

Machine Learning Model for Automatic Sleep Stage Classification



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Key Words: EEG; Automated sleep stage; HHT; Feature engineering; SVM

1. Background

Sleep plays a significant role in human health physically and mentally. So being able to monitor how well people sleep is vital. In this case, to understand which stage the brain is in during a sleep period provides valuable information in personal health.

Usually sleepers pass through four stages: 1,2,3 and REM sleep. These stages can be identified by the features extracted from the time series signal which are results of the experiment like EEG or ECG and so on. The process of classifying which stage the brain is in is called sleep stage scoring or sleep stage classification.

However, given the large amount of data, this manual approach is time-consuming. Thus, some methodologies have come out for a more accurate automatic sleep staging. We develop a method to better the classify process using multiple biological signals such as EEG, EMG, oronasal respiration and rectal body temperature and take a traditional way to extract the features in signals and get a satisfactory result.

2. Research methods

The implementation of the entire proposed system started by the pre-processing of the EEG signal followed by time–frequency analysis and feature extraction. The extracted features were then used to train and test the classifier; finally, the performance of the entire procedure was evaluated. The pre-processing, the time–frequency analysis, and the feature extraction steps were all implemented under MATLAB platform, while the classification procedure was done using Python.

2.1 dataset

EEG signal is the collective electrical activity of brain group neurons, which contains a large number of non-linear unit activity information. The collected background noise of sleep EEG signal is very strong, which seriously affects the analysis of EEG signals, so it needs EEG signals. Perform filtering and noise reduction processing. The purpose of the pre-processing step was to enhance the EEG signal. It starts by normalizing the EEG signal, removing the base-line drift, and eliminating any linear trends [1]. Then, the EEG signal was segmented (divided) into epochs of 30 s with each epoch corresponding to a single sleep stage.

We select data set Sleep-EDF Database from Physio Net and Sleep-EDF Database provides a data set on sleep stage scoring.

The *PSG.edf files are whole-night polysomnographic sleep recordings containing EEG (from Fpz-Cz and Pz-Oz electrode locations), EOG (horizontal), submental chin EMG, and an event marker. The SC*PSG.edf files (see the 'sleep cassette study') often also contain oro-nasal respiration and rectal body temperature.

The *Hypnogram.edf files contain annotations of the sleep patterns that

correspond to the PSGs. These patterns (hypnograms) consist of sleep stages W, R, 1, 2, 3, 4, M (Movement time) and? (not scored). All hypnograms were manually scored by well-trained technicians

More info:

<https://alpha.physionet.org/content/sleep-edfx/1.0.0/Polyman/Polyman/>

Subject	X F X Female 33yr		
Recording	Startdate 24-APR-1989 X X X		
Start	24 apr 1989	16:13:00	Duration 22:05:00

1	EEG Fpz-Cz	100 Hz
2	EEG Pz-Oz	100 Hz
3	EOG horizontal	100 Hz
4	Resp oro-nasal	1 Hz
5	EMG submental	1 Hz
6	Temp rectal	1 Hz
7	Event marker	1 Hz

Add->

Subtract->

Remove<-

Color

Fig. 1 – details about the EEG signals

2.2 Pre-processing

The EEG signal contains a frequency band component of 0.5 to 90 Hz, and is mainly focused on scientific research and clinical hospitals. 5 to 30 Hz, when studying sleep staging, I only pay attention to EEG signals below 30 Hz. Researchers at home and abroad generally believe that EEG signals mainly have four rhythm components: δ waves, θ waves, α waves, β waves, and some K-complexes, Sleep Spindles, and so on [2]. The following are the four main rhythm waveforms of the EEG signal:

δ waves: The frequency range is 0.5-4 Hz, and the amplitude is about 20 to 200 μ v. When people's brain frequency is at δ waves, for deep sleep, deep anesthesia, and unconscious state, there are no δ waves when healthy adults are awake.

θ waves: The frequency range is 4-8Hz, and the amplitude is about 20~100 μ v. When people's brain frequency is at θ waves, the human consciousness is interrupted, the body is deeply relaxed, and it is in a state of drowsiness. When an adult is awake, if it contains a large number of θ waves, it will be diagnosed with a malfunction of the brain.

α waves: the frequency range is 8 ~ 13Hz. The amplitude is about 20 ~ 150 μ v. When people's brain frequency is in α waves, the human consciousness is clear, but the body is relaxed. It provides a "bridge" between consciousness and subconscious. When in a quiet state, the amplitude will alternately appear in a fusiform state, when the eyes are opened. Or after being stimulated by the outside world, the α waves will disappear immediately. This phenomenon is called wave blocking.

β waves: The frequency range is 14~30Hz. The amplitude is about 5-20 μ v. When people are awake, most of the time, the brain frequency is in the state of β waves. It is generally believed that β waves is the brain electrical activity when the brain is in an

excited state.

K-complexes: It is more obvious in the top and central regions of the brain. It is one of the characteristic waves of NREM phase 2, which contains negative phase and positive phase, and the appearance time is greater than 0.5 seconds.

Sleep Spindle: The frequency is 12-14 Hz. The amplitude is less than 50 μ v, and the continuous appearance time is greater than 0.5 seconds, which is generally considered to occur during the light sleep period.

Table 1-Different waves and events embedded in the EEG signal and their frequency range.

<i>Waves and events</i>	Frequency range (Hz)
<i>Delta</i>	0.5 - 4
<i>Theta</i>	4 - 8
<i>Alpha</i>	8 - 13
<i>Beta1</i>	13 - 22
<i>Beta2</i>	22 - 35
<i>Sleep spindles</i>	12 - 14
<i>K-complex</i>	0.5 - 1.5

2.2.1 Time-frequency analysis

Many methods have been used to analyze the non-stationary EEG signal. Most of these methods are based on either frequency domain analysis or time domain analysis. This work employs a mixed approach (i.e., time–frequency analysis) to extract features from the EEG signal. Time–frequency analysis techniques are effective in analyzing non-stationary signals whose frequency distribution and magnitude vary with time, which is the case for the EEG signal [3].

