Improving protein structure prediction by generating high-quality decoys

Abstract

A fundamental and unsolved problem in computational molecular biology is to predict the structure of a protein, given sequence information. But none of the protein structure prediction algorithms have been so far, able to predict structures with satisfactory accuracy. It is imperative to improve the discriminatory functions of these algorithms. We propose a method to generate incorrect conformations very close to the native protein structure and then let the discriminatory function distinguish between correct and incorrect conformations. These structures, better known as protein decoys would help develop better protein modeling tools and high resolution decoys can help us solve structures of binding sites, interaction sites etc. A reduced representation protein modeling tool CABS has been extensively used in this project to generate the decoys and resolution of the resulting structures were compared with decoys of the published Decoys R Us database. The scope of this approach goes beyond generating high-resolution decoys. The applications of this method include ab-initio structure prediction, comparative modeling and loop modeling.

References: