World Scientific Research Journal (WSRJ) ISSN: 2472-3703
www.wsr-j.org

Application of User Identity Authentication Method Based on Spiking Neural Network

Chenyang Li [a]

School of Economics and Management, Beijing Jiao tong University, Beijing, China.

[a] 15711051@bjtu.edu.cn

Abstract: To authenticate the user's identity by the Spiking neural network, the prediction of protein secondary structure was studied. In addition, the Spike coding method of two amino acids was provided and applied to the study of secondary structure of proteins in a single Spiking neural network and cascade neural network. The research results showed that the first coding method can reduce the learning parameters of the network, but the accuracy of learning was not high. While in the second coding method, due to the introduction of amino acid characteristics, the nature of the problem can be better reflected. The accuracy of online learning was high. It is concluded that using the cascade neural network for secondary adjustment can improve the learning accuracy of the neural network and realize the user identification function.

Keywords: Spike neuron, learning model, pattern recognition, protein secondary structure prediction.

---

1. INTRODUCTION

Spike neurons are the third-generation model of artificial neuron development. Because it has the dynamic release characteristics of biological neurons and can deal with the problem of time patterns, research on Spike neurons has become an important issue in artificial neural networks (Li & Wu, 2014). The study of Spiking neural network learning model and algorithm can excavate its computational functional characteristics and is better used to solve practical problems. Artificial neural network is a high-tech research field that has re-emerged in recent years. It is also a hot topic in many disciplines such as information science, brain science, and neuropsychology (Li & Wu, 2014). As a pioneering technique of connectionist methods, people try to uncover the mysteries of the human brain through research on ANNs and establish an intelligent system that can simulate the structure and function of the human brain, enabling computers to perform information processing just like the human brain (Ruan, 2013).

In this paper, the functional properties of proteins are mastered by predicting protein secondary structure. A certain amount of research on the prediction of protein secondary structure is carried out. The Spike coding method of two amino acids is provided and applied to the study

of the protein secondary structure of a single spikes neural network and cascade neural network.

2. LITERATURE REVIEW

Artificial neural network has become an important subject in computer science research. The first generation of neuron models emerged more than 60 years ago. It is a simple model composed of McCulloch-Pitts threshold neurons. When the sum of the weighted input signals exceeds the threshold, the neuron sends a binary high signal (Zhuo, 2014). Although this neuron can only send digital signals, it has been successfully applied to multi-layer sensor networks and Hopfield networks. The second-generation neurons do not use threshold functions for output calculations. However, it uses continuous excitation functions that allow neurons to process the input and output of analog signals (Wang, 2014). The Sigmoid and Hyperbolic functions are commonly used excitation function models and are often used in feedforward and recurrent neural networks. They have more computational power than the first generation of neurons (Fan, 2013). The third-generation neural network uses a single neuron spike signal to maintain communication and calculations with temporary time information, as same as biological neurons (Zhang, 2013).

The structure and function of these three generations of neurons share similarities with biological neurons, simulating three of the more than 150 processing functions that can be performed by biological neurons (Liu, 2014). The first is that each input signal is processed to determine its strength (weighted). The second is that the combined effect (summation) of all input signals is determined. The third is that the output (transfer characteristics) is determined after the processing of the intermediate node and the output node. Figure 1 shows the basic structure of a neuron, which contains: input signal x_j from node j to node i, connection weight w_{ij}; neuron threshold ψ; transfer function f_i (x_i, w_{ij}); neuron excitation function and the response functions.

$$u_i = \sum_{i=1}^{m} x_i w_{ij} \ . \tag{1}$$

$$y_i = f(u_{rest} + u_i) \, . \tag{2}$$

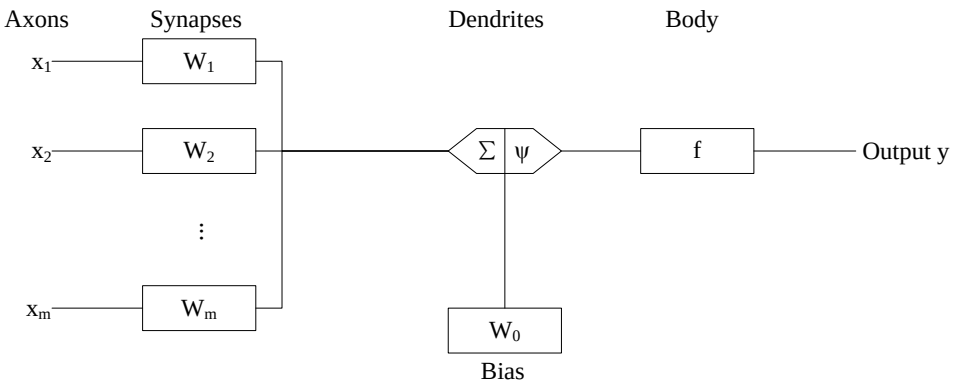

Figure 1. Artificial neuron model

3. METHODOLOGY

3.1 Spike prop algorithm based on traditional BP

Artificial neural network based on Spike neuron can use Spike Prop algorithm to conduct guided learning on the network, and some researchers have made some improvements based on Spike Prop algorithm.

A fully connected three-layer feedforward spiking neural network includes H input layer, I hidden layer and J output layer. Each pair of neurons contains k synaptic connection terminals. Each synapse connection can be considered as a single connection, and the connection weight is w^k_{ij}. The input sample set for a given problem is $\{P_i [t_1, ..., t_n] \}$, where $P_i [t_1, ..., t_n]$ represents the time-coded spike time set for the i-th input pattern using input layer neurons (the input neuron $n \in H$). For each pair of input modes, the correct output required by the network is $\{t^d_j\}$. t^d_j is the spike time point of the j-th output neuron, and the output neuron $j \in J$. The total error of online learning is defined as:

$$E = \frac{1}{2}\sum_i \sum_{j \in J} (t^a{}_j - t^d{}_j)^2 . \tag{3}$$

In the formula, t^a_j is the actual output of the network.

In the traditional BP rules, the neural network learning process adjusts the connection weights according to the following rules.

$$\Delta w^k{}_{ij} = -\eta \frac{\partial E}{\partial w^k{}_{ij}} . \tag{4}$$

In the formula, η is the learning rate. The Spike Prop algorithm is an improvement in the BP algorithm. The detailed algorithm is described as follows:

The δ_j is calculated for all output layer neurons j

$$\delta_j = \frac{\partial E}{\partial t^a{}_j} \cdot \frac{\partial t^a{}_j}{\partial x_j (t^a{}_j)} = \frac{t^d{}_j - t^a{}_j}{\sum_{i \in \Gamma_j} \sum_l w^l{}_{ij} [\partial y^l{}_i (t^a{}_j) / \partial t^a{}_j]} \tag{5}$$

The δ_i is calculated for all neurons i of other layers:

$$\delta_i = \frac{\sum_{j \in \Gamma_i} \delta_j \left\{ \sum_k w^l{}_{hi} [\partial y^l{}_i (t^a{}_j) / \partial t^a{}_i] \right\}}{\sum_{h \in \Gamma_i} \sum_l w^l{}_{hi} [\partial y^l{}_h (t^a{}_i) / \partial t^a{}_i]} . \tag{6}$$

The value of w^k_{ij} is adjusted for the output layer J:

$$\Delta w^k{}_{ij} = -\eta y^k{}_i (t_j) \delta_j . \tag{7}$$

The value of w^k_{hi} is adjusted for other layers:

$$\Delta w^k{}_{hi} = -\eta y^k{}_h (t_i) \delta_i . \tag{8}$$

The Spike Prop algorithm above combines the traditional BP algorithm with the Spiking neural network and uses the gradient information to adjust the network parameters to solve the actual classification problem. However, this algorithm is easy to fall into the local optimal solution.

At the same time, the neural network only allows positive connection weights; otherwise the Spike Prop algorithm will not converge.

3.2 Composition of protein molecules

The basic units that make up a protein molecule are amino acids, and there are 20 amino acids that make up the natural protein. Each amino acid consists of one amino--NH_2, one shuttle-COOH, one α carbon atom C^{α} and one R group. The amino group, the shuttle group and the carbon atom constitute the main chain of the amino acid. The R group is also called the side chain of the amino acid. The difference between different amino acids is that the chemical structure of the side chain R is different. In addition to proline, other amino acids both have the chemical structural formula shown in figure 2, and the proline structural formula is different in that its side chain is covalently bonded with the main chain N atom to form an imino acid shown in figure 3.

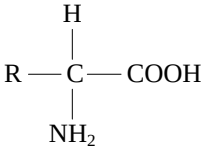

Figure 2. The chemistry structure of general amino acid

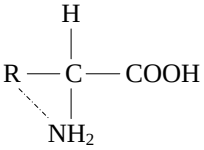

Figure 3. The chemistry structure of proline.

3.3 Protein secondary structure prediction

In evaluating various protein secondary structure prediction methods, the following evaluation indicators are commonly used in the world.

Overall accuracy Q_3:

$$Q_3 = \frac{P_\alpha + P_\beta + P_{coil}}{N}. \tag{9}$$

In the formula, N represents the total number of predicted amino acid residues, P_α represents the correctly predicted α-helix, P_β represents the correctly predicted β-segment, and P_{coil} represents the irregular curls that are correctly predicted.

Motthew coefficient:

The correlation coefficient of the α helix is defined as follows:

$$C_\alpha = \frac{p_\alpha n_\alpha - u_\alpha o_\alpha}{\sqrt{(n_\alpha + u_\alpha)(n_\alpha + o_\alpha)(p_\alpha + u_\alpha)(p_\alpha + o_\alpha)}}. \tag{10}$$

In the formula, p_α represents the total number of cases that are correctly predicted; n_α represents the total number of cases that are correctly negated; o_α represents the number of α-helix that are erroneously estimated; u_α represents the number of α-helix that are not predicted. The same calculation method is used for C_β and C_{coil}.

Three-state accuracy rate Q_i:

$$Q_i = P_i/(P_i + U_i) \qquad i \in \{H, E, C\}. \tag{11}$$

In the formula, P_i represents the number of residues that are correctly predicted as i-state, and U_i represents the number of residues that are incorrectly predicted as i-state. Q_i can be used to measure the lack of forecast.

4. RESULTS AND DISCUSSION

4.1 Spike coding method for protein secondary structure

In the protein secondary structure prediction model, the sliding window is a commonly used technique. The underlying assumption is that the identity of an amino acid and its neighboring amino acids determines the secondary structure of the neighborhood. As shown in figure 4, a continuous protein sequence formed by alanine and its 6 amino acid residues is a window. The length of the window is 13, and the secondary structure corresponding to this window is the type of secondary structure that alanine shows here.

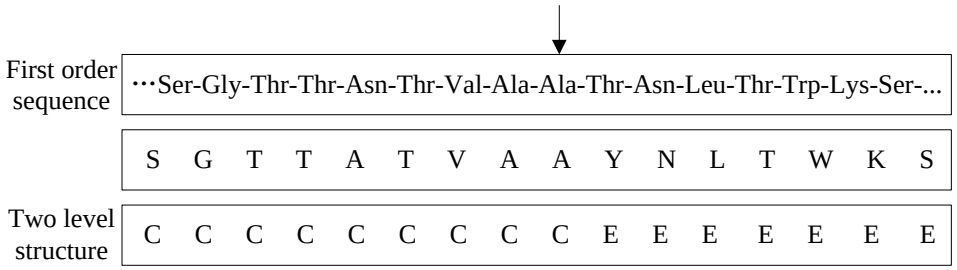

Figure 4. Example of sliding windows

The Spiking neural network is used to solve the problem of protein secondary structure prediction, and the key is also whether the network input and output coding can reflect the nature of the problem.

In the prediction of protein secondary structure, it is necessary to establish a protein database with a known secondary structure, and then extract the proteins one by one from the database for input and output coding. A key step in the entire coding process is how to group and encode the already coded proteins according to the length of the sliding window, and how to output the secondary structure of each group. As shown in figure 5, a detailed coding flowchart is provided. The get Protein Seq () function extracts protein data from the protein database based on the currently input protein name. Then, the get Seq Length () function is called to obtain the length of the current protein sequence and encode Protein () function. Therefore, the entire amino acid sequence is encoded to spike time. In addition, the bit-filling operation is performed. That is, at the beginning and end of the protein sequence, (windowsSize-1) / 2 bits are added. We will encode these bits into a larger spike time, meaning that the corresponding input neurons are not issued. The get Window Array () function is used to group the protein sequences. A length protein corresponds to a group of length amino acids (spike time series). Each group will serve as an input sample of neural network. The get Real () function calls the get Code () function to encode the secondary structure of a known protein and produce the

correct secondary structure output (represented by the output spike time) for each group, which is the correct output t_d of the network.

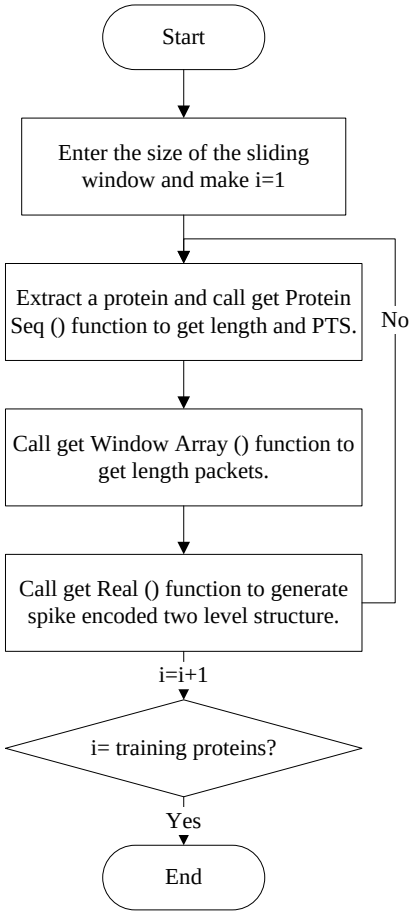

Figure 5. The input and output encoding of protein

The Spiking neural network input and output relationship under this coding is shown in figure 6. Assuming that the size of the sliding window is 13, the number of neurons corresponding to the neural network input layer is also 13. The current input primary amino acid sequence is ENLKLGFLVKQPE, and then the secondary structure corresponding to the "F" in the middle of the sequence is actually predicted. The secondary structure of the sequence is known as CCEEEEEECCCC, and the secondary structure of F is E, which is the structure of β-Strand. For the residues at the beginning and the end of the protein, complement method is used. That is, 6 complements are added before the first residue and after the last residue respectively. In actual coding, we encode the 12 complements into Spike neurons that do not issue (provide a larger spike time, such as 150 ms), so that the beginning and the end of the residue are only followed by the effect of the first 6 amino acid residues.

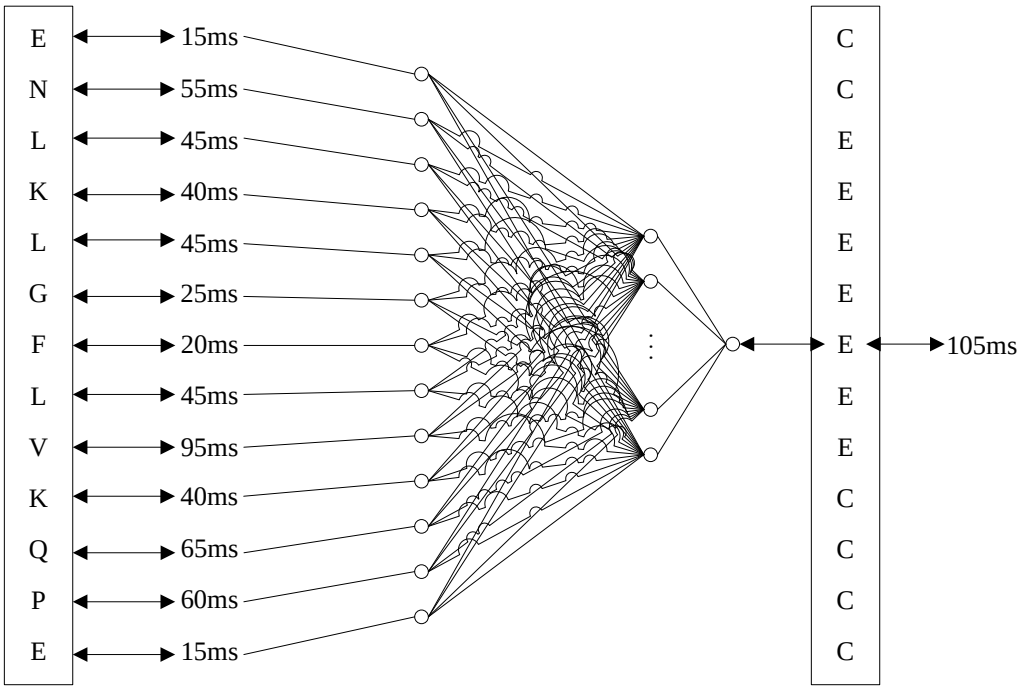

Figure 6. The relationship between input and output of the SNN

If we consider the structure information contained in the primary sequence of the protein, and encode the original sequence segment after preprocessing, we will increase the amount of input unit information included in the network. If the residue hydrophobicity, charge number, volume and other indicators quantized by real numbers are used to encode, we must consider the possible adverse impact on the defined input space. After the pre-processing of the original sequence segment encoding, the effect is better than the direct encoding of the input residue.

It is known that the structure and properties of the twenty amino acids that make up proteins are different, and each has its own characteristics. Due to this characteristic, the structure and function of protein molecules show diversified. The replacement of amino acids with similar physicochemical properties tends to preserve the structure and function of proteins, and thus the frequency of various amino acid substitutions varies greatly. Therefore, we consider the polarity and volume of amino acid molecules (as shown in table 1 and table 2). The two characteristic parameters are used to encode amino acids.

Table 1. The polarity value of 20 amino acids.

I	V	L	F	C	M	A	G	T	S
4.5	4.2	3.8	2.8	2.5	1.9	1.8	0.4	-0.7	-0.8
W	Y	P	H	E	N	Q	D	K	R
-0.9	-1.3	-1.6	-3.2	-3.5	-3.5	3.5	-3.5	-3.9	-4.0

Table 2. The bulk value of 20 amino acids.

