

Classification of Breathing Events Using Load Cells under the Bed

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Abstract—Sleep disturbances are prevalent, financially taxing, and have a negative effect on health and quality of life. One of the most common sleep disturbances is obstructive sleep apnea-hypopnea syndrome (OSAHS) which frequently goes undiagnosed. The gold standard for diagnosing OSAHS is polysomnography (PSG)—a procedure that is inconvenient, time-consuming, and interferes with normal sleep patterns. We are investigating an alternative to PSG in which unobtrusive load cells fitted under the bed are used to monitor movement, heart rate, and respiration. In this paper we describe how load cell data can be used to distinguish between clinically relevant disordered breathing (apneas and hypopneas) and normal respiration. The method correctly classified disordered breathing segments with a sensitivity of 0.77 and a specificity of 0.91.

I. INTRODUCTION

SLEEP disorders pose a huge financial, health, and quality of life burden worldwide. Estimates of the prevalence of sleep disorders in the US range from 50 to 70 million people [1], and as many as 9% of middle-aged American men suffer from sleep disordered breathing [2]. At least 80% of these people may not have received a clinical diagnosis [3]. Sleep disordered breathing leads to poor sleep quality, resulting in fatigue and day-time sleepiness that can lead to reduced cognitive capacity, ineffective work, accidents, and an increased risk of cardiac morbidity and stroke. The direct cost of treating sleep disorders has been estimated in the range of \$30-50 billion per year; indirect costs including absenteeism from work and fatigue-related accidents has been estimated to be \$210 billion [1].

Obstructive sleep apnea-hypopnea syndrome (OSAHS) is characterized by recurrent episodes of disordered breathing. The clinical diagnosis requires five or more obstructed breathing events per hour during sleep, accompanied by

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either daytime sleepiness or symptoms such as recurrent choking or waking during sleep. Disease detection and identification of severity need not distinguish apneas from hypopneas, and a single apnea-hypopnea index (AHI) is generally accepted for both clinical and research use [4, 5]. While obstructive apneas and hypopneas share the same cause and effects of sleep disturbance and oxygen instability, central apneas have a separate pathophysiology related to impaired respiratory control [4]. While these events are also included in the AHI, it is clinically useful to distinguish central apneas from obstructive respiratory events to distinguish obstructive sleep apnea from central apnea or patients with both disorders [4].

The gold standard for diagnosing sleep problems is overnight polysomnography (PSG), an obtrusive test in which patients spend a night in a sleep lab wired to up to 15 different devices for measuring airflow, movement, and electrical brain signals. The test is inconvenient, time-consuming, and interferes with normal sleep patterns [6]. Therefore, lower cost methods for testing may improve disease detection and access to care for a disorder that is highly prevalent and necessitates the testing of large numbers of patients.

Load cells placed under each support of a bed offer a unique opportunity to continuously and unobtrusively monitor patients while they sleep. The patterns of changing force at each support can be analyzed, and inferences about various sleep parameters can be made. Load cell data can be collected continuously in a person's home, giving physicians and researchers the ability to monitor a patient's sleep over time without interfering with the patient or their sleep.

Load cells have recently been used in our and other laboratories to detect [7, 8] and classify [9] movements in bed, as well as to assess sleep hygiene [10]. Recent studies have also shown the validity of using load cells placed under the supports of a bed to detect heart rate [7, 11] and respiration [7]. In the current study we have extended this previous work to evaluate the ability of load cells to detect clinically relevant disordered breathing such as apneas and hypopneas. We extracted features from the raw and filtered load cell signal and used these to train a Bayesian classifier to differentiate normal and disrupted breathing.

II. METHODS

A. Data collection and preparation

Load cells were placed under the supports of a bed in the

OHSU sleep clinic, one under each of the existing six supports. Data were collected on four patients admitted for regular polysomnography (PSG) evaluation. Both full polysomnography data and load cell data were collected for each patient and time-aligned for analysis.

