

Ab initio molecular dynamics

So far all simulation have been static or either minima or transition state search. So no real dynamics of the molecules have been considered. The ab initio molecular dynamics is still easy since we can use the BO approximation (the electronic Schrödinger equation can be solved with fixed atomic positions) which allows the classical treatment of the atoms. Now the dynamics can be described with Newton's equation

$$F = ma$$

With given atom configuration we can compute the forces and update the atomic positions with some algorithm. One of the simplest one is the Verlet algorithm

$$R_I(t + \Delta t) = 2R_I(t) - R_I(t - \Delta t) + \frac{F_I(t)}{m_I} \Delta t^2 + O(\Delta t^4)$$

The main point is that the position update have to be done very often. The Δt is very small, typically 1 fs. So to simulate 1 s we need 10^{15} steps! This is not possible but of course shorter simulation times are possible. In AIMD the simulation time scales are ca. 100 ps (and up to 1 ns). Naturally the size of the system affect a lot of the total time scale. In AIMD systems of few 100 water molecules can be simulated. (And this is hard to improve due to the at least N^3 scaling of the AI methods.)

The method above is called AIMD or BO-AIMD. It main bottle neck is the wave function optimization since at every MD step one need to solve the DFT (or equivalent) equations. So it is essential that the optimizer is fast and the information of the previous MD steps are used effectively.

We can mark the optimized as $\psi_{new} = \text{Opt}(\psi_n; R_I)$ which solves the new wave functions corresponding the atomic positions R and guess wave function ψ_n . In AIMD the simplest case is

$$\psi_n(t + dt) = \text{Opt}[\psi_n(t), R_I(t + dt)]$$

But this is not very effective. It is better to extrapolate the guess wave function. With two wave functions

$$\tilde{\psi}_n = 2 * \psi_n(t) - \psi_n(t - dt) + O(dt^2); \quad \psi_n(t + dt) = \text{Opt}[\tilde{\psi}_n, R_I(t + dt)]$$

Or more general (typically: $n=3,4$)

$$\tilde{\psi}_n = F_n[\psi_n(t), \psi_n(t-dt), \psi_n(t-2dt), \dots, \psi_n(t-ndt)]; \quad \psi_n(t+dt) = \text{Opt}[\tilde{\psi}_n, R_I(t+dt)]$$

This gives an extra complication to BO-AIMD. If the electronic structure of the system is difficult to converge the AIMD is slow. So the insulators and semiconducting materials are easy but metals are not.

There is also another way to do AIMD. In 1985 R. Car and M. Parrinello suggest so called Car-Parrinello (CP) method. In this methods all the parameters (atoms and electronic) are treated as dynamical variables (they can be updated with Newton's equations). The electronic parameters are the coefficients of the basis set $\psi_n(t) = \sum_i C_{n,i}(t) \xi_i(R)$. Now one can compute the forces for all parameters (E_{KS} is the Kohn-Sham energy)

$$R_I = -\frac{\partial E_{KS}}{\partial R_I}, \quad F(C_i) = -\frac{\partial E_{KS}}{\partial C_i} + \sum_j \Lambda_{ji} C_j; \quad F = M\ddot{R}, \quad F(C) = \mu\ddot{C}$$

The additional terms in the electronic force comes from the wave functions orthonormality constraints. If one optimize the wave functions at the beginning one can follow the CP dynamics ever since. The CP method works surprisingly well for insulators and semiconductors. Even metallic systems can be done but one need to keep the "temperature" of the electronic system in control. The key parameter in the CP method is the mass μ of the electronic parameters. This need to be much smaller that the mass of atoms. Typically value of 300 m_e (mass of electron) is used. Then the adiabatic effect is valid. This means that the light particles will follow the movements of heavier particles. (A classic example it the planetary system.) Unfortunately the light mass force the usage of small time step. The CP time step is typically 0.1-0.15 fs. Also in CP one electronic update is needed so if BO-AIMD method require less than ca. 10 iterations then it is faster. The algorithms used in BO-AIMD has improved and it is now better than CP. CP has also some problems with slow heating of the electrons, so CP is not used much. The CP is also problematic with atom centered basis functions.

