

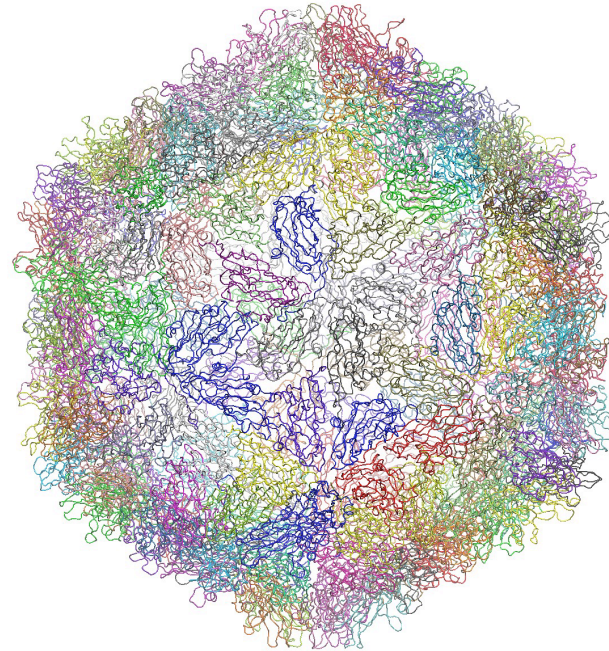
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AN $O(N)$ MULTI-SCALE N -BODY APPROACH FOR SIMULATING POLARIZABLE MICROSCOPIC SYSTEMS



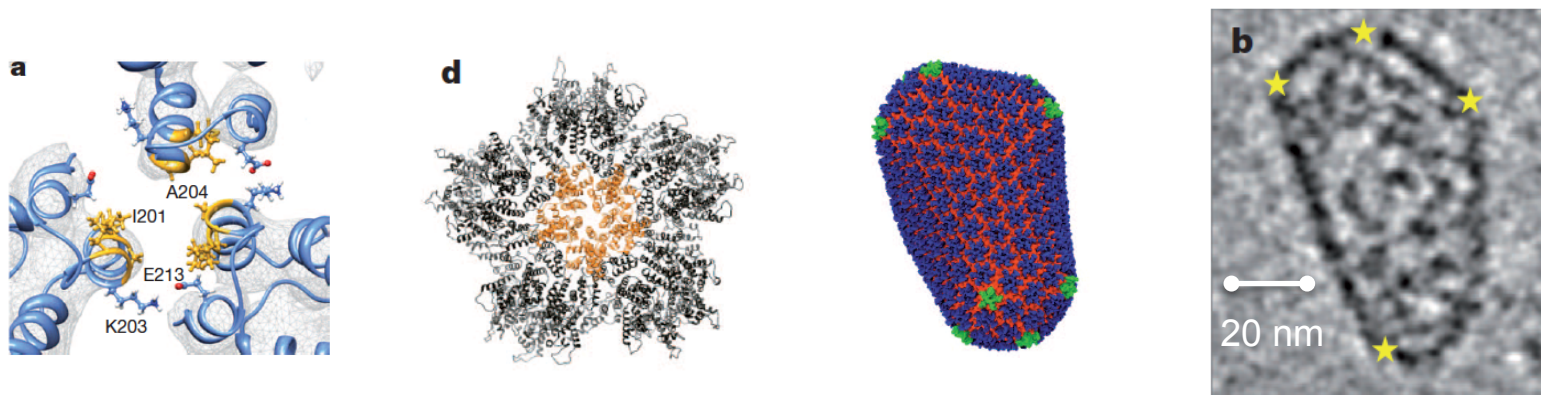
Workshop Maths/Industry | Michel Masella | Life Science Division

28 APRIL 2017

Why to use a classical formalism and empirical potentials to model protein systems in solution: efficiency

- Much faster computations compared to quantum approaches (DFT, MP2...)
- Large systems (thousands up to millions of atoms)
- Long simulations (from the ns up to the μ s scale)

Example : simulating the mature HIV-1 capsid structure

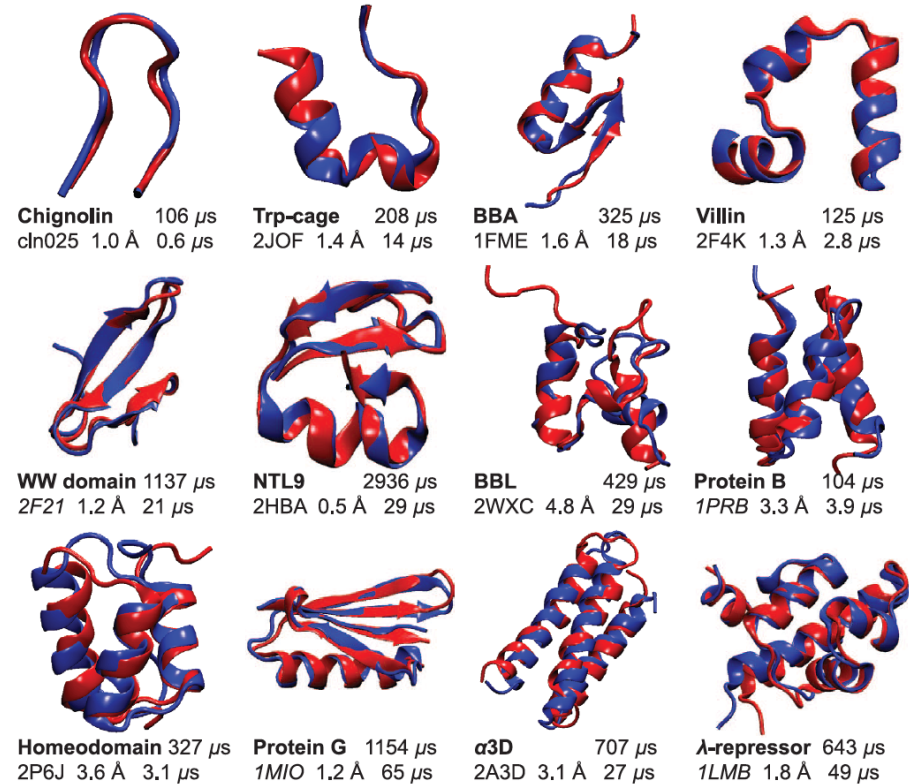


128 000 cores of the Cray “Blue Waters”, 300 ns, about $60 \cdot 10^6$ atoms ($50 \cdot 10^6 =$ water)

Zhao et al, Nature, 497 (2013) 643

Anton, a special-purpose machine for molecular dynamics simulation

Shaw et al, ACM SIGARCH, 35 (2007) 1-12



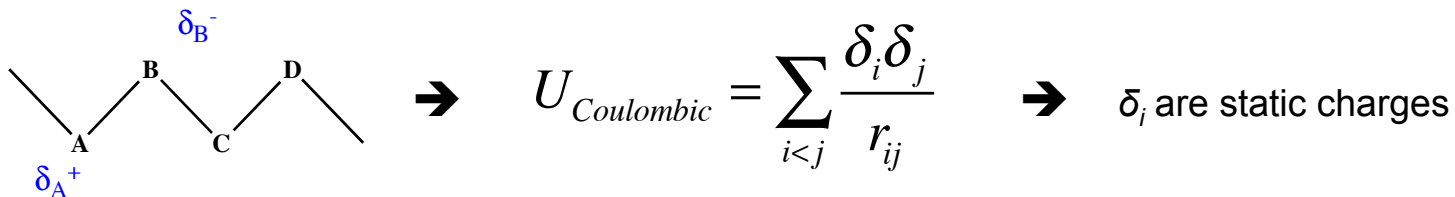
How fast folding proteins fold

Lindorff-Larssen et al, *Science*, 334 (2011) 517

The main drawback of MM approach: accuracy

Common force-fields are based on additive potentials (CHARMM, AMBER, OPLS ...)

