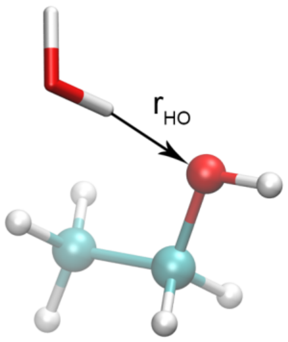
Improving SemiEmpirical (NDDO) methods for Born-Oppenheimer Molecular Dynamics

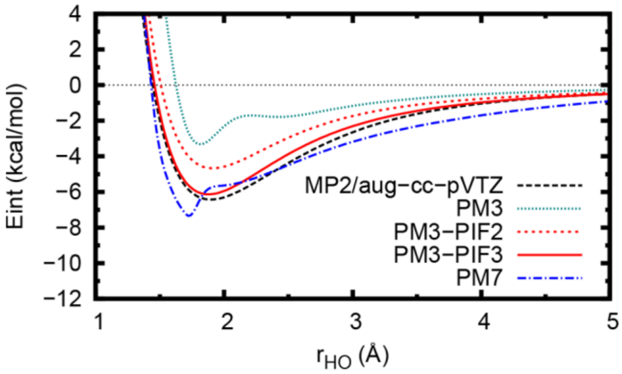
Antoine Marion,[1,2] Gérald Monard,[1,2] Manuel F. Ruiz-Lopez,[1,2] Francesca Ingrosso[1,2]
[1]SRSMC UMR 7565, Université de Lorraine, BP 70239 – 54506 Vandœvre-lès-Nancy
[2] SRSMC UMR 7565, CNRS, BP 70239 – 54506 Vandœvre-lès-Nancy
Presenting author: antoine.marion@univ-lorraine.fr

Modeling biomolecular systems by explicitly taking into account the quantum mechanical behavior of the electrons represents one of the greatest challenges for theoretical chemistry studies. Although outstanding progresses have been made in the past decades in performing molecular dynamics (MD) simulations with density functional theory based methods, long time scales and/or systems containing a large number of atoms still demand very high computational costs. A reasonable compromise is represented by the use of a lower level of quantum chemistry to model the electronic Hamiltonian. In particular, semiempirical (SE) methods based on the NDDO (Neglect of Diatomic Differential Overlap) approximation become appealing, since they can be reparametrized and improved.

We recently developed a new scheme allowing us to perform reasonably long MD simulations (up to nanosecond on commodity computer) of large systems (500-1000 atoms with periodic boundary conditions) with a full quantum description of the electrons at a SE level of theory, the so called SEBOMD methodology (SemiEmpirical Born-Oppenheimer Molecular Dynamics).[1] This technique has already been successfully applied to simulate liquid water [1] and N-methyl acetamide [2] in aqueous solution and aims at describing the time dependent behavior of proteins in water including key quantum effects (bond making/breaking, solvent induced polarization and IR shifts, charge transfer ...).

The major bottleneck for a more extensive use of SE methods for condensed phase studies is related to the fact that they were not originally developed to model intermolecular interactions. Some improvements were proposed in the past years for water and small hydrated systems (PM3-PIF2).[3] However, our recent work has shown that none of the SE methods in the literature is reliable to predict the properties of hydrophobic groups in aqueous solution. We have thus developed a new 'force field like' SE approach (PM3-PIF3), in which atom types are taken into account to reproduce high level *ab initio* interaction energy surfaces.[4] Here we shall discuss this methodology and present its application to a few model systems (from simple 1:1 solute-water complexes to biomolecules in aqueous solutions).





[1] G. Monard, M. I. Bernal-Uruchurtu, A. Van der Vaart, K. M. Merz Jr., and M. F. Ruiz-Lopez J. Phys. Chem. 109, 3425 (2005).
[2] F. Ingrosso, G. Monard, M. Hamdi Farag, A. Bastida, and M. F. Ruiz-Lopez J. Chem. Theory Comput. 7, 1840 (2011).
[3] W. Harb, M.I. Bernal-Uruchurtu, M.F. Ruiz-Lopez Theor. Chem. Acc. 112, 204 (2004).
[4] A. Marion, G. Monard, M.F. Ruiz-Lopez and F. Ingrosso (to be submitted).