The 100 ps time scale is very short for most of the chemical reactions. If realistic reaction attempt frequency is 1 ps, in room temperature ($RT=2.4$ kJ/mol) barrier of 11 kJ/mol will lead to reaction time scale of 100 ps ($\tau_0 \exp(-\Delta E/RT)$). Seldom it is

realistic to do AIMD simulations for chemical reaction and some constrained methods are needed. (We discuss them later.) But there are several systems in which the molecular movement is important. Of these the most important are liquids. In liquids it is essential that the molecules will move. At the moment only liquids consist of small molecules like water, methanol, ammonia, ethanol, are possible to simulate for reasonable time scales. Of course the key component is the number of electrons. In water there is 8 valence electron in methanol (14 valence e), ethanol (20 e), dichloro-ethane (26 e). These are doable but systems like ionic liquids are not (well even they have been simulated with AIMD).

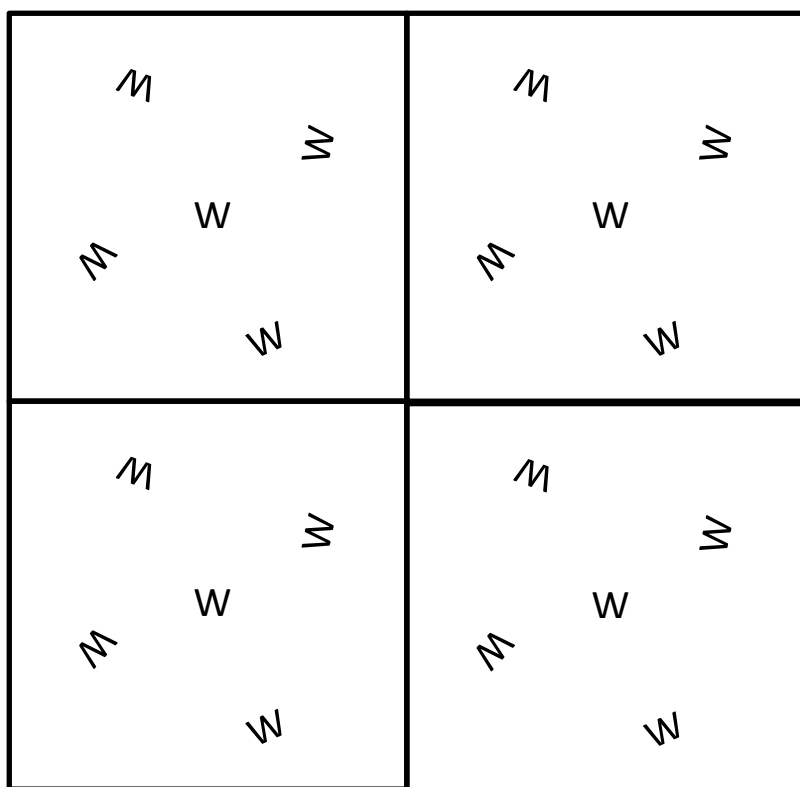
DFT Approximations

The AIMD simulations are mostly done with DFT-GGA models (BLYP, PBE). Also the hybrid simulations, like B3LYP, PBE0 are possible but they are time consuming. It is almost mandatory to use the empirical van der Waals corrections (Grimme generation 3, -G3). Because the DFT converge rapidly with the basis functions the key approximation is the used DFT model.

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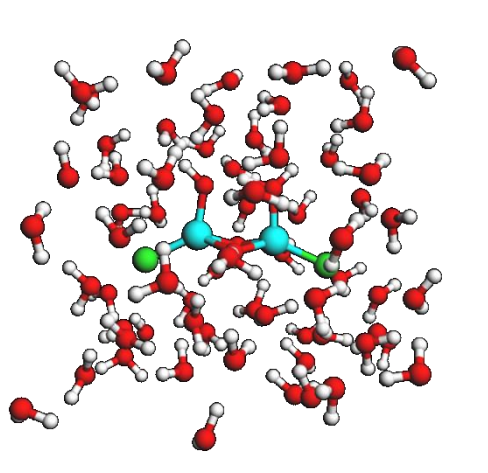
AIMD can be applied to any system but the solid systems are not very interesting since very little happen on the AIMD time scale. One can study light atom, like Li, diffusion but even that is better to do with some constraint. So one can push the atom to some direction and monitor the constraint force.

