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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

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

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

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

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

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

to the phase space of a system spanned by $\{\mathbf{r}_i\}$ and $\{\mathbf{p}_i\}$. 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.

References

- [1] H C Andersen. Molecular dynamics simulations at constant pressure and/or temperature. *The Journal of chemical physics*, 1980.
- [2] JW Dufty, JJ Brey, A Santos, G Ciccotti, and WG Hoover. Molecular dynamics simulation of statistical mechanical systems. In *Proc. Int. School of Physics Enrico Fermi, North-Holland, Amsterdam*, 1986.