Open Seminar of the Center for Informational Biology, Ochanomizu University

場所：お茶の水女子大学理学部3号館2階　第2会議室
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KIAS

Can one apply a principal-based method to the ill-defined problem of protein structure prediction to achieve the best protein modeling?

One of the fundamental goals of modern sciences is to understand the nature of life, and deciphering the protein structure and its working mechanism lies at the very heart of this agenda. Due to the tremendous success of many genome projects, the number of available protein sequences reached over 5.3 million as of 2007, but less than 1% of these protein structures are known. Reliable and accurate protein structure prediction using only the sequence information is greatly in demand, but it remains as an unsolved problem even after many years of efforts. We intend to establish a successful protein modeling method that is solely based on direct application of principles excluding human interference in modeling steps. This should be contrasted to the common conception in the field that human expertise accumulated by many years of protein modeling is the most important asset for accurate protein structure prediction. In this talk we will discuss recent progresses of our efforts in CASP [1] experiments. CASP stands for Critical Assessment of techniques for protein Structure Prediction, and it represents a combined community effort between protein experimentalists and theoreticians to create an objective way to assess protein modeling methods. It appears that our newly proposed method based on the rigorous optimization of relevant score functions can provide best 3D modeling of proteins in the category of High-Accuracy Template-Based Modeling.

[1] http://predictioncenter.org/