

A SLEEP APNEA DETECTION APPROACH BASED ON RECURRENCE PLOTS AND CONVOLUTIONAL NEURAL NETWORKS

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Abstract— This paper presents a new sleep apnea detection method based on the combination of recurrence plots (RPs) constructed from heart rate variability (HRV) data and convolutional neural networks (CNNs). RPs are built to present nonlinear dynamics of a complex cardio-respiratory system during sleep apnea reflected by HRV data, which is extracted from the electrocardiogram signals. The information contained in RPs are further extracted by CNNs to classify each RP as normal or apnea. This approach is shown to be good for sleep apnea detection since it can exploit dynamic characteristics of the cardiovascular system of human body during sleep and convert them into feasible features for classification processes. The use of CNNs are meaningful when it requires less domain knowledge for feature extraction and selection. Experimental results show that this newly proposed sleep apnea detection method is better than some other approaches based on RPs and HRV data in terms of the classification performance and due to the less complexity of the detection system. This also illustrates the capabilities of this study in real world applications since it is less dependent on domain knowledge, simple, low cost, and easy to implement.

Keywords— sleep apnea detection, recurrence plots, heart rate variability data, convolutional neural networks.

I. INTRODUCTION

Obstructive sleep apnea (OSA) is a periodic breathing disorder during sleep [1]. An obstructive sleep apneic event happens when there is a complete or partial absence of airflow for a short period of time, and may repeat multiple times during a night sleeping. It is reported that 10% of middle-aged people have sleep apnea, and most of them are unaware of its present [1]. Sleep apnea is the main cause of cyclic brain arousal, disruption of various stages of sleep, and sleep fragmentation, which leads to some health implications such as excessive daytime drowsiness, nonrestorative sleep, decreased memory, depression, and

even serious cardiac arrhythmias [2]. Sleep apnea is a treatable condition, and there needs to be a cheap and convenient way to monitor the presence of such problem.

Polysomnography (PSG), which is implemented in a sleep laboratory, is considered a standard approach to recognize sleep apnea. PSG is normally uncomfortable method since it requires a large number of wires and sensors connected to the subject's body, and an overnight stay in a lab for sufficient collection of signals related to OSA [3].

Various methods have been developed in the literature to solve for issues regarding the use of PSG for detecting sleep apnea. Among commonly used approaches are ones based on electrocardiography (ECG) data. ECG data requires a much less complicated and more convenient data collection procedure [4]. Almost all sleep apnea detection methods based on ECG data include two main stages: to extract useful features from ECG signals or its subsequence HRV data, and to apply a proper classification model to provide automatic apnea detection results.

A proper feature extraction and selection process usually plays an important role in the performance of current sleep apnea approaches based on ECG signals since it provides sufficient input information for further analysis steps or prediction models. Multiple feature extraction algorithms for sleep apnea detection have been presented in the literature such as statistical estimation [5], minimum redundancy maximum relevance (mRMR) [6], sequential forward selection [7], principal component analysis [8], and the genetic algorithm (GA) [9]. These features extracted from ECG signals are then usually fed to classification models for sleep apnea detection decision. Those classifiers include k-nearest neighbor [7], support vector machine [6, 10, 11], fuzzy logic [12, 13], neural network [6, 9, 14], and linear discriminant analysis [6, 15]. There are two main issues regarding this approach. The first problem is there are infinitely many ways to combine the available features for the input of detection models, and it is difficult to prove that any of those feature subsets is the best one for sleep apnea detection [16]. The next issue is how to apply background knowledge on sleep apnea and its effects on the cardiorespiratory system in human body into creating relevant features for sleep apnea detection.

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Recently, these two issues are tackled by using deep neural networks, which can automatically extract features by finding patterns in the input signals from the sensors. Basically, deep learning algorithms are initiated from image processing problems. Their different variants can further be applied to many other fields of study, resulting in different types of deep learning models [21].

In this study, a new approach to detect obstructive sleep apnea is presented. The new method is based on the combination of a convolutional neural network (CNN) [18] and recurrence plots (RPs) [17]. RPs are an efficient tool to visualize the relationship between different states in side one dynamic process. They are built based on the construction of phase states from time series of the process [19]. The input of this sleep apnea detection system is ECG signals. ECG signals are first preprocessed to extract heart rate variability (HRV) data, which includes a sequence of time intervals between consecutive R peaks of the ECG signal, so called RR interval data. HRV data reflects the heart's ability to identify, quickly respond, and adapt to changing intrinsic and extrinsic stimuli during sleep. Since apneic episodes cause changes to heart regulation during sleep, HRV data can be considered as a promising information source for sleep apnea detection [34]. RPs are constructed from HRV data to present the relationship between different phase states of HRV data, from which the dynamic characteristics of HRV data can be presented. CNN is adopted to automatically extract useful features from RPs, and then to classify each RP into either apnea or normal. This new sleep apnea detection approach has two main advantages. First, it exploits the use of HRV data, which is immune to the effects of the nonstationarity in nonlinear time series, by applying RP construction. Recurrence plots are useful for characterizing complex heart rate regulations. Second, CNN is a powerful tool to automatically extract distinctive features from RPs to detect the presence of apneic events from normal HRV data. The use of CNNs for feature extraction is meaningful since it does not depend much on background knowledge to select any particular feature of recurrence plots for the apnea analysis process like many current approaches on this problem. Experimental results show that this newly proposed sleep apnea detection method is effective in providing a good classification performance, and is promising for real-time sleep apnea detection implementation.

The structure of this paper is organized as follows. Section II provides all initial materials used in the research, including the description of the data as well as the background information of CRPs and CNNs. The detailed method for sleep apnea detection based on CNNs and CRPs is presented in Section III. Section IV includes all experimental results and discussion of the proposed approach. Section V concludes what have been accomplished in the study.

II. MATERIALS

Dataset

In this research, the Physionet Apnea-ECG Database [22] is used. There are 70 sleeping ECG records available

in the dataset, each of which is associated with one subject. The dataset includes a set of reference annotations that indicate the presence or absence of apnea during each minute of the sleep data. Here, 35 records are used for training and the remaining 35 are used for testing. Table I lists the basic properties of the subjects in both training and testing datasets. More details of the data can be found at [22].

Table I: Properties of all subjects in Physionet Apnea Database

	Training data		Testing data	
	mean	SD	mean	SD
Age (years)	46.6	10.07	43.83	11.55
Record length (min)	489.29	31.97	494.37	31.44

The ECG signal in each record is sampled at 100Hz. The HRV data, which contains RR interval series, is extracted from the ECG signals based on the thresholding method for QRS complex detection. The resulting RR intervals for each record are the input data for this study. The data is labeled as normal or apnea on 1-minute basis based on the occurrence of any apneic event in an 1-minute period of the ECG signal.

Recurrence Plots

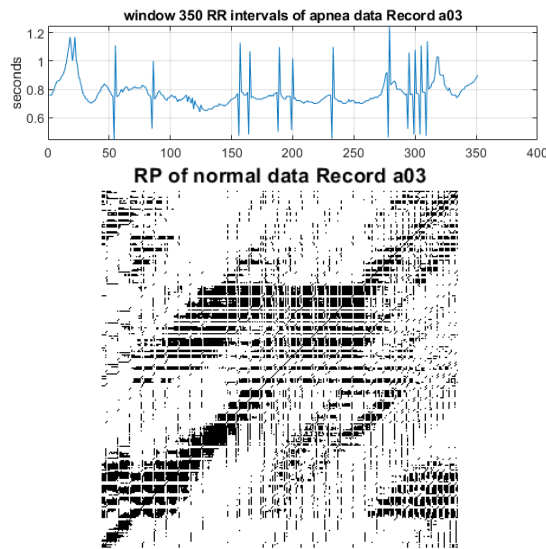
Recurrence [23] is an important property of a dynamic system. It can be visualized by recurrence plots [24]. By using RPs, the trends of complex dynamic systems containing in HRV data can be presented. Here, it is assumed that the complex cardiovascular system of a human body can be collected using HRV data as a time series $x(t)$, its working condition at the time t_i can be presented by a phase state defined as follows [25].

$$\vec{u}_i = [x(t_i), x(t_i + \tau), \dots, x(t_i + (m-1)\tau)] \quad (1)$$

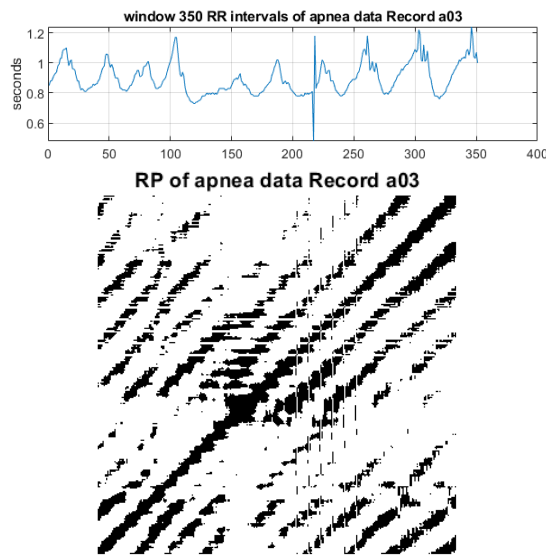
where τ is the delay and m is the number of dimensions of the embedding phase space. τ is chosen large enough to avoid the correlation between consecutive elements in one phase state, while m value is selected corresponding to the number of factors that directly influence the system states. A recurrence plot of $x(t)$ is an $N \times N$ binary matrix, whose each element is defined as:

$$R_{i,j} = \Theta(\varepsilon_i - \|\vec{u}_i - \vec{u}_j\|), \quad i, j = 1, 2, \dots, N \quad (2)$$

Where $\Theta(\cdot)$ is the unit step function, ε_i is the cut-off distance, and $\|\cdot\|$ is the distance between two phase states \vec{u}_i and \vec{u}_j . In this study, Euclidean distance is used. Formula (2) means that if the state vector \vec{u}_i is within the range of ε_i from vector \vec{u}_j , then $R_{i,j} = 1$, otherwise, $R_{i,j} = 0$. In the binary image presenting a Recurrence plot, each component value of one or zero in the matrix can be represented by a dot of black or white, respectively. The distance threshold ε_i can be either a predefined certain value or adaptively chosen such that there is a fixed number of neighbors (FAN) at every state \vec{u}_i . The value of ε_i is greatly based on the characteristics of the time series $x(t)$ as well as the applications of its recurrence plots. Recurrence plots are a powerful tool to visualize the recurrence behavior of nonlinear and dynamic systems and the arrangement of all recurrence points can be used to reconstruct the properties of the data [20]. Figure 1 illustrates two different sequences of HRV data and their corresponding recurrence plots for both normal sleep data and apneic sleep data.



(a) normal data



(b) apnea data

Figure 1: A visualization of RR intervals and corresponding recurrence plot of normal data (a) and apnea data (b).

Parameters for RPs: $m = 6$, $\tau = 10$, FAN 20%

Convolutional Neural Network

Convolutional neural network (CNN) [18] is a deep learning architecture and is commonly used for image processing. A CNN usually consists of multiple hidden layers for automatic feature extraction process. These hidden layers are mainly either convolutional layers or pooling layers. Figure 2 presents an example of a convolutional neural network with one convolution layer for feature extraction and one max pooling layer for feature reduction. A fully connected layer is adopted as the output layer to classify input image as apnea or normal.

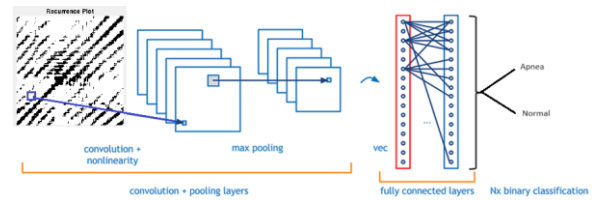


Figure 2: Illustration of a CNN with 1 convolution layer and 1 Max pooling layer combined with a fully-connected layer for Normal/Apnea classification.

