The Detection of Sleep Apnea Hypopnea Syndrome based on Improved BP Neural Network

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***Abstract*—The prevalence of sleep apnea hypopnea syndrome (SAHS) is increasing year by year and up to 14% in 2016.The disease poses a threat to human sleep safe. To detect the disease effectively and pre-alert, a method for the diagnosis of SAHS using respiratory signals was proposed. According to the characteristics of respiratory signal, nonlinear characteristics fractal dimension and sample entropy were introduced based on time-domain characteristics variance and clinical zero passing numbers as well as frequency-domain characteristics wavelet coefficients and wavelet energy. Then a 6-dimension feature vector was structured and input into the support vector machine (SVM), back propagation neural network (BPNN) and improved back propagation neural network (IBPNN) based on morphology. The method was verified by the 8 sets data including 3840 samples of the Physionet Apnea Database. Experimental results showed that classification accuracy of SVM and BPNN was 71.2% and 84.5% respectively. The IBPNN based on morphology improved the 85% of classification results and increased accuracy by 7.3%. It is very effective to detect the SAHS using the feature vector and IBPNN based on morphology proposed in this paper and provide an efficient and convenient method for the diagnosis of diseases.**

Keywords-sleep apnea hypopnea syndrome; nonlinear characteristics; morphology; back propagation neural network

I. INTRODUCTION

Sleep Apnea Hypopnea Syndrome (SAHS) refers to the sleep disorders that every night sleep apnea happens above 30 times or Sleep Apnea Hypoventilation index (AHI) is greater than or equal to 5 times per hour[1]. Epidemiological analysis showed that the prevalence of sleep apnea increased year by year. According to the latest data in 2016, the disease prevalence rate in male is as high as 14% and the prevalence in female has increased 2.5 times and rose to 5%. The disease causes serious damage to human health. Polysomnogram (PSG) monitoring is the golden standard for diagnosis of SAHS[2]. But the PSG inspection is tedious, costly, time-consuming and not convenient. In recent years, many scholars at home and abroad have started to study SAHS and are trying to simplify the detection of the disease and have made some achievements.

Even if SAHS is a respiratory disease, it is most common to use the characteristics of electrocardiogram (ECG) to determine whether develop the disease in detecting algorithm. Avci C, Correa L S, Al Ghunaimi B, professor Wen-long Xu and other scholars have proposed many new algorithms for detecting SAHS using ECG, the highest accuracy has reached more than 90%[3-6]. They mostly analyzed respiration signal derived from ECG signal and obtained a certain high accuracy. But SAHS is a respiratory disease and it must be easier and more convenient to detect the disease using signals that are directly related to it. In 2005, Fontenla-Romero O et al. used the respiratory signal to carry out five layers of wavelet decomposition and input the fifth layer of detail coefficients as the signal feature into the neural network. The classification accuracy was 83.78%+1.90%[1]. Tagluk et al. used the same method of wavelet decomposition in 2010. After seven layers of wavelet decomposition, they used the detail wavelet coefficients of the seventh layer as feature input and the classification accuracy of obstructive sleep apnea (OSA), central sleep apnea (CSA) and mixed sleep apnea (MSA) reached 73%, 94% and 73% respectively[7]. Thommandram A et al. input four characteristics according to clinical observation into k-Nearest Neighbor (KNN) network in 2013 and the classification accuracy reached 91.2%, specificity reached 88.1% and sensitivity reached 95.7%[8]. Aydoğan et al. used mean and energy of Multi-channel signals collected by PSG as characteristics and then input them into the neural network. They used morphological filter to improve classification effect and finally the classification result achieved 87.28% in 2016[9].

Because the chest respiration signal is easily disturbed by the beat of the heart pump blood [5], the nasal airflow signal detected by the nose thermistor was selected as the respiratory signal that we analyzed. On the basis of predecessors' research, we continued improving on the feature extraction and classifier of respiration signal. The nonlinear characteristics fractal dimension and sample entropy was introduced, then a new feature vector was built. And a new back propagation neural network (BPNN) structure based on morphology was also put forward. As a result, the classification result was improved of 85%. The algorithm framework is shown as Fig. 1.

