OPEN ACCESS
Journal of Mechanics in Medicine and Biology
Vol. 21, No. 5 (2021) 2140019 (13 pages)

DOI: 10.1142/S0219519421400194

ANALYSIS OF PHOTOPLETHYSMOGRAPHIC MORPHOLOGY IN SLEEP APNEA SYNDROME PATIENTS USING CURVE FITTING AND SUPPORT VECTOR MACHINE

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Received 16 September 2020
Accepted 5 January 2021
Published 8 April 2021

This paper develops a time-saving, simple, and comfortable method for detecting Sleep Apnea Syndrome (SAS). Seventy SAS patients and 17 healthy persons were randomly selected in this study, and nine analytical parameters (i.e., A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2}, and X_{C3}) of healthy persons and SAS patients during five sleep stages (i.e., W, R, N1, N2, and N3) were obtained to construct a SAS classification model based on logarithmic normal analytical parameters using the Support Vector Machine (SVM) method to fit Photoplethysmographic (PPG) signals. The results show that there were no statistical differences among the five sleep stages for either the healthy or SAS patients. However, there were significant differences in the measured logarithmic normal analytical parameters between the healthy persons and the SAS patients in each of the five sleep stages. The accuracies of the SAS classification model were 95.00%, 90.00%, 84.00%, 94.67%, and 90.77%, corresponding to the five sleep stages, respectively. The SAS classification model based on the SVM method of logarithmic normal analysis parameters can achieve higher classification accuracy for each of the five sleep stages. It can be considered to collect the patient's pulse wave during the awake period, but not necessarily during the sleep period to classify and identify the SAS; it provides an idea for a convenient and comfortable SAS detection.

Keywords: Sleep apnea syndrome (SAS); support vector machine (SVM); photoplethysmographic (PPG) signals; logarithmic normal function.

1. Introduction

An increasing number of people suffer from sleep disorders. According to the World Health Organization's statistics, about a third of the people in the world have sleep disorders. Previous studies show that 69% of college students have sleep disorders,[1] which seriously affect their health and academic performance.[2,3] Sleep apnea syndrome (SAS) is a common sleep disorder. Pathology and correct diagnosis of SAS are problems that should be solved urgently in clinical medicine.[4,5] Polysomnography is the accepted standard method for the diagnosis of SAS. However, more than a dozen sensors should be attached to the head, nasal cavity, eyes, and lower limbs of the tester to measure multiple parameters, such as brain electricity, snoring airflow, snoring, eye electricity, and limb movement during monitoring. Moreover, the monitoring time is usually more than 7 h at night. This makes the monitoring process complicated, time-consuming, and uncomfortable. The search for simple and comfortable diagnostic methods has always been the focus of research.[6] Thermal infrared imaging, RF architecture, and sound detection were all used for contactless detection for the comfort of the diagnostic process.[7–9] However, the measurement results were easily disturbed by limb movement, body position, and noise. The detection of patients at home with fewer sensors and using automatic diagnostic algorithms was another solution.[10] However, the diagnostic method is still being improved owing to its low accuracy.

Pulse monitoring has become an important method for clinical quantitative assessment of the risk of various diseases because of the convenience of obtaining

and containing a variety of information about the human body.[11,12] Pulse signals have also been widely used in the treatment of SAS. Pulse rate variability of SAS patients has been studied to simplify the diagnosis process of SAS.[13,14] Pulse wave amplitude was used to measure the difference between sleep events and nonsleep events in SAS patients.[15] However, these studies used local features of the waveform, and feature extraction was difficult when the signal was weak or disturbed. Global information of the signal was used by curve fitting, which was used to study the characteristics of pulse waves.[16,17] The Gaussian and log-normal functions are commonly used as fitting functions with low absolute error.[18–21] At present, there are few studies on SAS using the curve fitting method.

Support Vector Machine (SVM) is one of the most influential methods in machine learning. Its basic model was a linear classifier with the largest interval defined in the feature space. Its learning strategy was to maximize the interval, which could be formalized as a problem of solving convex quadratic programming, and it used the kernel function instead of nonlinear mapping to high-dimensional space. SVM could obtain better results than other algorithms on the small sample training set in the two-class classification problem. The SVM algorithm was employed in this study because it is a binary classification problem with a relatively small sample size.