Small molecular cluster are rather interesting. Especially water clusters but not much AIMD simulations were done. The most common systems are the liquids. In liquid systems the periodic boundaries are used. For the electronic structure the Γ -point $k=(0,0,0)$, is almost always used but other k-point sampling is possible. The system should contain at least 100 molecules and preferably 200+ molecules. The minimum time scale for pure liquids relaxations is ca. 5 ps water to 25 ps for ethanol. But if there is some ions in the system the equilibration time is much longer. Like 50-100 ps.

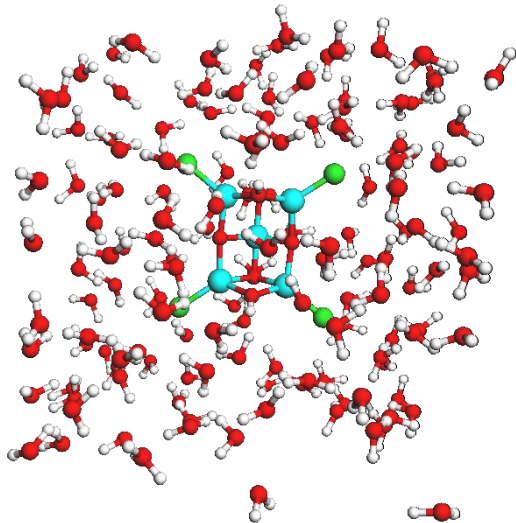


A very small system: Al₂-Cl₂-OH molecule + 65 water molecules.

This system is so small that the molecule will fit to the box but not the solvation layers of the Cl atoms. It is not so easy to see this from a static picture.



A larger system: Al₄-Cl₄-OH-O molecule and 144 water molecules.

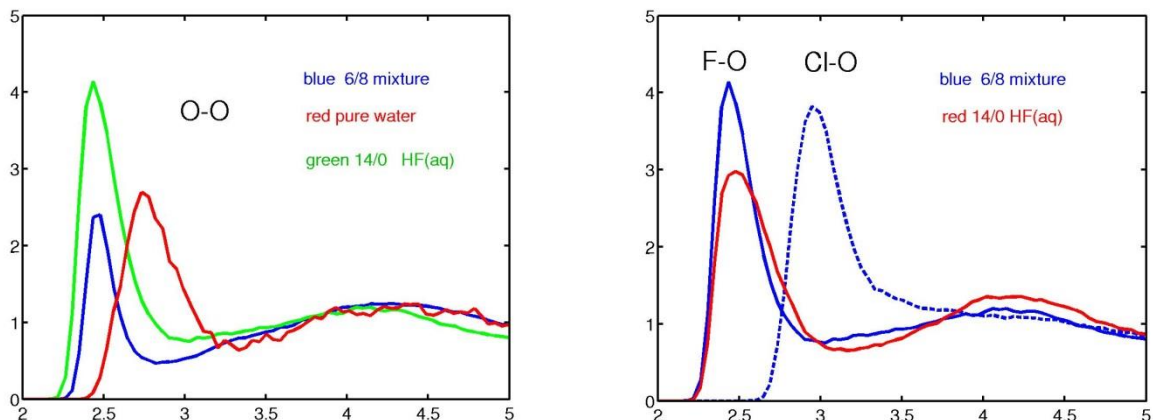


What can be learned from AIMD?

Almost anything.

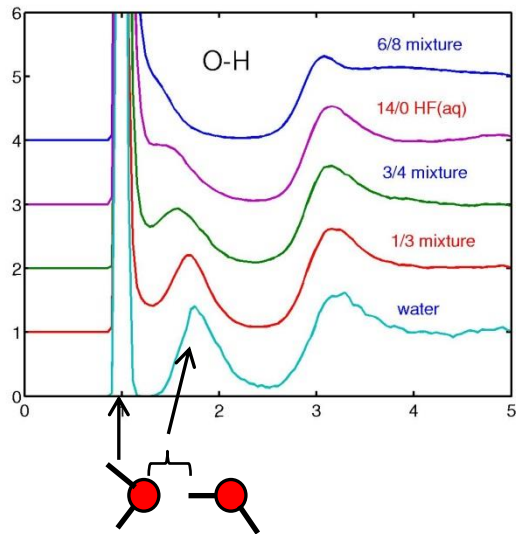
The most important quantity is the pair correlation function. It describes the atoms radial probability distribution. It tells how likely that atom B is at distance d from atom A.

