Scilight

1 February 2018

Graph theory model sets new accuracy benchmark for protein flexibility analysis

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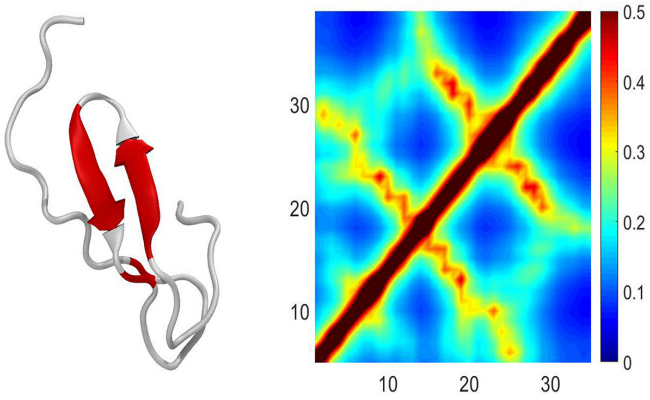
Multiscale weighted colored graph model promises a faster, simpler method for determining protein flexibility characteristics and achieves a significant increase in accuracy over widely used techniques.



Predicting protein flexibility is crucial to studying protein domains, entropy and stability. Several methods have been developed for predicting protein fluctuation features, such as B-factors for thermal motions, but a high-accuracy protein prediction model remains elusive. A newly introduced multiscale weighted colored graph (MWCG) model demonstrates results, reported in *The Journal of Chemical Physics,* that are significantly more accurate than current widely used methods. It leverages graph theory to accomplish these analyses in a fraction of the time.

Most interpretation of protein X-ray diffraction data so far has dealt with physical and molecular mechanics to derive protein structure from B-factors, measurements of protein X-ray scattering caused by thermal motions.

Instead, the authors modeled pairwise relations between atoms within a protein as graph edges. The approach placed atoms at coordinates as graph nodes that converted 3-D geometric information about element types and coordinates into protein connectivity. They defined multiscale subgraphs according to element types and use weighted edges to represent atom-atom interaction strength.

Applied to two protein data sets, one with 364 proteins, the MWCG model proved far more accurate than the classic Gaussian network model and more accurate than parameter-free flexibility rigidity index (FRI) techniques. It was able to predict the flexibility of all the atoms in each protein, not just alpha carbons — a feat that is new to the field. While characterizing some proteins using more sophisticated, less accurate models might take hours, the graph model is able to achieve more accurate results in a matter of seconds.

The group hopes to couple their multiscale color graph model with machine learning to use it to learn about how proteins interact with other biomolecules.

Source: "Multiscale weighted colored graphs for protein flexibility and rigidity analysis," by David Bramer and Guo-Wei Wei, *The Journal of Chemical Physics* (2018). The article can be accessed at https://doi.org/10.1063/1.5016562.