Abstract

The use of laboratory techniques such as X-ray Crystallography and Nuclear Magnetic Resonance (NMR) Spectroscopy for protein secondary structure prediction, although effective, are expensive and time-consuming especially when it is to be done in a large scale. Computational techniques are being employed to predict the structures of protein in order to overcome these limitations. Various methods such as HMM, SVM, ANN, etc. have been used for the prediction of the protein secondary structure with different accuracies, weaknesses, and strengths. The current prediction accuracy obtained from these existing tools has been between 60% and 80% over years and research is still ongoing to get better prediction accuracy in the prediction of the secondary structure of proteins. In this work, deep neural network with three (3) hidden layers and particle swarm optimization algorithms are combined to predict the secondary structure of proteins from their primary structures (Amino Acids Sequence). The basic particle swarm optimization algorithm was used in training a deep neural network as implemented using Java programming language with spring boot framework for generating the various APIs. The dataset used was retrieved from the JPred Server 1.2 which contained 1349 training set and
149 test set. The model had a maximum accuracy of 53.18% on epoch 180 due to the early convergence of the model at local minimal.

References


Index Terms

Computer Science Artificial Intelligence

Keywords
Deep Neural Networks, DNN, Protein Structures, Particle Swarm Optimization Algorithm, BPSO, Protein Secondary Structure Prediction, Swarm Intelligence.