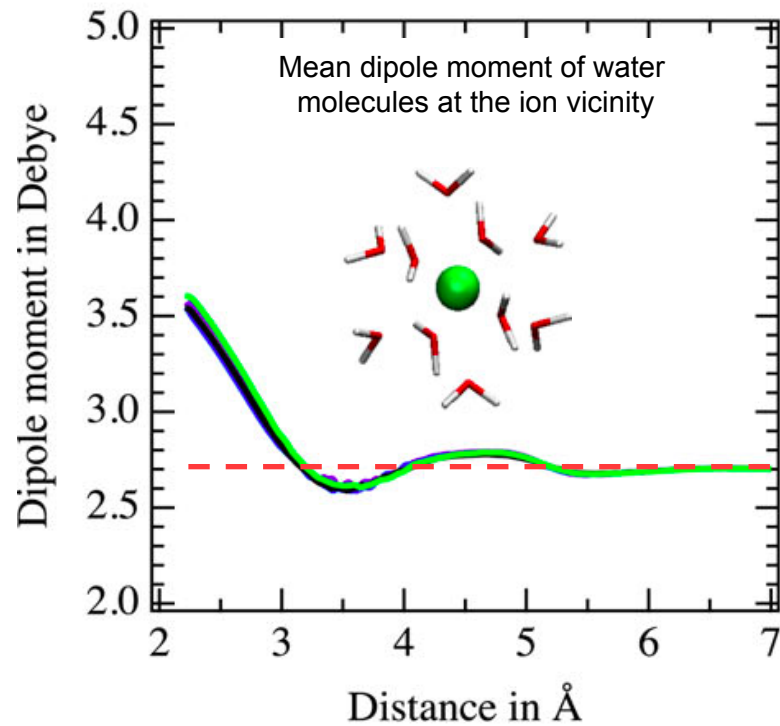
- 1 - The model parameters are constant along an MD trajectory
- 2 – Reliability of such an approach when mimicking microscopic electrostatic interactions



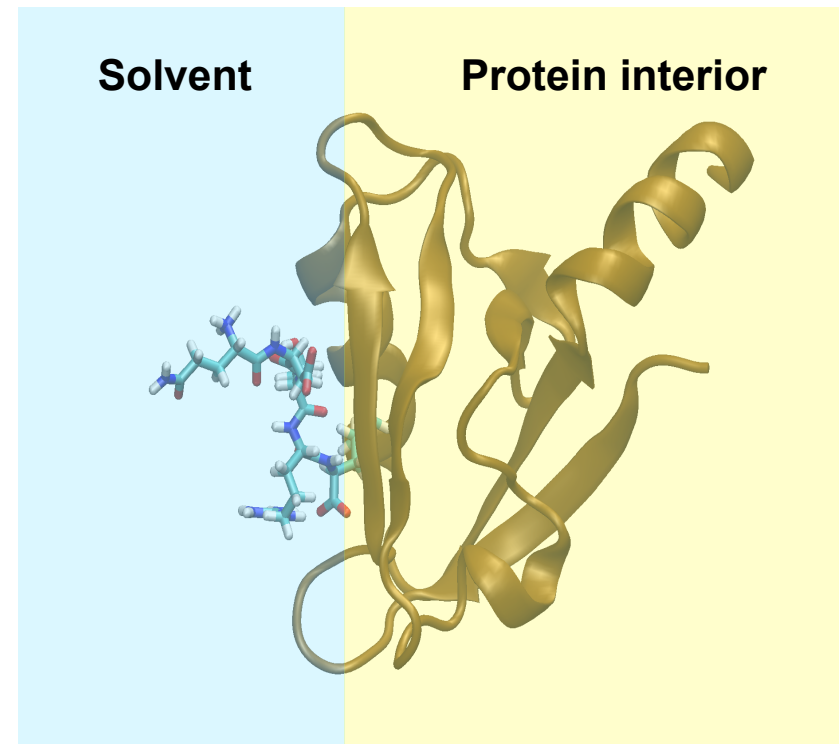
- 3 – Experimental results are commonly used for assigning/refining parameters, transferability ?
- 4 - Ok, you may say that for a homogeneous and isotropic system, you are using a mean field approach...

However, what about interfaces ?

The case of Cm(III) interacting with water



All protein/ligand interactions correspond to an interface problem



These phenomena can not be accounted for using static charges to model the molecular electronic cloud properties

They allow to account for environmental effects on electrostatic molecular properties considered in classical molecular dynamics

Many approaches have been proposed :

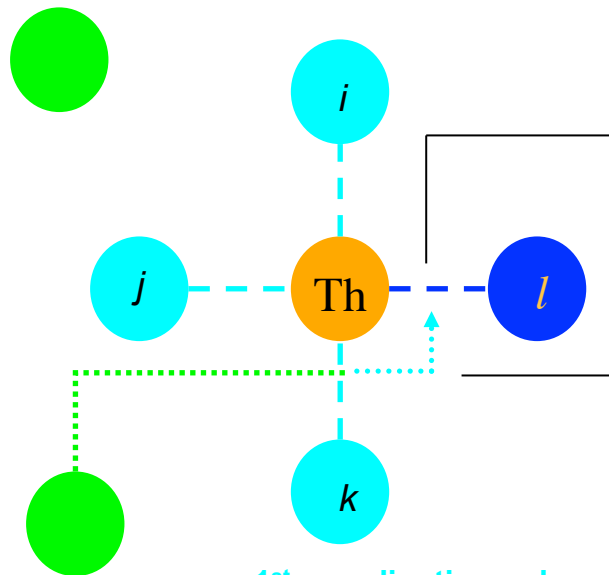
- Fluctuating charge approaches: the “static” δ_i charges are allowed to fluctuate
- Drude oscillators: “extra” atomic charges are introduced
- **Induced dipole moments: new degrees of freedom are introduced**

$$\boldsymbol{\mu}_i = \alpha_i \left(\mathbf{E}_i - \sum_{j=1, j \neq i}^N \mathbf{T} |\mathbf{r}_j - \mathbf{r}_i| \boldsymbol{\mu}_j \right) \Rightarrow \text{to be solved iteratively, } O(N^2)$$

\mathbf{T} is the dipolar tensor and α_i is the center i polarizability, usually isotropic
 \mathbf{E}_i is the electric field acting on center i
 $\boldsymbol{\mu}_j$ is the induced dipole moment on center j

Accounting for inter atomic interactions with a weak covalent character

2nd coordination sphere



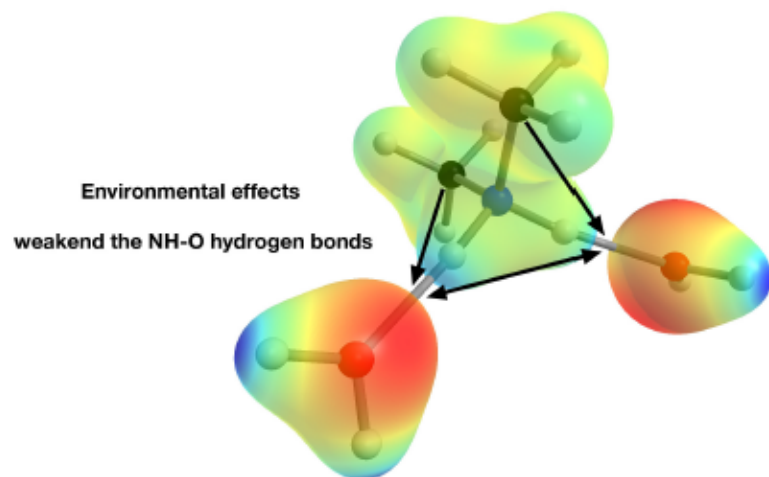
$$U_{ct} = \sum_{l \in \text{water}} D_e^c \exp(-\beta \cdot r_{Th-l})$$

$$D_e^c = D_e \left[1 - \xi \sum_{i \in \text{water}, i \neq l} \exp\left(-\frac{(r_{Th-i} - r_e)^2}{\gamma_r}\right) \right]$$

1st coordination sphere

Seems computationally demanding, however scales as $O(N)$

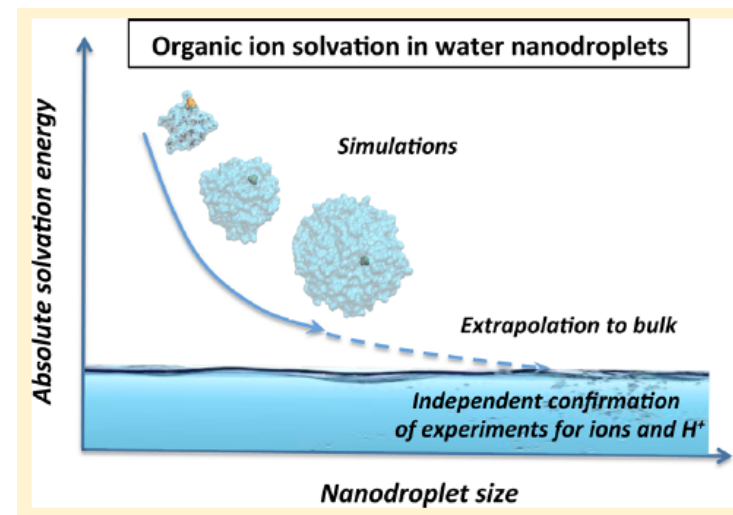
Benchmark binding energies of ammonium and alkyl-ammonium ions interacting with water. Are ammonium-water hydrogen bonds strong?