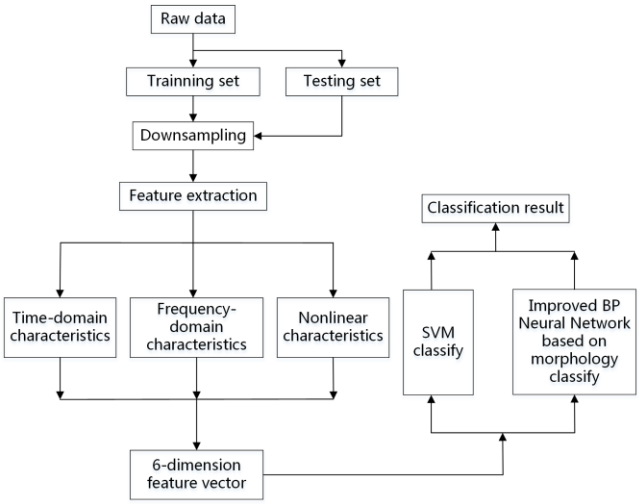

Figure 1. The framework of the algorithm including feature extraction and classification

II. METHOD

A. Feature Extraction

For all classification problems, the core problem is to construct a meaningful feature set. At present, the common features of signal research include time-domain characteristics such as peak, mean, variance as well as frequency-domain characteristics such as spectrum and power spectrum. In this paper, the effective respiratory signals were got after respiratory signals preprocessing. On the basis of summarizing the characteristics of the signals, the feature set was constructed which including time-domain characteristics, frequency-domain characteristics and nonlinear characteristics as shown in Fig. 2. Among feature set, the frequency-domain characteristics are obtained by wavelet transform.

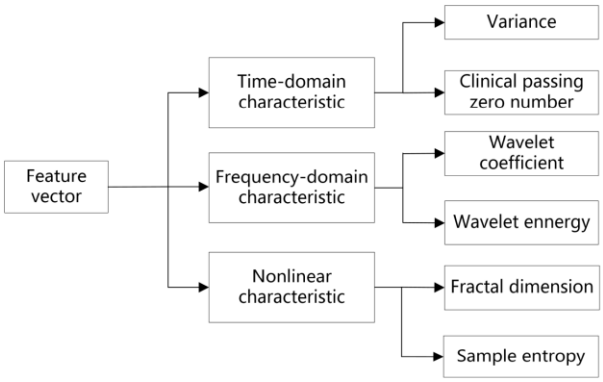

Figure 2. The feature vector including time-domain, frequency-domain and nonlinear characteristics

1) Wavelet Transform

Wavelet Transform (WT) is a time-frequency analysis method. Compared with the traditional Fourier Transform (FT) and short-time Fourier Transform (STFT), the WT overcomes the drawback that the window size is not change with frequency and realizes multi-scale analysis of signals by means of scaling and translation. It is a common method for analyzing non-stationary signals. After preprocessing, the sampling frequency of effective respiratory signal x(t) is still 100Hz. In order to facilitate the subsequent WT processing, we reduced the sampling frequency to 1Hz which is not very different from the main frequency component (0.2-0.4Hz) of the respiratory signal. It simplifies the process of wavelet decomposition.

For input signal x(t), the continuous wavelet transform (CWT) is defined as

$$CWT(a,b) = \int x(t)\psi^{*}_{a,b}(t)dt \tag{1}$$

where $\psi(t)$ is called the mother wavelet or a basic wavelet. A set of wavelet functions can be got by changing the scale parameter a and translation b. For real numbers (a,b), the CWT is defined as

$$\psi_{a,b}(t) = \frac{1}{\sqrt{a}}\psi(\frac{t-b}{a}) \tag{2}$$

In the process of applying WT, it is necessary to discretize the wavelet transform in order to simplify the calculation and reduce redundancy[7]. We usually choose binary wavelet whose expression is:

$$\psi_{j,k}(t) = 2^{\frac{-j}{2}}\psi(2^{-j}t-k) \tag{3}$$

2) Nonlinearity

a) Fractal dimension

The time-domain waveform of respiratory signals processed in this paper has self-similarity and shows periodicity and randomness. Theoretical researches and practices show that the fractal dimension of a set is very stable on a wide scale. That is, the fractal dimension is a constant for any kind of fractal[10]. This feature was used to describe and differentiate different fractal which in this paper is to distinguish respiratory signals between sleep apnea and sleep in normal conditions.

The dimension estimation method based on box-counting is widely used because it is simple and easy to use. Its definition is based on the idea of "measurement under the scale δ ".In the dimension estimation method based on box-counting, supposing an image's size is $M \times M$, and we divide it into the uniform grid whose size is $\delta \times \delta$. Place a column boxes whose size is $\delta \times \delta \times \delta'$ on every grid and height of the box δ' is $\left[\delta \times G / \mathrm{M}\right]$. G represents the biggest grayscale. On the (i, j) grid, if the pixels which have maximum and smallest gray value are respectively located in the v and u box, then we need $n_\delta(i,j)$ boxes to cover the grid. $n_\delta(i,j)$ is

$$n_\delta(i,j) = v - u + 1 \tag{4}$$

Therefore, the number of boxes required to cover the whole image surface can be approximately expressed as

$$N_\delta = \sum_{i,j} n_\delta(i,j) \tag{5}$$

At this time, the fractal dimension can be expressed as

$$D_H = \lim_{\delta \to 0} \frac{\ln N_\delta}{\ln(\frac{1}{\delta})} \tag{6}$$

According to the above equation, another definition of box-counting can be given. If $F \subset R^n$, for any $\delta > 0$ $N_\delta(F)$ represents the minimum number set covering F whose maximum diameter is δ [11]. Then if the limit

$$D_H = \lim_{\delta \to 0} \frac{\ln N_\delta(F)}{\ln(\frac{1}{\delta})} \tag{7}$$

exists, we call the D_H box-dimension for F.

b) Sample Entropy

Sample entropy is a measurement of time series complexity. The more complex the time series is, the greater the sample entropy is. That is, the probability of generating a new pattern in a signal is measured by measuring the complexity of time series. The accuracy of the sample entropy makes it able to be applied to the analysis of various biological time series signals[12].

The procedures of sample entropy algorithm given in the literature are as follows[13]:

(1) set the original data is N point as *u(1), u(2), …, u(*N*)*;

(2) according to the number of consecutive order, we form a m dimension vector from *Xm(1)* to *Xm(N-m)* which *Xm(i)=[u(i), u(i+1), …, u(i+m-1)](i=1~N-m)*.These vectors represent the continuous m u values from the ith point;

(3) define the distance between the vector *Xm(1)* and *Xm(N-m)* is *d[Xm(i),Xm(j)]* which is with the largest difference between two elements respectively in *Xm(1)* and *Xm(N-m)*. It means *d[Xm(i),Xm(j)]=max(|u(i+k)-u(j+k)|)*, and *k=0~m-1; i , j=1~N-m,i≠j*;

(4) given the threshold r, for each *i≤N-m* count the number of *d[Xm(i),Xm(j)]* when it is less than r (call it template matching) and calculate the ratio with the sum of distance number N-m-1. We define it as $B_r^m(i) = N^m(i)/(N-m-1)$. Calculate the average value for all i and get $B^m(r) = (N-m)^{-1} \bullet \sum_{i=1}^{N-m} B^m{}_r(i)$;

(5) increase the dimension to *m+1*, then repeat the procedures (2)~(4), finally get $B_r^{m+1}(i)$ and $B^{m+1}(r)$.

In theory, the sample entropy of this series is:

$$SampEn(m,r) = \lim_{N \to \infty}[-\ln \frac{B^{m+1}(r)}{B^m(r)}] \tag{8}$$

when *N* is a finite number, the above expression can be written as

$$SampEn(m,r,N) = \ln B^m(r) - \ln B^{m+1}(r) \tag{9}$$

The value of the sample entropy is related to the parameters *m, r* and *N*. And the sample entropy of different embedding dimension m and similar tolerance r is different. We usually take *r* as 0.1~0.25 times of the original data standard deviation. And when *m*=1 or *m*=2, the value of sample entropy has the best dependence on the length *N* of the series. The sample entropy calculated at this time has reasonable statistical characteristics.

B. Support Vector Machine

SVM is a supervised learning model and shows many unique advantages in solving the small sample, nonlinear and high dimensional pattern recognition. It can be applied to other machine learning problems such as function fitting.

SVM method is based on Vapnik-Chervonenkis (VC) dimension theory and structure risk minimum principle in statistical learning. In order to get the best generalization ability, it seeks the best compromise between the complexity of the model (i.e. the learning accuracy of specific training samples) and learning ability (i.e. the ability to recognize arbitrary samples without error) according to the limited sample information[14]. SVM wants to find a classification plane so that no data points exist near the two sides of the plane and the blank area is the largest. As shown in Fig. 3, solid and hollow points represent two types of data. H is the classification plane that we want to determine. Line H1 and H2 are parallel to the classification line and the points of two data closest to the classification are on line H1 and H2. SVM achieves the maximum interval between H1 and H2 which is the optimal classification line.

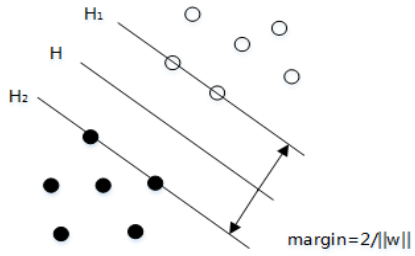

Figure 3. Schematic diagram of the support vector machine (SVM)

The classification problem is generally divided into linear separable and linear inseparable. The equation of classification plane is $\omega^T \bullet x + b = 0$, if the sample set (x_i, y_i) is linear separable, and satisfied

$$y_i[\omega^T \bullet x_i + b] - 1 \geq 0 \tag{10}$$

At this point, the classification interval is equal to $2/\|\omega\|$. We want classification interval biggest, in other

word, we want $\|\omega\|^2$ minimum. When (ω, b) is the optimal solution $\min \|\omega\|^2 /2$, there is a unique minimum point and the only optimal classification plane.

If the sample set (x_i, y_i) is linear inseparable, the input vector needs to be mapped to a higher-dimensional feature space through a nonlinear mapping (kernel function) and then construct the optimal classification plane. The kernel function has multinomial kernel, gaussian kernel and linear kernel, etc. According to the classification problem and different data, different kernel functions need to be selected.

C. Neural Network

Artificial Neural Network (ANN) is a hotspot in the field of artificial intelligence since the 1980s.A neural network (NN) is an operational model consisting of a large number of nodes (or neurons) connected to each other. Each node represents a specific output function called the activation function. The connection between each two nodes represents a weighted value of the signal through the connection, which is called the weight corresponding to the memory of the ANN. The output of the network depends on the network connection mode, the weight value and the excitation function.

As shown in Fig. 4, $a1, a2, ..., an$ is the components of the input vector, $\omega 1, \omega 2, ..., \omega n$ is the weight of each neuron, b is the bias, f is the transfer function and it is usually the nonlinear function, t is the output of this network, the equation is

$$t = f(\omega_n \bullet a_n + b) \tag{11}$$

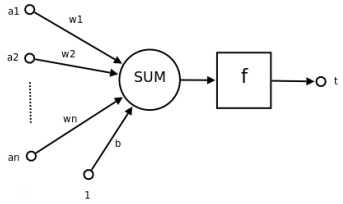

Figure 4. Simple schematic diagram of the artificial neural network (ANN).

This is a simple three-layer network including the input layer, the hidden layer and the output layer. In general, the number of vectors in the input layer is determined according to the number of features selected. The output layer generally outputs only one result and it is only one node. The number of hidden layers affects the classification of the network and we need to find the optimal number of hidden layers. In NN, the number of hidden layer is too little can lead to network work bad in complex nonlinear classification problems and the number of hidden layers too much can lead to training time increase and the tendency of "fitting". Based on the characteristics of respiratory signals, after a large number of experiments, an improved back propagation neural network (IBPNN) classification based on morphology was proposed. The framework is shown as Fig. 5. The IBPNN based on the morphology and the normal NN are different in the result of the output layer. The result was processed using the morphological filter to make the classification result more accurate.

