A New Algorithm for the Detection of Sleep Apnea Events in Respiration Signals

Jungyoon Kim, Hisham ElMoaqet, Dawn M. Tilbury, and Satya-Krishna Ramachandran

Abstract— **Sleep apneas are the most common type of sleep-related breathing disorders which cause a patient to move from a good sleep into an inefficient sleep. In addition, sleep apnea widely impacts the American population and is a large cost for healthcare. Traditional detection methods of sleep apneas are complex, expensive, and invasive to most patients. Among the various physiological signals, respiration signals are relatively easy to be monitored. However, not many studies are conducted using respiration signal only, and most of the previous algorithms are insufficient to detect apnea events. In this paper, we propose a new algorithm based on only the respiration signal to detect the apnea events during sleep and conduct experiments comparing the performance of our algorithm against two apnea detection algorithms. We use 20 patients' data, all of whom have severe Apnea Hypopnea Index (AHI≥30: over 30 events per hour). Our study shows that our algorithm outperforms the other two algorithms.**

I. Introduction

The appropriate breathing process is an important activity for human health, and abnormal breathing process may develop central nervous or physical disorders. When people are awake, breathing related disorders are easily recognized so that it can be cured. However, when people are going to sleep, most of the time the breathing disorders are hard to recognize. Thus, automatic respiration monitoring is a good solution for detecting breathing disorders during sleep. In addition, sleep disorders are popular and significant diseases that affect many people. The sleep disorders, which are medical disorders of the sleep patterns, affect on aspects, such as impacting suffers physically, psychologically and financially [1].

Among the different types of sleep disorders, sleep-related breathing disorder is the common disease that people have while sleeping. The sleep-related breathing disorder is defined as abnormal respiratory pattern or reduction in gas exchange during sleep [2]. Sleep apnea is the most common among the sleep-related breathing disorders. Sleep apnea is "*a sleep disorder characterized by pauses in breathing or instances of shallow breathing during sleep*" [3]. There are three types of sleep apnea, such as obstructive sleep apnea (OSA), central sleep apnea (CSA), and mixed sleep apnea (MSA). Among them, the most common disorder is OSA. In OSA, the airway repeatedly is blocked, reducing the amount of air impacts on patients' lung activity. When OSA happens, patients may snore loudly or make choking noises since the patients keep trying to breathe to increase the amount of air. The patient's brain and body are not getting enough oxygen and it may wake the patient up. This will interrupt the good sleep for recovering body fatigue so that daytime activities also get worse. [1]

OSA is a common sleep disorder found in 24% of adult men and 9% of adult women [4]. About 15 million adult Americans are affected and a large proportion of the patients have an experience of hypertension and other cardiovascular disorders, such as coronary artery disease, stroke, and atrial fibrillation [5]. Each sleep apnea event is defined as a respiratory pause lasting at least 10s. If the upper-airway obstruction is only partial and flow is lower than 50% of normal, the resulting airflow limitation is called a hypopnea. A patient with severe sleep apnea can have up to 600 apnea events per night, with a typical duration of 40s each, and few, if any, sustained periods of normal breathing.

Sleep related disorder affects the human body in several aspects. Sleep related breathing disorder is able to affect the overall sleep quality so that excessive daytime sleepiness occurs. In addition, if patients are treated at an early stage of the disease, their nighttime and daytime blood pressure can be lowered, and the adverse health effects can be reduced [6]. Sleep-related breathing disorder appears to contribute as a risk factor for stroke through hemodynamic and hematologic changes [7]. Sleep apnea may lead to the development of cardiomyopathy and pulmonary hypertension. Early recognition and treatment of sleep-related breathing disorders may improve cardiovascular function [8].