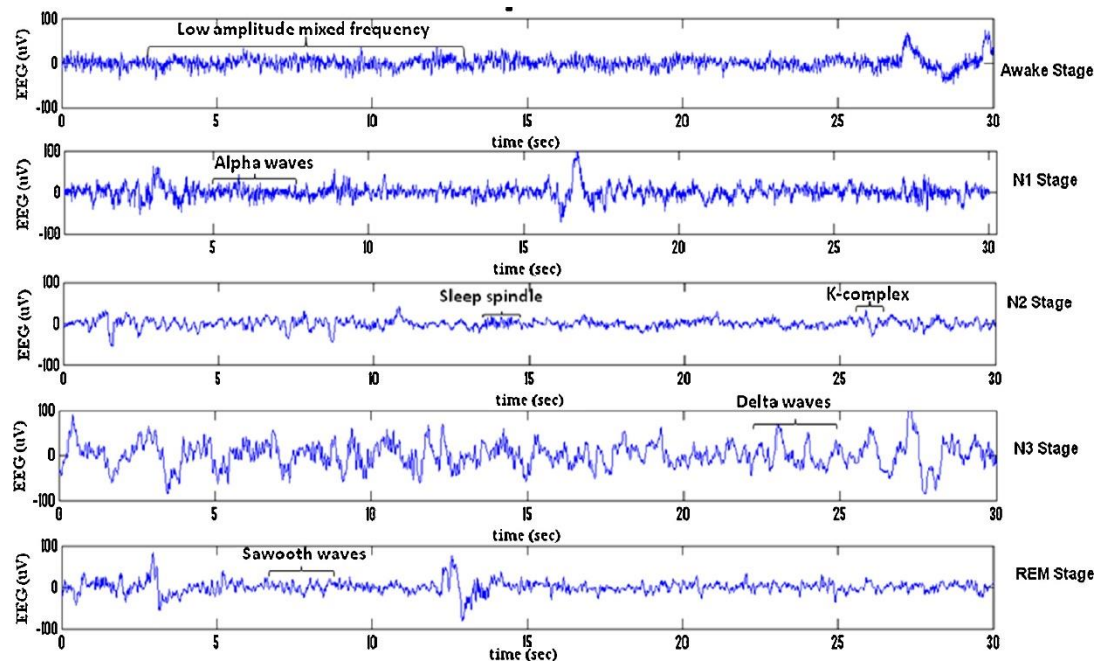


Fig. 2 – EEG signal for the different stages of sleep: N1, N2, N3, REM and the awake stage. The low amplitude mixed frequencies, Alpha waves, sleep spindles, K-complexes, delta waves, and sawtooth waves are shown in the figure.

i. *Choi–Williams distribution (CWD)*

CWD, which was proposed by Hyung-Il Choi and William J. Williams, is a member of Cohen's class distribution functions [4]. For a given time series $s(t)$, CWD is defined as:

$$\text{CWD}(t, f) = \int_{-\infty}^{+\infty} A_s \int_{-\infty}^{+\infty} (\eta, \tau) \phi(\eta, \tau) e^{j2\pi(\eta t - \tau f)} d\eta d\tau$$

Where $A_s(\eta, \tau)$ is called the ambiguity function given by:

$$A_s(\eta, \tau) = \int s^*(t - \frac{\tau}{2}) s(t + \frac{\tau}{2}) h(\tau) e^{-j2\pi\tau\eta} dt$$

Where $*$ is the complex conjugate operator.

$\phi(\eta, \tau)$ is called the kernel function defined as: $\phi(\eta, \tau) = e^{-\eta^2\tau^2/\sigma}$

where σ is the kernel width.

In CWD, the kernel function is a Gaussian window function used to eliminate cross product oscillations without applying kernels [5]. CWD is energy-conserved, real-valued, and retains both time and frequency offset, which makes CWD previously used in many applications, where the signals used are non-stationary [6].

ii. *Continuous wavelet transform (CWT)*

Wavelet transform is another form of time-frequency distribution, which has been widely used in many fields of signal processing and analysis in the past two decades [7]. There are two forms of wavelet transform: continuous wavelet transform (CWT) and discrete wavelet transform (DWT). In this work, continuous wavelet transform is used because it provides localization in time and frequency, which makes it a powerful tool for time-frequency analysis. The CWT of the signal $s(t)$ can be written as:

$$\text{CWT}(a, b) = \int s(t) \psi_{a,b}(t) dt$$

Where $\psi_{a,b}(t)$ is the dilation and transformation of the mother wavelet defined as:

$$\psi_{a,b}(t) = \frac{1}{\sqrt{|a|}} \psi\left(\frac{t-b}{a}\right)$$

Where $\psi(t)$ is called the mother wavelet, and b is the translation parameter that provides the time domain characteristics of the signal $s(t)$ (the time shift parameter), and $a(a \neq 0)$ is the scaling parameter that provides the scaling and compression of the parent wavelet function $\psi(t)$. It can be used to analyze the frequency characteristics of signal $s(t)$. The scaling parameter values are selected to cover the entire frequency range of different EEG waves and events based on the following equation that associates the scaling parameter a with the frequency f :

$$f = \frac{f_c}{aT_s}$$

where f_c is the center frequency of the mother wavelet, and T_s is the sampling period.

Many mother wavelets can be used to find the wavelet transform of signal $s(t)$,

such as Daubechies, Coiflets, Morlet, Gauss, Symlets, biorthogonal and reverse biorthogonal. In this work, the 20th order Daubechies wavelet is used.

iii. *Hilbert–Huang Transform (HHT)*

HHT is a two-step transform that was proposed by Huang et al. in 1998 [8]. The two steps are:

- a. The first step is called empirical mode decomposition (EMD). In this step, the signal is decomposed into a series of independent intrinsic signals or modes ($IM_i(t)$, $i = 1, 2, \dots, N$) where N is the number of intrinsic modes. Each mode must satisfy two requirements: (1) the number of zero crossings and the number of extremes should be equal or at most differ by one. (2) For any given point, the mean of the envelopes of the local minima and local maxima should be zero. The signal $s(t)$ can be decomposed using the EMD as:

$$s(t) = \sum_{i=1}^N IM_i(t) + r_N(t)$$

where $r_N(t)$ is the residue of the signal after which no intrinsic modes can be extracted. This residue is small but found to have significant high frequency information during EEG signal analysis.