Below there is O-O and FO pair correlation functions of water, concentrated HF (44 at%) and HF/HCl (HF 19 at%, HCl 25 at%). Here we see that that the O-O distance will reduce a lot.



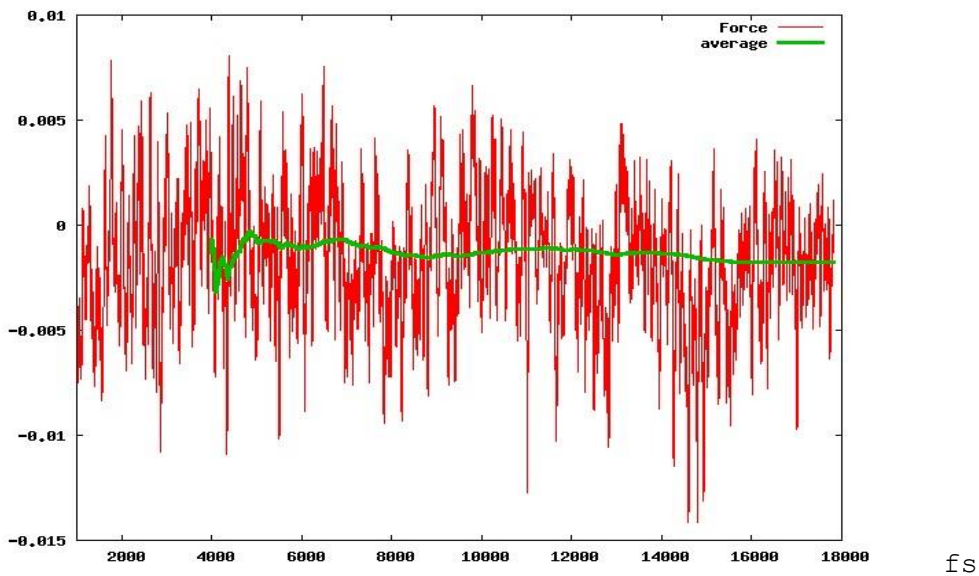
The OH pair correlation is even more interesting. The most interesting is the O...H-O peak. In pure water this peak is very clear but when the acid concentration (both HCl and HF) will increase this peak start moving towards the molecular O-H peak and highest concentration it merges to the H-O peak. This means that

the water molecules start losing their structure!! The hydrogen bonded hydrogen is almost as close to the O than the normal H.



Reaction in liquid

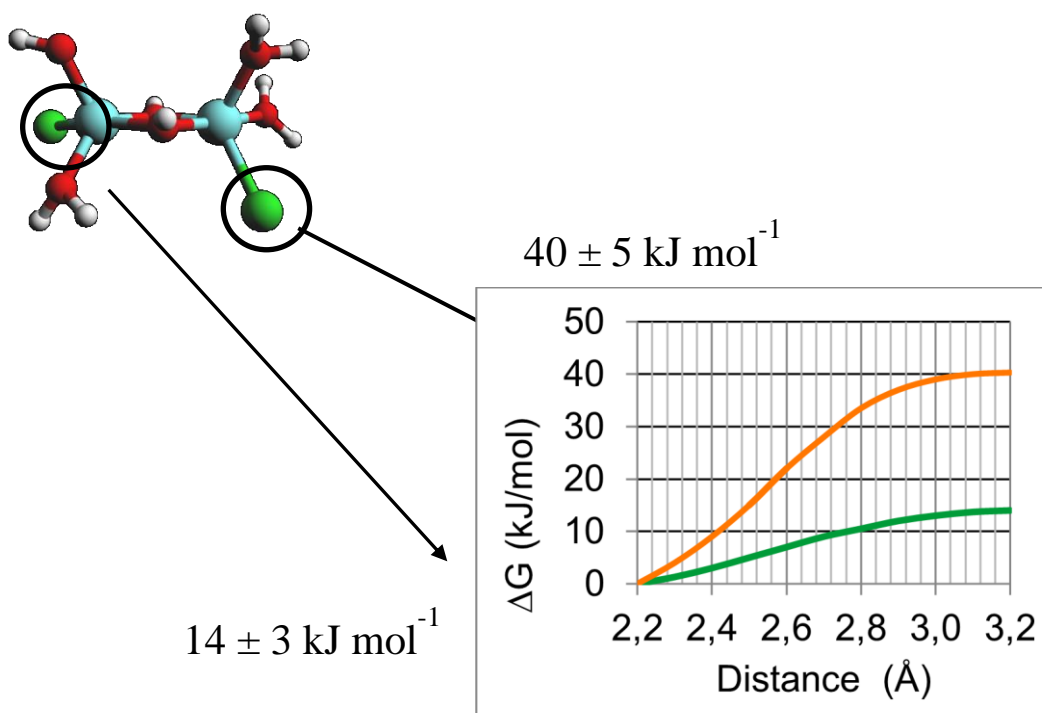
With AIMD one can study almost anything but one of the most interesting topic is the chemical reactions. As said earlier the direct simulations is usually far too slow and because all the atoms are moving the NEB type methods are not useful since they assume that everything else except than the path is in minimum. The simplest method is the constraint method where some constraint is imposed. The simplest constraint is the bond distance; $g = d(AB) - d_0$. ($d(AB)$ is the distance between the atoms and d_0 is the value of the constrain. Now one can do AIMD with this constraint and one need to monitor the force acting to the constraint. In this case it is easy $f_{\text{cons}} = (F_A - F_B) \cdot (R_A - R_B)$. Naturally the atoms will collide each other and this force is very noisy. One need to collect data for relatively long time (20-30 ps) to get a proper force; now we have $\langle f_{\text{cons}}(d_0) \rangle$.