A	R	N	D	C	Q	E	G	H	I
88.6	173.4	117.7	111.1	108.5	143.9	138.4	60.1	153.2	166.7
L	K	M	F	P	S	T	W	Y	V
166.7	168.7	162.9	189.9	122.7	89.0	116.1	227.8	193.6	140.0

Amino acid sequences are coded using amino acid polarity and volume values. Here, the characteristic values of amino acids are actually preprocessed. During coding, one amino acid

is coded with 8 neurons, 4 of which are used to encode the amino acid polarity value, and the other 4 are used to code amino acid volume values. Assuming that the size of the selected sliding window is window size, the neural network input layer neurons have (8*window Size). Similarly, the protein sequence should be patched in the same manner as the first coding. For the 12 bits to be supplemented, each one is coded with 8 neurons and encoded into a larger spike time. The input and output encoding process are the same as figure 4, excepting that the function of each function has changed. Among them, get Protein Seq () function extracts the corresponding protein from the established protein database according to the name of the input protein. It obtains the length of the protein without performing the encoding work of amino acid residues. The get Window Array () function first divides the protein sequence into length groups, and then calls encode Protein () function to encode each group. The detailed coding process is shown in figure 7. The get spike times () function uses the Gaussian coding method to perform the current input amino acid sequence. In the figure, the get spike times () function encodes the eigenvalues of the current input amino acid sequence using Gaussian coding. The get Real () function is unchanged and used to obtain the correct secondary structure output of each group (represented by the output spike time), that is, the correct output of the network t_d. The output secondary structure code is shown in table 3.

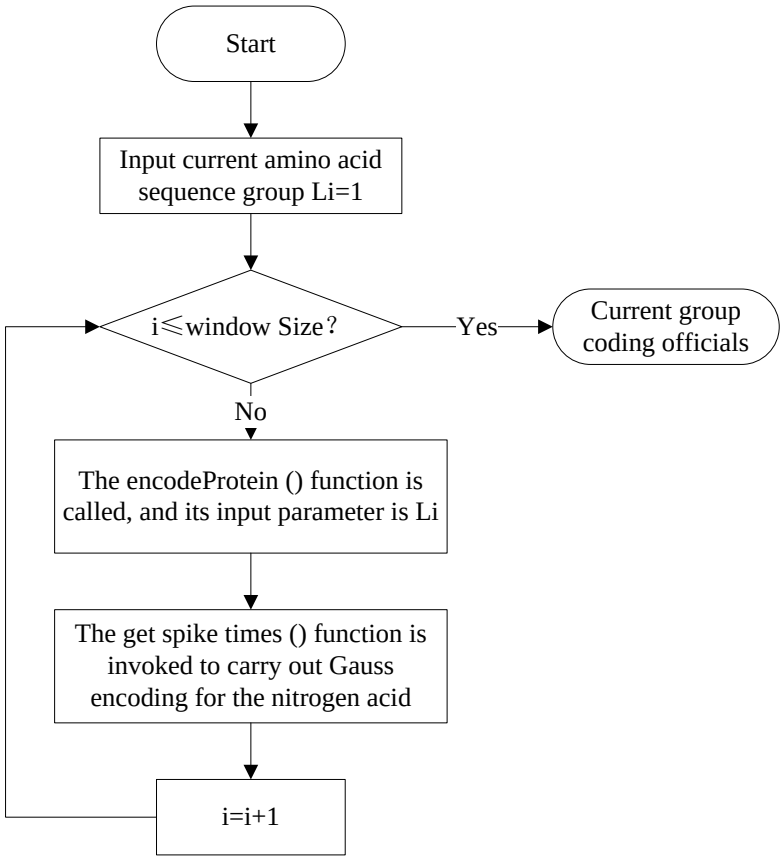

Figure 7. Encode the parameter of amino acids using Gaussian

A sample of the encoded amino acid sequence is poured into the input layer of the Spiking neural network. After the calculation of two layers of neurons, the actual output spike time t_a is obtained. If $t_a = t_d$, the prediction of the network is correct. Otherwise, the neural network

learning algorithm is used to adjust the weight of the network connection so that the error between t_a and t_d is within an allowable range.

Table 3. Encode the secondary structure.

Two level structure	Spike coding
H	5ms
E	10ms
C	15ms

4.2 Establishment of protein secondary structure learning model based on spiking neural network

According to the above two input and output encoding methods, Spicking neural network is used to learn the secondary structure of proteins. Prior to learning, protein data must be grouped in sequence to establish a spiking neural network learning sample set.

For a plurality of proteins in the training set, the proteins are divided into network learning input packets according to the flow chart of figure 4. The input coding of the grouping is performed using the above method, and each encoded input spike time is recorded in in_SpikeT [Total_ length] [Window Size] array. In this array, Total_length is the total number of amino acids in the training set, that is, the group number. The exact secondary structure corresponding to each group is also recorded in the output[Total_length] array. The in_SpikeT[][] array and output[] array constitute the input/output pattern pair for the network learning.

In this way, the neural network's input pattern set is $\{P_i [t_1, ..., w_{indow\ size}]\}$, $i \in [1, Total\_ length]$. $P_i [t_1, ..., w_{indow\ size}]$ is the input Spike time series of each protein group. For each input mode i, the correct output required by the neural network is output[i], and the actual output of the neural network is t_i. The total learning error of the neural network is the fitness value of the particle in the PSO algorithm:

$$E = \frac{1}{\text{Total\_length}} \sum_{i \in \text{Total\_lengh}} (\text{output}[i] - t_i)^2 . \tag{12}$$

4.3 Data selection

There are many ways to classify protein secondary structure, including dividing DSSP according to the repeating pattern of hydrogen bonds in the three-dimensional structural coordinates of the protein. According to the hydrogen, STRIDE divided by two kinds of dihedral angle data partition, the difference between the atomic distances in the coordinates of the structure and the standard atomic distance in the secondary structure, the secondary structure of DEFINE is determined.

In this paper, the DSSP classification method is used to classify the known structure of PDB database into three categories: Helices, Sheets and Coils. The protein structure in the PDB database is divided into eight categories: G, H, I, B, E, S, T and C. Among them, G, H and I belong to Helices and are denoted as H.B and E belong to Sheets and are designated as S. S, T and C belong to Coils and are designated as C.

Protein data of known secondary structure is randomly selected from the PDB database for neural network learning. The total number of residues is 17,953. It is also possible to generate 17,953 samples and enter the network for learning. Due to the limitation of experimental conditions, when we run on IBM Pentium 3.2G, 512MB of memory, the Spiking neural network takes about 3 to 4 months to learn. In the actual process, some parameters of the neural network and some of the initial settings of the PSO algorithm are adjusted and multiple learning are required. To accelerate the computation time, in the following experiments, only one protein is selected as the experiment, and the two encoding methods and the network learning model we gave are analyzed experimentally.

4.4 Experiment and analysis

In the experiments of this paper, Spike neurons of the SRM model are used. The selection of the membrane voltage constant should be slightly larger than the time interval of neural network coding. The Spiking neural network uses a single synaptic connection. At the initial stage of network initialization, the synaptic delay is randomly selected and fixed, and the connection weight is adjusted according to the learning model to optimize the network output. A three-tier Spiking neural network model is used, namely, an input layer, a hidden layer and an output layer. The three-layer network neurons use a single synapse full connection. The input and output relations of the neural network are shown in figure 5. The number of input nodes in the network structure is determined by the encoding method. In the first encoding mode, the size of the sliding window is chosen as 13, and the number of input neurons is 13. The number of nodes in the hidden layer is adjusted according to the input node, so as to obtain a better network performance. When the output node is 1, different output spike time is used to represent the three secondary structures. The time interval of spike encoding is 5ms. The network initial connection weight takes a random value between [-100, 100]. During the experimental process, we input the input layer of the neural network according to the amino acid grouping order of proteins. In addition, 30, 40 and 50 neurons are selected for the hidden layer respectively. The results show that the increase of the number of neurons in the hidden layer does not improve the accuracy of network learning. When the number of neurons in the hidden layer is 50, the best overall learning accuracy rate Q3 of the neural network is 49.6%.

To avoid the impact of using continuous input windows on performance, the protein sequence is used for network learning. The training group's sequence grouping is poured into the neural network in a random manner. The network connection method and the setting of neurons at each layer are the same as the previous experiment. The input and output coding use the first coding method. The size of sliding window is 13 and there are 13 neurons. The neural network overall learning accuracy rate Q3 can reach 52. 03%. This shows that the input of amino acid sequence grouping in a random way can improve the overall learning accuracy, but it is not very obvious.

We use the cascade Spiking neural network to learn the protein sequence. The network structure is shown in figure 8. The connection between neurons adopts a single synaptic full connection method, and the amino acid sequence encodes the first coding method. The size of

sliding window is Windows Size. First level neural network: input neurons windows size, 50 hidden neurons, 1 output layer neuron. Second neural network: input neurons windows Size, 50 hidden neurons, 1 output layer neuron. In the first step of the learning process, protein sequences are first grouped and the code is input. Then each group is input into the first level neural network in a random order to learn. The connection weights are adjusted according to the learning model to make the network output optimal solution. That is, the preliminary secondary structure of the sequence is obtained. If the length of the protein is length, there are corresponding length groupings. After the first-level network learning, length secondary structures corresponding to each group are generated. The second step is to group the length of the secondary structure in the same sequence grouping. There is also a need to do a bit-filling work, adding (windows Size-1)/2 bits at the beginning and end, respectively. Finally, each group is poured into the input layer of the second neural network in a random order for learning. After learning from the secondary neural network, the final secondary structure is obtained. The overall accuracy rate Q3 of the cascaded Spiking neural network after learning can reach 61.7%.

