Soft Computational Framework for Tertiary Protein Structure Prediction

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Abstract

Protein structure prediction is turning out to be one of the major challenges in the field of bio-informatics. It is highly important in medicine, especially in drug design and biotechnology. Proteins, being the basic building unit of all organisms, require experimental techniques for prediction of related structures. Among available methods, soft-computational tools provide readily available solutions for making predictions with less complexity, higher reliability and less time. The Artificial Neural Network (ANN) is one such tool which is used for structure prediction of proteins. This method is a machine learning approach in which ANNs are trained to make them capable of recognizing the 8-level subclasses of secondary structure. After the subclasses are recognized in a given sequence, their association with 3-level secondary protein structures is derived. The final structure is obtained from a majority selection from the protein structure. The work is also done in the reverse way, by predicting the 3-level secondary structure from the primary structure. This is done to confirm the accuracy of the prediction. In this work, ANNs are used as classifier to predict the secondary structure.
References


Index Terms

Computer Science
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Keywords

Protein structure prediction, proteinogenic amino acids, DSSP codes