Traditional detection methods of sleep related breathing disorders are complex and invasive to most patients. Esophageal pressure (Pes) measurement is the gold-standard technique for assessing respiratory effort and the identification of obstructive and central events [5, 9]. Diagnosing sleep apnea in the clinic requires the polysomnography (PSG), a test which is expensive, time-consuming, and a labor-intensive process [8]. There have been several studies using ECG signals to detect the sleep apnea [11-15]. However, ECG based detecting methods of sleep related breathing disorders still need to attach the electrodes to a patients' body. Researchers have been trying to develop methods for detecting apneas/hypopneas with less invasive tools based on the airflow signals, which is the measured values of the amount of air per sample that flows through the sensing device. Although the clinical adoption of these techniques has been

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JY Kim is with Mechanical Engineering Department, University of Michigan, Ann Arbor, MI 48109, USA (Corresponding author: phone: +1 7346605324; e-mail: bassjyki@umich.edu).

H. ElMoaqet is with the Mechanical Engineering Department, University of Michigan, Ann Arbor, MI 48109, USA, and also with the Mechatronics Engineering Department, German Jordanian University, Amman 11180, Jordan (e-mail: elmoaqet@umich.edu)

D. M. Tilbury is with Mechanical Engineering Department, University of Michigan, Ann Arbor, MI 48109, USA (e-mail: tilbury@umich.edu).

S. K. Ramachandran is with the Department of Anesthesiology, Medical School, University of Michigan, Ann Arbor, MI 48109, USA, (e-mail: rsatyak@med.umich.edu).

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limited because of the lack of validation in clinical aspect, it is a relatively convenient tool for initial screening of sleep related breathing disorders.

In this paper, we develop a new algorithm based on the respirational (air flow) sensor alone for detecting sleep apnea events including OSA, CSA, and MSA. This new approach uses the amplitude changes of peaks and compares the averaged values. For the performance comparison, we implement two previous algorithms based on (1) artificial neural network (ANN) with two features and (2) adaptive threshold for amplitude change. We select 20 patients who have a severe level of the apnea-hypopnea index (AHI) from the PSG dataset recorded at the University of Michigan Sleep Lab and compare the performance of three algorithms.

II. Data Sets and Annotation

This data set is composed of 20 patients. For these patients, we have full polysomnography (PSG) data that were recorded at the University of Michigan Sleep Lab. The PSG data for each patient consists of 21 signal channels, including electrocardiogram (ECG), Electromyogram (EMG), Nasal/Oral airflow, and others. The PSG monitors human body functions during sleeping period (usually at night). The breathing functions are monitored by Nasal/Oral airflow (NPRE and NO), typically measured using transducers fitted in or near the nostrils, are used to measure the rate of respiration and to identify interruptions in breathing.

The patients in this data set have annotations from clinicians for their apneas. They are diagnosed with obstructive sleep apnea, mixed apnea, central sleep apnea, or normal state. All three apneas are annotated as apneas, 'A' and normal states are annotated as normal, 'N'. We select 20 patients who have severe sleep apnea based on the apnea-hypopnea index (AHI). The AHI is an index used to represent the severity of sleep apnea. It is categorized as four states, such as normal ($AHI_{\leq 4}$), mild sleep apnea ($AHI_{\geq 5, \leq 14}$), moderate sleep apnea ($AHI_{\geq 15, \leq 29}$), and severe sleep apnea ($AHI_{\geq 30}$). Each state of AHI is determined by the number of apnea and hypopnea events per hour during sleep. The apnea, which temporally stops in breathing, should last for over 10 seconds. All 20 patients are categorized into $AHI_{\geq 30}$ (over 30 events per hour).

III. The Proposed Sleep Apnea Detection Algorithm

The proposed apnea detection algorithm is based on the respiration (Nasal/Oral airflow) signals including the evidence of apneas annotated by clinicians. Figure 1 shows how the amplitude changes of peaks (ACP) algorithm works. We use two windows W_p and W_m in Figure 1. At time t seconds, the range of the previous window (W_p) is from the lower bound ($t - \alpha$) to the higher bound ($t - \beta$). For the detection metric part, the range of the metric window (W_m) is from the lower bound of ($t - \beta$) to the higher bound of (t). Thus, the window size is α. We use 5s shifting time and the values of α and β are 130s and 10s respectively.