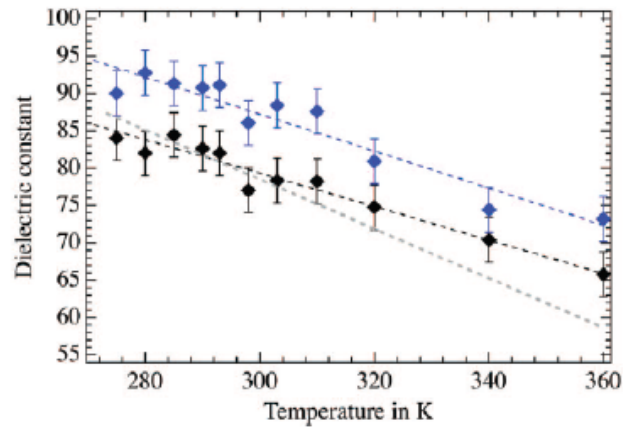
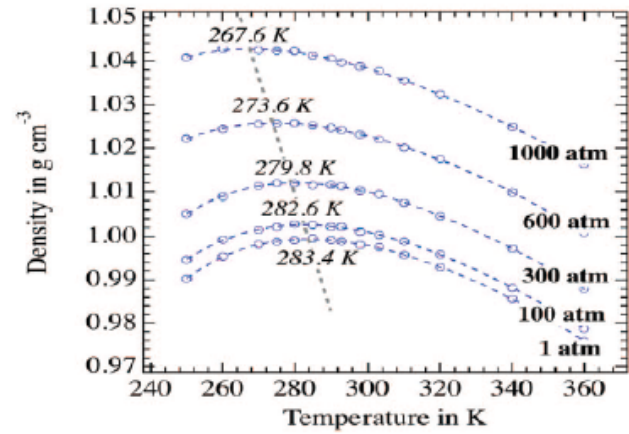
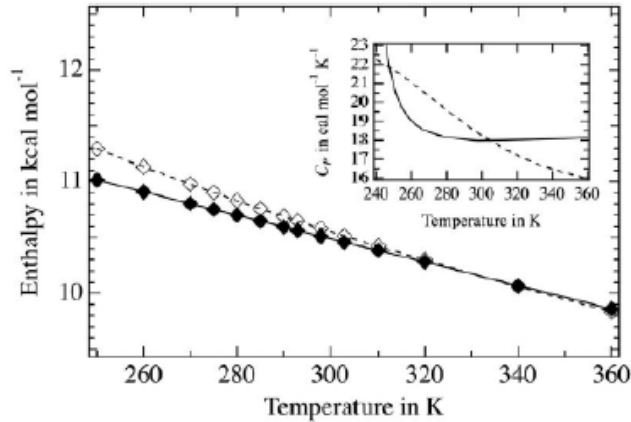
V. Vallet and M. Masella, CPL, 618 (2015) 168

Simulated Solvation of Organic Ions: Protonated Methylamines in Water Nanodroplets. Convergence toward Bulk Properties and the Absolute Proton Solvation Enthalpy

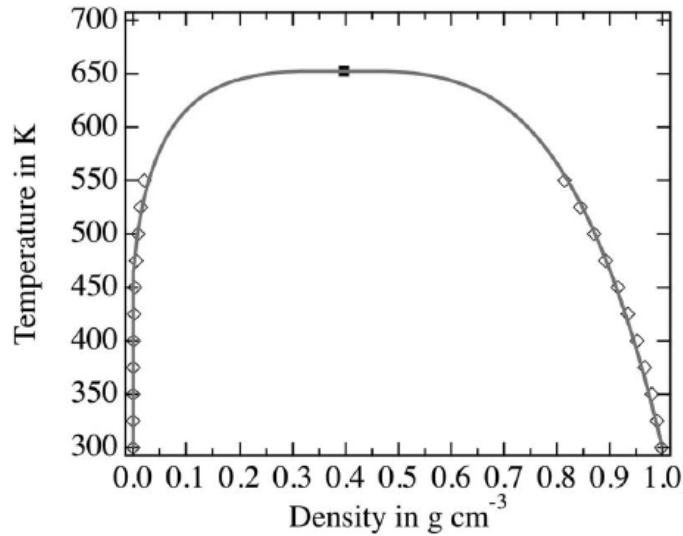
Céline Houriez,^{*,†} Michael Meot-Ner (Mautner),^{*,§} and Michel Masella^{||}



AB INITIO FORCE-FIELDS: LIQUID WATER

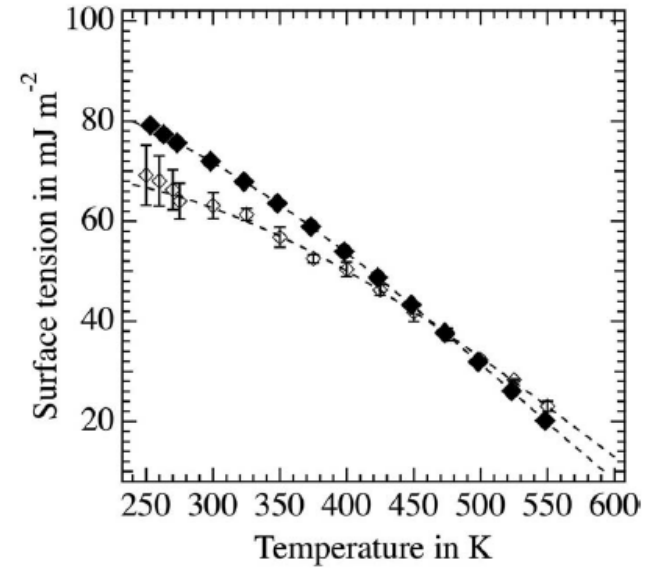


Water critical point



$$\rho_{\pm} = \rho_c + b_0|T - T_c| \pm (b_1|T - T_c|^{\beta_c} + b_2|T - T_c|^{\beta_c+1/2}),$$