- b. The second step is applying the Hilbert transform (H) to the signal $s(t)$ (the EMD of $s(t)$) and constructing the signal $z(t)$ defined as:

$$z(t) = s(t) + jH(s(t))$$

$$z(t) = \left[\sum_{i=1}^N IM_i(t) + r_N(t) \right] + jH \left[\sum_{i=1}^N IM_i(t) + r_N(t) \right]$$

or
$$z_i(t) = IM_i(t) + jH(IM_i(t)) = a_i(t)e^{j\theta_i}$$

where
$$a_i(t) = \sqrt{IM_i^2(t) + H^2(IM_i(t))}$$

$$\theta_i(t) = \tan^{-1} \frac{H(IM_i(t))}{IM_i(t)}$$

Then the instantaneous frequency is defined as:

$$\omega_i(t) = \frac{d\theta_i(t)}{dt}$$

Based on the above, the Hilbert–Huang Transform is defined as:

$$HHS(\omega, t) = \text{Real} \sum_{i=1}^N a_i(t) e^{j \int \omega_i(t) dt}$$

The HHT is a new tool for analyzing nonlinear and nonstationary signals. It was recently used in many applications in the biomedical field and other fields [9,10].

2.2.2 artifact removal

In the measurement of EEG signals, activities of human organs, such as blinking,

heartbeat, breathing, muscle movement, etc., change the potential of the scalp of the brain. When the scalp electrode collects an electric field change, artifacts are generated. Among various artifact components, the amplitude of the electro-optical artifacts is large, and the frequency overlaps with the frequency of the EEG signals, which makes it difficult to analyze the EEG signals. Therefore, it is necessary to remove the electro-optical artifacts and separate the electro-optical artifacts that are mixed with the EEG signals to ensure the quality of the EEG signals.

2.2.3 principle component analysis

Principal Component Analysis (PCA) is a multivariate statistical analysis method that uses multiple variables to linearly transform to select fewer significant variables. In the process of removing the electro-optical artifacts, it is assumed that the EEG signals and the EEG signals are orthogonal to each other, and the EEG signals are decomposed into a set of independent components by PCA, and the EEG artifacts are manually identified and removed, and then reversed. The projection obtains an EEG signal that removes the electro-optical artifacts.

In the principal component analysis process, it is necessary to find a linear transformation orthogonal matrix W , and orthogonally transform the vector X so that the variables of the output Y are not related to each other, that is, $Y=WX$:

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_N \end{bmatrix} = \begin{bmatrix} y_{11} & \dots & y_{1N} \\ y_{21} & \dots & y_{2N} \\ \vdots & \ddots & \vdots \\ y_{N1} & \dots & y_{NN} \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ \vdots \\ x_N \end{bmatrix}$$

Where the covariance matrix of Y is a diagonal matrix:

$$\begin{aligned} C_y &= E\{yy^T\} = E\left\{\begin{pmatrix} y_1 \\ \vdots \\ y_N \end{pmatrix} (y_1, \dots, y_N)\right\} \\ &= \begin{bmatrix} E(y_1^2) & \dots & E(y_1 y_N) \\ \vdots & \ddots & \vdots \\ E(y_N y_1) & \dots & E(y_N^2) \end{bmatrix} = \begin{bmatrix} \lambda_1 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & \lambda_N \end{bmatrix} \end{aligned}$$

The commonly used PCA calculation method is to perform feature decomposition on the covariance matrix C_x to obtain an orthogonal transformation matrix W , usually C_x is a symmetric matrix.

$$C_x = U \Sigma V^T$$

Where $U = [u_1, u_2, \dots, u_m]$, $V = [v_1, v_2, \dots, v_n]$, $\Sigma = \text{diag}(\lambda_1, \lambda_2, \dots, \lambda_p)$,

$P = \min(m, n)$, u_i is the eigenvector of the covariance matrix C_x , and the eigenvectors are orthogonal to each other.

After PCA transform, the signal energy is mainly concentrated in the first few principal components. Because the amplitude of the ectopic artifacts is large, it will also exist in the first few principal components, and it is necessary to manually identify the ocular artifacts. It is set to zero, and then the signal is restored by inverse transformation to obtain the effect of removing the electro-optical artifact.

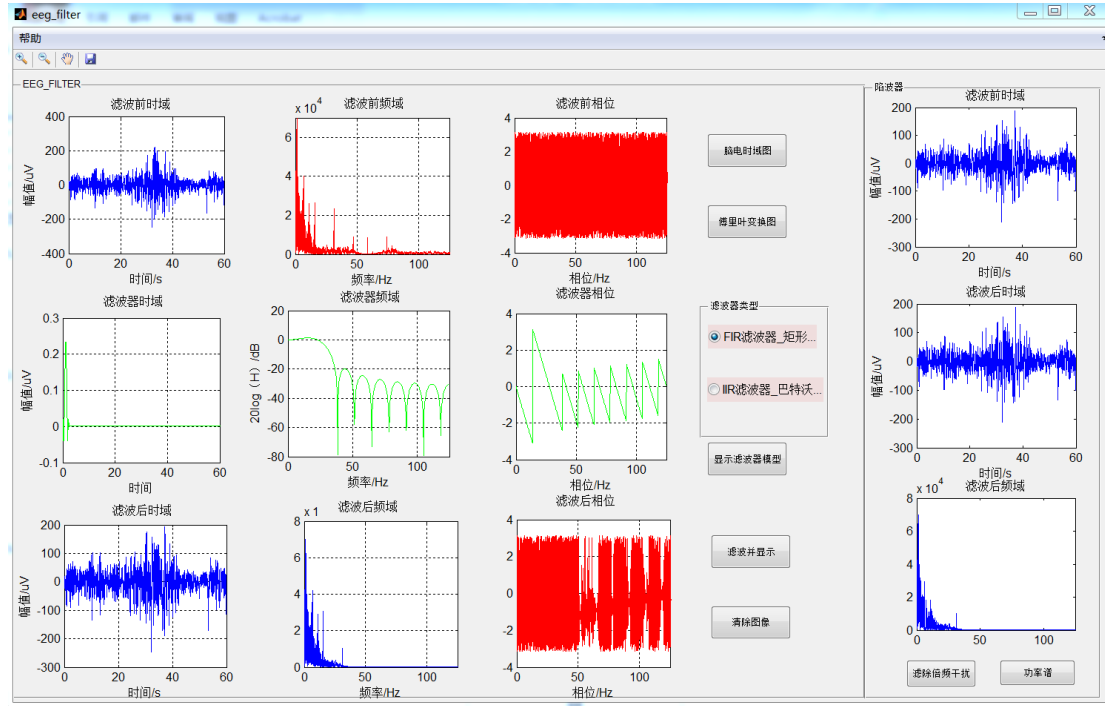


Fig. 3 – The EEG signal after filtering high frequency noise is compared with the original signal in time domain and frequency domain.

