Dissection of Mechanical Couplings in Biomolecules via a Multiscale Approach

Jhih-Wei Chu

Institute of Bioinformatics and Systems Biology
Department of Biological Science and Technology
Institute of Molecular Medicine and Bioengineering

jwchu@nctu.edu.tw

Abstract

Biomolecules such as protein and nucleic acids duplexes are of vital importance in biology. A key question for such systems is how do subtle differences in the chemical composition cause extended variation in structure and mechanical properties in the system. In this work, all-atom molecular dynamics simulations and multiscale coarse grained modeling were conducted to resolve the structures and mechanical couplings in dsDNA, dsRNA, and an enzyme system. The multiscale computational framework developed here allowed quantitative comparison of the strengths of mechanical couplings for the different interactions in a molecule as well as across different systems. It was thus established that dsRNA has significantly higher strengths for mechanical couplings in backbone and sugar puckering than those of dsDNA. For nucleobase interactions of hydrogen bonding and stacking, on the other hand, dsDNA exhibited stronger mechanical couplings. Moreover, we showed that the mechanical couplings in the protein structure can be utilized to capture the patterns of sequence correlation in a multiple sequence alignment.