

Holding a Microscope to Aggregation

Extension of Adaptive Resolution Path Integral Molecular Dynamics techniques to the study of hydrophobic molecules in and out of equilibrium

J. W. Whittaker, L. Delle Site, Institute for Mathematics, Freie Universität Berlin

In Short

- Non-equilibrium molecular dynamics (NEMD) will be introduced in the PI-GC-AdResS framework through the addition of a tunable electric field within simulations.
- Changes in the solvation shell structure and dynamics of a hydrophobic graphene surface will be explored via NEMD PI-GC-AdResS as a function of frequency and amplitude of the electric field.
- Massive PI-GC-AdResS simulations of fullerene in water will reveal how and why spherical hydrophobic particles tend to aggregate and how it may be possible to drive, halt, or reverse this process.
- Data from these simulations will yield important insights into the nature of hydrophobic particles in water.

Background and Motivation

The solvation and aggregation of hydrophobic molecules are the subjects of intense research in the fields of chemistry, physics, and biology [1]. Fullerene, for example, is one such molecule under this microscope due to its aggregation in water and the environmental implications of this process. For this reason, a microscopic model of solvation and aggregation of fullerene is highly-sought after [2]. The physio-chemical properties of aqueous solvation are particularly well-suited for study via molecular dynamics (MD). However, today's MD simulations of condensed matter systems are increasingly characterized by demands for higher accuracy, larger systems, and longer time scales—all at the expense of enormous computational resources. Our group attempts to circumvent this issue by developing and utilizing the grand canonical adaptive resolution simulation (GC-AdResS) approach [3]. This aims to eliminate the need for prohibitively large resources by representing only the region of specific interest in high resolution while the “bulk” of the simulation is represented by a low resolution description. This method allows for a significant speedup in calculation without sacrificing the accuracy and validity of

results pulled from the high-resolution region of interest. Over the past allocation period, our group has improved/simplified the GC-AdResS technique and successfully used it to simulate a complex, biologically relevant system: a lipid bilayer. This study validated our improvements to AdResS, resulting in a recent publication [4] (see fig. 1) and setting the stage for further applications of the method.

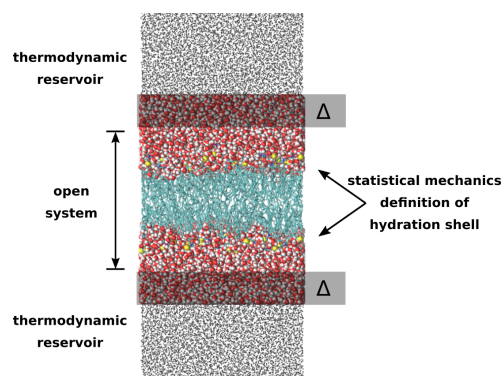


Figure 1: An illustrative example of the GC-AdResS method as applied to the lipid bilayer system of ref. [4]

In the context of studying with MD the solvation process, it is interesting to consider thermodynamic properties at the highest resolution possible, i.e., the quantum level, because quantum effects, namely delocalization of light atoms in space, is thought to have an impact on the structure of water, even at room temperature. A popular method for incorporating these delocalization effects in simulation, path integral molecular dynamics (PIMD) [5], increases computational load dramatically with respect to ordinary MD, inhibiting the sufficient study of large systems (for example, large solutes in aqueous baths). To combat this, the PIMD approach was integrated into the GC-AdResS framework, yielding path integral grand canonical adaptive resolution simulation (PI-GC-AdResS) which has aided in the study, at a quantum level, of static and dynamic properties of liquid water, large hydrophobic solutes, and more which would otherwise be impossible without massive computational effort [6]. In addition to the success of the work described in the paragraph above, PI-GC-AdResS has been updated and implemented within the newest version of GC-AdResS over the previous allocation period.