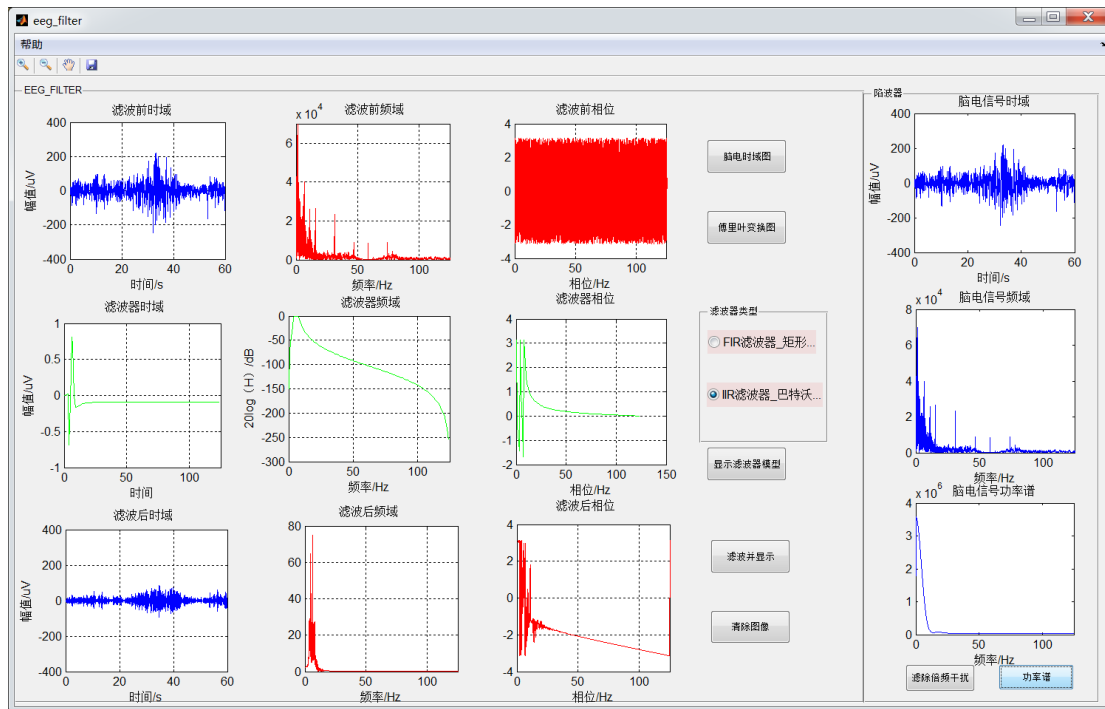


Fig. 4 – The EEG signal after filtering high frequency noise is compared with the original signal in time domain and frequency domain.

2.2.4 independent component analysis

Independent Component Analysis (ICA) is a blind source separation method that has been widely used in recent years. After processing by ICA, the resulting components are removed from correlation and are also independent Gaussian

distributed signals. ICA is a well-behaved blind source separation technique that effectively separates source signals from aliased signals when the model and source signals are not accurately known.

As shown in Fig.2, the vector $X = [x_1, x_2, \dots, x_N]$ is an observation signal of N -dimensional at t , which is mixed by M unknown and independent source signals $S = [s_1, s_2, \dots, s_N]$ through the mixing matrix Generated, ie $X=AS$. The purpose of ICA is to determine the de-mixing matrix M of $M*N$ based on the observed data vector X only if S and A are unknown, so that the output signal $Y=WX$ approximates the source signal.

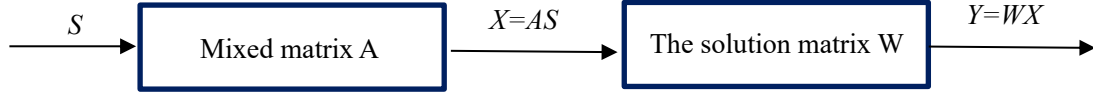


Fig. 5 – The principle of ICA

Assuming an independent variable is estimated, consider the linear combination x_i as follows:

$$y = W^T x = \sum w_i x_i$$

Here W is the required transformation matrix. Since we do not know the matrix A , we need to find a very approximate estimate of A .

If $z = A^T W$, then: $y = W^T x = W^T = W^T A = z^T s$

Y is a linear combination of s_i , The weight is given by z_i , so the sum of the two random variables is closer to the Gaussian distribution, and the $z^T s$ is closer to the Gaussian distribution than the human and a z_i . In this case, it is obvious that only one element in the z_i is non-zero. Therefore, we can think of W as a vector to maximize the non-Gaussian $W^T x$, such a vector corresponds to z , then there is an independent component of $W^T x = z^T s$. An independent component can be obtained by maximizing the non-Gaussian $W^T s$.

ICA artifact removal method has been widely used, but there are still some problems to be solved. When the number of observations is less than the number of source signals, how to separate the source signal; how to separate the source signal in the noisy environment; how to remove artifacts automatically without manual identification needs to be further solved.

