Improvement implementation a software to analysis polysomnography signal

- Le Quoc Khai
- Nguyen Thi Minh Huong
- Nguyen Vu Quang Hien
- Nguyen Le Trung Hieu
- Huynh Quang Linh

Ho Chi Minh city University of Technology, VNU-HCM

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ABSTRACT:

Sleep disorders have become nowadays one of the most important health issues in the community; they will affect many functions of the body and regular physical activities. The goal of our research is implementation the software *improvement* of for polysomnography signal analysis based on AASM standards published in 2014 to create a comprehensive assessment method for different abnormalities or pathologic symptoms. By using a combination of different learning machine algorithms, program can flexibly update threshold and characteristics of polysomnography signal for each people

and reduce errors in calculated results. The program is designed with friendly user interface without support of other special software. The results checked by comparative measurements with other facilities showed high reliability, which give the similarity over 83% for all data. The most advantage of the software is the ability to synchronize data and analysis results with other systems. Program can be decomposed in block modules, which can be easily integrated other equipment with to make independent and continuous diagnostic systems.

Key words: polysomnography analysis, learning machine, AASM standards

1. INTRODUCTION

Sleep is one of the most popular activities that people spend a third of life time. Insomnias or sleep disorders are often the cause of many other diseases. Besides sleep has a special role in clinical neurological studies. In 1929, Berger was the first scientist, who recognized the human brain electrical activity during sleep by recording electroencephalographic signals through attaching electrodes on the scalp and has showed the difference between the waking and relax states during sleep. Loomis et al. [1] have found that the scattered fragments of the Alpha waves start the sleep, then the appearance of the complex K, sleep spindles and slow waves. Initial sleep is divided into five different states with the stage as much as the later waves of low frequency and high amplitude. Kleitman and Dement, 1957 [2] has found rapid eye movement (REM) has led to the grouping of a specific sleep stages sleep called rapid eye movement or REM sleep.

In 1968, Rechtschaffen and Kales [3] has convened a group of experts to establish a unified detailed guidelines to standardize the classification of sleep stages. Sleep is divided into states: waking state, sleep state is not appear rapid eye movement (non-REM) sleep state with rapid eye movement (REM). In particular, the status of non-REM sleep consists of 4 stages, which are denoted respectively S1, S2, S3, S4. At least 1 EEG leads (electrodes placed at C3 or C4 position with the reference electrode in the opposite ear) as well as 2 and 1 lead EOG EMG leads were recorded. R & Κ rule recommendations sleep logs into segments of 30 seconds length or 1 "epoch". It is suitable for common scrolling speed of 10 mm/s, such as a resolution to detect the appearance of the Alpha waves and sleep spindles. Each epoch will be assigned to one particular state.

In 2004, the Academy of Medicine Sleep America - American Academy of Sleep Medicine (AASM) established the guidelines in detail, allowing control of some new features such as the micro-awakening (arousal), respiratory events, cardiovascular, and events related to the movement of patients. The establishment of these rules are standardized with specific guidelines. In 2007, the AASM officially publish detailed guidelines for the analysis of polysomnogrphy, also called AASM 2007 standards [4]. It is replacing R & K rule and become the main rule of any sleep study to this day. The latest calibration of the standard is AASM 2014 [5], with the main change in diagnostic characteristics related respiration disordes, the microwaves and the classification for infant sleep.

To analyzing any pathological disorders related to sleep, the requirement is exactly determine the state that a patient are experiencing. This is done through a detailed analysis of the structure of sleep, the pathology related to respiratory and cardiovascular disease is the information will be added to the pathological evaluation. The relation between sleep apnea syndrome and diseases such as hypertension, and cardiovascular diseases such as stroke, heart failure is increasing and getting the attention of researchers. It is important for cardiovascular physicians is to recognize and grasp heavy elements as sleep apnea syndrome have a direct negative impact on the cardiovascular system, and the doctors study of sleep is discontinued syndrome sleep apnea can increase the risk of cardiovascular disease. Susan Redline at el. [6] shows that the link between sleep apnea syndrome and heart rhythm disorders. Considering the whole, the study showed that the abnormal heart rate several times higher than in patients with manifestations of sleep apnea syndrome than subjects underwent sleep breathing was normal.