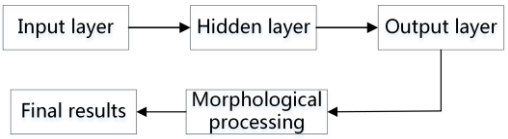

Figure 5. The flow diagram of improved BP neural network based on morphology.

III. RESULT

The calculation and evaluation process of the experiment in this paper was carried out in the MATLAB environment, and 8 data sets with 4 additional signals in the Apnea database were used for the experiment. The recording time length of 8 data sets was between 7 to 10 hours. The annotations experts marked is in every minute. The classification accuracy was got by comparing classification results of the algorithm this article put forward with classification results the expert marked.

A. Database

The PhysioNet Apnea-ECG database is used in this study. The database is divided into training set and test set. Each set contains 35 records of patient data and each recording has approximately eight hours (depending on patient the recording time ranges from 7 to 10 hours) of the ECG data. Each recording is accompanied with a set of reference apnea annotations. An annotation indicates the presence of apnea during one minute and was derived by human experts on the basis of simultaneously recorded related signals. As shown in Fig. 6, the length of time between the two "|" is 1 minute and "*" shows sleep apnea episodes. "N" and "A" are annotations marked by experts ("A" for apnea, "N" for non-apnea).

Figure 6. The annotations of the data collected from apnea database.

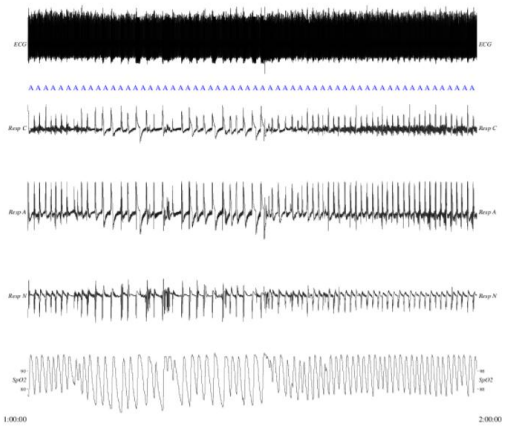

Figure 7. One-hour sample of an apnea recording.

Although the database is primarily a ECG database, eight of the recordings (a01 - a04 b01, c01 - c03) contains four additional signals. These are chest and abdominal respiratory effort signals (Resp C and Resp A) obtained using inductance plethysmography and oronasal airflow (Resp N) measured using nasal thermistors and oxygen saturation (SpO2). In this study, we focus solely on the signal Resp N.[15] An one hour sample of an apnea recording is shown in Fig. 7.

B. Feature Extraction

The features we extracted in this paper included time-domain characteristics such as variance and clinical features, frequency-domain characteristics such as wavelet coefficients and wavelet energy based on wavelet decomposition, as well as the nonlinear characteristics such as fractal dimension and sample entropy.

Variance is an indicator used to measure the dispersion degree of data. That the rhythm of human normal breathing and sleep apnea changed obviously and the centerline of exhale and inhale move will lead to significant difference in variance. From the point of frequency-domain, the center frequency of normal breathing signal is around 0.2-0.3 Hz by observing its spectrum, but the sleep apnea patients' will find a peak near the 0.02 Hz. Based on the differences of two signals in the frequency-domain, three layers wavelet decomposition is used after down-sample and the sampling frequency is about 1 Hz. In this way, the frequency range of the third layer approximation coefficient ca3 is between 0 and 0.125Hz, which including the central frequency of sleep apnea and not including the central frequency of normal respiratory signal. By analyzing the maximum value and energy value unit time of the approximation coefficient ca3 in the third layer wavelet decomposition, the difference between the apnea respiratory and normal respiratory can be obtained. Nonlinear characteristics generally reflect the irregularity and complexity of signals and they can better describe the characteristics of biomedical medical signals.