2.3 Data analysis and feature extraction

2.3.1 Exploratory Data Analysis (EDA)

- i. The two figures show that 7 signals in edfbrowser

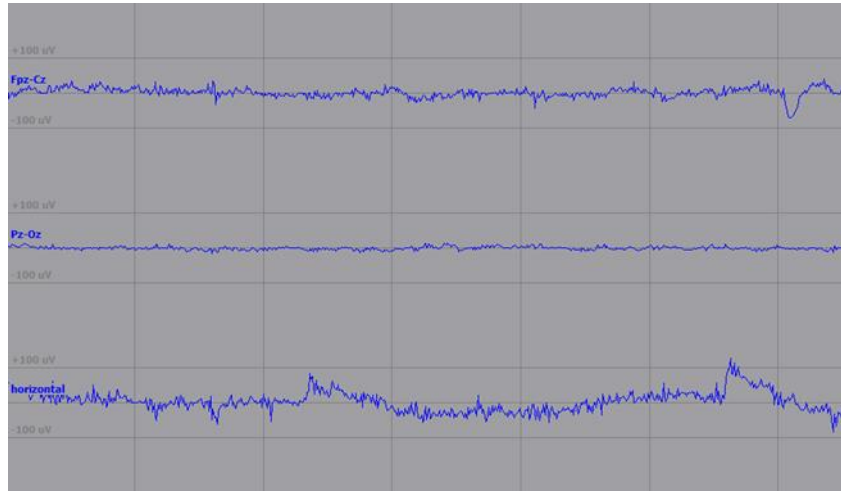


Fig. 6 – The first three signals 100Hz

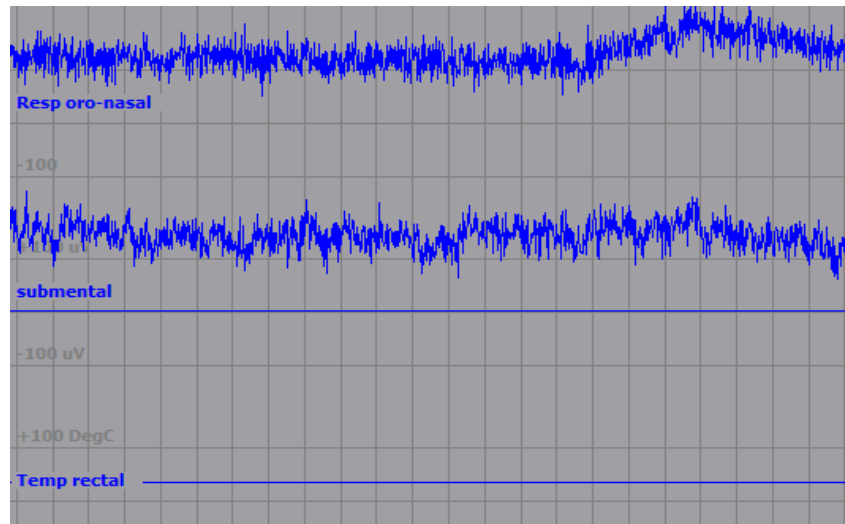


Fig. 7 – The last four signals 1Hz

- ii. We compute the correlation matrix for the 7 signal channels and make a thermogram to see the correlations between each pair in these 7 signals

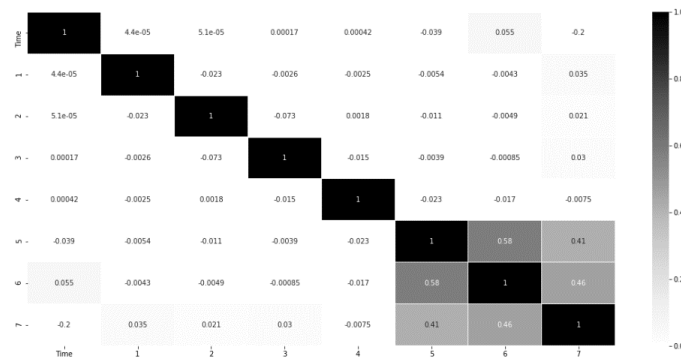


Fig. 8 – Signal correlation thermogram

- iii. We also make a 3D scatter graph to intuitively see the relation of the last 3 signals which have stronger correlations.

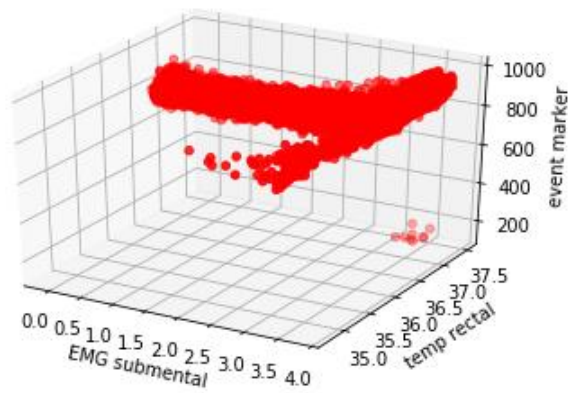


Fig. 9 – 3D Graph of 3 signals

- iv. We make 8 frequency distribution histograms to show the distribution of each signal.