Convolution layer is mainly used for feature extraction process. Here, a sliding kernel matrix is used to convolute with the input image to create a new matrix containing the convolution results from the input image and the kernel matrix. This process can be repeated multiple times using multiple convolution layers to generate more complex features of the input image. The outputs of each convolution layer is generally put into an activation function, which is commonly a Retified linear unit (ReLU) function. The activation function helps the neural network learn non-linear patterns and relationships in the data.

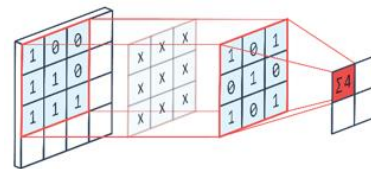


Figure 3: example of a convolution layer

Pooling layer is used to reduce the spacial size of the convolved results of the convolution layer. This is simply the down-sampling process of the convolved features, and helps reduce the computation requirements of the whole system while increasing the abstraction level of features. Two commonly used pooling methods in CNNs are Max pooling and Average pooling. Max pooling is generally preferable thanks to its ability to suppress noises during dimension reduction process.

The final layer of the network is the classification layer, which takes the resulting features of the previous convolution and pooling layers as its inputs and produces the classification decision on the data. Two main types of classification layers are fully-connected layers and global average pooling layers. Fully connected layers are more widely used for CNNs. This is a standard neural network that connects all the neurons in the input layer to all neurons in the output layer. There can be an option to add some more hidden neuron layers to increase the complexity of the fully connected layers.

There have been some well-known CNNs in the literature for image processing such as LeNet [26], AlexNet [27], VGGNet [28], ResNet [29], MobileNet [30]. In this study, in order to deal with a simple binary image classification problem, a traditional CNN that consists of some number of convolution layers and Max pooling layers. Based on the available training and testing datasets, the number of convolution layers are adjusted to explore the best figuration of the CNNs when dealing with this problem.

The following session presents the detailed apnea detection system based on RPs and CNN.

III. METHOD

Figure 4 depicts the workflow of the proposed approach for sleep apnea detection. There are two main phases of the method, which are training and testing phases, based on separated training and testing data subsets, respectively. In training process, the training data is divided into two different parts with two corresponding labels, i.e. Normal and Apnea, as provided in the database. The provided ECG data is labeled by experts as Normal or Apnea on a one-minute basis. In other words, each record contains a set of reference annotations, one for each minute of the recording that indicates the presence or absence of apnea during that minute. The apneic events usually occur continuously in clusters with periods of from 3 to 30 minutes. The HRV data is labeled accordingly with the original ECG signals. In training dataset, the recurrent plots are formulated based on HRV data separately for Normal and Apnea parts of the training data. Figure 5(a) illustrates the formulation of normal and apnea RPs. These RPs are labeled and provided to the CNN to train for a Normal/Apnea classifier.

In order to demonstrate a real-time sleep apnea detection scenario, in testing process, the HRV data is provided as sequences of original signal, and a sliding window of the same size as that for RP generation in training process is applied to create recurrence plots corresponding to the portion of the data being investigated. The RPs of the testing data are then input to the CNN classifier to produce the labels of the input data as normal/apnea detection results. The moving stepsize of the sliding window is set as 1 minute, which correspondingly matches with the annotations provided in the datasets for verification. The label (normal or apnea) for each data window of testing process is defined for the label of the last minute data. Specifically, if the RP of a data window is decided as Apnea, data of the final minute in that data window is labeled as Apnea, otherwise, it is labeled as Apnea. The testing process is illustrated in Figure 5(b).

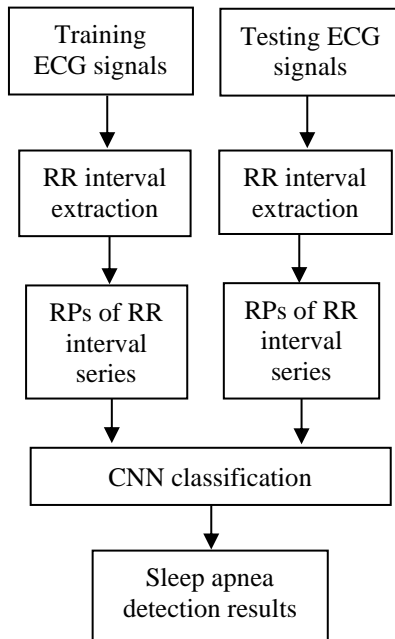


Figure 4: Flow chart of sleep apnea detection approach based on RPs and CNN.