This study was conducted with the goal of a complete software functional building classification and microscopic structure of sleep. The software is designed with friendly user interface and useful for doctors to use in examination and clinical treatment. It can be easily installed on conventional computers without installing special software. Therefore helping clinicians overview better of the relationship and influence between respiratory problems and cardiovascular disease. The development of an automated analysis tool is a useful contribution to the medical experts to shorten examination and treatment.

The most important thing in analyzing polysomography signal is handling all the physiological electrical signals recorded in the night. With advances in digital signal processing, a lot of research focused on developing treatment method spectral analysis [7], using artificial neural networks [8], processing or analyzing wavelet multicast [9] to develop an automated processing system analyzes the sleep state. In particular, the fractal is a method to examine the complex hiey credits. Handling fractal can characterize the EEG waves in the time domain [10], [11]. So we will describe the process of classifying the state by combining several different methods to detect specific to each state. After conducting classification and postprocessing, the result will be retested some errors by analyzing each individual epoch. A detailed description of the algorithm and the flowchart of the program will be interpreted in the specific section below.

2. MATERIALS AND METHODS

The software is built in modular function, the blocks can be customized and independent processing on the input data for each patient. This is the raw data obtain directly from polysomnography device. The first step is remove all kinds of noise and reducing the impact of electrophysiological signal to channel unwanted needs analysis.

Polysomnography signal often contain different types of noises, such as: drifting baseline, muscle activity noise, power source noise, exposed negative electrode.

The filters used in the program include: Lowpass with 45 Hz cutoff for ECG; without the use of low pass filters for respiratory signal. Highpass with 0.5 Hz cutoff for ECG and 0.1 Hz for the respiratory signal. Notch filters: remove artifacts from electrical power source at 50 Hz or 60 Hz. The ECG noise reduction with range 0.5 Hz to 45 Hz mainly to detect heart rate [12].

Analyze the microscopic structure of sleep



Figure 1. Algorithm of analyzing the microscopic structure of sleep using Support Vector Machine

Support Vector Machine (SVM), also known as classification method using support vector, is a new method in artificial intelligence (learning machine), developed by VN Vapnik et al. SVM is built on the principle of minimizing errors in a general way, ie minimize the overall error through error [13]. This is the appropriate method to classify the biological signal by characteristics such as high precision, application in multi-dimensional space, high flexibility [14].

SVM using linear equations in the ultra-flat space. Details of the topology selection and hardware design are provided in below sections [14], [15].

$f(x) = w^T \phi(x) + b$

EEG signals is a complex model of the

space include multidimensional feature space [15]. Therefore , the method uses artificial intelligence (learning machine) is considering using to analyze the characteristics of the EEG signal.

Using SVM to analysis K-complex [16], the system include the following steps (Figure 1.):

Identifying sleep apnea

Raw signal after filtering will be analyzed. We used Calib-data and Main-data in Identifying step. Calib-data is the data used to calibrate the object corresponding to each different measure, the receiver before the measurement. This is mandatory steps in all cases of measuring data, to create a data segment refine those standards mandatory tests according to the order and duration specified. Calib-data entirely conducted by the device automatically. Main-data: the actual measurement data from the patient after the machine has run Calib. The algorithm of this module as the Figure 2.



Figure 2. Algorithm of identifying sleep apnea

Analysis ECG signal



Figure 3. Algorithm of detect QRS complex

The way to identify the QRS complexes using extreme methods set thresholds as a method simple, popular, easy to implement. But huge drawback of this method, when we made the group determining the exact thresholds. Besides, some other techniques given by the researchers for the purpose of detecting the peak in the ECG wave [17], [18], special techniques using tools wavelet conversion efficiency high for signal analysis.

Wavelet Transform technique can identify the characteristic features of a signal signal to high precision, even with the presence of interference caused. Descrete Transform Wavelet (DWT) is used as a tool for analyzing ECG signals [19].

To extract the correct information, the output of the filter will signal to the wavelet transformation, the signal needs to be processed crude.

Here we use Wavalet Debauchies. ECG signal processing is performed by applying the

converter WT repeated, repeated. ECG signal is analyzed to level 4 and use them DB6 [20].

The signal is decomposed into two components A and D. A is the low frequency component, D is the high frequency components.

Low-frequency component is a useful component, shaped similar to the original signal. The identification of component-based crests A4, useful components.

