

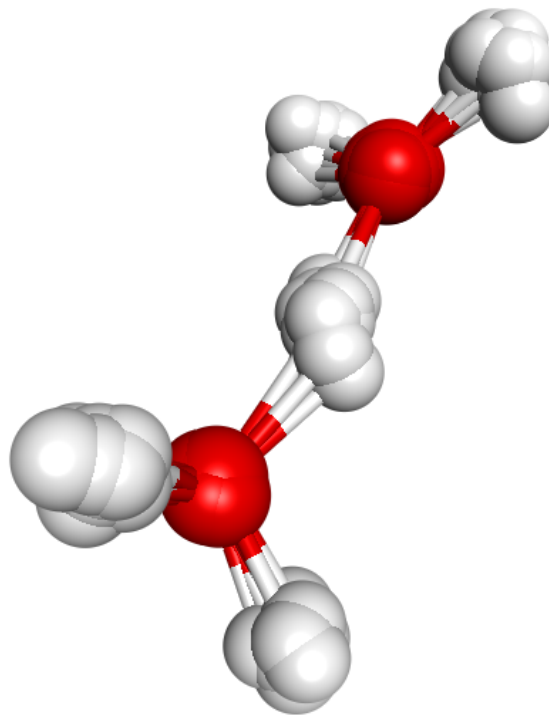
Path integral molecular dynamics (PIMD)

1. Calculation setup

The following setup is used.

- Method: PIMD
- Ensemble: NVT (canonical ensemble)
- Potential: SMASH (b3lyp/cc-pvdz)
- Number of beads: 16
- Boundary: free boundary condition
- System: protonated water dimer

A snapshot is shown below.



2. Results

As shown below, the total energy, the potential energy, the instantaneous temperature and the wall clock time of each step are printed in “standard.out”.

step	energy [au]	potential [au]	temp [K]	wall clock time
0	-152.18893397	-153.07017355	300.00	2016-04-25 月 09:12:32.28
1	-152.18894445	-153.07123665	302.08	2016-04-25 月 09:12:55.69
2	-152.18896233	-153.07337533	307.25	2016-04-25 月 09:13:18.87
3	-152.18898309	-153.07630145	314.45	2016-04-25 月 09:13:42.26
4	-152.18900223	-153.07961072	320.76	2016-04-25 月 09:14:05.64
5	-152.18901748	-153.08290248	324.19	2016-04-25 月 09:14:29.18
6	-152.18902891	-153.08590948	325.73	2016-04-25 月 09:14:52.62
7	-152.18903723	-153.08851938	326.82	2016-04-25 月 09:15:15.31
8	-152.18904302	-153.09070411	327.54	2016-04-25 月 09:15:38.60
9	-152.18904660	-153.09245733	327.80	2016-04-25 月 09:16:01.40
10	-152.18904804	-153.09377275	327.60	2016-04-25 月 09:16:24.70

...omitted...

The figure in the next page is the hydrogen bond fluctuation shown as the two-dimensional distribution with respect to the vertical axis Δr_{OH} (see below figure) and the horizontal axis r_{OO} .