Once we are happy with the $\langle f_{\text{cons}}(d_0) \rangle$ we can change the d_0 value. Then we collect statistics with this constraint etc. The free energy difference can be computed as an integral over the forces at each distance:

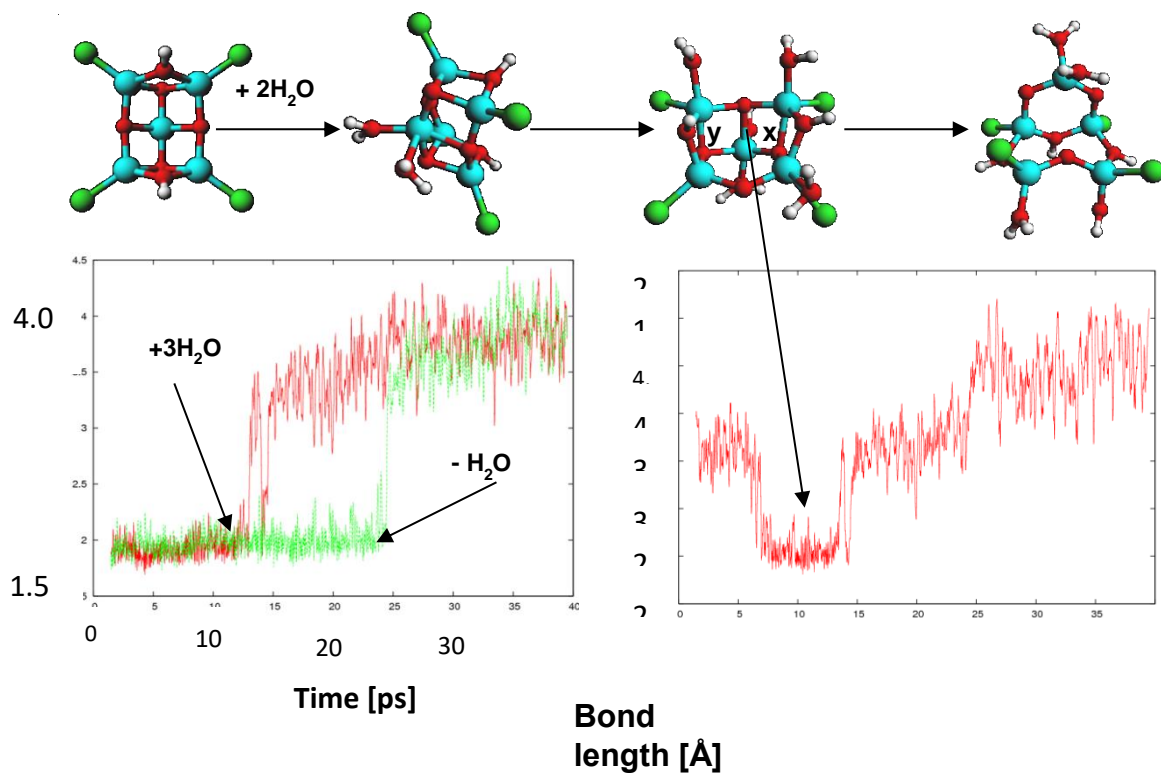
$$\Delta G = \int_{d_0}^{d_1} \langle f_{\text{cons}}(x) \rangle dx$$