Water surface tension

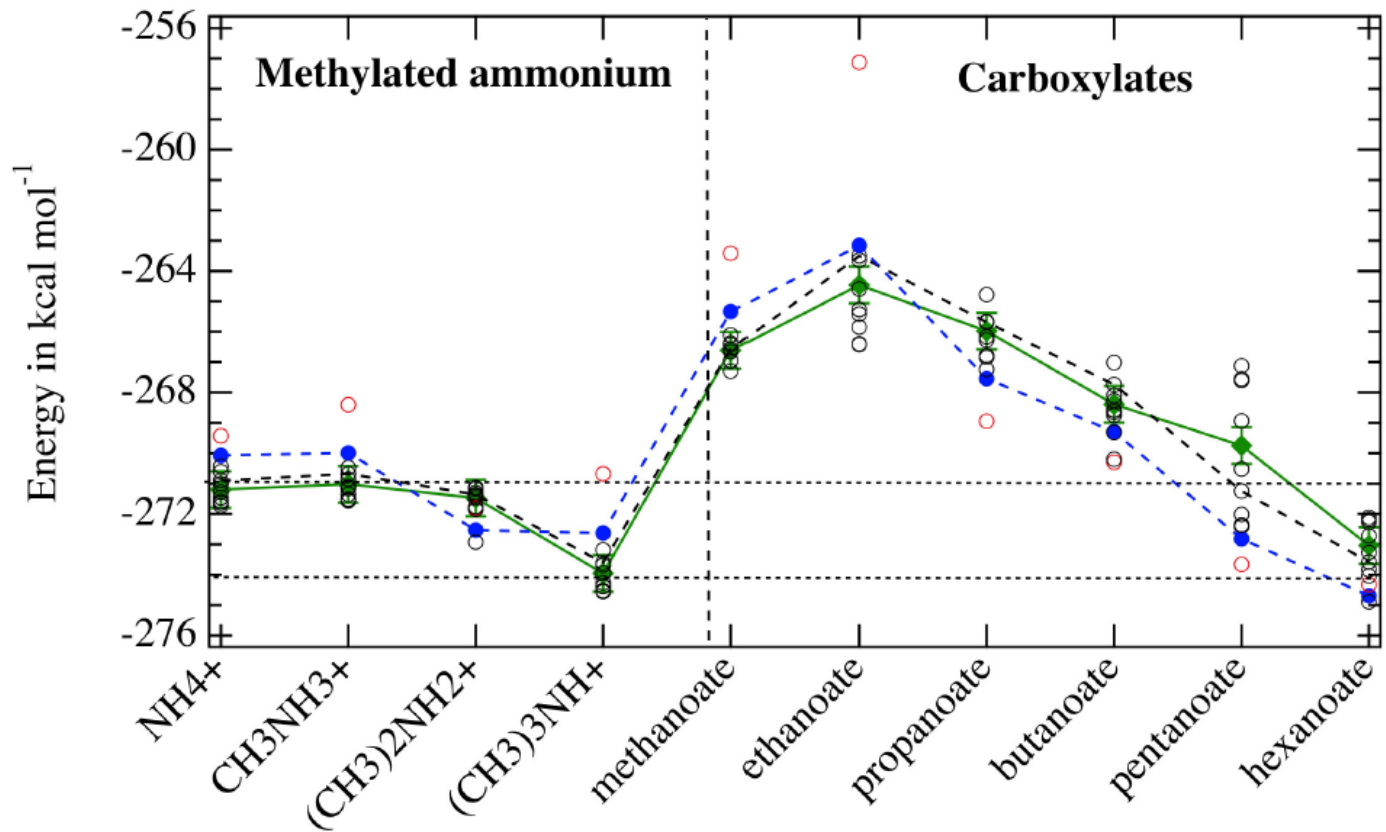


$$\gamma(T) = a_{\gamma}(T_c - T)^{5/4} + b_{\gamma}(T_c - T)^{9/4},$$

Real et al, J Chem Phys, 2013

ACCURACY OF AB INITIO FORCE-FIELDS

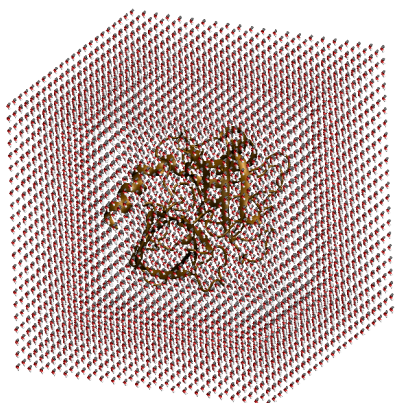
$$\Delta H_{solv}(H^+) = \Delta H_{g \rightarrow aq}(PH) - \Delta H_{g \rightarrow aq}(P) + \Delta H_g^{prot}(P) + \Delta H_{aq,dissociation}^0(PH)$$



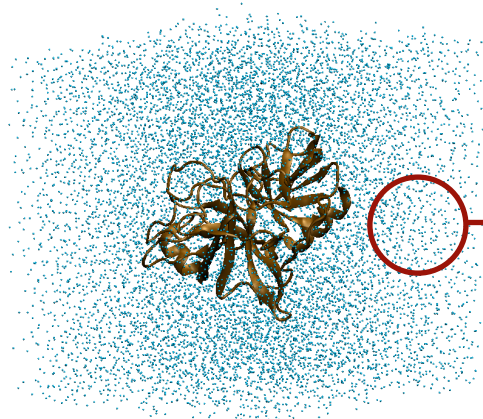
A multiscale solvent coarse grained approach

A SOLVENT COARSE GRAINED APPROACH

Explicit solvent approach, need of FFT !



Coarse grained approach
Efficiency and microscopic solvation properties



$$\alpha_s = \frac{1}{4\pi} \left(1 - \frac{1}{\epsilon_s} \right) \times \frac{1}{\rho_s}$$

i.e. $\alpha_s \propto \Delta v_s$

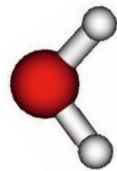
$$F_P[\mathbf{P}] = \frac{1}{2} \int \frac{\epsilon(\mathbf{r}) \mathbf{P}(\mathbf{r})^2}{\chi(\mathbf{r})} dV - \int \mathbf{P}(\mathbf{r}) \cdot \mathbf{E}_s(\mathbf{r}) dV$$

$$\mathbf{P}(\mathbf{r}) = \frac{\chi(\mathbf{r})}{\epsilon(\mathbf{r})} \mathbf{E}_s(\mathbf{r}) \longrightarrow \mathbf{p}_k^s = \Delta v \mathbf{P}(\mathbf{r}) = \frac{\mathbf{P}(\mathbf{r})}{\rho_s}$$

Implicit solvent approaches
Poisson-Boltzman
Warshell's grid approach

Haduong et al, J. Chem. Phys., 117 (2002) 541
Masella et al, J. Comput. Chem., 29 (2008) 1707

In the case of water, number of solvent atoms divided by 3



An explicit water molecule



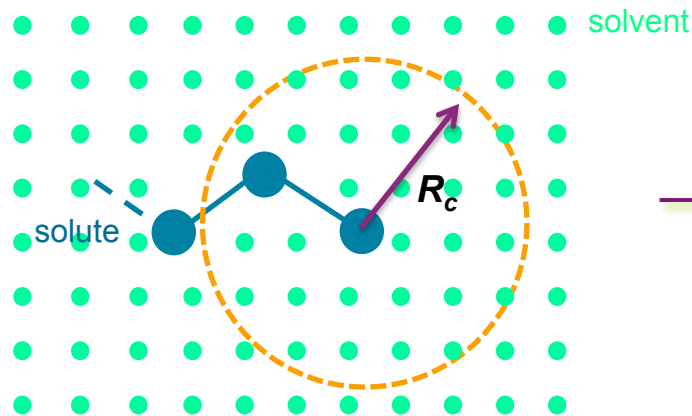
A nonpolar polarizable particle
= a water molecule



What about the liquid water hydrogen bond network ?

A solution from DPD

Systematic truncation of long tail electrostatic interactions

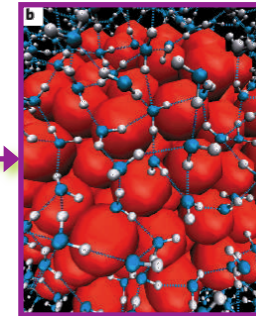
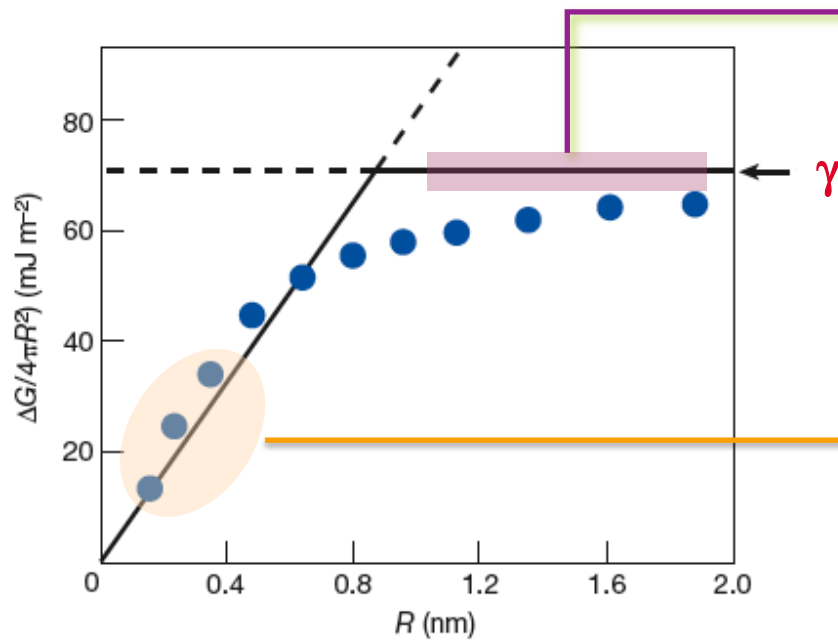


What about electrostatic long tail effects ?

