A Method of Classification and Recognition of Blue Copper Protein

Acep Purqon, Ayumu Sugiyama, Yuichiro Takamatsu, Hidemi Nagao, and Kiyoshi Nishikawa

Division of Mathematical and Physical Science, Graduate School of Natural Science and Technology, Kanazawa University, Kakuma, Kanazawa 920-1192, JAPAN

Abstract. Some proteins in blue copper proteins have similar properties. In some cases it is not easy to distinguish the proteins each other. The study to recognize and classify in blue copper proteins has important roles to recognize the difference of similar properties, for examples, structures and residue sequences in blue copper proteins. There are many methods being developed to predict protein structure from many approachs, which one still not satisfactory yet. Therefore it is a challenge for scientists to develop or improve their methods. One of promising method is artificial neural networks (ANN). ANN is learning machine methods consisted of input, hidden and output layer. ANN is tested to recognize secondary structure in blue copper protein. It is found that ANN can distinguish for 7-type of secondary structure and recognize 72% secondary structure in blue copper protein.

Keywords: blue copper protein, Artificial Neural Networks
PACS: 87.15.Aa; 87.15.Cc

INTRODUCTION

Blue copper protein is one of metalloproteins containing copper ion and showing blue color in EPR spectrum. Blue copper protein consists of various type of protein and can be found in biological system for example in animal, human, plants and so on. Until now this group is being explored. One of interesting problem in blue copper protein is similarity in structure and amino acid sequences. Sometime it is hard to distinguish protein each others. Therefore the study to recognize among the protein has important roles.

In this study we use artificial neural networks (ANN) method to predict and recognize the secondary structure in blue copper protein. As we know ANN has many various methods and applications in many areas especially for classification, recognition, prediction, simulation, analysis and so on. In this problem, we use ANN as classification and recognition methods. Some calculation using ANN for Secondary structure prediction can be found in some papers[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11].

METHOD

ANN is simply consists of input, hidden and output layers as shown in Fig.1. In this case we use ANN using backpropagation algorithm. This algorithm is as follow[12]. First, it is weight initialization which set all weights and node thresholds to small random numbers.

Second, it is calculation of activation determined by $O_j = F(\Sigma W_{ji} O_i - \theta_j)$, where W_{ji} is the weight from input O_i, θ_j is the node threshold, and F is sigmoid function $F(a) = 1/(1+exp(-a))$.

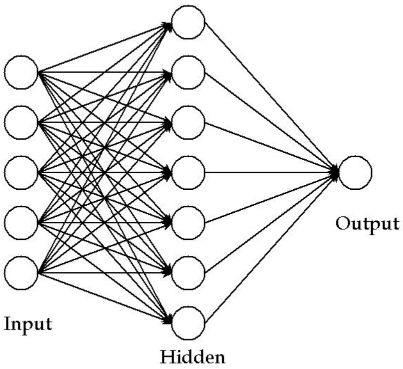

FIGURE 1. Schematic diagram of ANN with input, hidden and output layer. Input for this case is primary structure of blue copper protein and output is secondary structure of blue copper protein

Third, it is weight training which start at the output units and work backward to the hidden layers recursively. Adjust weights is determined by $W_{ji}(t+1) = W_{ji}(t) + \Delta W_{ji}$ where $W_{ji}(t)$ is the weight from unit i to unit j at time t (or tth iteration) and ΔW_{ji} is weight adjustment. The next is weight change which is computed by $\Delta W_{ji} = \eta \delta_j O_i$ where η is a trial-independent learning rate (0<η<1 e.g 0,3) and δ_j is the error gradient at unit j. The convergence is sometimes faster by adding a momentum term $W_{ji}(t+1) = W_{ji}(t) + \eta \delta_j O_i + \alpha[W_{ji}(t) - W_{ji}(t-1)]$ where 0<α<1.

Forth, it is the error gradient which is given by for the output units $\delta_j = O_j(1-O_j)(T_j - O_j)$ where T_j is desired (target) output activation and O_j is the actual output activation at output unit j. For hidden units is $\delta_j = O_j(1-O_j)\Sigma\delta_k W_{kj}$ where δ_k is the error gradient at unit k to which a connection points from hidden unit j. Fifth, Repeat iteration until convergence in terms of the selected error criterion. An iteration includes presenting an instance, calculating activation, and modifying weights.

