2 steps by scaling the sizes (interactions) of the particles from zero to their full value. The starting points for the growing particles are chosen to be the energetically most favourable points for the acceptance of a new particle determined by a MC procedure followed by a steepest descent energy minimization. A velocity of zero is assigned. This choice and the slow growing of the particle ensures that the system stays always close to equilibrium in order to minimize the influence of the starting configuration on the measured thermodynamic quantities of the suben- sembles. Accordingly, if particles have to be removed, the $N(t) - N(t + \Delta t)$ particles having the highest potential energies are chosen to be scaled down to zero interaction in n_2 MD time steps.
3. *Relaxation period.*
   The subensemble achieved after the creation respectively deletion of particles is then simulated during n_3 MD time steps.

4 SIMULATIONS

The algorithm has been applied and tested on a Lennard-Jones fluid. The simulation program is based on PROMDA, a GROMOS derivate [20]. The equations of motion are integrated using a leap-frog algorithm. Cubic periodic boundary conditions are applied. The Lennard-Jones interaction is neglected beyond a distance of 2.5. All quantities are given in reduced units. The calculated thermodynamic quantities are corrected for the neglect of the tails of the Lennard-Jones potential, assuming a pair correlation function of unity for distances larger than the cut-off. If not indicated otherwise, all simulations are performed at the temperature 1.3 around the density 0.75. The box size is chosen as to have 216 particles at the density 0.75. The time step of the integration is 0.002.

The simulations at constant energy are performed over 10^4 time steps, following an equilibration over 10^3 time steps. The temperature coupling is investigated using two different coupling schemes. The first scheme is the standard weak coupling, where velocity rescaling is carried out continuously after every MD time step. In the second scheme the velocities are rescaled discontinuously, i.e. they are only rescaled after a larger number of MD time steps. In the simulations with standard, i.e. continuous temperature coupling, the time constant $\tau_T = C_v \Delta t \alpha_T^{-1}$ for the temperature coupling is 0.1 if nothing else is indicated. Each simulation consists of 10^4 time steps. In the simulations with discontinuous temperature coupling, the velocities are rescaled every 500 time steps, using a time constant τ_T of 0.01. Here, every simulation consists of 10^5 time steps.

Several CPWC simulations at various chemical potentials were performed. The following parameters are set: $n_1 = 50$, $n_2 = 50$, $n_3 = 200$, $n_w = 100$. The coupling

constant α_N is either -5 or -3. The time constant of the (standard) temperature coupling is set to $\tau_T = 0.1$. Every simulation consists of 10^5 time steps starting from configurations obtained after an equilibration over 10^4 time steps.

5 RESULTS AND DISCUSSION

The distributions of the total energy per particle obtained from the WC simulations with coupling to a temperature bath are shown in Figure 1. They have roughly a Gaussian form. The width of the energy distributions depends on the time constant τ_T of the coupling. The distribution obtained from the standard weak coupling simulation with $\tau_T = 0.1$ closely approximates the distribution that is expected theoretically [14]. The theoretical distribution, a Gaussian with variance $\sigma^2 = k_B T^2 C_v N^{-2}$, is obtained using a value of $C_v (= 215.8)$ extracted from the equation of state of Nicolas *et al.* at $T = 1.3$, and $N = 216$ [21].

Figure 2.a) and 2.b) show the instantaneous temperatures averaged over all sampled configurations with the same total energy as a function of the total energy for the simulations with standard WC to a temperature bath. Figure 2.c) shows the same function for the simulation with discontinuous coupling. In all simulations, the averaged instantaneous temperatures as a function of the total energy fluctuate around the value imposed by the bath. The averages over all instantaneous temperatures differ less than 1% from the bath values.

It can be seen that the average instantaneous temperatures as function of the total energy depend on the coupling scheme but not on the time constant. Only if the velocities are not rescaled at every time step but after extensive sampling at fixed energy, the averages are distributed as imposed by the canonical ensemble.