The constraint method is very general and the constraint can be any function that depends on the atomic positions, like angle, torsional angle, coordination number, etc. The main problem of the method is that the real reaction coordinate is not a function of the constraint.



Al5O6Cl4 opening in water

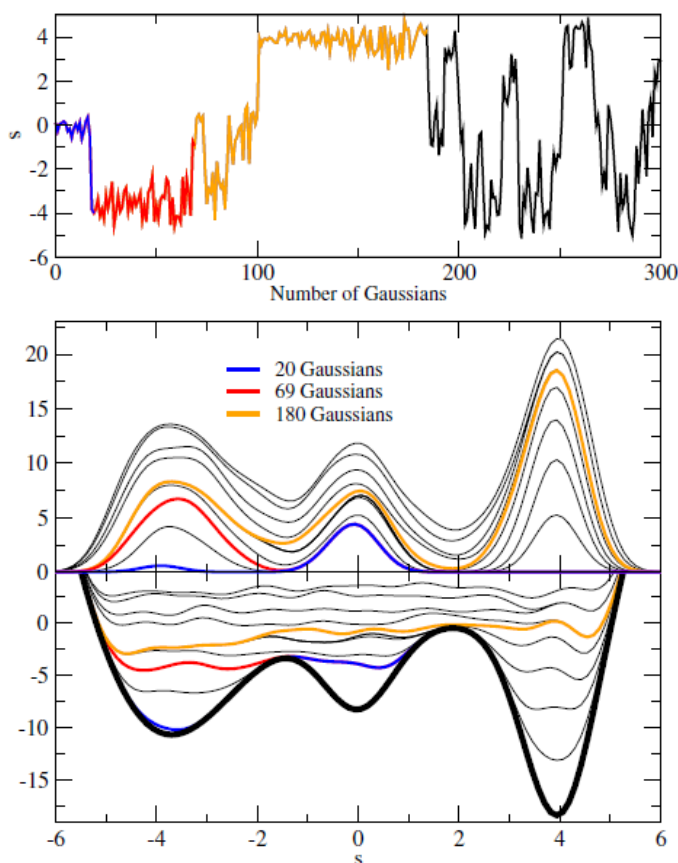
We noticed that a very symmetric Al5O6Cl4 structure dissociated in AIMD simulation. This is very surprising since the Al-O bond is very strong but this is a strong indication that the gas phase and solvation model calculations do not need to be reliable. We can do short simulations in water but this do not tell what the real structures in water really are.



Metadynamics

There are several methods for computing the Free energy barriers but we cannot go through all of them. I present one biased dynamics method, the Metadynamics. The Metadynamics has been developed by Laio and Parrinello (Laio ja Parrinello, PNAS, 2002). A good review article of the topic is Laio ja Gervasio, Rep. Prog. Phys. 71 126601 (2008))

The idea is to choose few collective variables (CV) to parametrize the reaction. The CV usually depend on atoms. Possible CV's can be atom distances, etc. The CV's have always some values and during the dynamics this value fluctuates. After some MD steps one adds a small repulsive Gaussian function to the CV's average value $\langle CV \rangle$. We will build a bias potential $V_{\text{bias}}(CV_1, CV_2, CV_3, \dots)$ during the simulation and this potential will push the system away from the starting minima. The smart thing is that we do not force the system to go any particular direction. We only "fill" the current minima. After the system has moved to a new minima we start filling that and the system will move to a new minima. After several steps we have a good map of the free energy. Providing that the CV have been reasonable. With one CV the Metadynamics is not very effective and same results can be found by scanning the CV with the constraint method. The key strength is that two (or more) CV's can be used. Naturally the Metadynamics become very time consuming with more CV's and typically two CV's are used.



Problem: why Metadynamics is not effective in 1-dim.

