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Sleep stage classification based on noise-reduced fractal property of heart rate variability

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Abstract

The aim of this study is to examine distinctive features related to sleep stages (wake, light sleep, deep sleep) from heart rate variability (HRV) and evaluate their usefulness in classifying sleep stages. To this end, we looked into DFA alpha1 sequence (DFAseq) in which DFA (Detrended fluctuation analysis) alpha1 values are calculated for every R points of HRV signal over time. This DFAseq can be interpreted as a variation of the fractal property of HRV over time. To investigate the DFAseq data, we reduced noise component from them using the empirical mode decomposition (EMD) method. For experiments, we used the CAP-sleep database from PhysioNet and evaluated the relevance between the noise-reduced DFA alpha1 sequence (NR-DFAseq) and the sleep stage sequence. Our results on 13 subjects showed that the correlation coefficient between sleep stage sequence and NR-DFAseq are 0.65 on the average, while the correlation coefficient without noise reduction is 0.42. For sleep stage classification, we constructed a prediction model that distinguish wake stage from the other sleep stages based on NR-DFAseq, and obtained 77% of sensitivity and 73% of specificity from the model. In addition, we constructed a model that distinguishes deep sleep from light sleep, and obtained 72% of the classification accuracy from the model. Interestingly, our prediction results only with NR-DFAseq are better than some recent study that employed multiple features extracted from heart beat signals. Therefore, it might be worthwhile to see that the noised-reduced fractal property of HRV could be highly correlated with the sleep stage.

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Keywords: Sleep stage; HRV; DFA alpha1; Fractal property; Noise reduction; EMD

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1. Introduction

As one of the important factors that greatly affect our physical activity, the quality of sleep also has a strong correlation with memory ability and learning ability [1]. Moreover, from a long-term perspective, the quality and quantity of sleep are related to disease development and immune function [2, 3]. Thus, it is essential to examine the quality of sleep for human health monitoring. PSG (Polysomnography) is a commonly used conventional method for sleep study based on variety of bio-signals related to sleep stages, such as ECG (electrocardiogram), EEG (electroencephalography), EMG (electromyography), and EOG (electro-oculography). Based on these signals, a sleep specialist judges whether the subject is in wake stage, light sleep stage, or deep sleep stage during a certain time period. However, it is not only time consuming and laborious task, but also requires big cost to run PSG method involving several equipment. Therefore, there is a need for a method that can automatically estimate the sleep stages in a more convenient way.

Among several vital signals, heart beat signals are relatively easy to detect in real life, and so various studies [4-10] have been conducted to use them for estimating the sleep stages. In most of such studies, the sleep related features (such as DFA alpha 1 [11]) were extracted based on the heart beat signal over a certain period of time, which were used later to estimate the sleep stage of the corresponding time period. That is, they divided the whole recording time into multiple time intervals and then used the signal data in each time interval for sleep stage estimation, without looking into whole time data.

In this study, for sleep stage classification, we extracted the DFA alpha1 value in each time interval from the heart beat signal and chained the values in chronological order to construct DFAseq for whole recording time. Then we developed a classification model for determining the sleep stage based on the NR-DFAseq, and evaluated the performance of the model.

Nomenclature

DFAseq	DFA alpha 1 sequence
NR-DFAseq	Noise-reduced DFA alpha1 sequence
RRI	RR-interval
HRV	Heart rate variability

2. Method

2.1. Data description and preprocessing

For experiments, we used the CAP-sleep database [12] from PhysioNet [13]. This database contains various bio-signals of 16 subjects without sleep related diseases, including ECG, EEG, and EMG. Among them, we only used the ECG data of 13 subjects because the rest are either irregular format data or too noisy. This database was originally recorded from a few minutes before the start of sleep to a few minutes after awake. Sleep experts assigned sleep stages to every 30 seconds of recording time according to the R & K rules [14]. This 30 second unit of data is called an epoch. That is, sleep experts manually labeled a sleep stage (wake, REM, S1, S2, S3, or S4) for each epoch. In this study, we considered S1 and S2 as *light sleep* stage, while S3 and S4 as *deep sleep* stage. The length of each recording data was 8.2 hours on the average. Table 1 shows the number of epochs included in each recording data for each sleep stage.

Table 1.The numbers of epoch used for our experiments.

Sleep stage	Wake	S1	S2	S3	S4	REM
epochs	1236	411	5136	1203	1996	2855

From each recording of ECG, we detected R-points and obtained RR intervals (RRIs). Among these RRIs, we excluded RRIs of less than 0.3 seconds or more than 3 seconds. Also, such RRIs were excluded that have less than