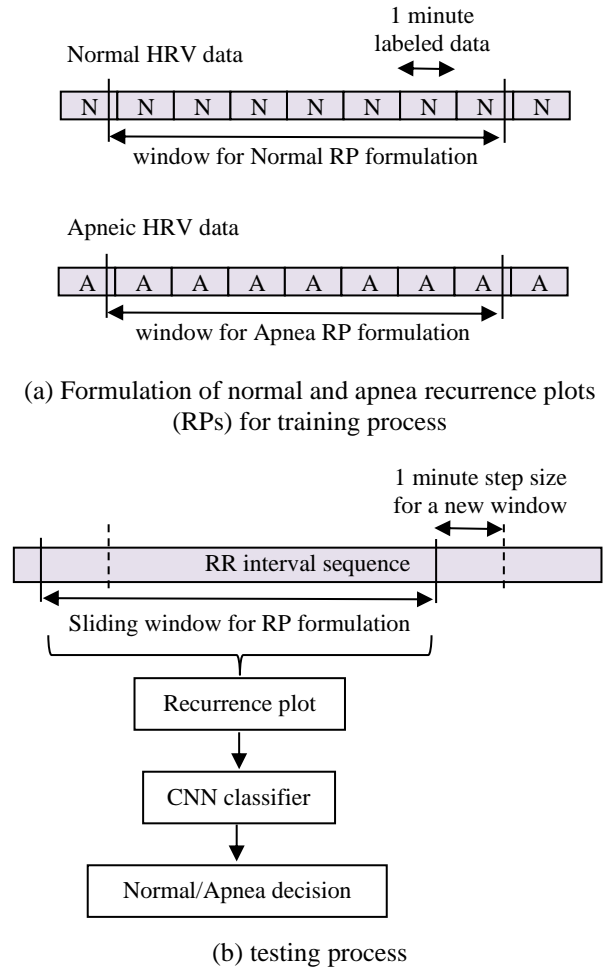


Figure 5: Formulation RPs of Training (a) and Testing (b) processes and the framework to detect sleep apnea.

In this study, the main use of recurrence plots is to present the dynamic properties of the HRV data, which also reflect the distinguishable characteristics of apneic data out from normal data. Convolutional neural networks helps automatically extract useful information from the recurrence plots based on multiple convolution and pooling layers. These features are then input to the classification layer to detect the present of apneic events. Here, any classifier can be adopted after the convolution and pooling layers. In order to simplify the system, a traditional fully connected classifier is used as the final layer of the CNN.

This proposed method requires that training data for apnea or normal events must contain sequences of data with the length of greater or equal to the data length of a RP formulation window. In other words, the choice for the data length to construct RPs must be small enough to match with the minimum duration of the apneic event clusters, while it must be long enough to capture the dynamic properties of the data. This is to ensure there are enough phase states in the window. In training process, the data is carefully separated into normal and apnea portions, then the RPs are well labeled as either Normal or Apnea. However, during testing process, the data in each window is no longer pure Normal or Apnea since the original sequence of ECG signals will be processed as a real time detection scenario, and some mixtures of normal and apneic data can be present in one processing window. As a

results, miss detection or false alarms are expected to happen more frequently in testing process than that of training process.

IV. RESULTS AND DISCUSSIONS

In this research, the window width to formulate RPs is set as 350 RR intervals, which corresponds to roughly 6 minutes. This data length is reasonable for presenting the dynamic properties of the cardiovascular system presented in HRV data while it is not too long to capture the short durations of sleep apnea events. There are more than 60 000 RPs of normal sleep data and more than 50 000 RPs of sleep apnea data created for training process. These RPs of both Normal and Apnea labels are used to train CNN classifiers. The binary classifier is trained using one third of the data (training set), and validated using the remaining two thirds of it (validating set). The structure of CNN is adjusted by changing the number of both convolution and pooling layers, as well as changing the size of the kernel matrices for convolutional layers. The resulting classifiers are then applied on testing data to verify their sleep apnea detection performances. The CNN structure with the best classification performance for testing data is selected as the final classifier. Table II summarizes some selected CNN classifier structures for sleep apnea detection based on RPs. Table III presents the testing performance of the selected CNN structures.