The algorithm finds all the peaks having widths of at least 30 samples (0.9375 seconds) in a window segment and peaks in W_p are sorted into descending order according to the size of amplitudes. Based on the cut-off filter value, F_l, the value of the selected top peaks, L_f, is calculated by the product of the cut-off filter value and the number of peaks in W_p as:

$$L_f = \lfloor F_l \cdot N_p \rfloor \quad (1)$$

where N_p is the number of peaks in the window (W_p). L_f is the number of the selected top peaks in descending order in the array of amplitudes, P_i.

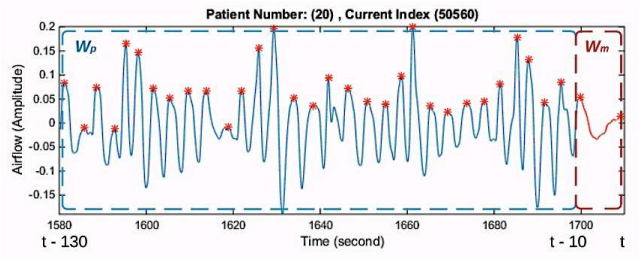

Figure 1. Airflow signal and sample windows (The unit of y-axis is Liters per second (L/s).)

The baseline values of the previous and posterior windows are calculated as follows:

$$B_{W_p} = \frac{1}{L_f}\sum_{i=1}^{L_f} P_i \quad (2)$$

$$B_{W_m} = \frac{1}{M_p}\sum_{j=1}^{M_p} P_j \quad (3)$$

where P_i is the amplitude of the i^{th} peak from the maximum to minimum peaks in descending order in W_p, P_j is the amplitude of the j^{th} peak in W_m, and M_p is the number of peaks in W_m. Specifically, the changed peak value for detecting apnea is calculated as:

$$P_c = \frac{B_{W_p} - B_{W_m}}{B_{W_p}} \quad (4)$$

If the value of P_c is bigger than the certain threshold, P_{th}, P_c is classified as apnea events. The values of F_l and P_{th} were empirically determined as 0.45 and 0.55, respectively.

IV. Algorithms for Apnea Detection

A. Várady et al (2002) [16]

Várady et al (2002) proposed an algorithm for detecting apnea and hypopnea events based on respiration signal. Initially, the original airflow signal, s, is resampled using adaptive baseline correction and normalization within the n^{th} window. Baseline correction, d_n, and scale factor, f_n, can be calculated by following equations:

$$d_n = d_{n-1} - \frac{1}{4}\left(d_{n-1} - \frac{\max(s)+\min(s)}{2}\right) \quad (5)$$

$$f_n = min\left\{f_{n-1} - \frac{1}{8}(f_{n-1} - \max(s) + \min(s)), k\right\} \quad (6)$$

where k = 100,…,500 is specific to the type of airflow sensor. The initial normalization of original signal with values based on the specific sensor is not clear and [16] didn't provide the exact type of sensors and how to select the value of k. The resampled airflow signal, r, is generated using equation (7).

$$r = \frac{s - d_n}{f_n} + \frac{1}{2} \quad (7)$$

where $f_0 = 2k$ and $d_0 = 2048$ and the values remaining outside the range [0, 1] are cut out. Our original airflow signal ranges between -4 to +4 so that if we truncate the original signal into 0 to 1, we lose major signal. Thus, we use a signal without the proposed normalization for r.

This algorithm basically uses two features, such as an instantaneous respiration amplitude (IRA) and instantaneous respiration interval (IRI). Using the local maximum (peak) and minimum (valley) values, differences of intervals and amplitudes between adjacent peaks and valleys. Figure 2 (a), (c) and (d) shows that respiration signals with the process of obtaining IRI and IRA values. After obtaining the IRI and IRA features, both features are resampled at 1.5625Hz based on the anti-aliasing filter in Figure 2 (e) and (f). Thus, a window segment of 16s includes 25 sample points of IRI and IRA, respectively. The total number of inputs in an input layer of the ANN is 50 values of IRAs (25) and IRIs (25).