The PSG data were scored clinically by a single sleep technician following American Academy of Sleep Medicine (AASM) guidelines. This scoring was then reviewed by a sleep medicine physician. Polysomnographic records were then analyzed for periods of central apnea, obstructive apnea, and hypopnea. The clinically determined times and durations of these events were used to segment the load cell data for analysis. Because the majority of events are obstructive in nature [5], and because during routine PSG measures for discriminating central from obstructive hypopneas are not available [4], we grouped hypopneas and obstructive apneas for the analysis. Across the four subjects, a total of 300 representative samples of hypopneas/obstructive apneas (N=150) and of central apneas (N=150) were segmented from the load cell data. An additional 150 samples of normal breathing that did not contain respiratory events were selected across all four subjects and segmented from the load cell data. The duration of the normal breathing segments was chosen to be 20 seconds, which was the average length of the 300 apneic events.

For each subject, the digital load cell signal $x^i(t)$ was

sampled at 2KHz for each load cell i , which was more than double the 60dB point of the anti-aliasing filter. The load cell signals were then low-pass filtered to 5Hz and then decimated to 10Hz for data reduction purposes. The resultant signal $x_d^i(t)$ was further band-pass filtered using a combination of 7th order high and low-pass Chebyshev Type II filters to isolate frequencies (0.2 – 0.33 Hz) expected to contain the respiration signal [12]. The high-pass filter had a stop-band edge frequency of 0.05 Hz, was monotonic in the pass-band, and attenuated the stop-band by 40 dB. The low-pass filter was similar to the high-pass filter but with a stop-band edge frequency of 0.45 Hz.

The resultant decimated ($x_d^i(t)$) and band-pass filtered ($x_{BP}^i(t)$) signals for each load cell i were then segmented based on the polysomnography data as described above. Fig. 1 shows sample signals from the PSG, the decimated load cell segment $x_d^i(t)$ and the filtered load cell segment $x_{BP}^i(t)$, for each class of breathing data (normal breathing, central apnea, and hypopnea).

B. Feature Extraction

Eight features were extracted from each of the load cell segments for each load cell i . From each segment of the decimated signal $x_d^i(t)$ we extracted the following features. In the descriptions below, the subscript k represents the k^{th} segment for the particular load cell; we have dropped the subscript i (indicating which of the six load cell signals the