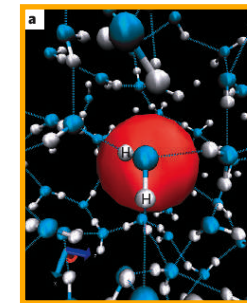
with $R_c = 12 \text{ \AA}$, the solvent cost represents 10 to 30% of the total cpu time

Free energy cost ΔG for creating a cavity within liquid water (Monte-Carlo SPC/E simulations)

D. Chandler, Nature, 437 (2005) 640



« *Dry* »



« *Wet* »

Computing γ with VdW potentials : large cutoff (15 Å) for estimating it within 10%

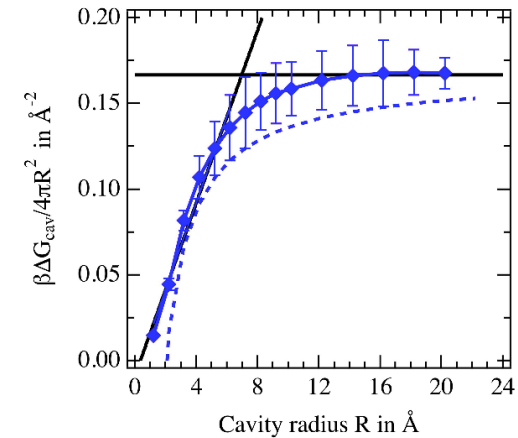
Mecke *et al*, J. Chem. Phys, 107 (1997) 9264

$$U_{pp}^{density} = \sum_{1 \leq i \leq N_s} \epsilon_s^0 (n_i^0 - \bar{n}^0)^2 + \epsilon_s^1 (n_i^1 - \bar{n}^1)^2$$

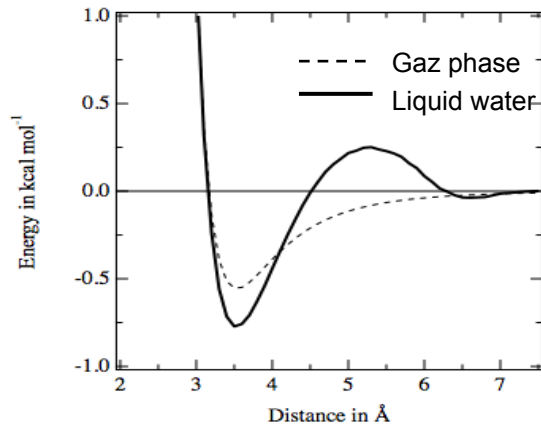
n_i : solvent local density at the vicinity of a particle
 0 → 1st shell ; 1 → 2nd shell

→ solvent/solvent interaction truncation : 7 Å

Masella et al, J. Comput Chem, 2011



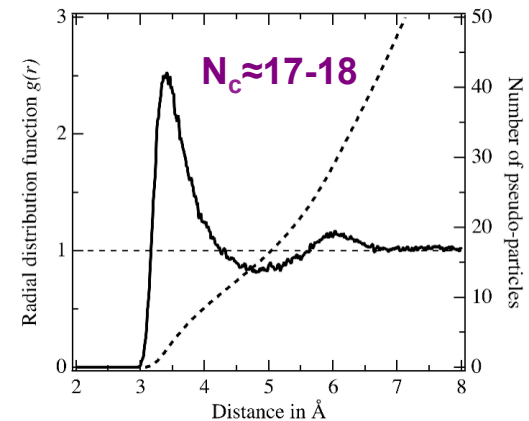
PMF of the methane dimer (300 K, 1 atm)



Agreeing with the theory of the hydrophobic effect ...

Pratt and Chandler, J. Chem. Phys., 67 (1977) 3683

Methane : solvent structure

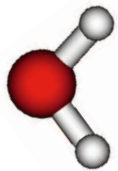


...and all atom simulations

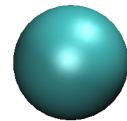
Asthaqari et al, J. Chem. Phys., 128 (2008) 244152

Particle polarizability proportional to their individual volume : $\alpha_s \propto \Delta V_s$

