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Molecular

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1 Some algorithm for molecular dynamics

1.1 Closed methods

1.1.1 Euler's method

1.1.2 Modified Euler's method

1.1.3 Gear algorithm

1.2 Open methods

1.2.1 Verlet algorithm

1.2.2 Leap-frog algorithm

1.2.3 Beeman algorithm

2 Invariant molecular dynamics with variable cell shape

2.1 Andersen's approach

It was Anderson who first extends the molecular dynamics field to ensembles other than micro-canonical ensemble.[1] In his ground-breaking paper, he proposed ways to calculate properties average over isoenthalpic-isobaric (NPH) ensemble. In the article, he introduced a Lagrangian

$$\mathcal{L}(\rho, \dot{\rho}, Q, \dot{Q}) = \frac{1}{2}mQ^{\frac{2}{3}} \sum_{i=1}^N \dot{\rho}_i \cdot \dot{\rho}_i - \sum_{i<j=1}^N u(Q^{\frac{1}{3}}\rho_{ij}) + \frac{1}{2}M\dot{Q}^2 - \alpha Q, \quad (1)$$

where $\rho_i = \mathbf{r}_i/V^{\frac{1}{3}}$, $i = 1, 2, \dots, N$, is called scaled coordinates. Here α and M are constants, $\frac{1}{2}M\dot{Q}$ now is regarded as a kinetic energy with fictitious mass M , and αQ is regarded as a potential energy for the motion of Q . The generalized momentum conjugate to ρ is

$$\pi_i = \frac{\partial \mathcal{L}_2}{\partial \dot{\rho}_i} = mQ^{\frac{2}{3}}\dot{\rho}_i, \quad (2)$$

and which for Q is

$$\Pi = \frac{\partial \mathcal{L}_2}{\partial \dot{Q}} = M\dot{Q}. \quad (3)$$

The Hamiltonian is thus

$$\begin{aligned} \mathcal{H}(\rho, \pi, Q, \Pi) &= \sum_{i=1}^N \pi_i \cdot \dot{\rho}_i + \Pi \dot{Q} - \mathcal{L}_2(\rho, \dot{\rho}, Q, \dot{Q}) \\ &= \frac{1}{2mQ^{\frac{2}{3}}} \sum_{i=1}^N \pi_i \cdot \pi_i + \sum_{i<j=1}^N u(Q^{\frac{1}{3}}\rho_{ij}) + \frac{1}{2M}\Pi^2 + \alpha Q. \end{aligned} \quad (4)$$

So the equations of motions are

$$\dot{\rho}_i = \frac{\partial \mathcal{H}}{\partial \pi_i} = \frac{\pi_i}{mQ^{\frac{2}{3}}} \quad (5)$$

$$\dot{\pi}_i = -\frac{\partial \mathcal{H}}{\partial \rho_i} = -Q^{\frac{1}{3}} \sum_{\substack{j=1 \\ j \neq i}}^N \frac{u'(\rho_{ij})}{|\rho_{ij}|} \quad (6)$$

$$\dot{Q} = \frac{\partial \mathcal{H}}{\partial \Pi} = \frac{\Pi}{M} \quad (7)$$

$$\dot{\Pi} = -\frac{\partial \mathcal{H}}{\partial Q} = -\frac{1}{3Q} \left(-\frac{1}{mQ^{\frac{2}{3}}} \sum_{i=1}^N \pi_i \cdot \pi_i + Q^{\frac{1}{3}} \sum_{i<j}^N \rho_{ij} u'(Q^{\frac{1}{3}}\rho_{ij}) + 3\alpha Q \right) \quad (8)$$

With these equations, the trajectory of the scaled system are given by $\rho(t)$, $\pi(t)$, $Q(t)$, and $\Pi(t)$.

Use this trajectory, any function's time average are given by

$$\overline{G} = \lim_{T \rightarrow \infty} \frac{1}{T} \int_0^T dt G(\rho(t), \pi(t), Q(t), \Pi(t)), \quad (9)$$

and this can be given by the average of an NE ensemble. That is,

$$G_{NE}(N, E) = \frac{1}{N! \Omega(N, E)} \int d\rho \int d\pi \int dQ \int d\Pi \delta(\mathcal{H}(\rho, \pi, Q, \Pi) - E) G(\rho(t), \pi(t), Q(t), \Pi(t)), \quad (10)$$

where

$$\Omega(N, E) = \frac{1}{N!} \int d\rho \int d\pi \int dQ \int d\Pi \delta(\mathcal{H}(\rho, \pi, Q, \Pi) - E). \quad (11)$$

The scaled system has a correspondence

$$V = Q, \quad (12)$$

$$\mathbf{r}_i = Q^{\frac{1}{3}} \mathbf{p}_i, \quad (13)$$

$$\mathbf{p}_i = \boldsymbol{\pi}_i / Q^{\frac{1}{3}} \quad (14)$$

to the phase space of a system spanned by $\mathbf{r}_i, i = 1, \dots, N$ and $\mathbf{p}_i, i = 1, \dots, N$, where \mathbf{r}_i is the particle coordinate, \mathbf{p}_i is its momentum. Thus the trajectory $\rho(t), \pi(t), Q(t)$, and $\Pi(t)$ have its correspondence $V(t), \mathbf{r}_i(t)$ and $\mathbf{p}_i(t)$ by (12). Since the time average \overline{F} of any function F derived by this trajectory is the same as an isoentahpic-isobaric ensemble average of F_{NPH} , and $\overline{G} = \overline{F}$, thus we get the NPH ensemble average. The ensemble pressure P is α in (1) indeed.