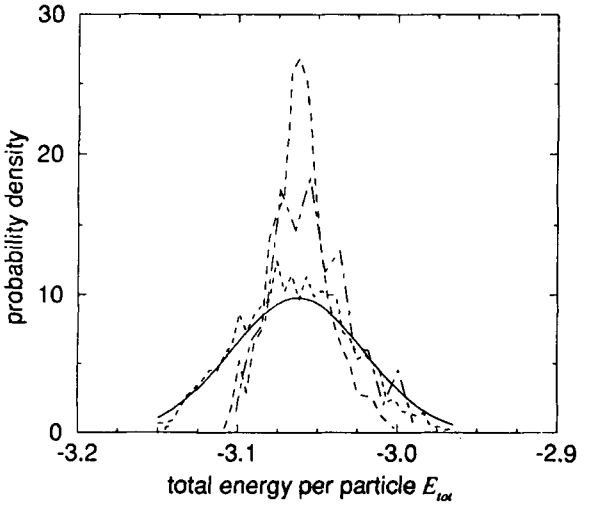

Figure 1 Energy distribution produced by weak coupling to a temperature bath ($T = 1.3$). Short-dashed: standard weak coupling, $\tau_T = 0.1$; long-dashed: standard weak coupling, $\tau_T = 0.5$; short-long-dashed: discontinuous coupling; full line: theoretically expected distribution. All values are in reduced units.

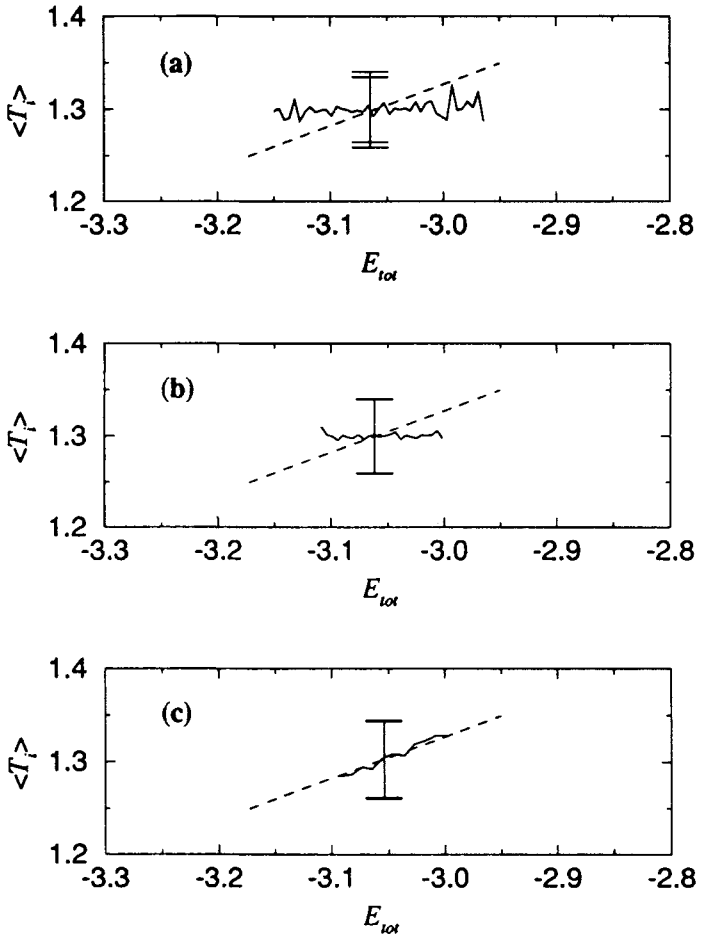

Figure 2 Average temperature as function of the total energy per particle of systems weakly coupled to a bath of constant temperature (full lines). a) Standard weak coupling, coupling time constant $\tau_T = 0.1$; b) standard weak coupling, $\tau_T = 0.5$; c) discontinuous coupling. Dashed: expected average temperature (according to the data of Nicolas *et al.* [21]). Outer error bars: width of the fluctuations extracted from a microcanonical simulation. Inner error bars: width of the fluctuations in the weak coupling simulations. All values are in reduced units.

The distributions of the instantaneous temperatures are quenched by the coupling, as can be seen from the same figures. The outer error bars correspond to the standard deviations of the instantaneous temperatures from their average values determined from microcanonical simulations, while the inner error bars show the standard deviations measured in the simulations with coupling to the temperature bath. It can be seen that the quenching decreases with increasing time constant. At a time constant of $\tau_T = 0.5$, almost no quenching is perceptible any more. Furthermore, in the discontinuous WC simulation, the quenching is reduced as well.

