

Metadynamics: a rare events exploration method

CLABAUT Paul

ENS de Lyon

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1 Why Metadynamics ?

- The problem of pure Ab Initio Molecular Dynamics (AIMD)
- The Metadynamics idea

2 How to choose a set of Collective Variables (CV)

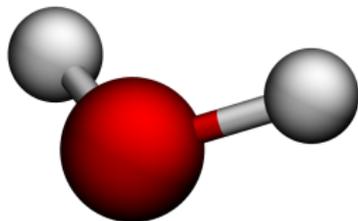
- What is a good CV ?
- Usual kinds of CV

3 Technical limitations and evolutions

- Error on the estimated free energy
- Advanced methods

Why Metadynamics ?

A problem of time scale



$$\nu_{\text{stretching}} \approx 10^{15} \text{ s}^{-1}$$

Typical times:

Simulation step: $t \approx 10^{-15} \text{ s}$

Simulated time: $t \approx 10^{-10} \text{ s}$

Simulation time: days to weeks

But:

Rare events: t up to 10^{-5} s

Rare events examples:

Chemical reactions

Phase transitions

Protein mechanisms

Beyond pure AIMD

Or

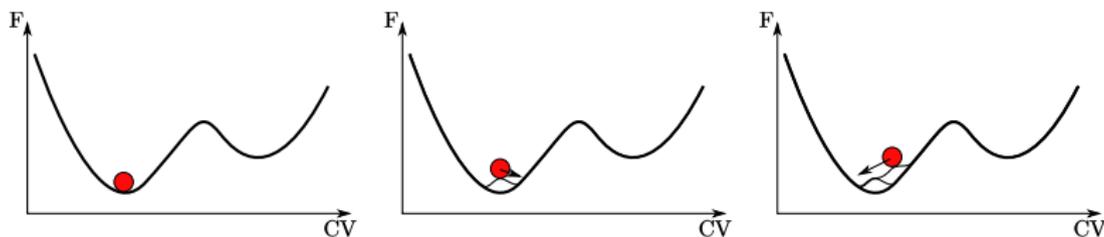
Coarse-grained models

Need of a detailed previous knowledge of the system

Rare events acceleration

- * Enhancing sampling along collective variables (CV)
- * Transition and reaction mechanism exploration
- * Potential energy surface exploration
- * Multiple temperature phase space exploration

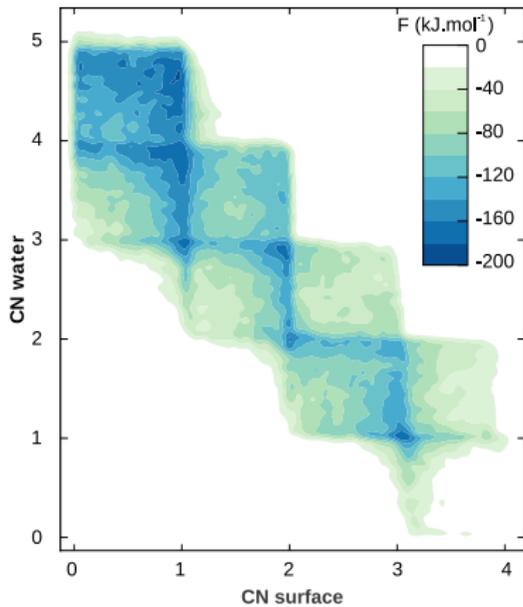
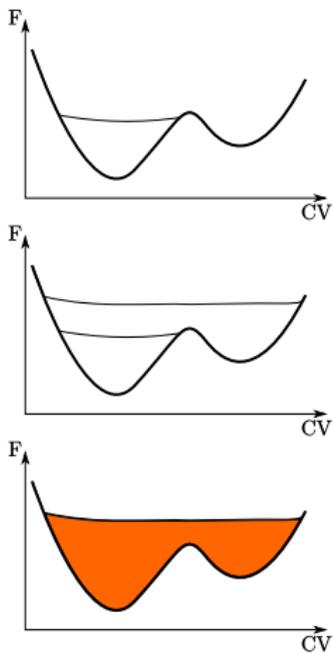
General idea



Steps:

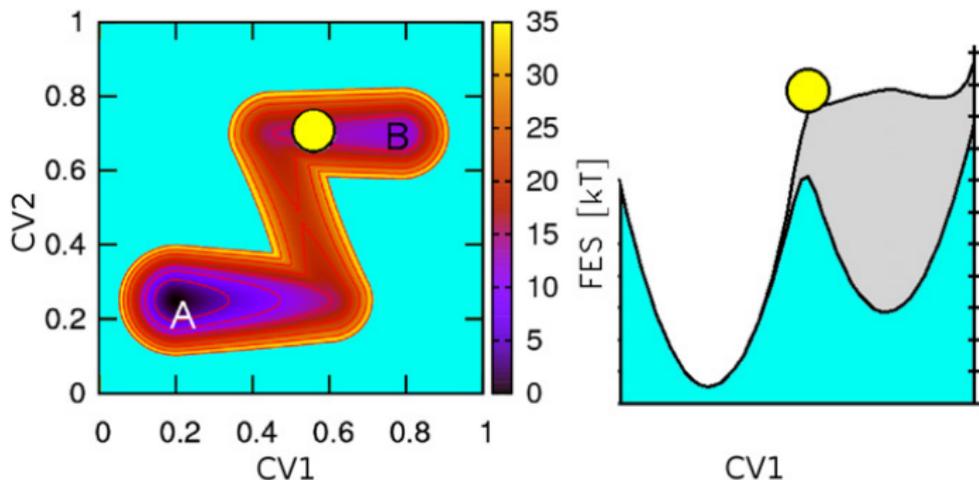
- I Computation of a step of length t of AIMD
- II Calculation of the position of the system in the reduced coordinates of the CVs and addition of it to the previous position list
- III Computation of the forces corresponding to the modification of the true potential energy by the gaussians and addition of them to the AIMD calculated forces.
- IV Moving to the next MD step with the biased force.