→ a multi-scale coarse grained approach to handle long tail bulk electrostatic



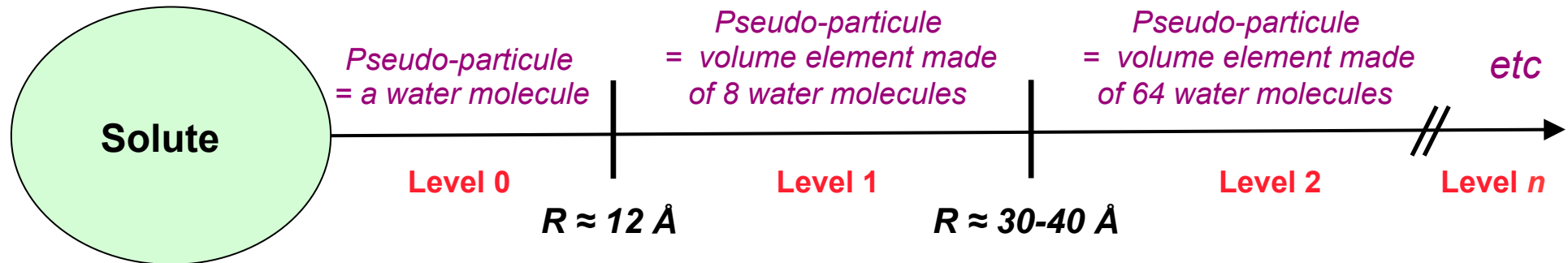
An explicit water molecule



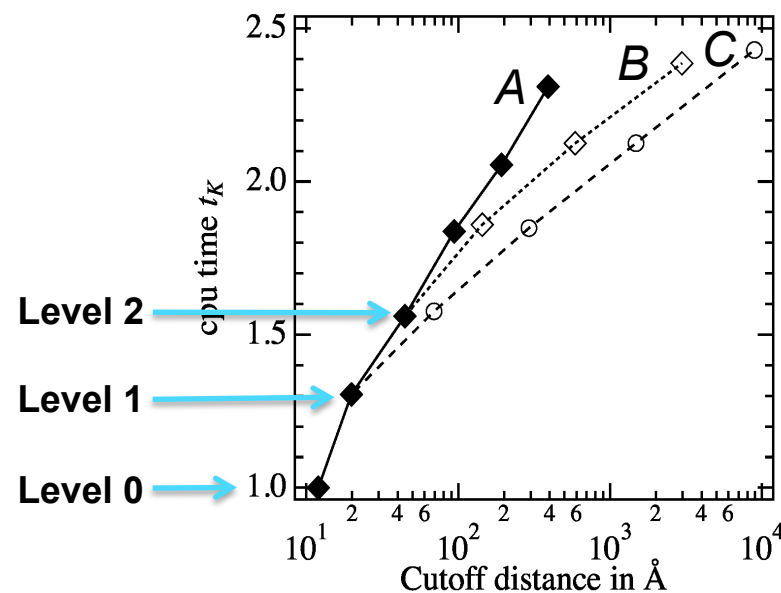
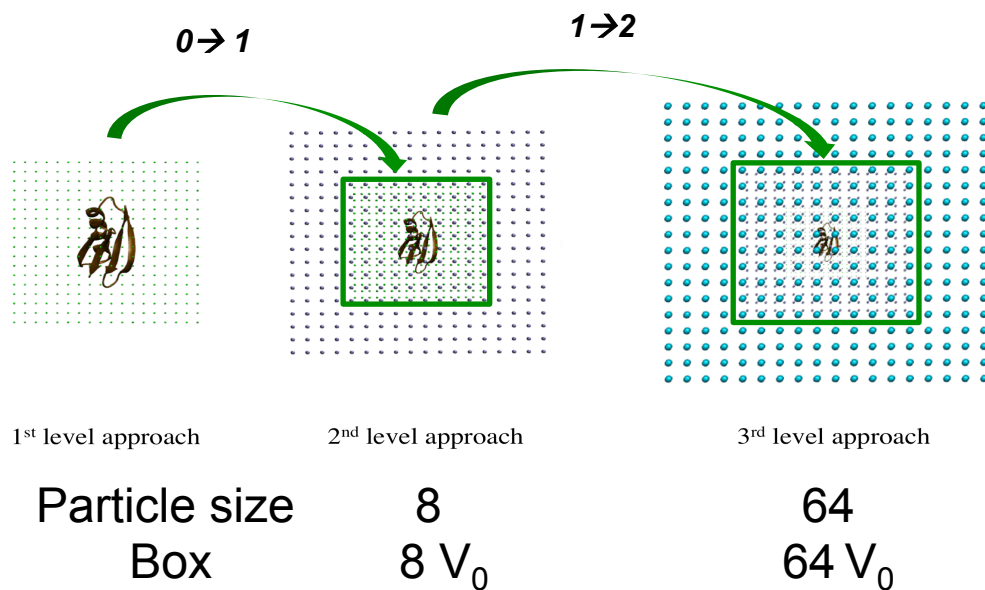
A polarizable pseudo-particle
= a water molecule



A larger polarizable pseudo-particle
= a volume element of liquid water



M. Masella et al, *J. Comput Chem*, **32** (2011) 2664; *ibid*, **34** (2013) 1112

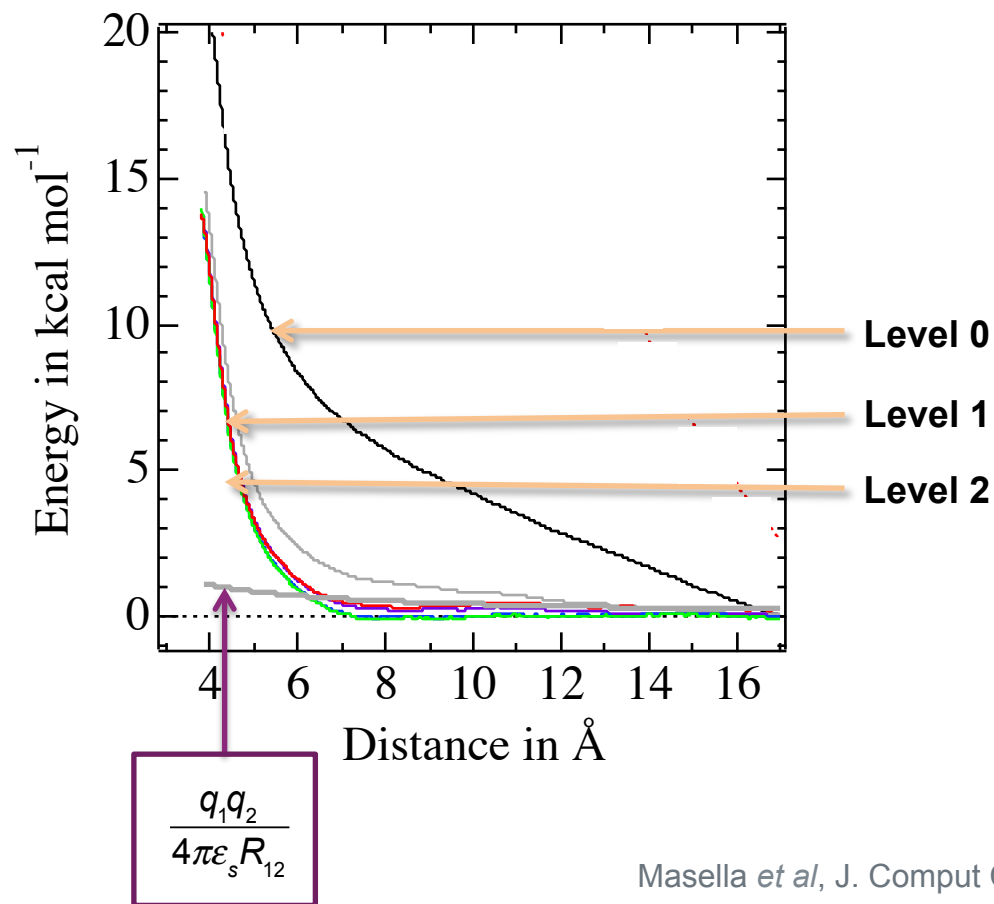


Boxes	0→ 1	1→ 2	2→ 3	3→ 4
A	x2	x2	x2	x2
B	x2	x2	x3	x4
C	x2	x3	x4	x5

Now, the bottleneck is handling the interactions within the solute...

Potential of mean force of Cl-/Cl- and the coarse grained approach level

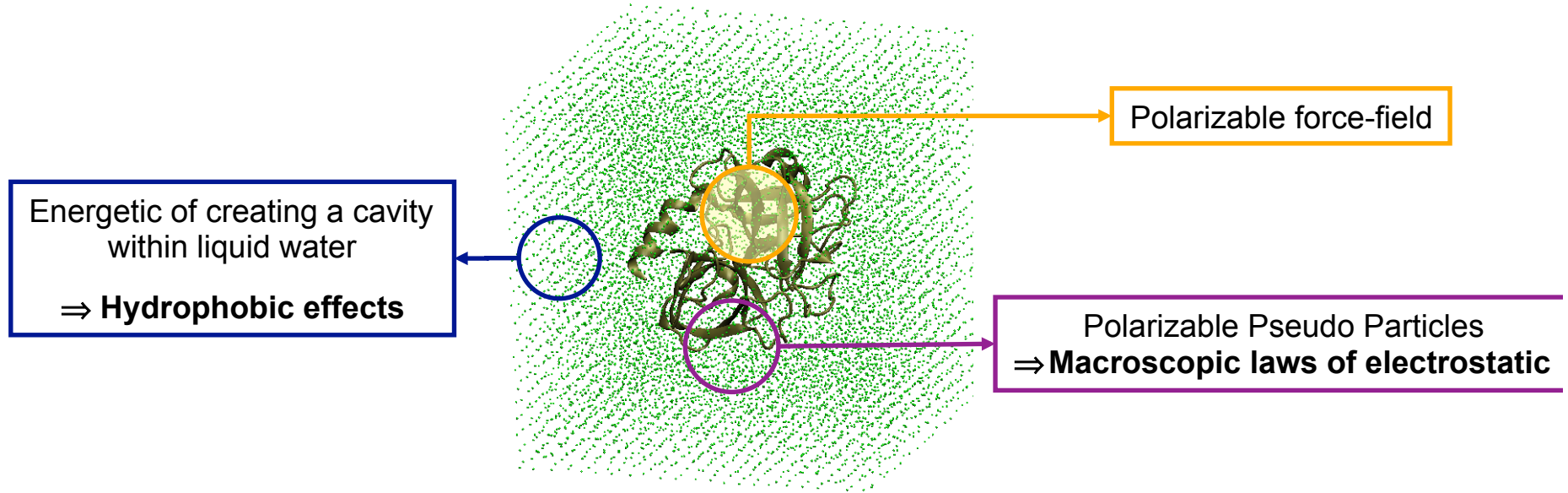
(1ns simulation, solvent boxes made of 4096 particles, umbrella sampling, etc...)