SVM was used in the study of neurocognitive impairment in SAS patients and was also used to classify heartbeat interval signals and respiration signals derived from Electrocardiogram (ECG) to realize the detection of SAS through ECG signals.[22] Research on SVM-based oxygen measurement and airflow for testing SAS at home has been conducted.[23] In this study, the curve fitting method is used to extract the pulse wave characteristics of SAS. The SAS classification model based on the SVM method of analysis parameters is constructed, expecting to provide a new idea for SAS detection.

In our previous research, the Photoplethysmographic (PPG) signals of 87 subjects were fitted using Gaussian signals, and the differences between the analysis parameters of SAS patients and those of healthy people were analyzed during five sleep stages (i.e., W (Wake) and R (Rapid eye movement) stages, and three sleep stages (N1, N2, and N3) according to sleep depth in the NonRapid Eye Movement period).[24] In this study, the above data were fitted by logarithmic normal functions, and an SVM model based on lognormal analytical parameters was constructed to identify SAS patients. The performance of this classification model was compared with that of the SVM model based on Gaussian analysis parameters.

Our results showed that the SVM model based on analytical parameters has a satisfactory classification performance for SAS. This means that SAS can be classified and identified using PPG signals through the analysis method and SVM model; this could make the SAS monitoring process time-saving, convenient, and comfortable.

2. Methods

2.1. *Subjects*

In this study, 70 patients with SAS and 17 healthy individuals were enrolled. The clinical information of the 87 subjects is shown in Table 1. Before participating in the test, none of the subjects smoked or drank wine for a week. This study was approved by the Shandong Provincial Hospital ethical committee, and all subjects provided their written informed consent.

2.2. *Data acquisition and processing*

The PPG measurements were described in detail by Jiang *et al.*[24] In short, all measurements were made in the sleep medicine center of Shandong Provincial Hospital by the Alice 5 Sleepware Polysomnographic System. At a sampling frequency of 100 Hz, the finger PPG signals of the subjects were recorded and automatically identified by the system in five sleep stages (W, R, N1, N2, and N3) for 8 h on average at night. During each sleep stage of each subject, the PPG signal without the sleep apnea events was intercepted for 30 s. Because some people's sleep only contained several stages in five stages, the number of data segments obtained by the healthy persons and the patients in the five stages (W, R, N1, N2, and N3) are 16, 13, 17, 17, 15, and 64, 45, 55, 56, and 46, respectively. The foot points of each pulse period of each data segment were marked and 10 successive cardiac cycles of signals were selected and normalized to 10 single-cycle signals (amplitude and length were 1 and 1000, respectively).

2.3. *Curve fitting*

The logarithmic normal function was used to analyze PPG signals in this study, and it was defined as follows:[20]

$$f_k(n) = \frac{1000 \times A_k}{\sqrt{2\pi} \times W_k \times n} \exp\left(- \frac{\left(\ln\left(\frac{n}{1000 \times X_{ck}} \right) \right)^2}{2W_k^2} \right), \tag{1}$$

where three parameters were $A_k (0 < A_k < 1)$, W_k $(0 < W_k < 1)$, and $X_{ck} (0 < X_{ck} < 1)$, respectively. The subscript k indicates different logarithmic normal functions with $k = 1, 2, 3$, and n is the length of the logarithmic normal function

Table 1. The clinical information of 87 subjects.

Variable	Mean ± SD	95% Confidence interval
Age (year)	42 ± 15	39–46
Gender (Male/Female)	59/28	—
Height (cm)	169 ± 7	167–170
Weight (kg)	74 ± 12	71–76
BMI (kg/m^2)	26 ± 4	25–27

with $n = 1, 2, \ldots, 1000$. According to previous studies,[21] three logarithmic normal functions were used to fit the PPG signals as fitting kernels and nine parameters (i.e., A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2}, and X_{C3}) for the three logarithmic normal functions obtained.

