Modeling Supramolecular Dynamics at Atomic Detail

Pemra Doruker

Boğaziçi University, İstanbul

A mixed coarse-graining technique has been developed for elastic network models (ENM) in order to describe the harmonic dynamics of biological supramolecules at atomic detail. This technique forms an elastic network composed of high-resolution (atoms) and low-resolution (coarse-grained residues) nodes that are inter-connected by harmonic springs. Normal mode analysis of biomolecular systems including proteins, DNA, and/or RNA can be performed with high computational efficiency to extract biologically important collective dynamics. This new methodology is first validated on a homo-dimeric enzyme triosephosphate isomerase (TIM) and later applied to the supramolecular assemblage ribosome. A complimentary technique called reverse-mapping has also been introduced to perform conformational sampling around the native state of TIM by performing energy-minimization on deformed structures along the collective modes of ENM. Combining the two techniques can effectively provide alternative conformers for supramolecular assemblages that can further be utilized in flexible drug design.