In this study, the input of ANN are amino acid/residue sequences of blue copper protein, especially classification of type 1 Cu Protein from PDB files references [13, 14]. For this study we adopt 28 proteins of blue copper proteins.

From the viewpoint of chemistry, the kind of secondary structure formed depends on how the residue and its neighbours in the sequence are interacting. The pattern is arranged in the window of neighbouring amino acids around a residue. For this problem we use 5 residue [15] by the procedure as shown in Fig.2.

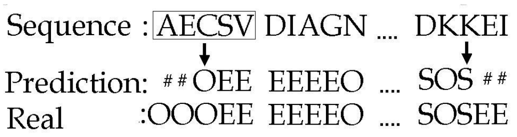
Sequence : AECSV DIAGN .... DKKEI
Prediction: ##OEE EEEEO .... SOS##
Real :OOOEE EEEEO .... SOSEE

FIGURE 2. window 5 amino acid to predict one secondary structure protein to distinguish H;Helix, B;Residue, E;Extended Beta Strand, G;310 Helix,I;Pi Helix, T;Hydrogen Bonded Turn, or S;Bend. Mark(#) is meant the strings is not involved as input pattern

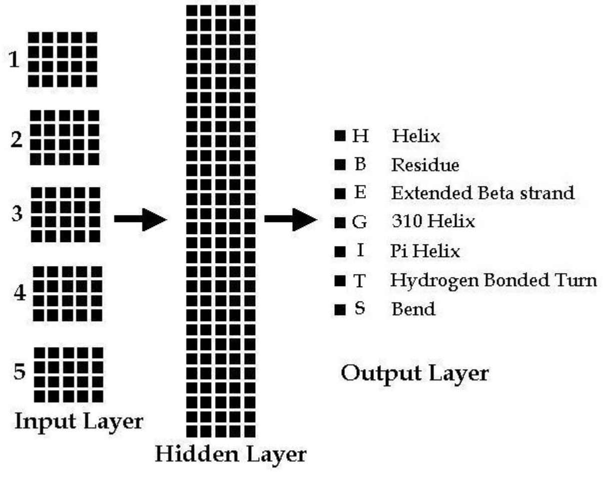

FIGURE 3. composition of matrix for input, hidden and output layer. input layer 100 node representing 5 amino acid ×20 element vector, hidden layer is 150 node (variable), output layer consists of 7 node representing secondary structure protein

TABLE 1. PDB files for blue copper protein for input of ANN [11]. The input represents variation types of animal, plant, bactery and so on

No	Protein	PDB
1	A. *xylosoxidans* azurin I	1RKR
2	A. *xylosoxidans* azurin II	1ARN
3	P. *aeruginosa* azurin	5AZU
4	A *denitrificans* azurin	2AZA
5	P. *putida* azurin	1NWP
6	C. *sativus* stellacyanin	1JER
7	A. *denitrificans* (M121Q) azurin	1URI
8	A. *denitrificans* (M121H) azurin	1A4C
9	P. *aeruginosa* (M121E) azurin	1ETJ
10	cucumber basic protein	2CBP
11	A. *xylosoxidans* nitrite reductase	1BQ5
12	A. *sylosoxidans* nitrite reductase	1NDT
13	S. sp. PCC 6803 plastocyanin	1PCS
14	M. *extorquens* pseudoazurin	1PMY
15	U. *pertusa* plastocyanin	1IUZ
16	P. *laminosum* plastocyanin	1BAW
17	A. *cycloclastes* pseudoazurin	1ZIA
18	A. *faecalis* pseudoazurin	8PAZ
19	P. *aeruginosa* (M121A) azurin	2TSA
20	S. *pratensis* plastocyanin	1BYO
21	A. *faecalis* pseudoazurin	1PAZ
22	C. *reingardtii* plastocyanin	2PLT
23	P. *nigra* plastocyanin	1PLC
24	T. *ferrooxidans* rusticyanin	1RCY
25	S. *oleracea* (G8D)plastocyanin	1AG6
26	P. *denitrificans* amicyanin	1AAC
27	E. *prolifera* plastocyanin	7PCY
28	D. *crassirhizoma* plastocyanin	1KDJ

TABLE 2. Vector for input. All characters/strings of amino acid are converted to be value/number. The simplest way is arranged by 20 element vector. For examples, vector no.4 is meant the value of element vector no.4 is 1 and another is zero, etc