2.4. *Classifier and evaluation indicators*

As a machine learning algorithm, SVM was effective not only in high-dimensional spaces but also in cases where the number of samples was smaller than the number of dimensions. In this study, the SVM classifier was based on the Radial Basis Function (RBF) (Scikit-learn machine learning package: Ver. 0.19.1; Spyder software, Ver. Python 3.6) that was used to identify healthy and SAS patients. The penalty coefficient C and kernel function parameter γ are parameters of the RBF-SVM model. Grid search was used to determine the proper C and γ, and the search range of the parameters C was $10^{-7} \leq C \leq 10^5$; the number of grid points was 13, the range of γ was $10^{-7} \leq \gamma \leq 10^7$, and the number of grid points was 15. Finally, the best two parameters, C and γ, were obtained.

To avoid over-fitting in machine learning, five-fold cross validation was used to build the SVM model, and the performance of the model was evaluated using three indicators: sensitivity (Se), specificity (Sp) and accuracy (Acc). These three indicators were defined as follows:

Sensitivity (Se):

$$\mathrm{Se} = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}} \times 100\%. \tag{2}$$

Specificity (Sp):

$$\mathrm{Sp} = \frac{\mathrm{TN}}{\mathrm{TN} + \mathrm{FP}} \times 100\%. \tag{3}$$

Accuracy (Acc):

$$\mathrm{Acc} = \frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{FP} + \mathrm{FN} + \mathrm{TN}} \times 100\%, \tag{4}$$

where TP was True Positives, FP was False Positives, FN was False Negatives, and TN was True Negatives, respectively.

2.5. *Statistical analysis*

In each of the five sleep stages, by averaging the analysis parameters of 10 normalized PPG signals of each subject, the mean value of each logarithmic normal parameter of each subject was obtained, and then the overall mean of each logarithmic normal parameter for the healthy persons and SAS patients was calculated at each sleep stage. To study the differences in analysis parameters during the five sleep stages, the overall means of logarithmic normal parameters for the healthy persons and SAS patients were compared at each sleep stage. To study the

variability of analysis parameters between SAS patients and healthy subjects, the logarithmic normal parameters of SAS patients and healthy subjects were compared at each stage by two-way Analysis of Variance (ANOVA). Statistical significance was considered at $P < 0.05$.

3. Results

3.1. *Results based on logarithmic normal analytical parameters for the healthy subjects and SAS patients*

Table 2 shows the overall means and SDs of nine Logarithmic normal analysis parameters of three Logarithmic normal functions in five sleep stages for the healthy subjects and SAS patients. In Table 2, ↓ and ↑ indicate a significant decrease or a significant increase among the healthy subjects and SAS patients at the same sleep stage by T test at $P < 0.05$.

Table 2 shows that the analysis parameters A_3 in five sleep stages, and the parameters W_1 and W_2 in four sleep stages except stage N1 for W_1 and except stage W for W_2 of SAS patients are significantly lower than those of the healthy subjects; while the parameter X_{C1} in five sleep stages and the parameter X_{C2} (except stage N2) in four sleep stages of the SAS patients are significantly higher than those of the healthy subjects; for the parameters A_1, A_2, W_3, and X_{C3}, the SAS patients' are significantly smaller or larger than those of the healthy patients.

With patient types as the main factor and sampling sleep stages as sub-factors, two-way ANOVA for nine logarithmic normal parameters are shown in Table 3. The results of "sleep stages" in Table 3 show, except for parameter W_3, that there were no statistical differences among the five sleep stages for the healthy subjects or SAS patients. The results of "Patient types × Sleep stages" showed that there were no statistical differences in the interactions among the healthy subjects and SAS patients. However, the results of "patient types" showed significant statistical differences among the healthy subjects and SAS patients in five sleep stages for logarithmic normal parameters.

3.2. *Evaluation of SVM based on logarithmic normal analytical parameter indicators*

Considering the logarithmic normal analysis parameters as characteristic indicators to identify the healthy subjects and SAS patients using the SVM model, Table 4 shows the optimal solutions for the five sleep stages in nine combinations of logarithmic normal analysis parameter indicator combinations from 1 to 9 (A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2}, and X_{C3}). In Table 4, the maximum value of Acc for each sleep stage and the corresponding combination of characteristic indicators are marked in bold. Moreover, the proposed SVM model has suitable classification results in the five sleep stages. Although the classification results yield the worst in the N1 stage, the accuracy rate Acc can reach 84.00%.