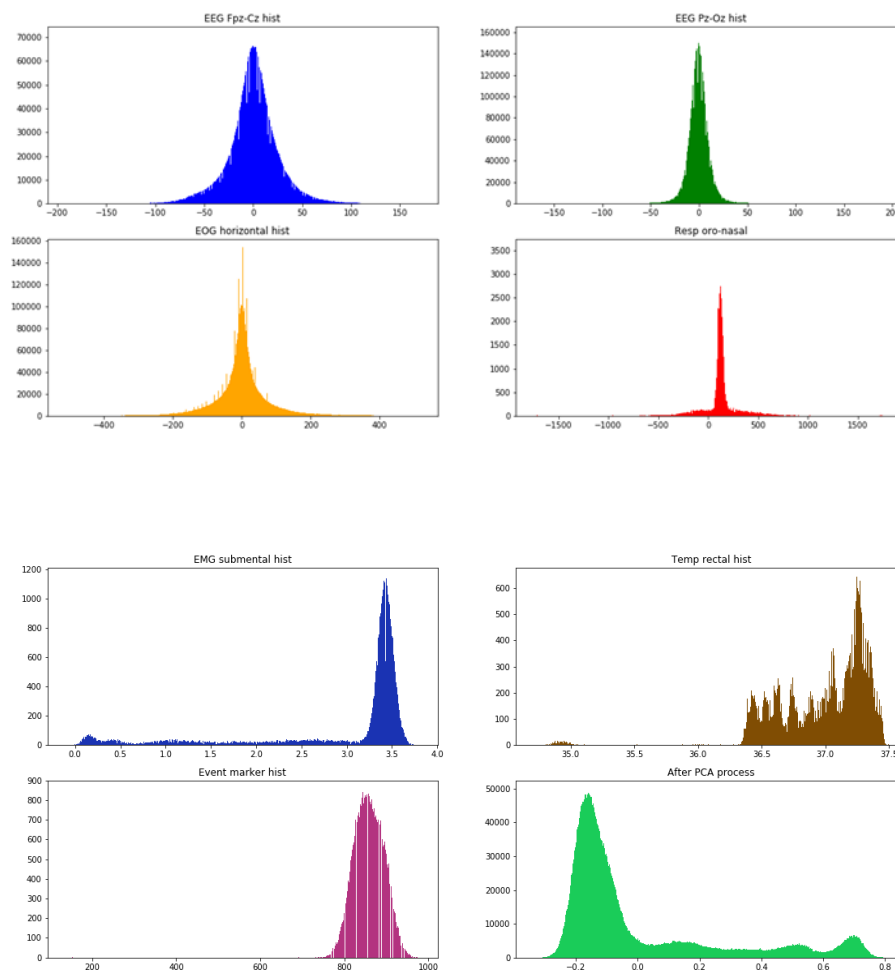


Fig. 10 – all signals Frequency distribution histogram

The correlation of the last three signals can be seen from the 3D scatter plot and the related thermodynamic plot that they have more redundant information, so we apply PCA on these signals

According to PCA on last 3 signals, the first principal component accounted for 76.7% of the total, so we use PCA to reduce the dimension and get the first principal component as a signal channel.

However, the first four signals are not highly correlated, so the overlapping information of these four signals is not much. They all approximate to the Gauss distribution.

2.3.2 Discrete Fourier Transform (DFT)

Because they are time series, the discrete Fourier transform (DFT) is proposed to be applied to transform them to extract the features of the signal frequency. we utilize real-input FFT to extract time-invariant features

A fast Fourier transform (FFT) is an algorithm that computes the discrete Fourier transform (DFT) of a sequence, or its inverse (IDFT). Fourier analysis converts a signal from its original domain (often time or space) to a representation in the frequency domain and vice versa. The DFT is obtained by decomposing a sequence of values into components of different frequencies.

$$X_k = \sum_{n=0}^{N-1} x_n e^{-i2\pi kn/N} \quad k = 0, \dots, N-1$$

the time-sequence data after DFT is like this:

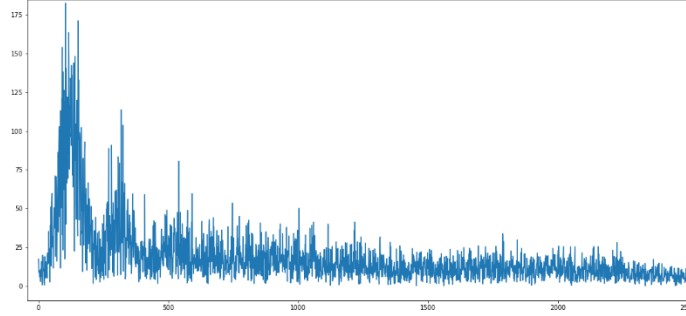


Fig. 11 – time-sequence data after DFT

2.3.3 Data equalization

In order to better describe the frequency signal, we smoothed the frequency sequence after discrete Fourier transformation. We finally extract 7 features from each frequency sequence.

After Fourier transform, we are not interested in the frequency with the largest amplitude, but in the frequency range with larger amplitude (area), because at the same stage, there may be a frequency with very high amplitude, and this situation may decrease the stability of the features. In addition, after Fourier transform, there are many

burrs in the spectrum, which are not conducive to the intuitive analysis of the characteristics of the frequency amplitude, so we need to do further processing.

we use a sliding window with size K to averaging the spectrum. Each point of the spectrum, is replaced by the average value of the previous K-1 value, which can make the data smoother and eliminate burrs. Each point contains the information of the nearest K points; thus, we can enhance the stability and intuition of the data.

$$Y_i = \begin{cases} \frac{1}{k} \sum_{i-k}^i X_i & i > k \\ \frac{1}{i} \sum_1^i X_i & 0 < i \leq k \end{cases}$$

In this experiment K=15.

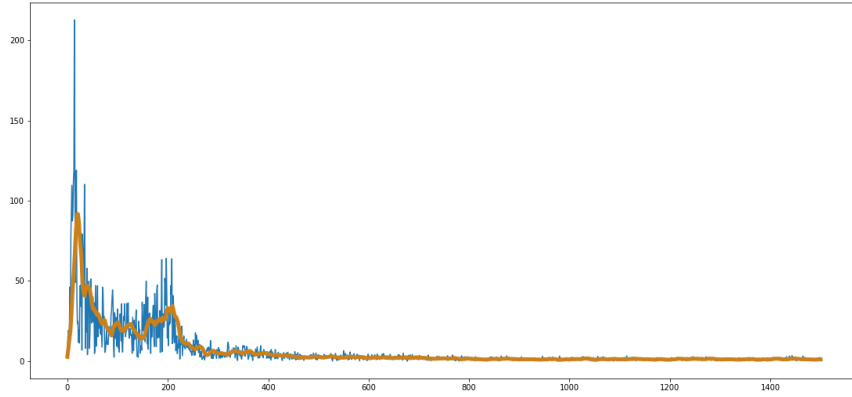


Fig. 12 – yellow line shows data after equalization

we extract 7 features from the final data, they are the first and second largest amplitudes in channel 1,2,3 and the amplitudes of frequencies 10 in channel 4.

2.4 The Algorithm Based on SVM

After feature extraction of signals during sleep, we need to analysis these feature vectors to evaluate the quality of sleep, which is also the key to automatic sleep recognition. To achieve higher accuracy rate, we should use the feature parameters obtained in the previous chapter as input features. Then we will apply SVM on sleep staging.

2.4.1 Brief introduction to SVM

Support Vector Machine is a new category proposed by Vapnik. It is a set of related supervised learning methods, which are popular for performing classification and regression analysis using data analysis and pattern recognition. Methods vary on the structure and attributes of the classifier. The most commonly known SVM is a linear classifier, predicting each input's member class between two possible classifications. A more accurate definition would state that a support vector machine builds a hyperplane or set of hyperplanes to classify all inputs in a high-dimensional or even infinite space. The closest values to the classification margin are known as support

vectors. The SVM's goal is to maximize the margin between the hyperplane and the support vectors.

