Protein Tertiary Structure Prediction by a Multiobjective Optimization and Neural Network Approach

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Abstract : Protein structure prediction is a challenging task in the bioinformatics field. The biological function of all proteins majorly relies on the shape of their three-dimensional conformational structure, but less than 1% of all known proteins in the world have their structure solved. This work proposes a deep learning model to address this problem, attempting to predict some aspects of the protein conformations. Throughout a process of multiobjective dominance, a recurrent neural network was trained to abstract the particular bias of each individual multiobjective algorithm, generating a heuristic that could be useful to predict some of the relevant aspects of the three-dimensional conformation process formation, known as protein folding.