Table 2. Overall means and SDs of nine parameters of Logarithmic normal functions in five sleep stages for the healthy and SAS patients.

Patient types	Sleep stage	A_k			W_k			X_{Ck}		
		A_1	A_2	A_3	W_1	W_2	W_3	X_{C1}	X_{C2}	X_{C3}
Healthy	W	0.226 ± 0.03	$0.177 \pm 0.03\downarrow$	$0.172 \pm 0.04\uparrow$	$0.697 \pm 0.04\uparrow$	0.469 ± 0.09	$0.273 \pm 0.04\uparrow$	$0.224 \pm 0.01\downarrow$	$0.355 \pm 0.04\downarrow$	$0.625 \pm 0.02\downarrow$
	R	$0.186 \pm 0.04\downarrow$	0.192 ± 0.02	$0.181 \pm 0.05\uparrow$	$0.709 \pm 0.04\uparrow$	$0.537 \pm 0.10\uparrow$	$0.277 \pm 0.04\uparrow$	$0.223 \pm 0.02\downarrow$	$0.323 \pm 0.05\downarrow$	$0.616 \pm 0.03\downarrow$
	N1	0.210 ± 0.04	0.182 ± 0.03	$0.165 \pm 0.04\uparrow$	0.688 ± 0.06	$0.506 \pm 0.11\uparrow$	$0.270 \pm 0.04\uparrow$	$0.220 \pm 0.02\downarrow$	$0.345 \pm 0.05\downarrow$	0.625 ± 0.02
	N2	0.208 ± 0.05	0.187 ± 0.03	$0.162 \pm 0.03\uparrow$	$0.707 \pm 0.03\uparrow$	$0.503 \pm 0.10\uparrow$	0.270 ± 0.03	$0.219 \pm 0.02\downarrow$	0.342 ± 0.04	0.622 ± 0.01
	N3	0.199 ± 0.05	0.180 ± 0.03	$0.158 \pm 0.03\uparrow$	$0.712 \pm 0.04\uparrow$	$0.540 \pm 0.10\uparrow$	0.266 ± 0.02	$0.224 \pm 0.02\downarrow$	$0.322 \pm 0.04\downarrow$	$0.615 \pm 0.02\downarrow$
Sleep apnea	W	0.225 ± 0.05	$0.198 \pm 0.03\uparrow$	$0.130 \pm 0.03\downarrow$	$0.669 \pm 0.04\downarrow$	0.435 ± 0.08	$0.239 \pm 0.04\downarrow$	$0.245 \pm 0.02\uparrow$	$0.379 \pm 0.04\uparrow$	$0.645 \pm 0.03\uparrow$
	R	$0.219 \pm 0.04\uparrow$	0.203 ± 0.02	$0.145 \pm 0.04\downarrow$	$0.670 \pm 0.03\downarrow$	$0.430 \pm 0.07\downarrow$	$0.248 \pm 0.03\downarrow$	$0.240 \pm 0.02\uparrow$	$0.379 \pm 0.04\uparrow$	$0.636 \pm 0.02\uparrow$
	N1	0.216 ± 0.04	0.194 ± 0.03	$0.135 \pm 0.03\downarrow$	0.675 ± 0.04	$0.442 \pm 0.06\downarrow$	$0.247 \pm 0.04\downarrow$	$0.241 \pm 0.02\uparrow$	$0.367 \pm 0.03\uparrow$	0.637 ± 0.03
	N2	0.212 ± 0.04	0.193 ± 0.03	$0.139 \pm 0.03\downarrow$	$0.670 \pm 0.03\downarrow$	$0.455 \pm 0.07\downarrow$	0.251 ± 0.04	$0.238 \pm 0.01\uparrow$	0.361 ± 0.04	0.631 ± 0.03
	N3	0.217 ± 0.03	0.194 ± 0.02	$0.137 \pm 0.03\downarrow$	$0.674 \pm 0.03\downarrow$	$0.454 \pm 0.05\downarrow$	0.249 ± 0.03	$0.236 \pm 0.01\uparrow$	$0.366 \pm 0.03\uparrow$	$0.633 \pm 0.03\uparrow$

Note: A significant decrease or a significant increase among the healthy and SAS patients at same sleep stage by T test at $P < 0.05$ indicates by $\downarrow$ and $\uparrow$.

