

A Method of classification and Recognition of Blue Copper Proteins

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Some proteins in blue copper proteins have similarity of properties. In some cases it is not easy to differentiate the proteins each other. The study to recognize and classify in blue copper proteins has important roles to differentiate the similarity of properties for examples structures and residue sequences in blue copper proteins.

There are many methods have been developed to protein structure prediction from many approaches, but still not satisfied yet. Therefore it is a challenge for scientists to develop or improve their methods. One of promising methods is artificial neural networks (ANN) [1,2]. ANN is learning machine methods consist of input, hidden and output layer. This method has many various methods and applications in many areas especially for classification, recognition, prediction, simulation, analysis etc. In this problem we use ANN as classification and recognition methods.

Besides for classification and recognition, combination ANN and Fuzzy logic can be used to analysis the result and improve the accuracy. One of the combination method is ANFIS (adaptive Neuro-fuzzy inference systems[3]. The combination makes sense because ANN is learning method and fuzzy logic is efficient decision maker. The combination makes the methods powerfull and can be used in this problem.

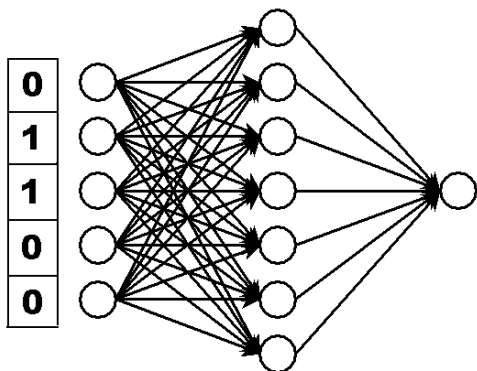


Figure 1: Schematic diagram of ANN with input, hidden and output layer.

In this study, the inputs of ANN are residue sequences of blue copper protein especially Classification of type 1 Cu Protein from Pdb files[4,5]. For

Table 1: PDB files of blue copper protein for input.

[57] 1RKR	[65] 1A4C	[74] 1ZIA	[83] 2PLT
[58] 1ARN	[66] 1ETJ	[75] 8PAZ	[84] 1AAC
[59] 5AZU	[67] 2CBP	[76] 2TSA	[85] 7PCY
[59] 4AZU	[68] 1BQ5	[77] 1BYO	[86] 1KDJ
[60] 1IJOI	[69] 1NDT	[78] 1PAZ	[87] 1KCW
[61] 2AZA	[70] 1PCS	[79] 1PLC	[88] 1A65
[62] 1NWP	[71] 1PMY	[80] 1AOZ	[87] 1KCW
[63] 1JER	[72] 1IUZ	[81] 1RCY	
[64] 1URI	[73] 1BAW	[82] 1AG6	

this study we will use 34 proteins of blue copper proteins. We have to make preprocessing in order to reduce time and avoid overfitting. For this reason we analysis number of residues, arrangement of residues and check of different residues. The output targets are secondary structure prediction i.e. α -helix, β -sheet and coil. ANN has to be trained to make this machine works. The method is also tested to classify and analysis protein classification of blue copper protein in human, animal and plant. Finally the method will be used to recognize and classify from residue sequence to determine types, class and name of the protein. Some of analysis i.e using correlation coefficient and SSE (sum square error) is required to make comparison and get better result.

The aim of this study is to make classification and recognition of blue copper proteins based on bioinformatics approach[6]. We try to analysis some characteristics and properties of blue copper protein using the methods.

References

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