Abstract

Protein structure prediction plays a vital role in drug design and biotechnology. Understanding protein structures is necessary to determine the function of a protein and its interaction with DNA, RNA and Enzymes. Experimental techniques such as NMR Spectroscopy and X-ray Crystallography have been the main source of information about protein structures. But these conventional methods are now replaced by Machine learning methods such as Artificial Neural Network (ANN) and Support Vector Machine (SVM)s. In this paper, ANNs are used as a two level classifier to estimate the tertiary structure of proteins. ANNs are trained to make them capable of recognizing the primary sequences and DSSP codes of protein structures and their association with the secondary structure is derived. Based on majority selection, the final secondary structure is evaluated. These secondary structures can be further used as inputs to classify between the basic tertiary folds and subclasses of tertiary folds.

References

- H. Bordoloi and K. K. Sarma, "Protein Structure Prediction Using Multiple Artificial Neural Network Classifier", as a Chapter of a volume titled Soft Computing


Index Terms

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