Table 3. Two-way analysis results of variance with patient types as main factor and sampling sleep stages as sub-factor. F/P values were given.

Measured parameters of logarithmic normal functions		Patient types	Sleep stages	Patient types times × Sleep stages
A_k	A_1	4.91/0.027*	1.92/0.11	1.21/0.31
	A_2	13.15/< 0.001***	1.11/0.35	0.59/0.67
	A_3	51.74/< 0.001***	1.20/0.31	0.77/0.55
W_k	W_1	41.66/< 0.001***	0.77/0.55	1.12/0.35
	W_2	45.93/< 0.001***	2.47/0.04*	1.73/0.14
	W_3	75.37/< 0.001***	22.51/0.001***	30.03/0.001***
X_{Ck}	X_{C1}	74.18/< 0.001***	0.94/0.44	0.58/0.68
	X_{C2}	44.49/< 0.001***	2.32/0.06	2.03/0.09
	X_{C3}	19.36/< 0.001***	1.21/0.31	0.36/0.84

Notes: Patient types — healthy and sleep apnea patients; Sleep stages — five sleep stages of W, R, N1, N2 and N3; $^*P< 0.05$, $^{***}P< 0.01$.

The classification result at the W stage is the best, and the accuracy rate Acc can reach 95.00%. Table 3 also shows that in each sleep stage, the highest classification effect does not come from using one or all nine characteristic indicators for classification but from combinations of parameters that contain significant differences, such as the parameter X_{C1} in the "optimal combination" in Table 4.

Table 4. Classification results of RBF-SVM model with nine lognormal analytical parameters characteristic indicators in five sleep stages.

Sleep stage	Number of indicator combinations	Optimal combination	Se ± std (%)	Sp ± std (%)	Acc ± std (%)
W	1	A_3	100.00 ± 0.00	66.67 ± 21.08	93.75 ± 3.95
	2	A_1, A_3	100.00 ± 0.00	66.67 ± 21.08	93.75 ± 3.95
	3	$\boldsymbol{A_3}$, $\boldsymbol{W_1}$, $\boldsymbol{X_{C1}}$	**100.00 ± 0.00**	**73.33 ± 13.33**	**95.00 ± 2.50**
	4	A_2, A_3, W_3, X_{C3}	100.00 ± 0.00	66.67 ± 21.08	93.75 ± 3.95
	5	A_1, A_3, W_1, W_3, X_{C2}	100.00 ± 0.00	66.67 ± 21.08	93.75 ± 3.95
	6	A_1, A_2, A_3, W_1, X_{C2}, X_{C3}	100.00 ± 0.00	66.67 ± 21.08	93.75 ± 3.95
	7	A_1, A_3, W_1, W_2, X_{C1}, X_{C2}, X_{C3}	96.92 ± 3.77	73.33 ± 13.33	92.50 ± 4.68
	8	A_1, A_2, A_3, W_1, W_2, X_{C1}, X_{C2}, X_{C3}	96.92 ± 3.77	66.67 ± 0.00	91.25 ± 3.06
	9	A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	93.85 ± 5.76	66.67 ± 21.08	88.75 ± 6.12
R	1	W_2	97.78 ± 4.44	60.00 ± 13.33	88.33 ± 4.08
	2	$\boldsymbol{A_1}$, $\boldsymbol{W_1}$	**97.78 ± 4.44**	**66.67 ± 29.81**	**90.00 ± 6.24**
	3	$\boldsymbol{A_3}$, $\boldsymbol{X_{C1}}$, $\boldsymbol{X_{C2}}$	**93.33 ± 5.44**	**80.00 ± 26.67**	**90.00 ± 6.24**
	4	W_1, W_2, W_3, X_{C3}	95.56 ± 5.44	60.00 ± 13.33	86.67 ± 4.08
	5	A_2, W_1, W_2, W_3, X_{C2}	93.33 ± 5.44	60.00 ± 13.33	85.00 ± 3.33
	6	A_1, A_2, W_1, X_{C1}, X_{C2}, X_{C3}	91.11 ± 8.31	80.00 ± 26.67	88.33 ± 6.67
	7	A_1, A_2, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	95.56 ± 5.44	53.33 ± 16.33	85.00 ± 3.33
	8	A_1, A_2, W_1, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	93.33 ± 5.44	60.00 ± 24.94	85.00 ± 6.24
	9	A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	88.89 ± 12.17	53.33 ± 16.33	80.00 ± 6.67
N1	1	X_{C1}	98.18 ± 3.64	25.00 ± 31.62	78.67 ± 7.77
	2	X_{C1}, X_{C2}	94.55 ± 4.45	50.00 ± 22.36	82.67 ± 6.80
	3	$\boldsymbol{A_2}$,$\boldsymbol{A_3}$, $\boldsymbol{W_2}$	**98.18 ± 3.64**	**45.00 ± 29.15**	**84.00 ± 6.80**