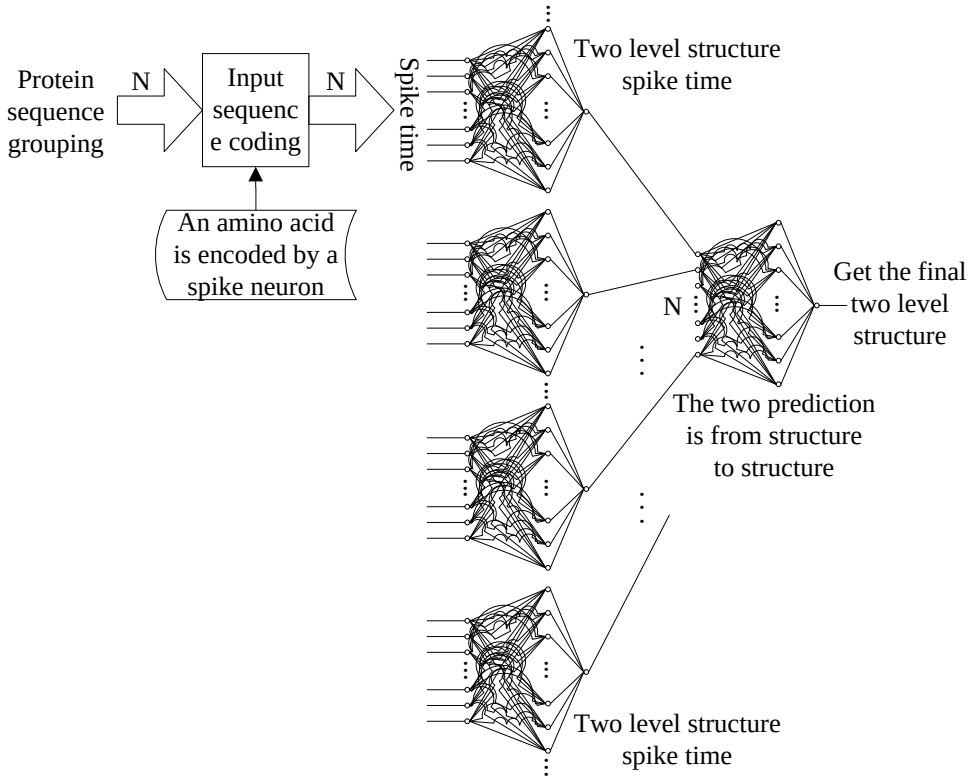

Figure 8. SNN with multi-levels while amino acid encoded by the first method.

The following experiment uses Gaussian coding. The cascade Spiking neural network is used to learn the selected protein data. In this way, the cascading neural network structure is shown in figure 9. The number of neurons in each layer is the same as the previous experiment. In the first step, protein sequences are first grouped and the code is input. One amino acid in the grouping sequence here will be coded with 8 neurons. Assuming that the size of sliding window is windows Size, and the input neurons of the first layer neural network have (8 *

windows Size). Then, the encoded packets are input into the input layer of the first-level neural network in a random order for learning, and the connection weights of the network are adjusted by using the learning model, so that the network output is optimized and a preliminary secondary structure of the sequence is obtained.

If there are length sequence groups, the length of the corresponding secondary structure will be generated after the first layer is learned. In the second step, we group these length secondary structures using the same grouping method. Here we also need to do a bit-filling work, adding (windows Size-1)/2 bits at the beginning and end, respectively. Then, each group is poured into the second-level neural network in a random order for learning. Similarly, since the output of the first-level neural network is the spike time corresponding to the secondary structure, there is no need to perform spike coding when inputting the second-level neural network learning, and the input layer neuron of the second-level neural network is Windows Size. Without the use of cascading, the overall preparation rate for online learning Q3 can reach 54.4%, which is an improvement over the first encoding method. After the secondary learning of the cascaded Spiking neural network, the overall accuracy rate Q3 can reach 70.7%, which is a relatively high accuracy rate.