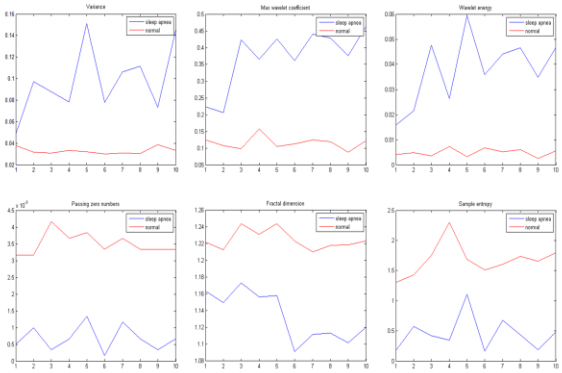

Figure 8. Schematic gram of 6-dimension feature vector.

In addition, by observing the characteristics of the signal, the clinical characteristic number of zero points which is clinical standard doctor diagnosing the sleep apnea was proposed. As shown in Fig. 8, six characteristics of normal respiratory signals and sleep apnea respiratory signals were drawn respectively, and there were significant differences between the two signals.

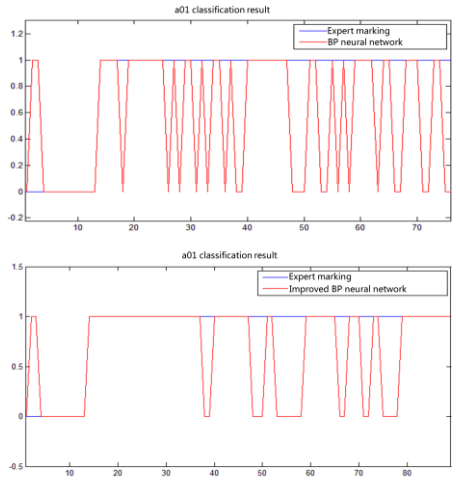

Figure 9. Comparison of classification result (the above was BPNN classification result and the below was IBPNN after morphology)

The above characteristics are used as input vectors of the support vector machine and neural network classifier to help distinguish the normal and apnea respiratory signal.

C. Support Vector Machine Classification

The kernel function of the SVM used in this paper is the radial basis function (RBF). The RBF belongs to the local kernel function[16]. When the data points are further away from the center point, the value will become smaller and the equation is:

$$K(x,z)=\exp(-\gamma \| x-z \|^2) \tag{12}$$

The gaussian kernel function can be regarded as another form of the radial basis kernel function

$$K(x,z)=\exp(-\frac{-\| x-z \|^2}{2\sigma^2}) \tag{13}$$

The gaussian radial basis function has good ability to noise anti-interference in the data. Because of its strong locality, the parameters determine the scope of function decreasing with parameter σ increasing.

Input above six characteristics including variance of the signal, a maximum and energy of the third layer approximation coefficients of wavelet decomposition A3_max and A3_ener, clinical characteristics the number of signal passing zero zero_num, the nonlinear characteristics of fractal dimension D and sample entropy SampEnVal in one minute into SVM respectively and as a feature vector $\vec{x}$. Comparing the classification results with the annotations experts marked, classification accuracy is shown in Table 1. According to the results of table 1, the sensitivity of each data set is different because different characteristics and the

classification performance of different characteristics is different. This results in a large difference in classification results.

TABLE I. THE CLASSIFICATION RESULTS OF SVM

	Var	A3_max	A3_ener	zero_num	D	SampEnVal	$\vec{x}$
a01	22.4949%	37.8323%	16.5644%	80.1636%	83.0266%	20.8589%	21.27%
a02	56.0606%	64.5833%	55.6818%	66.6667%	61.3636%	41.2879%	43.56%
a03	54.7206%	61.4644%	53.7572%	74.3738%	63.9692%	87.0906%	86.71%
a04	26.4228%	17.4797%	9.14634%	26.2195%	23.1707%	32.5203%	28.25%
b01	93.8144%	96.0825%	96.0825%	96.0825%	96.0825%	95.8763%	95.88%
c01	100%	100%	100%	97.0954%	96.888%	97.5104%	97.51%
c02	99.8%	99.8%	99.8%	96%	95.8%	96.8%	96.6%
c03	99.7788%	100%	100%	100%	100%	100%	99.78%