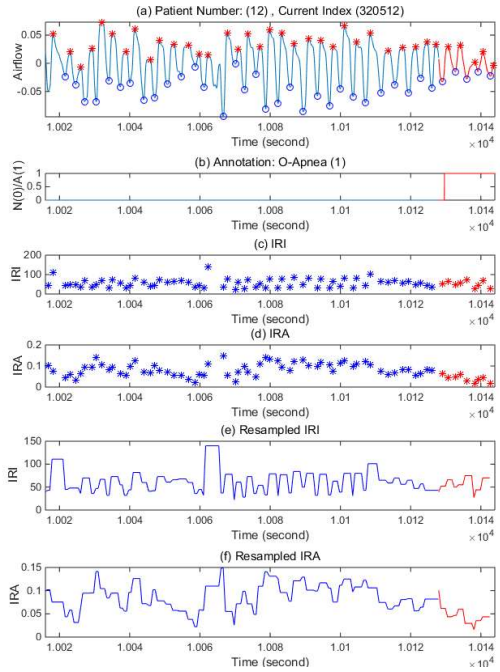

Figure 2. Respiration patterns detected by ANN with IRI and IRA containing (a) airflow signals with peaks (marked as '*') and valleys (marked as 'O'), (b) annotations (normal as 'N' and apnea as 'A') by clinicians, (c) IRI and (d) IRA values at each point of peaks and valleys, and (e) resampled IRI and (f) IRA at 1.5625Hz.

In order to classify the apnea events, a feed-forward artificial neural network (ANN) was designed and implemented. The network structure consists of 50 inputs (25 IRIs and 25 IRAs), 10 hidden nodes in the 1st hidden layer, 4 hidden nodes in the 2nd hidden layer, and 2 output units (N and A). The sigmoid-type activation functions are used for the hidden and the output nodes, and the back-propagation algorithm with gradient descent and momentum was used for training the ANN with 20 pieces of normal and apnea fragments [16]. However, [16] didn't provide the detail information of the selected fragments. Thus, we apply 10% of all data for training ANN. The epoch value to train the ANN sets as 1000.

B. *Fontenla-Romero et al (2005) [17]*

Although this algorithm is designed to classify the types of apneas, it also includes a detection module to find sleep apnea events. The basic idea of this algorithm is to find 10s consecutive airflow signal below a certain threshold, γ. Initially, the original airflow signals, $s(t)$, are preprocessed as the absolute values, K, of the difference between the original signal and the average airflow signal in each sliding window (W_0). $K(t)$ can be calculated as follows:

$$M(t) = (s(t) + |\min(\forall s)|) \quad (8)$$

$$K(t) = |M(t) - mean(\forall M)| \quad (9)$$

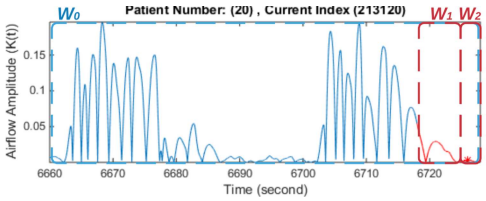

Figure 3. The preprocessed airflow signals and three windows (The unit of x-axis is second.)

Two windows are used that have different sizes (W_1 and W_2) to take the possible difference between maximum amplitude of W_1 and mean amplitude of W_2. The adaptive threshold is the changing value in the respiratory flow of the patient to detect the apneas. The adaptive threshold value, γ_i, at i^{th} sample, is calculated as follows:

$$\gamma_i = \gamma_0 \left(1 - \frac{\max(W_1) - mean(W_2)}{\max(W_1)}\right) \quad (10)$$

where $\gamma_0$is the initial threshold. The original algorithm uses the value of 55 as the empirical value, and we determine the value of γ_0 based on the equation, because the amplitude scales of datasets are different and the original algorithm determined the initial value empirically. We determine the initial value (γ_0) using the following equation:

$$\gamma_0 = \varepsilon(max(W_0) - \min(W_0)) \quad (11)$$

where ε is 1.75 for balancing the sensitivity and specificity.

V. Results

We first conduct comparative analyses over three sleep apnea detection algorithms: ANN algorithm using IRI and IRA features [16], adaptive threshold based algorithm [17], and ACP algorithm. All three algorithms are analyzed in terms of common quality metrics -- sensitivity (*Sn*), specificity (*Sp*), positive predictivity (*PP*), negative predictivity (*NP*), accuracy (*Ac*) and the area under curve (*AUC*) using the 20 patients' respiration signals from the University of Michigan.