2.2 Rahman and Parrinello's approach

Rahman and Parrinello then proposed a method to perform MD simulations which allows volume and shape of the MD cell to change with time.[2] If the MD cell edges are \mathbf{a}, \mathbf{b} and \mathbf{c} , which are time dependent. Stack them to form a matrix $h = \{\mathbf{a}, \mathbf{b}, \mathbf{c}\}$, and the volume of a cell is then $\Omega = \mathbf{a} \cdot \mathbf{b} \times \mathbf{c}$, the metric tensor is $g = h^T h$. Let $\mathbf{r}_i = \xi_i \mathbf{a} + \eta_i \mathbf{b} + \zeta_i \mathbf{c} = h \mathbf{s}_i$, where \mathbf{s}_i store its coordinates ξ_i, η_i , and ζ_i , each from 0 to 1. Then they introduced a Lagrangian

$$\mathcal{L} = \frac{1}{2} \sum_{i=1}^N m_i \dot{\mathbf{s}}_i^T g \dot{\mathbf{s}}_i - \sum_{i=1}^N \sum_{i < j} \phi(r_{ij}) + \frac{1}{2} W \text{Tr}(\dot{h}^T \dot{h}) - P \Omega, \quad (15)$$

where $r_{ij}^2 = (\mathbf{s}_i - \mathbf{s}_j)^T g (\mathbf{s}_i - \mathbf{s}_j)$, P is the external hydrostatic pressure, $\phi(r_{ij})$ is the pair potential, W is the fictitious mass.

Then the equations of motion are

$$\ddot{\mathbf{s}}_i = \frac{1}{m_i} \sum_{j \neq i} \frac{\phi'(r_{ij})}{r_{ij}} (\mathbf{s}_i - \mathbf{s}_j) - g^{-1} \dot{g} \dot{\mathbf{s}}_i, \quad i, j = 1, 2, \dots, N, \quad (16)$$

$$\ddot{h} = \frac{1}{W} (\Pi - P) \sigma, \quad (17)$$

where $\sigma = \{\mathbf{b} \times \mathbf{c}, \mathbf{c} \times \mathbf{a}, \mathbf{a} \times \mathbf{b}\}$, matrix Π is given by

$$\Omega\Pi = \sum_{i=1}^N m_i \mathbf{v}_i \otimes \mathbf{v}_i + \sum_{i=1}^N \sum_{i<j} \frac{\phi'(r_{ij})}{r_{ij}} (\mathbf{r}_i - \mathbf{r}_j) \otimes (\mathbf{r}_i - \mathbf{r}_j), \quad (18)$$

with $\mathbf{v}_i = h\mathbf{s}_i$. Then Andersen's case is a special one of (16), where $h = \text{diag}(\Omega^{\frac{1}{3}}, \dots, \Omega^{\frac{1}{3}})$ and $g^{-1}\dot{g} = \frac{2\dot{\Omega}}{3\Omega}$. Though his equation for \ddot{V} cannot be obtained from (17). But this Lagrangian also results in a isoenthalpic, isobaric ensemble, though with a small correction from the third term.

2.3 Wentzcovitch's approach

Wentzcovitch stated that R and P's method is dependent on the choice of cell edges.[3] For different \mathbf{a} , \mathbf{b} , and \mathbf{c} , the fictitious kinetic energy K_L term could be different. For MD simulation of $\sim 10^2$ particles the problem may not be too serious. But if the cell experience a modular transformation, the nominal value of K_L , and the resulted forces and trajectories will be dependent on the choice of h . Then she proposed a new Lagrangian

$$\mathcal{L} = \sum_{i=1}^N \dot{\mathbf{q}}_i^T d \dot{\mathbf{q}}_i - \sum_{i=1}^N \sum_{i<j} \phi(r_{ij}) + \frac{W}{2} \text{Tr}(\dot{\epsilon} \dot{\epsilon}^T) - P\Omega, \quad (19)$$

where ϵ is the strain, \mathbf{q}_i is the defined as $\mathbf{r}_i = (1 + \epsilon)\mathbf{q}_i$, thus $d = (1 + \epsilon)^T(1 + \epsilon)$. The equations of motion are

$$\ddot{\epsilon} = \frac{\Omega}{W} (\Pi - P) ((1 + \epsilon)^T)^{-1}, \quad (20)$$

$$\ddot{\mathbf{q}}_i = -\frac{1}{m_i} \sum_{\substack{i,j=1 \\ j \neq i}}^N \frac{\phi'(r_{ij})}{r_{ij}} (\mathbf{q}_i - \mathbf{q}_j) - d^{-1} \dot{d} \dot{\mathbf{q}}_i. \quad (21)$$

An equivalent form of (19) is

$$\mathcal{L} = \frac{1}{2} \sum_{i=1}^N m_i \dot{\mathbf{s}}_i^T g \dot{\mathbf{s}}_i - \sum_{i=1}^N \sum_{i<j} \phi(r_{ij}) + \frac{1}{2} W \text{Tr}(\dot{h} f_0 \dot{h}^T) - P\Omega, \quad (22)$$

with $f_0 = \sigma_0^T \sigma_0$, where $\sigma_0 = \{\mathbf{a}_0 \times \mathbf{b}_0, \mathbf{b}_0 \times \mathbf{c}_0, \mathbf{c}_0 \times \mathbf{a}_0\}$.

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