The discontinuous energy coupling is computationally less efficient. The correlation length of kinetic energy fluctuations is long. 500 time steps between the scaling steps

proved to be necessary in order to have a kinetic energy, which is independent of the previously visited subensembles. In order to have the same convergence of the averages as in the continuous coupling, the simulations had to be performed one order of magnitude longer. Thus, the gain in stability and efficiency of a continuous coupling scheme results in a loss of information on the system and in a decline of the quality of sampling of the ensemble. In the following, the corresponding analyses for the trajectories produced by the CPWC algorithm are presented. As reference values for the extracted thermodynamic quantities serve data obtained from the equation of state of the Lennard-Jones fluid by Nicolas *et al.* [21].

The choice of the simulation parameters n_1, n_2, n_3 did not prove to be critical for the stability of the algorithm within the investigated range. However the quality of the reproduction of the thermodynamic quantities suffers if they are chosen much smaller than in the present simulations. The values of n_1, n_w and the coupling constant α_N control mainly the fluctuations in the number of particles. The efficiency of the sampling along the particle number degree of freedom is affected by their choice, and the quality of the approximation of the GCE distribution is influenced as well.

The number of particles during a typical simulation is shown in Figure 3. The observed density distributions in two typical simulations are shown in Figure 4. In all three simulations the excess chemical potential μ^{ex} is set to -0.8. The observed probability distributions are shown together with the theoretically expected distribution, a Gaussian with variance $\sigma_\rho^2 = \langle N \rangle^2 k_B T \kappa_T V^{-3}$. $\langle N \rangle (= 216)$ denotes the average number of particles and $V(= 288.0)$ is the volume of the simulated box. The isothermal compressibility $\kappa_T (= 0.0945)$ is extracted from the equation of state of Nicolas *et al.* [21]. The width of the distribution depends on the parameters. With all residual parameters being equal, $\alpha = -5$ yields density fluctuations of $\sigma_\rho = 0.025$ and

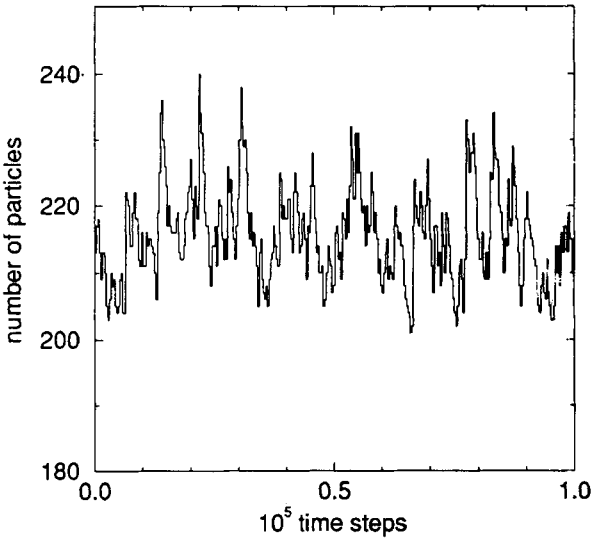

Figure 3 Evolution of the number of particles during a typical chemical potential weak coupling (CPWC) simulation ($T = 1.3$, $\tau_T = 0.1$, $\mu^{ex} = -0.8$, coupling constant $\alpha_N = -5$).

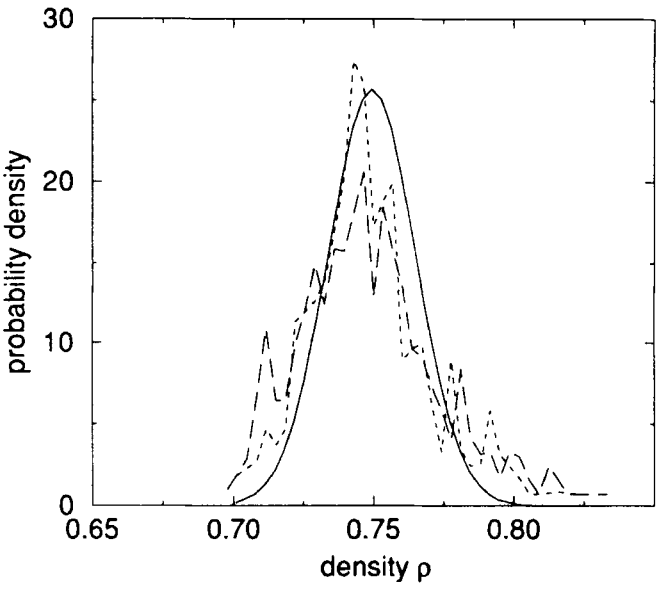

Figure 4 Density fluctuations in chemical potential weak coupling (CPWC) simulations at $T = 1.3$, $\tau_T = 0.1, \mu^{ex} = -0.8$; short-dashed: coupling constant $\alpha_N = -3$; long-dashed: $\alpha_N = -5$; full line: theoretically expected distribution.