In more complex reaction the Metadynamics with 2 CV's is a good choice. But choice of the CV's is non-trivial. They need to represent well the real reaction coordinate which we do not know.

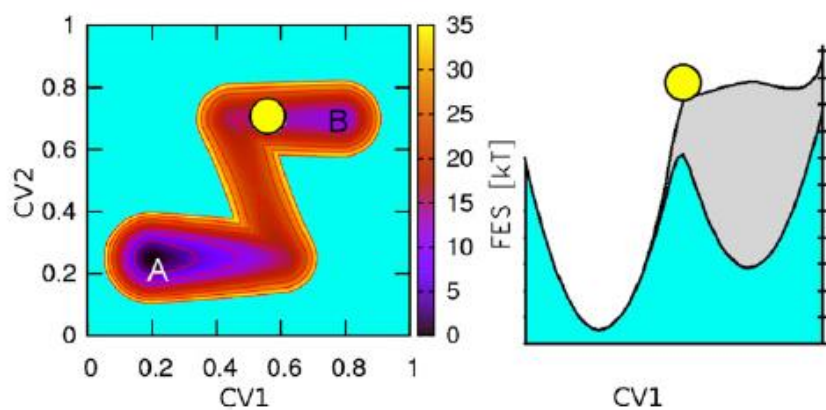
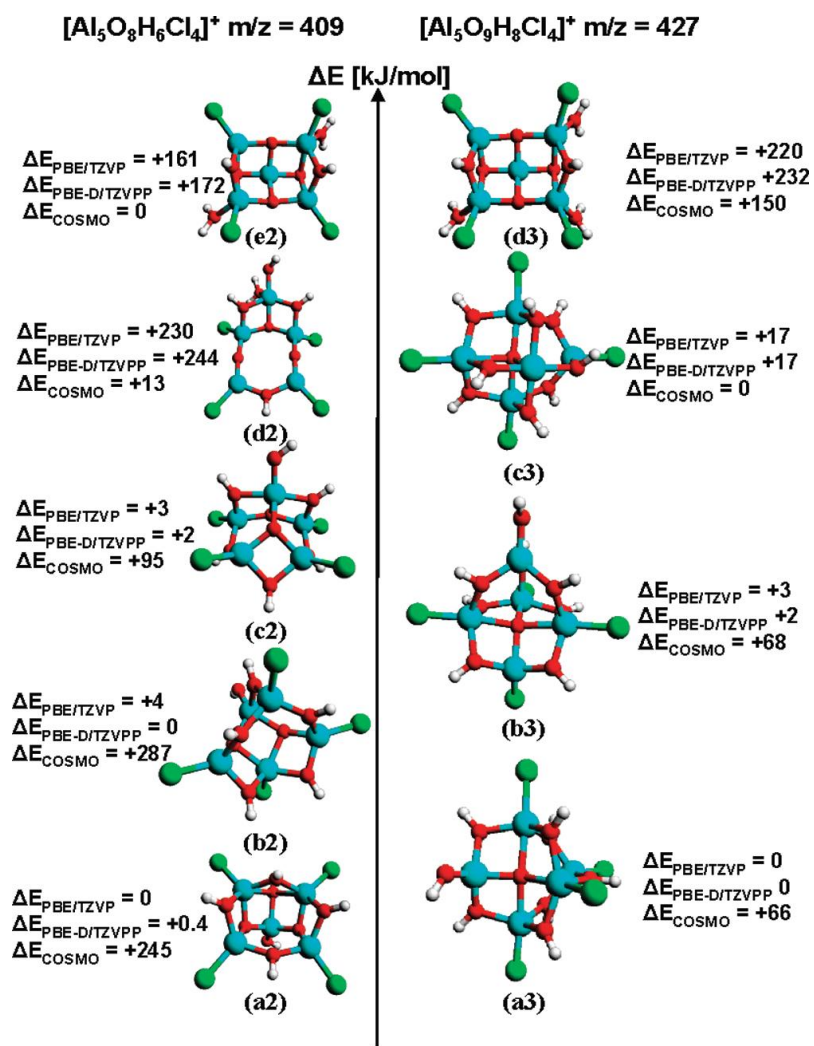


Figure 2. The effect of neglecting a relevant degree of freedom. Left side: 2D Z-shaped potential. Right side: the trajectory of a metadynamics simulation generated using only s_1 as CV. Transitions from A to B are properly described by CV1, causing strong hysteresis in the reconstructed free energy.