In addition to the technical refinements outlined above, PI-GC-AdResS as a tool to better understand the structure and thermodynamics of aqueous solvation would benefit greatly from its extension to

the study of non-equilibrium situations. Here, the system is perturbed by an external agent and the effects of this perturbation are observed and quantified. In the case of the solvation of a solute such as fullerene, the perturbation on the system could take the form of a localized electric field acting on the water molecules of the solvation region. The relevancy of an electric field acting as the perturbing agent stems from the idea that its modulation of the solvation shell surrounding a hydrophobic molecule will likely encourage or discourage interaction with similarly-solvated molecules within close proximity. Thus, introducing non-equilibrium capabilities to PI-GC-AdResS will allow our group to gather novel information about aggregation of hydrophobic molecules valuable to many researchers across multiple disciplines.

Aim

Our goal is to move towards the use of the PI-GC-AdResS approach to investigate, at the quantum level, the aggregation propensity of a large system of hydrophobic molecules. In order to achieve this, we will (1) develop and refine non-equilibrium methods for PI-GC-AdResS in order to introduce a tunable electric field and apply this method to a solvated hydrophobic molecule such as graphene. (2) Investigate an unprecedented system of two hydrophobic molecules (fullerene) (fig. 2) at PI-GC-AdResS resolution and use information gathered from our first goal to speculate how changes in the character of solvation may have an impact in the process of aggregation.

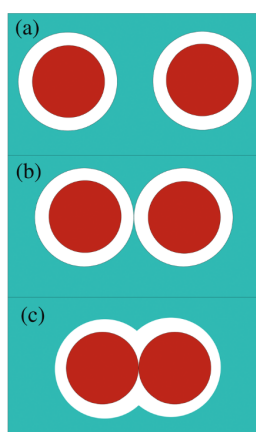


Figure 2: (a-c) An illustration of the possible behavior of two fullerene molecules and their solvation shells as they aggregate. We will shed more light on this process in the final phase of this project.

Method

All simulations will be performed using a home-modified version of the molecular dynamics software package GROMACS. The NEMD approach in PI-GC-AdResS will be implemented and applied to system of a single-atom-thick graphene sheet solvated in water. We will investigate how the solvation shell structure surrounding the hydrophobic molecule changes as a function of frequency and amplitude of the electric field. Following this, we will use PI-GC-AdResS to examine a system of two fullerene molecules immersed in a large bath of water. We will use the umbrella sampling method to gain insight into the aggregation process of these toxic particles and use information gained in the first phase to speculate on how this process can be modulated.

Despite the improvements to GC-AdResS and further PI-GC-AdResS over the past year, the cost of the planned simulations is still extremely expensive. Although the GC-AdResS method reduces computational cost, it must still be noted that PIMD techniques in the high-resolution region of these adaptive resolution simulations increase the number of calculations by at least $\sim 32x$. In addition to this, both NEMD and umbrella sampling simulations require multiple nearly-identical simulations in order to produce meaningful values of a given quantity of interest. For all simulations, this represents a considerable computational roadblock for our project unless extensive highly-parallel computing resources are available. Thus, we believe that our project will benefit greatly from resources allocated by the HLRN.

WWW

<https://userpage.fu-berlin.de/dellesite/>

More Information

- [1] H. Meng, et al., *ACS Nano* **4**, 5 (2010). doi:10.1021/nn100448z
- [2] J. D. Fortner, et al., *Environ. Sci. Technol.* **39**, 11 (2005). doi:10.1021/es048099n
- [3] H. Wang, et al., *J. Chem. Theory Comput.* **8**, 8 (2012). doi:10.1021/ct3003354
- [4] J. Whittaker, et al., *Phys. Rev. Research* **1**, 3 (2019). doi:10.1103/PhysRevResearch.1.033099
- [5] M. E. Tuckerman, et al., *J. Chem. Phys.* **99**, 4 (1993). doi:10.1063/1.465188
- [6] A. Agarwal, et al., *Phys. Chem. Chem. Phys.* **19**, 13030 (2017). doi:10.1039/C7CP01629H