Machine Learning Potentials Illuminate Nuclear Quantum Effects in Water

Nuclear Quantum Effects in Liquid Water Are Marginal for Its Average Structure but Significant for Dynamics

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Water is essential for life, actively participating in the molecular processes that sustain living organisms and serving as a universal solvent in chemical and biological systems [1]. Despite the apparent simplicity of a single H_2O molecule, the behavior of liquid water is surprisingly complex, including diverse effects such as negative thermal expansion, autoionization and the associated Grotthuss mechanism [2] and even a hypothesized liquid-liquid phase separation [3]. Many of the peculiar properties of water are related to the dynamically rearranging network of hydrogen bonds in the liquid, and the features of macromolecules and salt ions are often dictated by interactions with this network. Accordingly, understanding the behavior of water is of fundamental importance to soft matter physics.

Substituting the protons in regular water with deuterium creates heavy water (D_2O) , which is toxic to many organisms [4]. Experimentally, it is well-established that D_2O differs from H₂O in a number of key physico-chemical properties, including the melting temperature, viscosity, acidity and diffusion coefficient [5]. For example, the self-diffusion coefficient of H₂O is approximately 23% larger than that of D₂O. This isotope effect is much more pronounced than predicted classically due to the different particle masses, suggesting that the quantum mechanical nature of the nuclei significantly affects the dynamics of water. However, while dynamical nuclear quantum effects (NQE) in liquid water are unequivocal, the experimental situation regarding NQEs on water structure is less clear—there are discrepancies regarding the magnitude and even the sign of NQEs on bond lengths. Moreover, water is an especially subtle system, because competing NQEs may partially cancel each other out.

Given this experimental uncertainty, computer simulations are a helpful tool to gain a microscopic understanding of NQEs on water structure. In principle, NQEs can be modeled using Ring-Polymer Molecular Dynamics (RPMD), which is a method based on the path integral formalism of quantum mechanics [6, 7]. However, there is always a trade-off between accuracy and computational cost when calculating the interactions between the nuclei. Classical force fields are comparatively fast, but they neglect quantum effects of the electrons.

Conversely, ab initio methods, such as density functional theory and coupled cluster theory, account for these effects to various degrees of approximation, but are limited to comparatively small length and time scales. Lately, Machine Learning (ML) potentials promise ab initio accuracy at a significantly reduced computational cost.



Figure 1: Left panel: Radial distribution functions for H_2O and D_2O , showing only marginal differences in the water structure. Right panel: Diffusion coefficients of H_2O and D_2O as a function of the inverse simulation box length. The results extrapolated to the infinite system limit are in close agreement with experimental results. Figures adapted from the recommended paper.

Three years ago, Daru et al. presented a highly accurate ML potential for liquid water, using a training set based on coupled cluster calculations [8]. In the recommended paper, the same authors perform extensive RPMD simulations of both H_2O and D_2O using this model, with the aim of studying the impact of NQEs on both structure and dynamics. Crucially, the employed ML potential allows for the simulation of comparatively large systems (up to 256 water molecules) and time scales $(100 \, \text{ps})$. The authors calculate radial distribution functions for both H_2O and D_2O (left panel of Figure 1), which are almost identical. However, the radial distribution functions for H_2O are slightly more diffuse than for D_2O , which is attributed to the more delocalized nature of the protons as compared to the deuterons. Based on their simulation data, the authors also calculate the average lengths of covalent bonds and hydrogen bonds, both of which are approximately $5 \cdot 10^{-3}$ Å longer in H₂O than in D₂O. Thus, the overall impact of NQEs on the *average* water structure is predicted to be only minimal. A more detailed analysis of the hydrogen bonding shows that the hydrogen nuclei in H_2O are more delocalized both along hydrogen bond axes and in the perpendicular direction. Because these NQEs compete against each other, a partial cancellation occurs, leading to an overall more classical behavior and only small differences in the average structure.

In contrast, dynamical properties are found to be strongly affected by isotope substitution. Most notably, H_2O is predicted to diffuse faster than D_2O , which is in agreement with experiments. An extrapolation of the diffusion coefficients to the infinite system size limit yields predictions that are in remarkable agreement with experimental results (right panel of Figure 1). Similarly, the orientational relaxation time of H_2O is predicted to be shorter than in D_2O , and the ratio of the relaxation times also agrees with experimental measurements. The authors explain the accelerated dynamics of H_2O as a consequence of increased hydrogen delocalization, which lowers free energy barriers and enhances the rate of barrier crossing. Because the NQEs "soften" the free energy landscape, but do not significantly shift the positions of the free energy minima, the overall isotope effect is thus much more pronounced on dynamical quantities than on structural properties.

To summarize, the recommended work demonstrates that NQEs are generally insignificant for the structure of liquid water, but strongly affect dynamical quantities. Given the ubiquity and importance of water, it will be intriguing to explore how the presented simulation approach can be applied to more complicated features of aqueous systems in a biological context. In a recently published follow-up, Malik et al. study the impact of isotope effects on the dynamics of hydrogen bonds [9]. They find that D_2O exhibits substantially slowed down hydrogen bond dynamics, which they relate to its toxic nature. However, this conclusion being based on studies of pure bulk water—is still largely speculative. Simulations that directly address the interactions between water and biomolecules could provide mechanistic insights into the biological implications of isotope substitution in water.

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