2.4.2 How SVM work

The SVM method is developed from the optimal classification surface in the case of linear separability. The basic idea can be illustrated by this diagram.

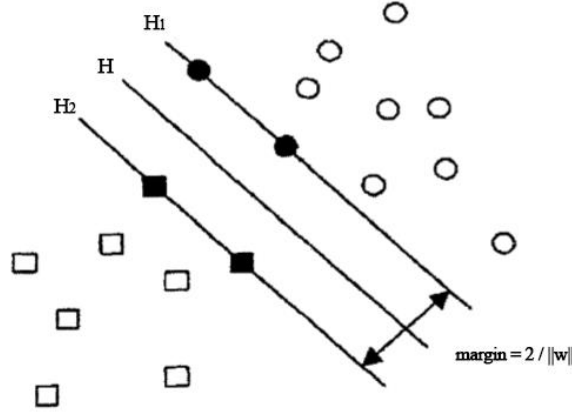


Fig. 13 – Support vector and interval

In this picture, circles and squares respectively represent two types of samples, and the two lines near circles and squares are the edges which classify the two types with no errors. The distance between them is called classification interval, so the optimal classification line which not only could classify the two types correctly, but also have the largest classification interval.

The former is to guarantee the minimum of experience risk, the latter is to minimize the confidence range in the generalization bound, which minimize the real risk.

We assume that we have n examples x_i and their types y_i , which is represented as

(x_i, y_i) , $x_i \in R^d$, $y_i \in \{-1, +1\}$ ($i=1, \dots, n$), hyperplane equation $w \cdot x + b = 0$ could classify the two types correctly, and the problem of maxing the classification interval can be represented as minimizing $\hat{N}(w) = \frac{1}{2} \|w\|^2 = \frac{1}{2} (w \cdot g \cdot w)$ during $y_i (w \cdot x_i + b) - 1 \geq 0$. Considering that there may be some examples can't be classified correctly, we got relaxation factor $\xi_i \geq 0$ ($i=1, \dots, n$). Now the constraint has changed to $y_i (w \cdot x_i + b) - 1 + \xi_i \geq 0$ ($i=1, \dots, n$), and optimization objective function has changed to

$\hat{N}(w) = \frac{1}{2} (w \cdot g \cdot w) + C \sum_{i=1}^n \xi_i$. The $C > 0$ is a constant which control the penalty degree of

right and wrong sample distribution and achieve the tradeoff to the distinction between

school-based ratios and the complexity of the algorithm. This problem could be transform to getting the maximum of a_i , while $\sum_{i=1}^n a_i y_i = 0, 0 \leq a_i \leq C, (i=1, \dots, n)$

2.4.3 Kernel function

a. Polynomial kernel function:

$$K(xgy) = [(xgy) + 1]^d \quad (d=1,2,3\dots)$$

b. Gaussian radial basis kernel function:

$$K(xgy) = \exp\left\{-\frac{\|x-y\|^2}{2\sigma^2}\right\} \quad \sigma > 0$$

c. Sigmoid kernel function:

$$K(xgy) = \tanh(b(xgy) + c)$$

2.4.4 Multi-class classification of support vector machine

The classical support vector machine algorithm only provides the binary classification algorithm. However, in the practical application, generally needs to solve Multi-class classification

At present, multi-class classification algorithm is a research hotspot in the field of support vector machine. One-to-many methods and one-to-one methods are applied more. In addition, scholars at home and abroad also proposed the global optimization of multi-classification methods and decision tree multi - classification method.

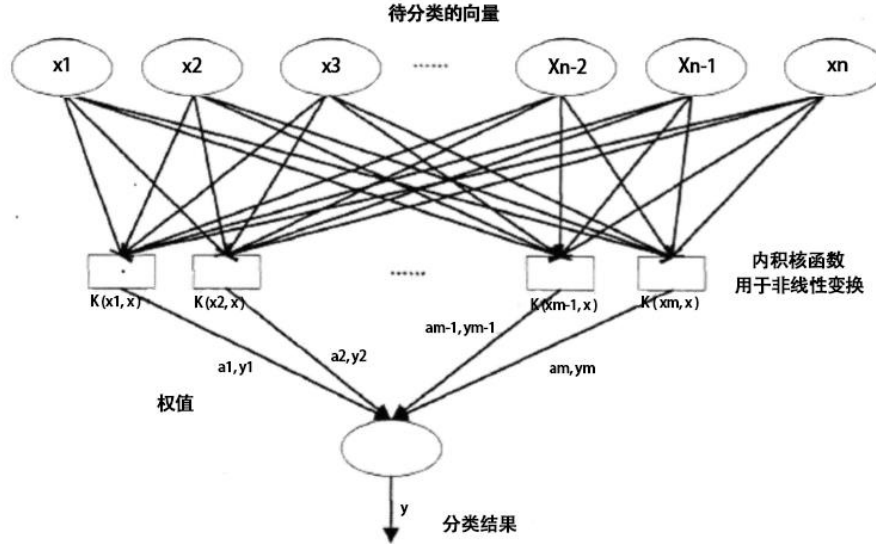


Fig. 14 – multi-class classification algorithm is a research hotspot in the field of support vector machine

3. Results

The data we use comes from Sleep-EDF Database Expanded. The sleep-edf database contains 197 whole-night Polysomnographic sleep recordings, containing EEG, EOG, chin EMG, and event markers. Some records also contain respiration and body temperature. Corresponding hypnograms (sleep patterns) were manually scored

by well-trained technicians according to the Rechtschaffen and Kales manual, and are also available.