$\alpha = -3$ yields $\sigma_\rho = 0.02$. These numbers have to be compared with the theoretical value of $\sigma_\rho = 0.015$.

The thermodynamic quantities pressure, total energy per particle and number of particles are reproduced correctly, as can be seen from Figure 5. The slight deviations can be attributed to the non-linear behaviour of the mean Boltzmann factor as a function of the density and to insufficient sampling. The energies and the densities are averages over the total trajectory. The pressure is the average over all sampling periods of n_1 steps. If the pressure is calculated fom all time frames, the resulting value is up to 15% above the equilibrium value. This artefact is due to the overlap of particles during the insertion of new particles. In spite of the scaling, the insertion of particles disturbs the system locally. A slower scaling (i.e. growing or shrinking) of these particles would keep the system closer to equilibrium. However, a slow scaling rate results in a slow equilibration. Since the energy is not affected, as can be seen in Figure 5.a), and since the deviations from the equilibrium value of the virial decay very fast, it is not worthwhile reducing the scaling rate. In order to have an efficient simulation procedure, it is advantageous to use a fast scaling and to sample quantities that are highly sensitive to the insertion of new particles only during the n_1 MD steps of the sampling period of the algorithm.

In Figure 6, the instantaneous values of the $MBF(N(t))$ averaged over all values obtained from configurations having an identical density are shown as a function of the density. The plots are shown for two simulations at $\mu^{ex} = -0.8$ with coupling constant $\alpha_N = -3$ (a) and $\alpha_N = -5$ (b). It can be seen that the solid line, representing the averaged $MBF(N)$, fluctuates around the dashed line, representing the expected

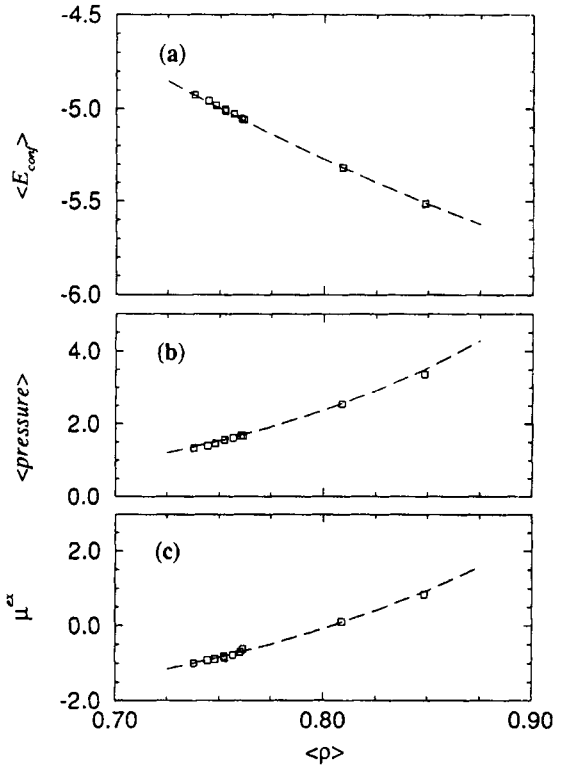

Figure 5 Comparison of thermodynamic quantities as a function of density ρ obtained by chemical potential weak coupling (CPWC) at the temperature $T = 1.3$ to values from the literature. a) Configurational energy per particle; b) pressure; c) excess chemical potential. Dashed: curves corresponding to the equation of state of Nicolas *et al.* [21]. □: values computed using chemical potential weak coupling (CPWC) with a coupling constant $\alpha_N = -5$. The quantities in brackets denote ensemble averages, all values are in reduced units.

average according to the equation of state of Nicolas *et al.* [21]. Since the isothermal compressibility κ_T can be expressed as [14]

$$\kappa_T = \left(\rho^2 \left(\frac{\partial \mu}{\partial \rho}\right)_T\right)^{-1} \tag{12}$$

using (eq.8) and

$$\frac{\partial \mu^{id}}{\partial \rho} = \frac{k_B T}{\rho} \tag{13}$$

and respecting (eq. 7) it is possible to extract κ_T from the averaged $MBF(N)$. By taking the slope of a linear regression through $-k_B T \ln(MBF(N))$ as approximation of μ^{ex}, one finds for simulation (a) in Figure 6 $\kappa_T = 0.160$ and for simulation (b) $\kappa_T = 0.101$. These values have to be compared with the value extracted from the equation of state of Nicolas *et al.* [21]: $\kappa_T = 0.0945$. The deviations are due to the limited simulation time which was not sufficient to obtain the averaged $MBF(N)$ completely converged.