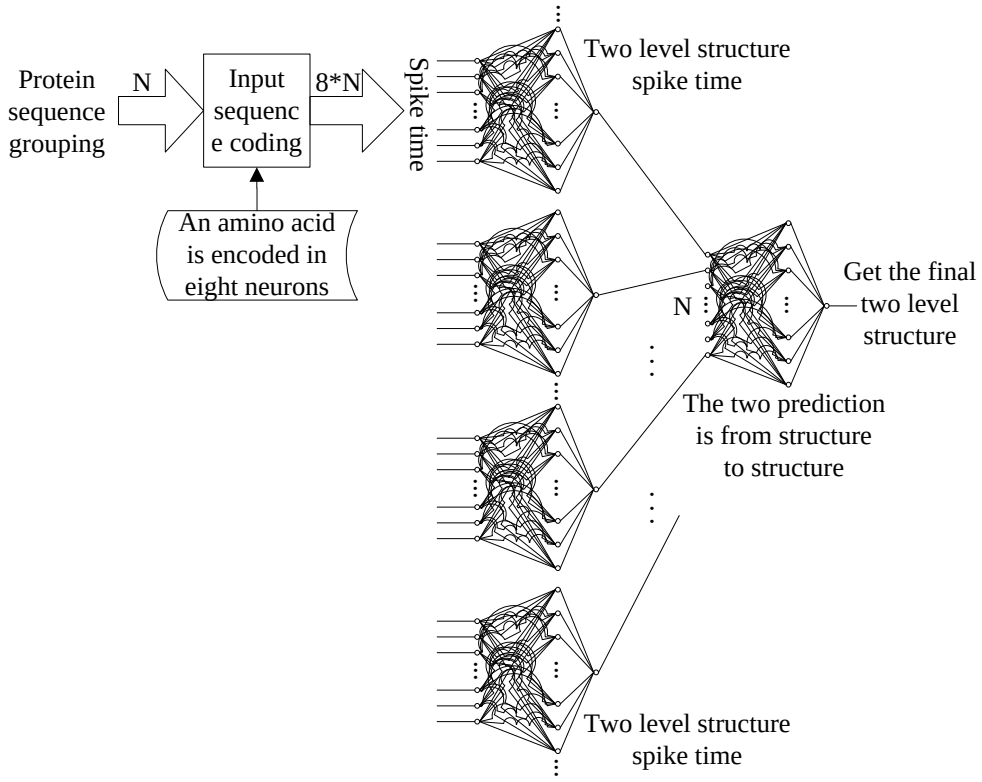

Figure 9. SNN with multiple levels encoded by the first method.

From the above several experimental results, it is known that although the first encoding method reduces the number of input neurons compared with the traditional amino acid orthogonal encoding method, it greatly reduces the network parameters and accelerates the speed of network learning. However, due to the fact that no biological information is added during coding, the overall network learning accuracy is not very high. At the same time, the

random input method is used to learn the network, which can avoid the influence of the sequential input window on the performance to a certain extent and improve the accuracy of learning. Cascading neural networks can further improve the performance of neural networks. In the second coding method, some characteristic values of amino acids are added. Although the number of input neurons in the network is increased, the ability of network learning is greatly improved. In general, if the orthogonal coding method is used, the number of input neurons is 13×21 for a window size of 13 and the first encoding method requires only 13 input nodes. The second encoding method also requires only 13 x 8 input nodes.

It is known that some sequences in the primary sequence of a protein are mainly composed of a certain structure. Therefore, to obtain a higher prediction accuracy, the selected training set must be large enough and include a certain number of various structures. However, due to the limitations of the experimental environment, we can only extract a protein from the international protein database to analyze its spike coding and learning model based on Spiking neural network.

5. CONCLUSION

Protein structure prediction is the most basic problem in biological information processing. Artificial neural network is also used to predict protein structure and has been a persistent hot issue in bioinformatics research. In this paper, based on the prediction of protein secondary structure, the Spiking neural network model based on particle swarm optimization algorithm is used. In addition, a certain amount of research has been done on the prediction of protein secondary structure. Two kinds of amino acid encoding methods are provided, including Spike time encoding of amino acids and Gaussian coding of amino acid properties. These two encoding methods are orthogonal to the traditional amino acid encoding, simplifying the complexity of the encoding, and the network learning accuracy is higher. At the same time, the cascaded Spiking neural network is used for secondary adjustment, which can further improve the neural network learning accuracy.

REFERENCES

[1] Li, H., Wu, Q. (2014). The hardware implementation of neuron synapse in pulse neural network (pp.125-126). Application of computer system.

[2] Li, H., Wu, Q. (2014). The implementation of neural network activation function in smart sensors (pp.111-112). Sensors and microsystems.

[3] Ruan, C. (2013). Research on learning algorithm of pulse neural network based on STDP (pp.210-211). Fujian Normal University.

[4] Zhuo, Z. (2014). Research on image processing algorithm of pulse neural network based on GPU (pp.154-155). Fujian Normal University.

[5] Wang, X. (2014). Color edge gradient segmentation and corridor ground extraction based on pulse neural network (pp.123-124). Fujian Normal University.

[6] Fan, L. (2013). Comprehensive neural network and facial expression recognition

algorithm based on multi feature fusion (pp.201-202). Fujian Normal University.

[7] Zhang, Y. (2013). Research and implementation of video-based traffic flow detection technology (pp.130-131). University of Electronic Science and technology of China.

[8] Liu, J. (2014). Synchronization of neural networks with impulses and infinite distributed delays (pp.110-111). Yangzhou University.