TABLE II. THE CLASSIFICATION RESULTS OF BP NEURAL NETWORK

	Var	A3_max	A3_ener	zero_num	D	SampEnVal	$\vec{x}$
a01	70.55%	86.09%	83.03%	84.05%	93.46%	31.49%	82.21%
a02	71.21%	81.06%	77.27%	69.7%	78.22%	52.65%	67.61%
a03	62.81%	86.71%	82.85%	77.46%	81.31%	90.37%	89.98%
a04	59.55%	45.53%	25.41%	29.47%	49.39%	45.33%	44.72%
b01	89.9%	96.08%	95.88%	96.08%	95.67%	96.29%	96.08%
c01	100%	99.79%	99.59%	97.1%	95.23%	97.3%	98.34%
c02	99.8%	99.8%	99.6%	96%	93.6%	96.8%	97%
c03	99.78%	100%	100%	100%	99.56%	100%	100%

D. Neural Network Classification based on Morphologic

Input above six characteristics including variance of the signal, a maximum and energy of the third layer approximation coefficients of wavelet decomposition A3_max and A3_ener, clinical characteristics the number of signal passing zero zero_num, the nonlinear characteristics of fractal dimension D and sample entropy SampEnVal in one minute into BPNN classifier respectively and as a feature vector $\vec{x}$. Comparing the classification results with the annotations experts marked, classification accuracy is shown in Table 2.

Compared with the classification results of SVM, the accuracy of classification results of BPNN is improved obviously. The classification results of BPNN are shown in Fig. 9. Since we are classifying in minutes, the classification results per minute are biased according to the patient's respiratory characteristics. In Fig. 9, the blue line shows the experts marking information carried by the data itself, red line shows classify result information by BPNN classifier, the number "1" on behalf of sleep apnea episodes, "0" on behalf of normal breathing. As can be seen from the Fig. 9, many classification results belong to the outliers and there is no continuity between the individual judgment result and its surrounding points. It is misjudged.

Based on the thought of dilation and erosion in the morphological operation, the result that belongs to outliers and is no continuity between itself and its surrounding points was taken place by the classification result one minute before. The result is shown in Fig. 9. As you can see, the classification results based on morphological operation obviously reduced the existence of single meaningless point, but it also can increase the misjudgment. Generally speaking, it improves the classification accuracy.

The classification results of three ways are shown in Table 3. By contrast, we found that morphological operation is helpful to improve the classification accuracy of sleep apnea especially for some individuals, but for some individuals it does not work well. In general, morphological operation improves the classification accuracy to a certain extent and the range of improvement ranges from 0.3% to 8%. It is necessary to introduce it in the classification process.

TABLE III: COMPARISON OF CLASSIFICATION ACCURACY

	SVM classifier	BP NN classifier	Improved BP NN classifer
a01	21.27%	82.21%	89.57%
a02	43.56%	67.61%	67.99%
a03	86.71%	89.98%	91.33%
a04	28.25%	44.72%	41.67%

b01	95.88%	96.08%	96.08%
c01	97.51%	98.34%	97.93%
c02	96.6%	97%	97%
c03	99.78%	100%	100%

IV. CONCLUSION

Nonlinear characteristic was introduced in this paper and a feature vector including variance, wavelet coefficients, wavelet energy, clinical zero passing point, fractal dimension and sample entropy was structured. Input the feature vector into SVM and BPNN classifier, the classification accuracy of sleep apnea is 71.2% and 84.5% respectively. It can be seen that the classification effect of BPNN is obviously better than that of SVM. In addition, an IBPNN based on morphology was put forward in this paper. It improved the 85% of classification results and increased accuracy by 7.3%. In a word, a new method of recognition sleep apnea and a solution for sleep respiration signal detection and prediction was provided. However, the classification can only distinguish between SAHS and health, and cannot accurately diagnose which kind of SAHS. This is the direction of our next work.

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