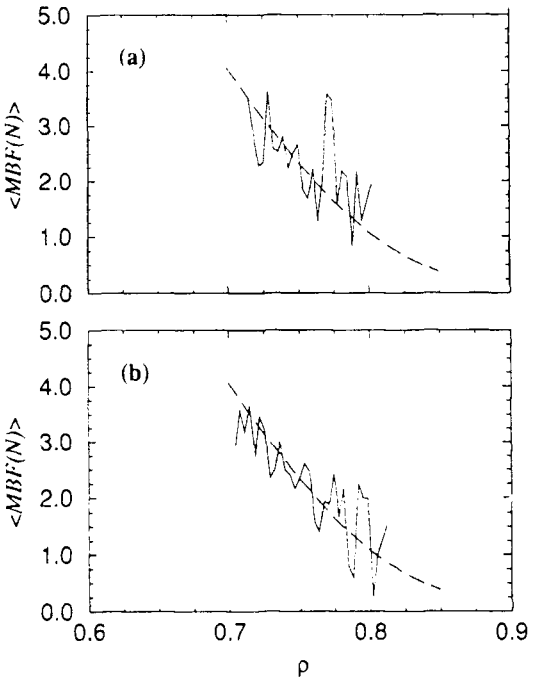

Figure 6 Comparison of expected with observed density dependence of the instantaneous measure of the chemical potential ($\langle MBF(N(t))\rangle$) during two typical chemical potential weak coupling (CPWC) simulations at $T = 1.3$, $\mu^{ex} = -0.8$. a) Coupling constant $\alpha_N = -3$; b) $\alpha_N = -5$. Dashed: expected dependence (mean Boltzmann factor (MBF) according to the equation of state of Nicolas *et al.* [21]); full line: observed dependence. All values are in reduced units.

6 CONCLUSION

A new method, chemical potential weak coupling (CPWC), has been developed to perform MD simulations at constant chemical potential. The presented method is applied and tested on a Lennard-Jones fluid. The thermodynamic quantities known from the literature are accurately reproduced.

The approach is based on a first order coupling to a particle bath, yielding a fast and easy to control convergence of the thermodynamic averages. The spurious oscillations found in the second-order extended system approach [6], are avoided. The applied gradual insertion of particles by scaling their Lennard-Jones interactions from zero to their real values tends to preserve dynamical quantities as in the extended system approach.

Both types of weak coupling (WC) simulations, the CPWC and the constant temperature WC simulations, show that the reproduction of thermodynamic averages is not sensitive to the particular choice of the coupling parameters. The sizes of the fluctuations, however, are affected by their choice. In WC, the direct relation between the width of the fluctuations and the related susceptibility is lost in favour of an improved convergence of the averages. However, the information on the susceptibility

in WC is not lost a priori. Provided that the scaling of the velocities and the number of particles, respectively, are performed after extensive sampling of a subensemble, the analysis of the distribution can still yield their values.

From the simulations with coupling to a temperature bath, it can be seen that both, the continuous and the discontinuous coupling, yield the correct total averages. However, in the case of continuous coupling, the slope of the average kinetic energy as a function of the total energy has no relation to C_v any more. It can be concluded that simulations with continuous coupling to a temperature bath have the advantage of being highly efficient and stable, but that they have the disadvantage of lowering the quality of the sampling.

The influence of the coupling parameters on the fluctuations can also easily be seen in the weak coupling to a temperature bath, as demonstrated in this paper. The sampling of the ensemble can be optimized. With a judicious choice of the coupling parameters, the width of the fluctuations can be adjusted to the one expected from ensemble theory and the corresponding experimental susceptibility. However, since the averages of most thermodynamic quantities are not affected by the choice of the parameters, it is not worthwhile to pursue a further optimization of the coupling parameters.

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