Masella *et al*, J. Comput Chem, 2013

The code POLARIS(MD) © CEA/DSV

Masella, Mol. Phys., 2006 ; Masella *et al*, J. Comput Chem, 2008; *ibid*, 2011; *ibid*, 2013



Supported by the Exascale Computing Research Laboratory



energie atomique • energies alternatives



Reference : Intel Sandy-Bridge octo-cores 2.7 Ghz (CURIE)

All atom simulations+ PME summation techniques

A water box of 1000 molecules → **3.0 ns per day** (1 cpu)
4.5 ns per day (2 cpu)

Coarse grained simulations + solute interactions $O(N^2)$

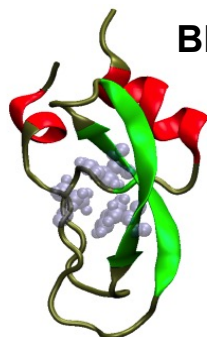
6000 particles + solute = 900 atoms → **15 ns per day** (level 0 + 1 cpu)
13 ns per day (level 1 + 1 cpu)
11.5 ns per day (level 2 + 1 cpu)
9.5 ns per day (level 3 + 1 cpu)

Largest system simulated :

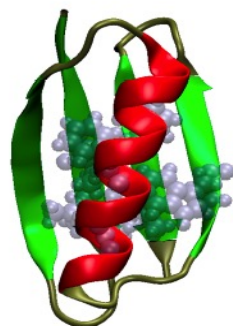
8400 atoms solute + 51 000 particles, **850 ps per day** (level 0 + 1 cpu)

→ **Fast Multipole Method !!!**

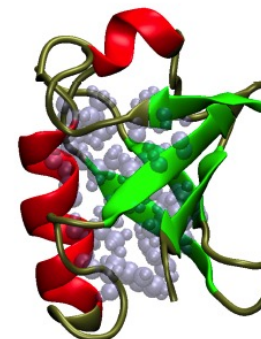
10x20 ns simulations of three small solvated proteins (240 SB cores/36 h)



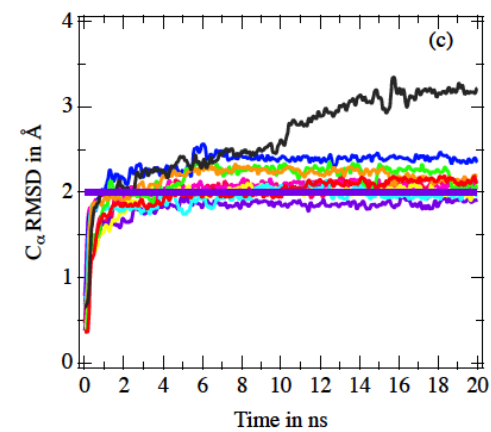
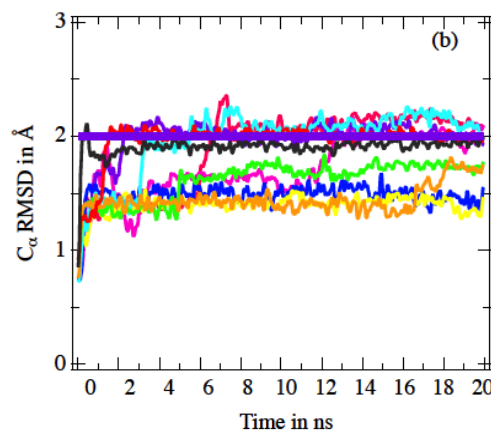
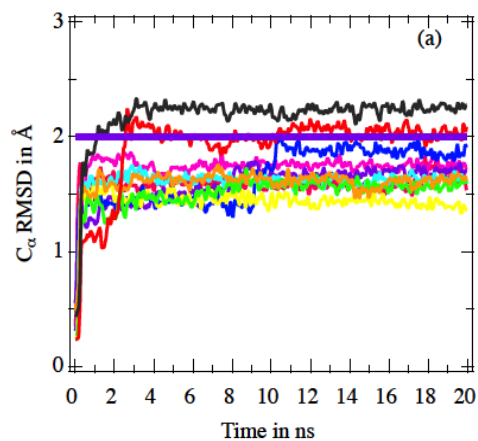
BPTI



PGB



UBL



Masella et al, J. Comput Chem, 2011

No parameter assigned to reproduce protein structures

An $O(N)$ multi-scale N -body approach for simulating polarizable microscopic systems

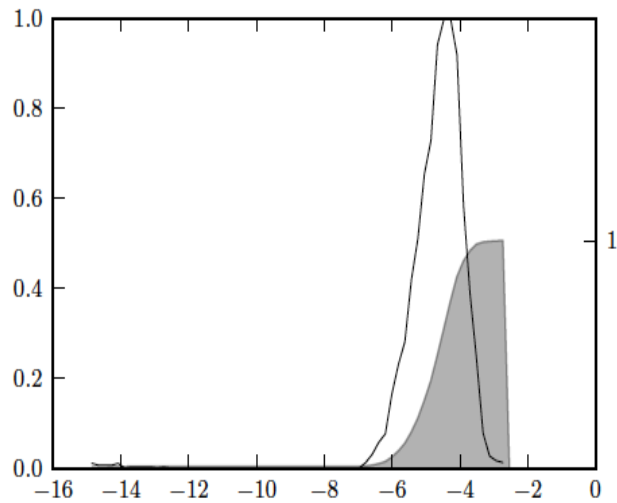
A O(N) FFM APPROACH



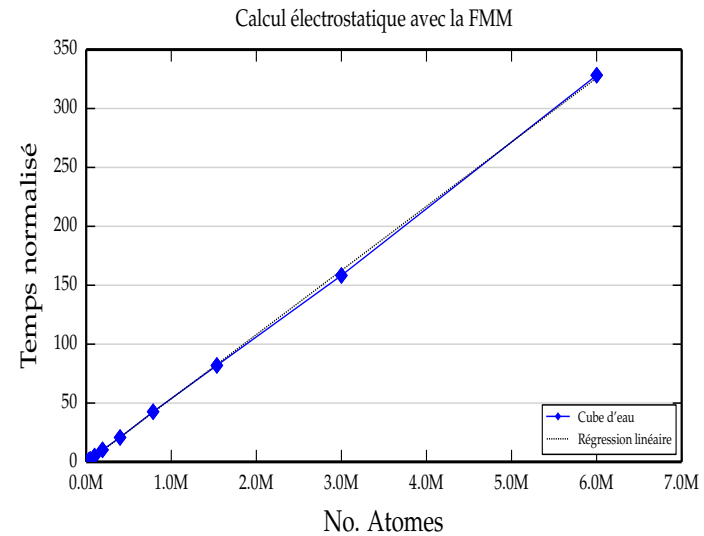
$$\phi(\mathbf{x}_b - \mathbf{x}_a) = \frac{q_a}{|\mathbf{x}_b - \mathbf{x}_a|}$$