Name	Vect	Name	Vect
Glycine (G)	1	Methionine (M)	11
Alanine (A)	2	Tryptophan (W)	12
Valine (V)	3	Tyrosine (Y)	13
Leucine (L)	4	Asparagine (N)	14
Isoleucine (I)	5	Glutamine (Q)	15
Phenylalanine (F)	6	Aspartamic Acid(D)	16
Proline (P)	7	Glutamic Acid (E)	17
Serine (S)	8	Lysine (K)	18
Threonine (T)	9	Argenine (R)	19
Cystine (C)	10	Histidine (H)	20

ANN is trained to recognize the target/output pattern based on input pattern. After training, ANN can be tested for real conditions. We make a conversion from string/character of primary structure become value/number. The simplest way of representing the 20 possible amino acid letters is arranged by 20 element vector. Each element corresponds to one letter, so particular one is encoded by setting it is element to 1 and the rest are set at zero. For a window of 5 amino acids,

TABLE 3. Vector for ouput. All characters/strings from 7 secondary structure are converted to be value/number

Letter	Secondary Structure	Output vector
H	Helix	1 0 0 0 0 0 0
B	Residue	0 1 0 0 0 0 0
E	Extended Beta Strand	0 0 1 0 0 0 0
G	310 Helix	0 0 0 1 0 0 0
I	Pi Helix	0 0 0 0 1 0 0
T	Hydrogen Bonded Turn	0 0 0 0 0 1 0
S	Bend	0 0 0 0 0 0 1

TABLE 4. Training data: (75% data) representing animal, plant, and bactery in blue copper protein

1RKR	1ETJ	1PMY	2TSA	1AG6
5AZU	2CBP	1BAW	1BYO	2PLT
2AZA	1BQ5	1ZIA	1PAZ	1AAC
1JER	1NDT	8PAZ	1RCY	1KDJ
1URI				

the input of the network is then a vector with 5 × 20 elements.

To make ANN work we train this algorithms and make preprocessing in order to reduce time and avoid overfitting. Training data consists of 2851 residue sequences and testing data 751 residue sequences. in matrix form there are 100 × 2851 for training data and 7 × 751 for testing data. The output pattern is much simpler because we only need to encode only 7-vector as shown in table 3. the 7-vector of output are Helix (H), Residue (B), Extended Beta strand (E), 310 Helix (G), Pi Helix (I), Hydrogen Bonded Turn (T) and Bend (S). The consideration and determination of hidden layer number depend on situation. In this case to make comparison, we use 50 hidden layer and 150 hidden layer. Figure 3 shows the architecture of the corresponding 5 window neural networks for recognizing and distinguishing 7-type of secondary structure.

In this case we to make prediction based on input, we start from no. 1 to 5 of primary structure of the sequence to predict secondary structure no.3. Then, no.2 to 6 to predict secondary structure no.4, and so on. Therefore we do not involved two data in the first secondary structure and two data in the last secondary structure as part of prediction (see again Fig.2). We divide 28 proteins of blue copper protein into 21 protein which involve azurin, plastocyanin an so on for training data and 7 proteins for testing data which also involve azurin, plastocyanin an so on(see table 4 and 5).

TABLE 5. Testing data: (25% data). The testing data are chosen so that the output data representing animal, plant, and bactery in blue copper protein

PDB	type	PDB	type
1ARN	Animal	1IUZ	Plant
1NWP	Plant	1PLC	Plant
1A4C	Animal	7PCY	Plant
1PCS	Bactery		

TABLE 6. Recognition using 150 hidden layer. Mark (*) has two meaning categories: the secondary structure prediction is out of pattern and the others one is false interpretation