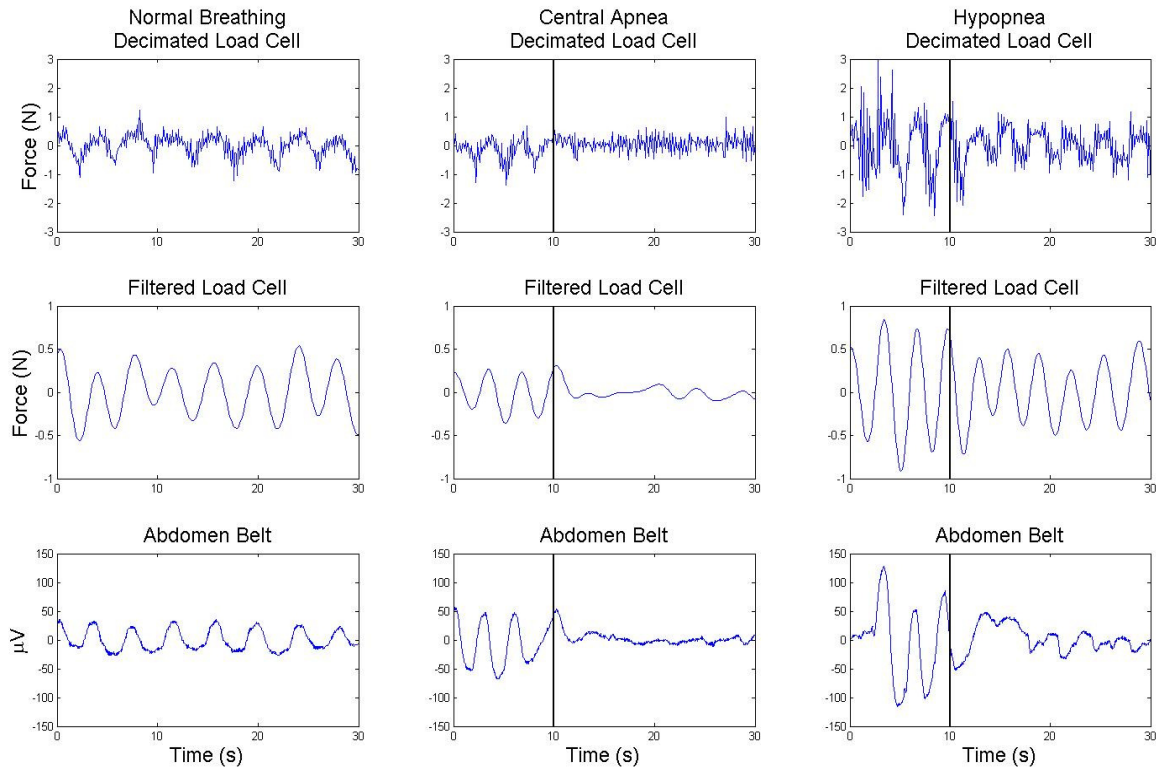


Fig.1. Patient data from three different 30 second epochs during the sleep study. The left column depicts an epoch of normal breathing, the middle column depicts a central apnea, and the right column depicts a hypopnea. The upper row contains decimated data from the load cell placed under the upper middle support of the bed. The middle row contains filtered load cell data from the same sensor. The bottom row contains data from the PSG respiratory inductive plethysmography abdomen belt during the 30 second epoch. The vertical line indicates the time point where the respective respiratory event was scored by an OHSU sleep lab technician.

segment came from) for clarity.

(1) Variance s_k^2 in the signal over all samples of the decimated respiratory segment.

(2) Normalized average power of the signal in each of the three frequency bands: [0-0.5 Hz], [0.6-0.75 Hz], and [0.75-5 Hz]. These measures provide us with information about the relative frequency content in each of these bands. To calculate the average power, we treated each individual signal segment as weakly stationary. The power spectral density (PSD) S_k of each segment was calculated by first high-pass filtering to remove the trend, then multiplying the filtered segment by a Blackman window to get $x_B^k(t)$, and finally using the normalized and squared absolute value of the Fourier transform (1024 point) on this modified segment:

$$S_k(e^{j\omega}) = \frac{1}{n} \left| \sum_{t=1}^n x_B^k(t) e^{-j\omega t} \right|^2. \quad (2)$$

The Blackman window reduces the side-lobe amplitude in the estimated spectrum by about 58dB, and has a roll-off of about 18dB per octave. The average power P_k in a given frequency band $[F_1, F_2]$ was calculated as

$$P_{k F_1 F_2} = 2 \sum_{f=F_1}^{F_2} S_k(f). \quad (3)$$

(3) Spectral entropy, SE_k , of the signal calculated by finding the PSD of $x_B^k(t)$ as shown in (2), segmenting the PSD into 100 equal frequency bins, f , normalizing each bin's average power to find its probability density p_f , and using the equation:

$$SE_k = \sum_{f=1}^{100} p_f \log_{10} \left(\frac{1}{p_f} \right). \quad (4)$$

From the filtered signal segments $x_{BP}^k(t)$ we extracted the following additional features:

(1) Variance s_k^2 in the signal over all samples of the filtered respiratory segment.

(2) Range, R_k , of the data values in the period calculated using the maximum and minimum data values:

$$R_k = \max(x_{BP}^k(t)) - \min(x_{BP}^k(t)). \quad (5)$$

(3) Respiration amplitude, RA_k , estimated by dividing each segment into overlapping 5 second windows that have starting points offset by 0.1 seconds, finding the range of the data in each window, and then taking the median of all the ranges. A simple peak detection algorithm could not be utilized since peaks are not always easily identifiable in disordered breathing, especially in cases of central apneas.

C. Classification

Classification of the respiratory segments was done separately for each of the six load cells. First, the features described above were calculated for each segment and the data were separated into training and testing sets. Let the vector of classes (central apnea, obstructive apnea/hypopnea, and normal breathing) be \mathbf{W} , and our feature set be \mathbf{X} . We

want to estimate the probability that a given segment in our test set \mathbf{X} comes from a particular class w_i , $P(w_i|\mathbf{x})$. By Bayes rule, we know

$$P(w_i|\mathbf{x}) = \frac{p(\mathbf{x}|w_i)P(w_i)}{\sum_{j=1}^3 p(\mathbf{x}|w_j)P(w_j)}$$

We assumed that can use our training sample set D to estimate the prior probabilities $P(w_i)$ as $P(w_i|D)$. Then, we used Bayesian learning to determine the class-conditional probabilities $P(\mathbf{x}|w_i)$ by fitting the features from each class with a multivariate normal density. We assumed that our feature set \mathbf{X} is distributed according to a multivariate normal distribution with expectations $\boldsymbol{\mu}$ and a variance-covariance matrix $\boldsymbol{\Sigma}$ and used our sample set D to fit the distribution. Likelihood ratios were used to assign each observation to one of the groups [13].

