A183 · Differentiable Learning of Nuclear Magnetic Responses with NequIP-NMR

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Nuclear Magnetic Resonance (NMR) provides atomistic insights into the structures, dynamics and interactions of molecules and proteins under near-native conditions. NMR observables, such as chemical shifts and J-couplings, are highly sensitive to the local electronic environments that nuclei experience within a molecule, and they can provide structural insights into atomic connectivity and molecular conformation. However, directly mapping these local environments to NMR observables is challenging, thereby motivating highly accurate prediction methods. We develop NequIP-NMR, a physics-informed machine learning framework to predict chemical shielding tensors and J-coupling tensors, as well as energies and forces, from atomic coordinates. The formalism extends the E(3)-equivariant NequIP architecture to NMR and ensures that exact differential relationships between these quantities are satisfied: by learning a generalized potential function and taking derivatives with respect to a magnetic field and nuclear magnetic moments, the NMR observables arise as response functions. To prepare training datasets, we compute energies, forces, chemical shieldings and J-couplings using Density Functional Theory (DFT) for several biologically relevant systems: two natural products, vindoline and 24-epibrassinolide, as well as the neutral dipeptides from the SPICE dataset. Individual models trained on natural products demonstrate sensitivity to conformation across complex ensembles, while a multi-system model trained on the dipeptides demonstrates predictive ability over hundreds of molecules. High-accuracy predictions of NMR observables may enable more robust chemical and biophysical structure determination approaches.

Differentiable Learning of Nuclear Magnetic Responses with NequIP-NMR

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