1ARN (80%)	OEEEEEEO TTSOB*O**E EE*TTOSEE* EEEEEOSOOO HHHHO*O*EE EE***HH*H* HHH*T*T*** TTTTTTT**B SEEOOO*OTT OEEEEEEEG* ***TTOOE*E EOOSTTTTTT SEEEEEE
1NWP (60%)	OEEE***O T**O**OS*E E**TTOSEEE EEEE*OS**O HHHHO*O*EE EE******** ********** ****TT*TTB *EOOO*OTT OEEEEEEEG*GTTT** EEE *OOSTT**** *EEEEE
1A4C (85%)	OEEEEEEO **SO*SOSEE EE*TTOSEEE EEEEEOSSOO HHHHOBOOEE EEG****HHH HHHH**TGGG TTTTTTT*** SEEOOO*OTT OEEEEEEEG* G*T*TOEEEE EOOSTTTTT* *EEEEE
1PCS (57%)	*EEE**** *OO**EES*E EEE**T**EE EEEO***OBO *EEO********HHHH**** *****TOE*EE *EOSOEEEE EEO***TTTT OEE*EE
1IUZ (74%)	*EE**OTT *OOSEESS*E EE*TT*E*EE EEOSSOOBO* EEO*****TT ***HH***OS O**STTOEEE EE*O*OEEEE EEO******T **EEEEE
1PLC (74%)	E*ESOTTO O**EES*EEE **TT*EEEEE EOSSOOBO*E EO****OTTT ******OOTT OOB*S*T**E EEE*OS*EEE EEEO*GGTTT TOEEEEE
7PCY (73%)	EEE**OTT OO*SEE*S*E EE*TTOEEEE EEOSS*OBO* EEO*****TT ***HHHO*** O**S*TO*EE EEOOSOEEEE EEOS*TTTTT *EEEEE

RESULTS AND DISCUSSION

The performance of prediction and recognition using ANN for each protein is shown in Table 6. ANN can recognize each letter or 7-types of secondary structure with the exception using the mark (*) which means they have two catagories. The first category, the secondary

TABLE 7. Performance of recognition between 50 hidden layer with SSE=0.01 and 150 hidden layer with SSE=0.0001

PDB	50 hidden	150 hidden
1ARN	76%	80%
1NWP	58%	60%
1A4C	85%	85%
1PCS	59%	57%
1IUZ	55%	74%
1PLC	73%	74%
7PCY	60%	73%
AVERAGE	**66.4**%	**72**%

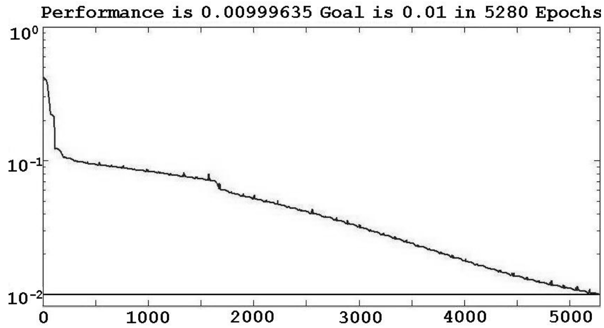

FIGURE 4. Example of SSE calculation using parameter 150 hidden layer and SSE=0.01 which can be reached after 5280 epoch

structure prediction is out of pattern and the second one is false interpretation.

Table 7 shows The prediction result for each protein is variated, for example, starting from the highest prediction respectively are A. *denitrificans* (M121H) azurin, A. *xylosoxidans* azurin II, P. *nigra* plastocyanin, U.*pertusa* plastocyanin, E.*prolifera* plastocyanin, P.*putida* azurin, and S.sp PCC 6803 plastocyanin. On the other hand A. *denitrificans* (M121H) azurin is the highest prediction result with 85%. It is meant that sequence pattern in this protein have been recognized by ANN. Meanwhile S.sp PCC 6803 plastocyanin is the lowest prediction result with 57%, probably the pattern in this protein can not well be recognized or there are new pattern in this sequence residue of the protein. However the result still can be improved using variation of hidden layer number, addition of blue copper protein data, and then we make better preprocessing/conversion and make better rules in neighbourhood rules and so on.

The average of prediction can be compared between ANN using 50 hidden layer with 66.4% and 150 hidden layer with 72%. In this case increasing hidden layer can improve the prediction result. we make comparison with another paper which the prediction result is 64% [10]. In addition, in this paper we calculate the output of prediction for 7 types of secondary structure. Meanwhile in another paper [3, 9, 10] use 3 types, there are Helix, Beta strand and Coil. Althought prediction of 7 types of secondary structure is more difficult, but the ANN still can predict for this problem.

CONCLUDING REMARKS

From this result, we can make conclusion that ANN method can be used to make prediction and recognition for secondary structure in blue copper protein. This method can be alternative method for recognition and prediction problem. The result for this case showes that ANN can distinguish for 7-type of secondary structure and recognize 72% secondary structure in blue copper protein.

ACKNOWLEDGMENTS

H.N. is grateful for financial support from the Ministry of Education, Science and Culture of Japan (grant 15550010).

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