Table I shows the comparative results in terms of the six quality measures across the three sleep apnea detection algorithms, where the best results are highlighted. As shown, the proposed algorithm performs better than in terms of *Sn*, *Sp*, *Ac*, and *AUC*.

TABLE I. Comparison of Performance for Three Sleep Apnea Algorithms

Algorithms	Sn. (%)	Sp. (%)	PP. (%)	NP. (%)	Ac. (%)	AUC. (%)
ACP	**78.47**	**79.86**	22.88	97.99	**79.76**	**79.17**
[16]	63.50	66.63	**34.95**	86.60	65.94	65.06
[17]	70.16	64.47	13.62	96.43	64.89	67.31

Table II shows the comparative results for 20 patients. As shown, the lowest AUC is 61.38% (patient #7) and the highest AUC is 95.50% (patient #1). The highest PP is 41.49% (patient #8).

TABLE II. COMPARISON OF PERFORMANCE FOR 20 PATIENTS

P#	Sn. (%)	Sp. (%)	PP. (%)	NP. (%)	AC. (%)	AUC. (%)
1	100.00	90.99	0.47	100.00	91.00	**95.50**
2	92.77	77.28	6.59	99.84	77.54	85.02
3	78.13	64.03	3.45	99.44	64.26	71.08
4	74.34	88.49	31.30	98.00	87.56	81.42
5	92.31	80.16	6.76	99.85	80.34	86.23
6	90.00	81.05	9.12	99.74	81.23	85.52
7	50.00	72.77	0.18	99.93	72.75	*61.38*
8	70.49	78.31	**41.49**	92.40	76.91	74.40
9	95.45	91.01	5.51	99.97	91.03	93.23
10	88.07	86.71	24.97	99.31	86.78	87.39
11	80.00	79.44	3.50	99.77	79.44	79.72
12	84.86	78.98	18.82	98.91	79.30	81.92
13	83.33	71.76	2.65	99.79	71.86	77.55
14	86.36	87.81	20.59	99.44	87.76	87.09
15	88.24	94.96	6.64	99.95	94.93	91.60
16	50.00	77.51	0.57	99.83	77.44	63.75
17	91.14	78.51	7.69	99.78	78.75	84.82
18	100.00	80.60	0.60	100.00	80.62	90.30
19	73.33	59.58	0.57	99.86	59.62	66.46
20	91.62	77.00	13.50	99.58	77.55	84.31

VI. DISCUSSION

The proposed peak values based apnea detection algorithm was based on the processing of respiration signals. In order to optimize the overall result, we tried several cases of the sliding windows, such as 1s, 5s, and 10s. Although the 1s of sliding window generates slightly better performance of sensitivity and specificity, the value of positive-predictivity becomes below 10%, and 10s of sliding window reduced sensitivity and specificity. In addition, the proposed algorithm has two control parameters that are the cut-off filter value and threshold of peak change. We have computed the combination of 18 cut-off filter values and 10 peak changes. Among the 180 cases of combination, we select over 79% of AUCs and balanced values of sensitivity and specificity for overall results. This is because [18] mentions that AUC is a single measure that can determine which classifier provides better performance.

We implemented two other algorithms for comparing the detection performance. [16] discarded the breaths that include the IRIs are smaller than 4s and IRAs are below 0.1. However, we include all signals because the other algorithms didn't remove any signals for the performance comparison.

VII. CONCLUSION

In this paper, we proposed a new algorithm that uses filtering peak values to detect sleep apneas events. Our comparative analyses show that based on 20 patients with severe AHIs the proposed algorithm performs better than two other algorithms in terms of common quality measures. Our study shows that our algorithm improves upon the ANN based algorithm in the four other quality measures, 79.17% of the area under curve (AUC), 78.47% of sensitivity, and 79.86% of specificity.

Future work will include applying more patients' data and turning the threshold to maximize the detections accuracy. In addition, the proposed algorithm can be further utilized as the module for auto-detection to develop the prediction algorithm for sleep apneas.

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