Table 4. (*Continued*)

Sleep stage	Number of indicator combinations	Optimal combination	Se ± std (%)	Sp ± std (%)	Acc ± std (%)
	4	A_1, X_{C1}, X_{C2}, X_{C3}	90.91 ± 9.96	60.00 ± 20.00	82.67 ± 6.80
	5	A_1, A_2, A_3, W_2, X_{C1}	96.36 ± 4.45	45.00 ± 18.71	82.67 ± 3.27
	6	A_1, A_2, W_2, X_{C1}, X_{C2}, X_{C3}	92.73 ± 3.64	50.00 ± 15.81	81.33 ± 2.67
	7	A_1, A_2, A_3, W_1, X_{C1}, X_{C2}, X_{C3}	94.55 ± 7.27	35.00 ± 25.50	78.67 ± 11.47
	8	A_1, A_2, A_3, W_1, W_3, X_{C1}, X_{C2}, X_{C3}	85.45 ± 14.77	50.00 ± 31.62	76.00 ± 10.83
	9	A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	100.00 ± 0.00	0.00 ± 0.00	73.33 ± 0.00
N2	1	X_{C3}	100.00 ± 0.00	40.00 ± 24.94	88.00 ± 4.99
	2	A_1, X_{C2}	96.67 ± 4.08	80.00 ± 16.33	93.33 ± 4.22
	3	A_1, A_2, X_{C1}	100.00 ± 0.00	60.00 ± 24.94	92.00 ± 4.99
	4	$\boldsymbol{A_1}$, $\boldsymbol{A_2}$, $\boldsymbol{X_{C1}}$, $\boldsymbol{X_{C3}}$	$\mathbf{98.33 \pm 3.33}$	$\mathbf{80.00 \pm 26.67}$	$\mathbf{94.67 \pm 4.99}$
	5	A_1, A_2, W_3, X_{C1}, X_{C2}	96.67 ± 4.08	80.00 ± 16.33	93.33 ± 5.96
	6	A_2, W_1, W_2, W_3, X_{C1}, X_{C3}	98.33 ± 3.33	73.33 ± 24.94	93.33 ± 4.22
	7	A_1, A_2, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	100.00 ± 0.00	66.67 ± 21.08	93.33 ± 4.22
	8	A_1, A_2, W_1, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	98.33 ± 3.33	60.00 ± 24.94	90.67 ± 6.80
	9	A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2},X_{C3}	86.67 ± 4.08	93.33 ± 13.33	88.00 ± 4.99
N3	1	W_2	100.00 ± 0.00	53.33 ± 26.67	89.23 ± 6.15
	2	$\boldsymbol{W_2}$, $\boldsymbol{X_{C1}}$	$\mathbf{100.00 \pm 0.00}$	$\mathbf{60.00 \pm 24.94}$	$\mathbf{90.77 \pm 5.76}$
	3	W_2, W_3, X_{C1}	98.33 ± 3.33	60.00 ± 25.04	90.67 ± 6.80
	4	A_1, W_1, W_2, X_{C3}	100.00 ± 0.00	53.33 ± 26.67	89.23 ± 6.15
	5	A_3, W_2, W_3, X_{C1}, X_{C2}	96.00 ± 4.90	53.33 ± 16.33	86.15 ± 5.76
	6	A_2, A_3, W_2, W_3, X_{C1}, X_{C3}	96.00 ± 4.90	60.00 ± 24.94	87.69 ± 9.23
	7	A_1, A_2, A_3, W_3, X_{C1}, X_{C2}, X_{C3}	94.00 ± 4.90	73.33 ± 32.66	89.23 ± 7.84
	8	A_1, A_2, A_3, W_2, W_3, X_{C1}, X_{C2}	92.00 ± 4.00	73.33 ± 32.66	87.69 ± 9.23
	9	A_1, A_2, A_3, W_1, W_2, W_3, X_{C1}, X_{C2}, X_{C3}	88.00 ± 14.70	66.67 ± 21.08	83.08 ± 13.23