Result



How to choose a set of Collective Variables (CV)

The slow motions and the hysteresis problem



[Laio and Gervasio(2008)Laio, and Gervasio]

The rules of the CVs

3 rules for the CVs:

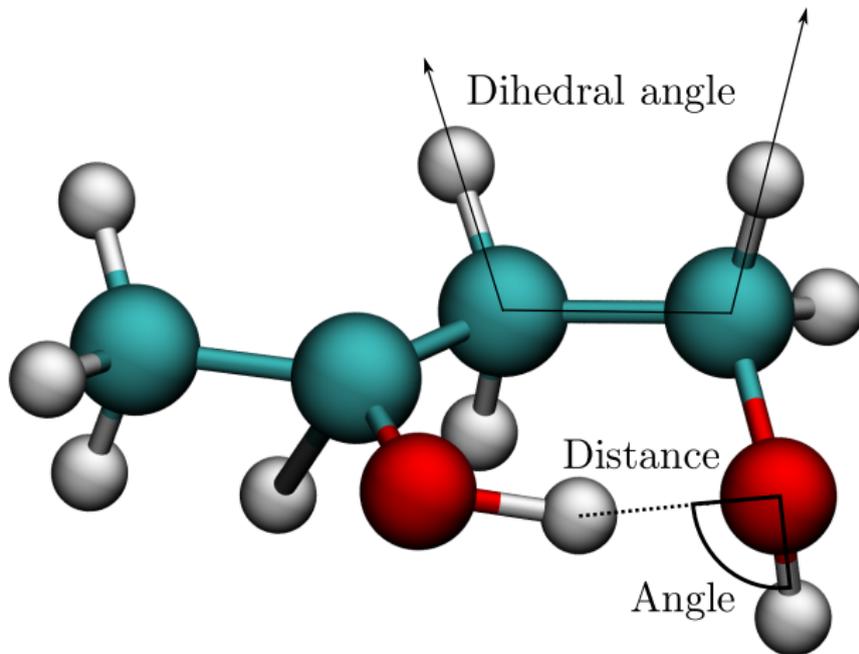
The chosen collective variables should clearly distinguish between the initial state, the final state and all the relevant intermediates.

They should describe all the relevant slow motions of the process.

Their number should be around 2 or 3 to involve a decent calculation time.

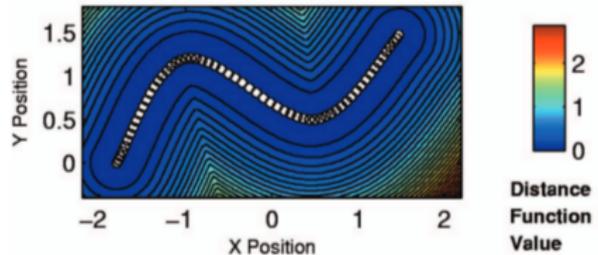
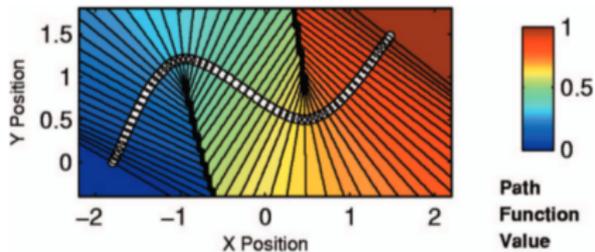
To choose the amplitude on which to sample the CV (and hence the width of the added gaussians along those CVs, a preliminary run at finite temperature should always be used).

Some classical types of CVs ...



... and some less usual...

Coordination number, number of H-bonds, potential energy, protein specific variables, normal modes, path coordinates...



[Branduardi et al.(2007)Branduardi, Gervasio, and Parrinello]

Technical limitations and evolutions

Error estimate and Well Tempered metadynamics (WT)

For a standard algorithm and with constant height gaussians:

$$\epsilon \propto \sqrt{\frac{\omega \cdot k_B \cdot T}{D}} \quad \text{with } \omega = \frac{W}{\tau_G}$$

But the Well Tempered method proposes a rescaling of W during the run:

$$W = \omega \cdot \tau_G \cdot e^{-\frac{V_G(S,t)}{k_B \cdot \Delta T}}$$

→ The dynamics gets closer to thermodynamic equilibrium along the run

→ Possibility to tune the exploration extent with ΔT

(ordinary MD $\xleftarrow{0} \Delta T \xrightarrow{\infty}$ ordinary metadynamics)

[Barducci et al.(2008)Barducci, Bussi, and Parrinello]

Scaling and multiple walkers

Method	Multiple walkers ¹	Parallel Tempering ²	Bias exchange ³
Difference between the walkers	None	Temperature	CVs considered
What is exchanged ?	Position of gaussians	System coordinates	Bias potential at a certain probability
Benefits	Highly parallelized calculation	Slow motion capture	Exploration of a great number of CVs

¹[Raiteri et al.(2006)Raiteri, Laio, Gervasio, Micheletti, and Parrinello],

²[Hansmann(1997)], ³[Piana and Laio(2007)Piana, and Laio]

Thank you for your attention !
Questions ?

References

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