An example Al₃O_nH_m cluster

We have studied a lot of small Al_nO_mH_k clusters. Even a given cluster in gas phase have several structures and very little is known in their structures in water. The Mass Spectra data suggest also that there are huge amount of different clusters but the MS do not give information of the structures.



The clusters are prepared from $AlCl_3$ that is added to water. From this solution one can observe a huge amount of clusters (several hundreds) and they are of various sizes. Thus the $AlCl_3$ clusters will react rapidly in water. We wanted to understand what happens to the $Al_3O_nH_m$ cluster in water and we used Metadynamics for it. We had a good collection of the gas phase cluster structures but the clusters interact very strongly with water. So we start with the best gas phase cluster and placed that in water. We choose two CV's ($d(Al1-Al2)-d(Al2-Al3)$ and RMS deviation from the starting structure) and start a Metadynamics (MetaD) simulation.

The Free energy surface from the MetaD is below. It is not very reliable but it is indicative and it shows that this cluster has very many structures that are not very different in Free energy. It also shows that the MetaD is a good tool to map complex surfaces and we do not need to decide how the system will behave. There are also some problems in the structure A the cluster has broken and we do not think that the CV's can handle this.

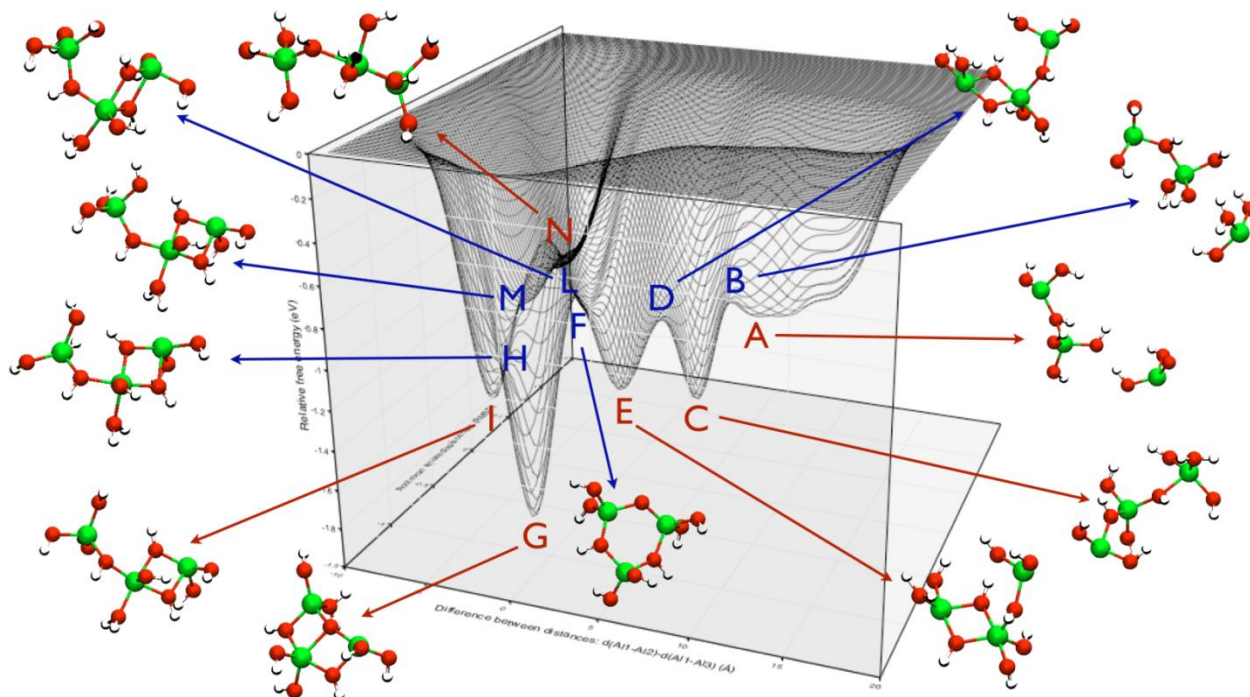


Figure: Free energy surface of Al₂O_nH_m in water, Lanzani et al. JPCC (2017)