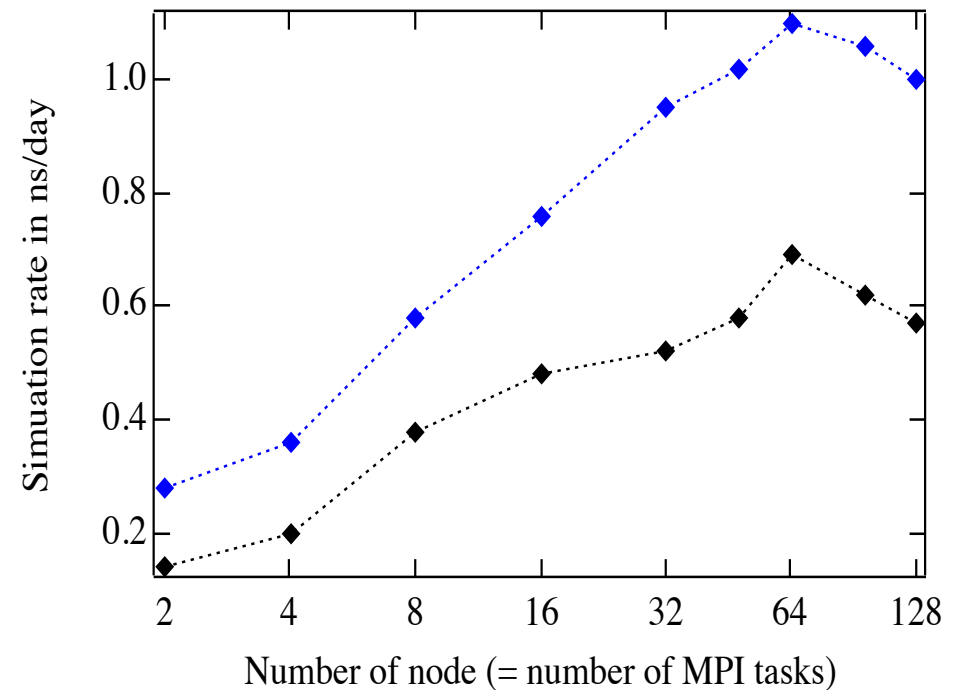
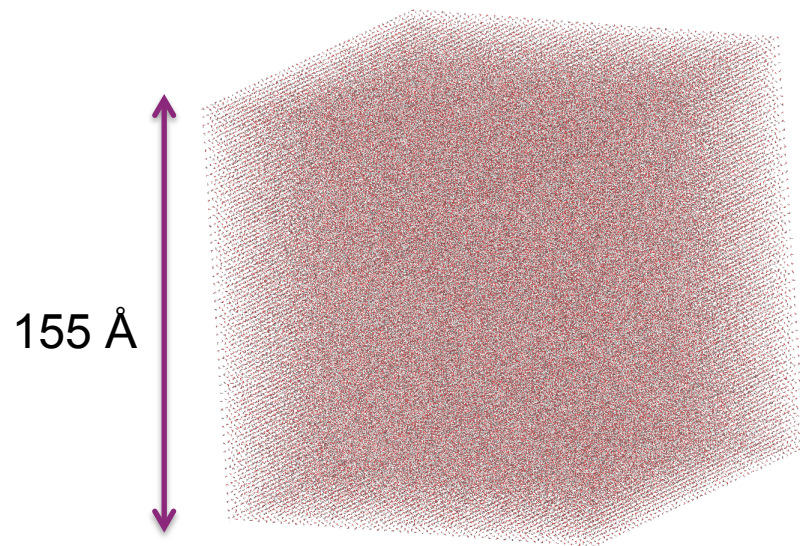
$$\begin{aligned} \rightarrow \phi(\mathbf{x}_b - \mathbf{x}_a) &\approx \sum_{|n| \leq p} \sum_{|m| \leq p - |n|} \frac{(-1)^{|n|}}{n!m!} r_b^n r_a^m \nabla^{n+m} \phi(z_B - z_A) \\ &+ \mu_a = 2q_q^\mu \delta l_a \end{aligned}$$

+ atoms organized via a kd-tree spatial decomposition



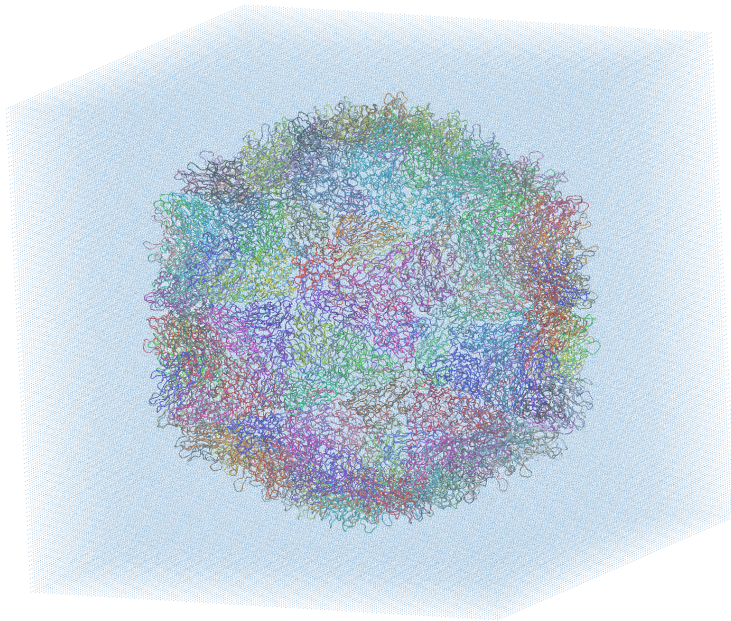
Mean error on the forces





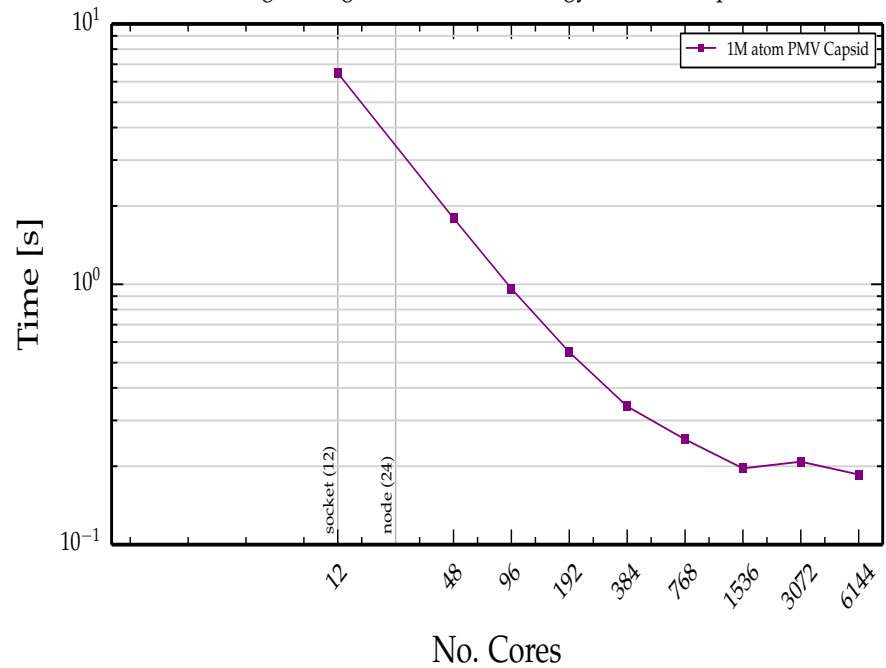
Dipoles solved iteratively; MTS (2f/4fs); black: CURIE@CEA (node = 16 cores); blue: OCCIGEN@CINES (1 node 24 cores)

A SOLVATED VIRUS CAPSID



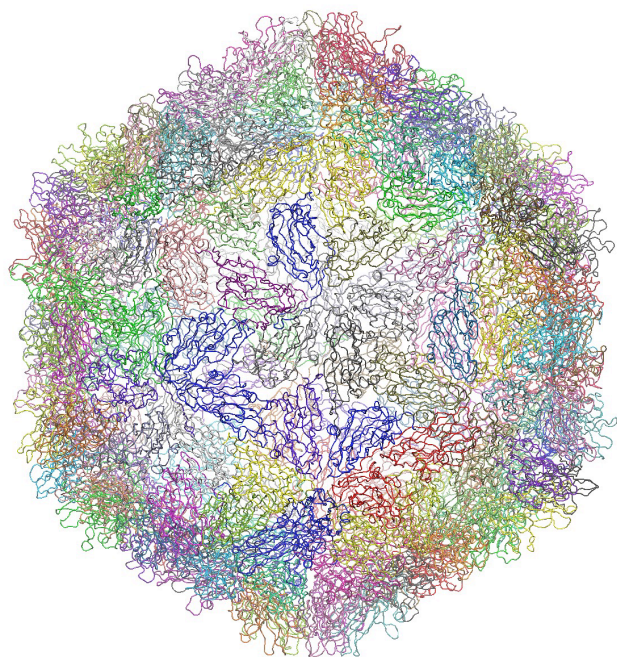
Mosaic Panicum virus capsid
 0.6 M atoms + 1.8 M coarse grained
 solvent particules
 Equivalent to a 6.5 M atom systems

Strong Scaling of Electrostatic Energy for PMV Capsid



Method scalability
 Hazelhen supercomputing system
 (HLRS, Stuttgart, Gemany)





29 MARCH 2016

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