The performance of the classifier was assessed using 10-fold cross validation [14]. The 150 data segments from each class were divided into 10 disjoint sets of 15 samples. The classifier was trained 10 times, each time with one set of samples held out for validation. The 10-fold cross validation was performed for each of the six load cells, and each load cell was allowed to 'vote' for the classification of each event. The class with the most votes was selected as the predicted class. In the case where more than one class shared the most votes, the class predicted by the load cell under the upper middle of the bed was selected. Finally, the sensitivity and specificity of the classifier were averaged over the ten iterations for each class.

Clinically, the measure most often used to assess sleep disordered breathing is the Apnea-Hypopnea Index (AHI), which does not differentiate between types of apneas or hypopneas. Therefore, we also separated the load cell respiratory segments into two classes: periods of disordered breathing (combined data of the hypopneas, obstructive apneas, and central apneas, N=300), and periods of normal breathing (N=150). The average sensitivity and specificity for this classifier were also found using 10-fold cross validation, with 10 disjoint sets of 30 samples that were randomly sampled without replacement. The 150 normal breathing segments were divided as already explained.

III. RESULTS

Table I shows the sensitivity and specificity obtained for each type of breathing event. While the specificity is reasonably high for the disordered breathing events (central

TABLE I
SENSITIVITY AND SPECIFICITY FOR ALL CLASSES

	Sensitivity	Specificity
Hypopnea/Obstructive Apnea	0.65	0.90
Central Apnea	0.82	0.92
Normal Breathing	0.84	0.84

TABLE II
CONFUSION MATRIX FOR ALL CLASSES

Estimated Class	Actual class		
	Hypopnea /Obstr. Apnea	Central Apnea	Normal Breathing
Hypopnea/Obstr. Apnea	97	15	16
Central Apnea	17	123	8
Normal Breathing	36	12	126

apneas and hypopneas/obstructive apneas), it is clear that the sensitivity for detecting hypopneas/obstructive apneas is poor. The confusion matrix (Table II) shows that hypopneas/obstructive apneas were primarily confused with normal breathing, although some were confused with central apneas. The feature that best differentiated the hypopneas/obstructive apneas from other classes was the normalized power in the [0.6-0.75 Hz] frequency band.

Results were better when the disordered breathing events were considered as a single group, as is done clinically when calculating AHI. The sensitivity and specificity for discerning disordered breathing segments was 0.77 and 0.91 respectively, and the sensitivity and specificity for discerning normal breathing segments was 0.91 and 0.77 respectively.

IV. DISCUSSION

Our research indicates that using load cells under the supports of a bed has significant potential for automatically detecting sleep apnea. The overall performance of the classifier in separating normal breathing from disordered breathing was acceptable, although we are continuing to add features to improve the classification. We are currently investigating features that provide information about the time course of the signal during the event, such as features derived from wavelets. We are also in the process of training and testing our classifier using data collected from approximately 20 patients in the sleep lab, and we plan to test the performance of other classification methods such as support vector machines in the future.

Other methods have been used to unobtrusively detect respiration of individuals lying in bed. One method has been to attach a mechanical sensor to a mat that can be placed on top of the bed [15]. The technique has high accuracy in detecting heart and respiration rates; however, it has a few limitations. The sensor is used in consort with a thin mat that alters the sleeping surface of the bed, and it must be placed near the thorax of the patient.

The current research focused on the classification of different breathing events from load cell data segmented using the PSG data as a gold standard. We are now working on combining our previous work on automatic segmentation of continuous load cell data into quiescent periods and periods of movement with our classification of breathing segments. Our ultimate goal is to develop an algorithm that utilizes our classifier to automatically detect disordered breathing episodes from the quiescent periods of load cell

data collected over an entire night. This is a necessary next step to be able to use the approach to estimate the apnea-hypopnea index from in-home data.

The true potential of this technology for assessing sleep disorders lies in its unobtrusive nature, and on the fact that it could be used to assess disrupted sleep in a person's own bed. Once in place, multiple nights of data may be obtained without a significant increase in cost. The potential cost savings in a tool that could be used to pre-screen for sleep apnea, or to follow treatment, is significant. Load cells may make informative longitudinal unobtrusive monitoring of sleep a reality.

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