4. Conclusion and Discussions

In this study, logarithmic normal functions were used to fit PPG signals of healthy subjects and SAS patients during five sleep stages. Differences in the healthy subjects and SAS patients based on analytical parameters were compared using the two-way ANOVA. Statistical results showed that there were no significant differences between the five stages in both the healthy subjects and SAS patients; however, at each of the five stages, there were significant differences between them. Using the machine learning method based on SVM, a SAS classification model can achieve higher classification accuracy in each of the five sleep stages. This means that we can collect the patient's pulse wave during the awake period (not during the sleep period) for the classification and identification of SAS, thus, making the detection of SAS convenient and comfortable.

Gaussian functions are also often used for PPG fitting functions.[17,18] In our previous work, a Gaussian function was used to fit the PPG signals, and compared the difference between healthy subjects and SAS patients based on Gaussian fitting parameters.[24] However, the SVM model based on Gaussian parameters was not constructed to identify healthy subjects and SAS patients. In this study, an SVM

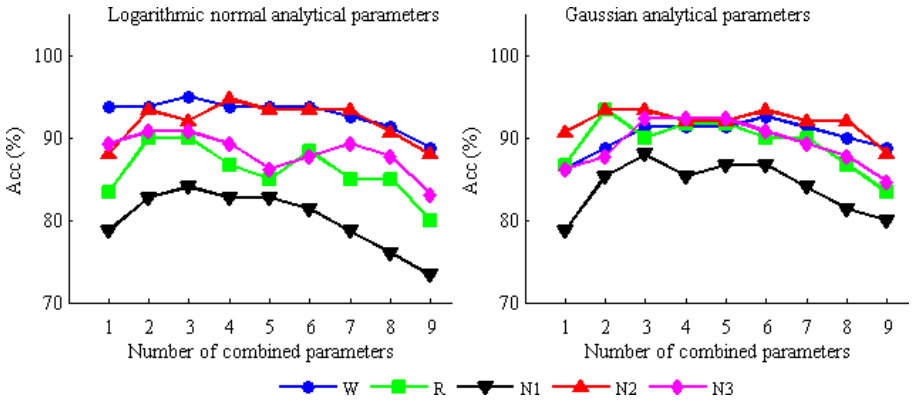

Fig. 1. Optimal Accs of five sleep stages with different number of parameter combinations. W, R, N1, N2, and N3 refer to the five sleep stages of W, R, N1, N2, and N3, respectively.

model based on Gaussian analytical parameters was employed, and the accuracy of the two models based on Gaussian analytical parameters and logarithmic normal analytical parameters was compared. Figure 1 shows the optimal solutions for the five sleep stages in nine combinations of logarithmic normal analysis parameter indicators and Gaussian analysis parameter indicators (the numbers of combined parameters are from 1 to 9). As can be seen from Fig. 1, the SVM model based on Gaussian analysis parameters also exhibits a suitable classification effect in the five sleep stages.

Figure 2 shows the maximum value of the optimal Accs in five sleep stages for logarithmic normal functions and Gaussian functions, respectively. Figure 2 shows that for logarithmic normal functions, the highest Acc is 95.00% in the W stage and the lowest is 84.00% in the N1 stage. For Gaussian functions, the highest Acc is 93.33% in the R and N2 stages and the lowest Acc is 88.00% in the N1 stage.