First, the signal component A4 segmented into short segments. To assess the performance of the heart rate, people often divide each segment is one minute (60 seconds), employment will increase accuracy, reduce work in process calculate wave identification.

In this section, the QRS complexes acquired from the combination of transformations Wavalet with appropriate threshold peak detection and the comparison wave after wave peak detected signal components on A4 with credits ECG ECG.

Q and S are the two smallest peak amplitude before and after peak R an 0.1s . To identify the exact location of the peak Q and S , starting from the top R on ECG ECG we select a frame size from position R - R + 0,1s and 0,1s to find extreme values before and after the position profile R. the minimum value before and after the position R respectively peak position Q and S.

3. RESULTS & DISCUSSION

There are some examples before and after signal preprocessing step. Summary results for the implementation of a noise in Figure 4.



Figure 4A. Respiratory signal



Figure 4B. Electrocardiography signal

Figure 4: Signal before and after preprocessing

Signals are applied to the correct base line. However appearance latancy time in the ECG. While not observed in the respiratory signal. Appearing decrease in amplitude ECG . Whereas, in the respiratory signal attenuation is negligible. Signal after treatment was smooth than rough initial signal .

Identification microwave

Initial implementation of applied research SVM method on microscopic structural analysis is the study of sleep using SVM method to identify the K –complexes. SVM training consists of 2 process data and data classification, use the following syntax: svmstruct = svmtrain (training, group, name, value).

Training : Data used for training. The data is data training consists of 2 columns. The first column is the value of time , column 2 is the voltage value. Group : 1 column matrix , with the number of rows equals the number of training products . Matrix only 2 values ([1, -1] or [1,0]). Name and value : as minor , supporting more training correctly . Without the program values will be interpreted as the default value.

For example, we obtained results that detection a K-complex in Figure 5. The K-complex detected will be change to the green color and saved the location in time axes.





Analysis the relationship between respiratory signal and ECG signal.

From the graph in Figure 6, the user will know the total distance apnea is defined as standard document AASM Scoring Rules of version 2.1 released in 2014 - left panel

Location apnea segment will be marked to start position and end position while delimiting mark again . On the picture is positioned apnea No. 7, at 259 minutes .



Figure 6A: Respiration and ECG signal in normal



Figure 6: The relationship between respiratory signal and ECG signal

The program determines the exact location of the peak of the QRS complex. Green squares: Q peak. Red triangle: R peak.Golden Triangle: S peak.

This is the result of extreme methods set threshold with automatic threshold is established automatically. Despite the fluctuation signal to the electrodes , the program algorithm still correctly identify the QRS complexes.

From the identification of the exact location of R peak, from which we determine the interval between two consecutive R peaks and ultimately determine heart rate. From the graph in Figure 6A, users can see the variability of heart rate in the entire range of data.

This is one special case (Figure 6B). This piece of data occurs due to the measurement process, the patient was moved out from Polygraph test chamber. Segment data will not be counted in the diagnosis of doctors. In fact, the electrical signals associated with brain and muscle signals electrical current along with the other data channel, the data segment will be automatically removed.

In order to accurately assess the relationship between breathing and ECG, after detecting breathing another greenhouse trial position, we take the middle position of the previous paragraph and stopped breathing after every 30 seconds to determine the total heart rate during that minute.

Therefore, the results obtained below, toward the overall assessment of the process of achieving the results of this study.



signal and ECG signal with warning function

From the chart in Figure 7, the user can easily determine the relationship between changes in heart rate with time apnea. On the form, the user will easily notice increased heart rate at 262 minutes, minute apnea condition occurs in 13 seconds. Since heart rate graph , users also easy to see, heart rate changes constantly and dramatically across from 259 minutes to 267 minutes .

Figure 8 and Figire 9 show some accesibilities for user when using this program, the user will know the number of central apnea events occur in each hour. Aims to users review results amenities as well as archived data back to

serve future research, our software will extract and record data file format * .xls



Figure 8: Structure in detail of *.xls result file



Figure 9: Notificate the quantity and duration of apnea events

4. CONCLUSION

Based on the results of the study were previously deployed on building software analyzes the state of sleep [21], [22]; in this study, we focused on the analysis of the microwave, the problem abnormalities present cardiovascular relationship between and respiratory system during sleep. This is the additional content needed to complete a signal analysis program sign a complete majority. The software is built in module, so can be flexibly used and is compatible with different types of hardware as needed to establish a new system of analytic functions related to sleep disorders sleep.

