Abstract

Protein secondary structure prediction is a problem related to structural bioinformatics which deals with the prediction and analysis of macromolecules i.e. DNA, RNA and protein. It is an important step towards elucidating its three dimensional structure, as well as its function. Secondary structure of a protein can be predicted from its primary structures i.e. from the amino
Protein Structure Prediction using Artificial Neural Network

acid sequences or from the residues though challenges exists. For these four methods are used. These are Statistical Approach, Nearest Neighbor method, Neural Network Approach and Hidden Markov Model Approach. The Artificial Neural Network (ANN) approach for prediction of protein secondary structure is the most successful one among all the methods used. In this method, ANNs are trained to make them capable of performing recognition of amino acid patterns in known secondary structure units and these patterns are used to distinguish between the different types of secondary structures. This work is related to the prediction of secondary structure of proteins employing artificial neural network though it is restricted initially to three structures only.

Reference

- S. A. Malekpour, S. Naghizadeh, H. Pezeshk, M. Sadeghi, C. Eslahchi; Protein secondary structure prediction using three neural networks and a segmental semi Markov model; “Elsevier Inc. All rights reserved.2008”.
- Protein Structure Image Gallery at “Biochemistry Department Website of Duke University. USA”. (http://kinemage. biochem.duke.edu/).
- Mona Singh; Introduction to computational biology;11/16/2000
- Kandarpa Kumar Sarma; Speech Corpus of Assamese Numerals for Recognition using Artificial Neural Network; “September 5, Springer”
- Aramak Afzal; Applications of neural networks in protein structure prediction.

Index Terms

Computer Science

Information Technology
Key words

Protein structure prediction

Artificial Neural network
Amino acids