Table II: Some selected CNN classifier structures

Structure	Convolution layers	Pooling	Kernel size	Fully connected size
1	1	Average	3x3	30
2	1	Average	5x5	50
3	2	Max	3x3	30
4	2	Average	3x3	50
5	2	Max	3x3	50
6	2	Max	5x5	50

Table III: Classification performance of some selected CNN structures

Structure	Precision	Recall	Accuracy
1	76.33	93.47	82.97
2	75.16	96.33	83.17
3	83.58	92.18	87.9
4	77.36	90.14	82.88
5	72.9	92.51	81.74
6	78.06	92.96	86.67

Since the recurrence plots are binary images where the dynamic characteristics are mainly presented by diagonal, vertical and horizontal structures, which are unlike many other real-life images, the structure of the CNN for feature selection does not need to be too complicated. This claim is supported by the results in Table III, where the CNN with a simple structure (structure number 3) can provide a really good precision outcomes together with a high accuracy. In addition, the input binary image size of RPs can be flexibly selected by changing the data length in each window as well as the parameters to formulate phase states of the system. A less complex structured CNN can be applied accordingly to facilitate the computational performance of

the whole system while a good detection performance can be maintained. Here, with the select window size of 350 RR intervals, the RPs has a size of 300x300 binary pixels. As a result, there is no need to apply a too complexity CNN for sleep apnea detection. Experimental results also show that the classification performance is not significantly improved if the structures of the CNN is adjusted to be more complicated, while the computational cost for the increase of the CNN complexity is significantly growing. Tables II and III illustrates the possibility of using small sized CNN for feature extraction and binary classification for sleep apnea detection. If the complexity of the network is increased, the detection performance is not significantly improved.

In this research, based on the classification performances of different CNN structures, a good and low complexity CNN classifier for sleep apnea based on RPs of HRV data is identified as the one with two convolution layers, two max pooling layers, and a fully connected layer with 30 neurons. This sleep apnea classifier structure is further compared to some selected sleep apnea systems in the literature. The comparison results are presented in Table IV.

Table IV: Comparison between different sleep apnea detection systems

Systems	Precision (%)	Recall (%)	Accuracy (%)
Sleep apnea detection based on RQA statistics of HRV [31]	86.37	83.47	85.26
Bagging.REPTree using ECG data [32]	69.82	80.29	77.74
KNN applied on temporal and spectral features of HRV [33]	85	90	88
1-D CNN on ECG data [35]	81.1	92.0	87.9
LeNet-5 CNN [36]	83.1	90.3	87.6
CNN classifier based on RPs of HRV data	83.58	92.18	87.9

The results in Table IV show that the proposed method that applies CNN for feature extraction and binary classification based on recurrence plots constructed from HRV data is promising and effective. In this study, the properties of dynamic systems contained in the recurrence plots are automatically extracted by CNN, which are then fed to the classifier for the final decision on the presence of apneic events. These results also illustrate that a less complex CNN can effectively successfully extract useful features from RPs, then a simple classifier at the final stage is enough to provide the final sleep apnea detection decision. This is meaningful in real scenarios where less computational complexity is an important factor in selecting an applicable solution.

It is also presented in Table IV that the performance scores of the proposed method are generally good, but not yet perfect for sleep apnea detection in a real-world scenario where there are many unfamiliar cases during the testing process in which the normal and apneic data are mixed in one data window. Specifically, testing procedures in this study are made illustrating real sleep apnea detection scenarios where input data is provided as realtime sequences of HRV data and the sliding windows for RPs

construction and subsequent sleep apnea detection based on RPs processes are formed naturally. This results in a wider range of feature values for RPs, which is slightly different from training data, where normal and apneic events are separated. The data segments in the overlap regions of normal and apneic events are the main reasons for that low accuracy score of the proposed method.