The program has functions: identification full range central apnea - apnea central standard version aasm scoring rules of 2014. Mark fully about apnea and offer statistics on the index of apnea / reduction of breath - AHI.

Using wavelet analysis method ECG for good results. Determine full peak in the qrs complex with almost perfect precision for many patient data in multiple age, gender, health status.

During sleep, the body is put into sleep mode ie body to rest completely. when in sleep mode, the brain is restored, the cells in the body is repaired, the body produces important hormones. thereby, we can see enough and deep sleep is very important for your body. As the graph of heart rate and respiration, we found that:

The phenomenon apnea occurs in both men and women, of all ages, the older more common. according to studies of aasm, for every 100 people between 30-50 years of age, having from 1 to 3 people with apnea condition. besides, those who are obese or snore during sleep apnea common condition better. Apnea is represented by 1 contiguous series apnea, every apnea from a minimum of 10 seconds during normal beating. after each apnea, the patient suddenly strong breathed out. If apnea occurs too many times in one medium binhh prolonged sleep 8 hours will reduce oxygen levels in the blood.

Patients experiencing apnea condition: in one night, often have trouble sleeping, so often awakened after each apnea. and abnormal heart thumping with reduced oxygen levels in the blood light up patients feel headache lasts for many years , patients with a high risk for complications of chronic respiratory failure and cardiovascular disorders such as hypertension , heart attacks, arrhythmia...

Determine microscopic structure of sleep follow standards of the AASM scoring rules 2014 edition central apnea segments. The program implementation creating .exe file program can be used on other machines, without the need to support programs MATLAB this is a further improvement that our team has carried out for this valuable software more practical value for users as well as other study subjects.

Create file notice results .xls file format for storing patient information and patient data of patients. User-friendly interface, easy to perform the operation to interact with the user interface needs to provide more information (see in the appendix). Develop program analysis and microscopic structure of sleep using matlab software (write algorithms and use some toolbox). analysis of channel disorders abnormal respiration and SpO2. Analysis of channel disorders abnormal ECG. Statistics and evaluate the pathology of respiratory and ecg channels.

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Hoàn thiện triển khai chương trình phân tích tín hiệu đa ký giấc ngủ

- Lê Quốc Khải
- Nguyễn Thị Minh Hương
- Nguyễn Vũ Quang Hiển
- Phạm Lê Trung Hiếu
- Huỳnh Quang Linh

Khoa Khoa học Ứng dụng, Trường Đại học Bách khoa, ĐHQG-HCM

TÓM TẮT:

Giấc ngủ và những bệnh lý liên quan đến giấc ngủ ngày nay đã trở thành mối quan tâm hàng đầu của cả công đồng: một rối loạn liên quan đến giấc ngủ khi xảy ra sẽ ảnh hưởng lên hầu hết các chức năng khác của cơ thể. Mục tiêu của đề tài là xây dựng hoàn thiên một chương trình phân tích tín hiệu đa ký giấc ngủ theo tiêu chuẩn AASM xuất bản năm 2014, mang đến phương pháp đánh giá toàn diện về những dấu hiệu bất thường hoặc bệnh lý của đối tượng khảo sát. Bằng cách sử dụng kết hợp nhiều thuật toán với cơ chế tự học, chương trình có thể linh hoạt cập nhật ngưỡng và các đặc trưng tín hiệu riêng cho từng đối tượng khảo sát khác nhau, làm giảm

sai số tối đa trong kết quả phân tích. Chương trình được xây dựng có tính linh hoạt cao, không cần cài đặt các phần mềm chuyên dụng, giao diện thân thiện với người sử dụng. Kết quả phân tích mang độ tin cậy cao, đã được đánh giá độc lập từ các bác sĩ chuyên khoa sử dung, mức độ tượng đồng bình đạt trên 83% cho các dữ liệu đã xử lý. Ưu điểm lớn của chương trình là khả năng đồng bộ dữ liệu và kết quả phân tích để có thể theo dõi trên nhiều thiết bị ngoại vi; có thể dễ dàng phân tích riêng rẽ theo từng khối chức năng để kết hợp với các thiết bị khác thành một hệ thống chấn đoán độc lập và liên tục.

Từ khóa: phân tích, tự học, đa ký giấc ngủ, AASM

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