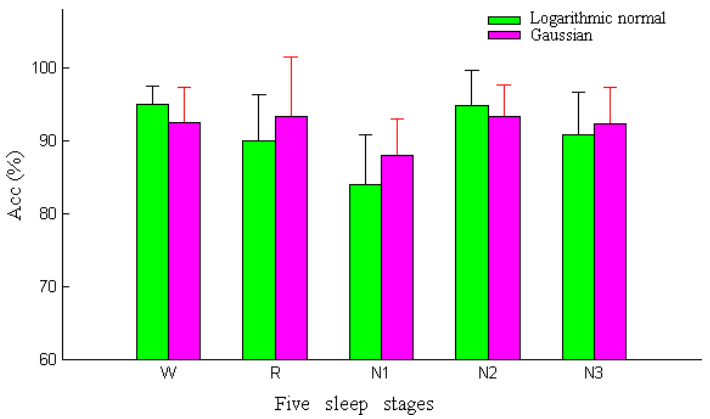

Fig. 2. The maximum value of the optimal Accs in five sleep stages for logarithmic normal functions and Gaussian functions.

Polysomnography is the accepted standard method for diagnosing sleep apnea; however, its diagnostic process takes approximately 8 h at night, and the tester is very uncomfortable because of the bundled dozen sensors. Considerable research has been conducted to find convenient and comfortable SAS detection methods. For instance, Bluetooth transmission has been used for the detection of SAS, with an accuracy of approximately 90%.[25] In addition, random forest and regularized logistic regression methods have been used in SAS recognition, and their recognition accuracy reaches more than 80%.[26] Furthermore, electrocardiogram-based algorithms have been used to identify SAS, and the classification accuracy of hypopnea index severity is 84.9%.[27] Moreover, the classification accuracy of identifying SAS with the ensemble of bagged tree classifiers based on electrocardiography signals reaches 86.27%.[28] However, among the aforementioned methods, some take a long time, some require many sensors, and the accuracies of some are very low. In our research, we mainly studied PPG signals of SAS without sleep events; moreover, we studied the PPG signals of patients when they were awake. Our results show that there are no significant differences between the analytical parameters of the awake and sleep phases. This means that the diagnosis of SAS can be achieved by the PPG of SAS obtained when SAS patients are awake, and the detection requires only approximately 10 min.

Our study has some limitations. First, the healthy subjects are mainly young people aged 20–30 while the patients include not only young people but also elderly people. However, age can affect PPG signals.[29–31] Second, the PPG signals of the patients we collected did not include sleep events, but the signals of some heavy apnea patients whose entire sleep was almost occupied by sleep events may be affected by sleep events owing to the close distance to the event. Finally, the number of samples is small, and the number of healthy people is significantly different from the number of patients. Furthermore, more subtypes are not separated in SVM for the use of SVM machine learning methods. Therefore, the classification results of the SVM model have a huge room for improvement.

In conclusion, we used the analysis parameters of the lognormal function as characteristic parameters to establish an SVM model for classifying SAS, and compared the performance of the model with the performance of the SVM model established by the analysis parameters of the Gaussian function. The results show that for healthy individuals or patients, there was no significant difference between them in each stage; however, significant differences existed between healthy subjects and patients in five stages. Both SVM models based on lognormal analytical parameters and on Gaussian analytical parameters have good classification performance for classifying SAS. Our results indicate that the patient's pulse signal can be collected during the awake period, not necessarily in the sleep period, and the number of the used sensors and the monitoring time can be reduced or shortened significantly. Our research provides a new method for the convenient, time-saving, and comfortable SAS detection method.

Acknowledgments

This work was supported by the National Natural Science Foundation of China (Grant Nos. 82072014 and 61901114), the National Key R&D Program of China (Grant No. 2019YFE010670), the Shandong Province Natural Science Foundation (Grant No. ZR2020MF028) and the Key R&D Program of Shandong Province (Grant N0.2020CXGC010110). The authors thank the support from the Southeast-Lenovo Wearable Heart-Sleep-Emotion Intelligent monitoring Lab.

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