Accuracy score of the proposed method is higher than previous studies based on recurrence plots. However, it is still out-performed by another approach where a careful feature selection and extraction method is used. If the feature extraction process is fine-tuned based on domain knowledge to perfectly match with both training and testing datasets, the classification performance of one detection method can be very high, but its generalization capability is limited, which is not the case in this study. The main advantage of the proposed method over other approaches is the simplification of feature extraction and classification processes. In other words, there are not many fine tuning steps in this algorithm compared to some other approaches in the literature. As a result, the proposed algorithm is believed to be easily generalized in real-life applications.

As discussed above, the proposed approach is expected to work well with the data containing purely normal or apneic data, and it is more favourable to other methods thanks to its simplicity and efficiency to maintain good sleep apnea detection performance. The performance of the proposed system can be further improved if the training data can be carefully generated with more data windows having different mixtures of normal and apneic data. This issue can be solved if a more proper approach to label the data as apnea or normal for those mixed windows is developed. This will be the future work of this study and the solution for it will be soon presented.

V. CONCLUSIONS

In this research, a new sleep apnea detection approach is introduced based on recurrence plots constructed from HRV data and convolutional neural networks. The cardiovascular characteristics of the human body during sleep apnea events reflected by the heart rate variability data can be successfully presented by recurrence plots. CNNs are then used to automatically extract useful information from RPs for classification process. This method is shown to be efficient for sleep apnea detection and is a cheap approach since it does not require much domain knowledge for feature extraction and analysis as many other methods in the literature. This study can be further improved if a better procedure to build training data that contains a wider range of normal and apnea combinations with proper data labels is developed. This will be a topic for the future work of this research.

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MỘT PHƯƠNG PHÁP NHẬN DIỆN CHỨNG NGỪNG THỞ KHI NGỦ DỰA TRÊN ẢNH HỒI QUY VÀ MẠNG NƠ RON TÍCH CHẬP

Tóm tắt: Bài báo này trình bày một phương pháp mới trong phát hiện chứng ngưng thở khi ngủ dựa trên sự kết hợp của ảnh hồi quy (RP) được xây dựng từ dữ liệu biến

đổi nhịp tim (HRV) và mạng nơ ron tích chập (CNN). RP được xây dựng nhằm diễn tả các đặc tính động và phi tuyến của hệ thống tim - hô hấp của cơ thể người trong giấc ngủ có sự xuất hiện của chứng ngưng thở khi ngủ, được phản ánh qua dữ liệu HRV. HRV được trích xuất từ tín hiệu điện tâm đồ. Các đặc tính này sau khi được diễn đạt bởi RP được CNN tiếp tục trích xuất và biến đổi nhằm gán nhãn cho từng RP là bình thường hoặc ngưng thở. Cách tiếp cận này được chứng minh là tốt cho việc phát hiện chứng ngưng thở khi ngủ vì nó có thể khai thác các đặc tính động của hệ thống tim mạch của cơ thể con người trong khi ngủ và chuyển chúng thành các thuộc tính hữu ích cho quá trình phân loại. Việc sử dụng CNN có nhiều ý nghĩa khi nó đòi hỏi ít kiến thức chuyên môn trong việc trích xuất và lựa chọn các đặc tính hữu ích. Kết quả thực nghiệm cho thấy phương pháp phát hiện ngưng thở khi ngủ mới được đề xuất trong nghiên cứu này tốt hơn các phương pháp khác cũng dựa trên dữ liệu RP và HRV dựa trên hai khía cạnh là hiệu suất phân loại tốt hơn và độ ít phức tạp hơn của hệ thống. Điều này cũng minh họa cho khả năng của phương pháp này trong các ứng dụng thực tế vì nó đơn giản, chi phí thấp và dễ thực hiện

Từ khóa: chứng ngưng thở khi ngủ, ảnh hồi quy, dữ liệu biến đổi nhịp tim, mạng nơ ron tích chập.



systems, data mining, and machine learning.

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