After feature extraction of signals during sleep, we normalize the features by Min-Max Normalization:

$$x' = (x - X_{\min}) / (X_{\max} - X_{\min})$$

Finally, we use Linear SVC to train the classifier, and get the result as follow:

```
print(clf.score(x_train, y_train)) # 精度
y_hat = clf.predict(x_train)
show_accuracy(y_hat, y_train, '训练集')
print(clf.score(x_test, y_test))
y_hat = clf.predict(x_test)
show_accuracy(y_hat, y_test, '测试集')
```

0.8520667150108775

0.8239130434782609

Fig. 15 – The training and test score of linear SVC classifier

```
import matplotlib.pyplot as plt
plt.bar(time, Y, 30)
plt.show()
```

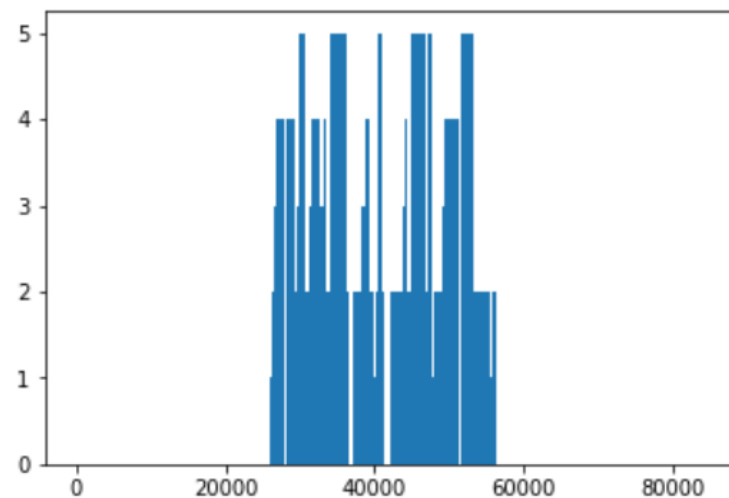


Fig. 16 – The staging made by experts

And this is the staging made by us:

```
plt.bar(time, y, 30)
plt.show()
```

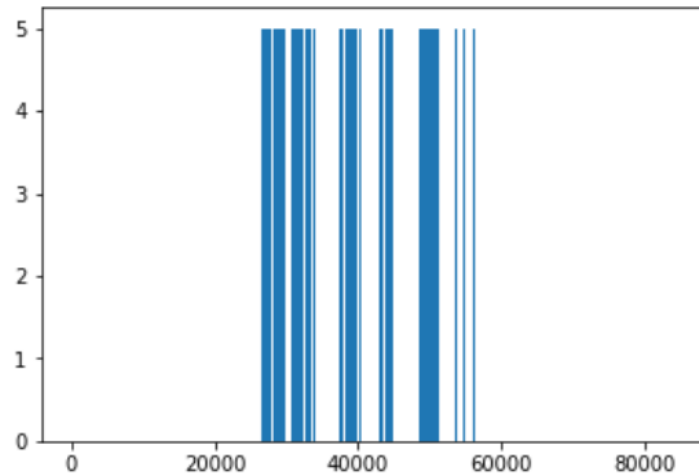


Fig. 16 – The staging made by us

We can see this picture shows a good classification of wake stage and sleep stage, but the classification of different sleep stages is really bad. However, a very interesting thing is that we can get a better classification if we use the feature directly without data normalization. Just like this:

```
plt.bar(time, y, 30)
plt.show()
```

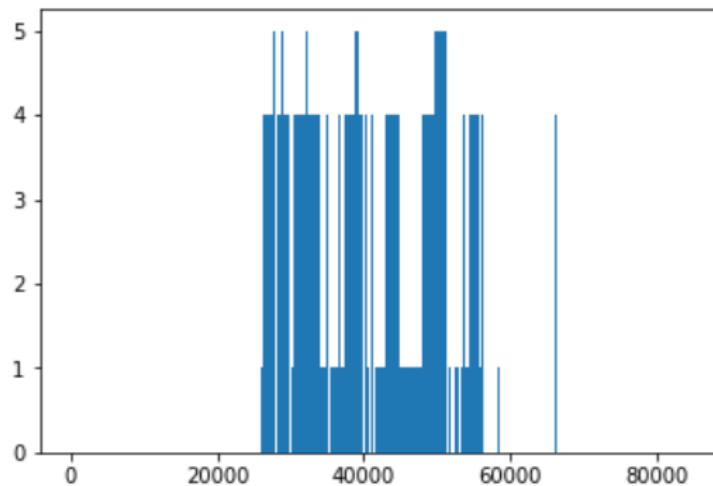


Fig. 17 – The classification when we use the feature directly without data normalization

4. Top research groups/labs

4.1 Sleep and Chronobiology Laboratory

4.1.1 Research interests

Health and safety.

- a. Consequences of sleep and circadian disruption.

- b. Influence of sleep and circadian rhythms on human physiology (neuroendocrine, metabolic and immune function) and behavior (sleepiness, memory, learning, mood, cognitive and motor performance) with application to public health and safety.
- c. Countermeasures to improve sleep, wakefulness, and health.

4.1.2 Current research projects

- a. Impact of sleep and circadian disruption on the human microbiome and related changes in human physiology and cognition.
- b. Biomarkers for insufficient sleep and circadian rhythm disruption (metabolomics and proteomics).
- c. Tissue specific alterations in response to insufficient sleep and circadian misalignment.
- d. Influence of sleep loss, sleep inertia and circadian disruption on cognitive function.
- e. Countermeasures to improve sleep and wakefulness.
- f. Physiological and behavioral mechanisms by which insufficient sleep and circadian misalignment contributes to metabolic dysregulation.
- g. Countermeasures to improve cardiometabolic health during insufficient sleep.
- h. Student-athlete sleep, health and performance.

4.2 Sleep medicine at Harvard medical school

4.2.1 Mission

The Division of Sleep Medicine at Harvard Medical School is dedicated to establishing the model program in sleep and circadian biology. Toward this goal, the Division of Sleep Medicine works to mobilize the intellectual and scientific resources at Harvard to create and sustain groundbreaking programs that will educate the medical and lay populations, impact public policy, foster collaborative research, and set new standards of clinical practice.

4.2.2 Goals

- a. To establish permanence of Sleep Medicine at HMS
- b. To create a model program in sleep and circadian biology
- c. To enable evidence-based policy making through research
- d. To educate physicians and their patients about the importance of sleep and the impact and treatment of sleep disorders
- e. To enhance medical education in the area of sleep and sleep medicine through new and novel materials and channels
- f. To foster collaborative research
- g. To develop guidelines and raise standards for clinical practice

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