A Robust Detection Algorithm to Identify Breathing Peaks in Respiration Signals from Spontaneously Breathing Subjects

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Abstract

Assessing respiratory and cardiovascular system coupling can provide new insights into disease progression, but requires accurate analysis of each signal. Respiratory waveform data collected during spontaneous breathing are noisy and respiration rates from long term physiological experiments can vary over a wide range across time. There is a need for automatic and robust algorithms to detect breathing peaks in respiration signals for assessment of the coupling between the respiratory and cardiovascular systems. We developed an automatic algorithm to detect breathing peaks from a respiration signal. The algorithm was tested on respiration signals collected during hemorrhage in a conscious ovine model (N=9, total length = 11.0h). The breathing rate varied from 15 to as high as 160 breaths/min for some animals during the hemorrhage protocol. The sensitivity of the algorithm to detect respiration peaks was 93.7% with a precision of 94.5%. The developed algorithm presents a promising approach to detect breathing peaks in respiration signals from spontaneously breathing subjects. The algorithm was able to consistently identify breathing peaks while the breathing rate varied from 15 to 160 breaths/min.

1. Introduction

Continuous monitoring of respiratory activity is important to understand disease progression [1, 2] and is performed via a multitude of methods [3]. Identifying breathing peaks in respiration waves is a critical first step in respiratory activity monitoring and can be done using conventional peak detector algorithms [4]. However, respiration waves from spontaneous breathing subjects are noisy, which gives rise to erroneous peak detections when noise peaks are present [5] causing high false alarm rates. Critical conditions can result in respiration rates beyond normal expected limits. Respiration rate from long term measurements and under changing physiological conditions can vary over a wide range across time, which presents the need for automatic and adaptive breathing peak detection algorithms. We developed an automatic algorithm to detect breathing peaks from noisy respiration signals with a varying respiration rate over time. To demonstrate our approach, we apply the algorithm to a set of respiration signals collected in conscious ovine undergoing hemorrhage during spontaneous breathing.

2. Algorithm

The breathing peak detection algorithm consists of several parts. The preprocessing consists of a band pass antialiasing filter, power line noise filter, baseline wander correction, and down sampling. A 10s moving window which slid along the signal in 5s steps identified the frequency peak (f_i) between 0.2-5Hz for the window using the fast Fourier transform. The window is then preprocessed with a low pass filter with the cutoff frequency of f_i + 1Hz.This low pass filtered signal is then down sampled to 20Hz. The distribution of f_i was constructed using f_i over all 10s windows of signal. To remove the baseline wander, the signal is then filtered through a high pass filter where the cutoff frequency is the 2.5^{th} percentile of the distribution of f_i.

The 10s low pass filtered and baseline wander corrected signal is then applied to the breath detection algorithm, presented as a flow diagram in Fig.1. At each sample i, signal slope (S_i) and the slope at proceeding sample (S_{i+1}) was calculated. Depending on the sign of the slope at sample i and i+1, the sample is identified to be a potential valley ($S_i<0$ and $S_{i+1}>0$), potential peak ($S_i>0$ and $S_{i+1}<0$) or none of the above. The following state variables were used to keep track of immediate past state of the signal; valley detected (VD): before the current sample a valley following a breathing peak was detected, peak detected (PD): before the current sample a breathing peak was detected, height threshold (HT): 10% of the mean height of previous 100 breathing peaks, depth threshold (DT): 10% of the mean depth of the previous 100 valleys, baseline (BL): mean of the samples from

previously detected valley to the current sample. Using these state variables an adaptive thresholding criterion was developed to validate whether the detected peak is a true breathing peak. The algorithm starts with following initial conditions; height threshold (HT) = 0.1, depth threshold (DT) = 0.1, baseline (BL) = 0, valley detected (VD) = false, peak detected (PD) = false. When a valley is detected it is flagged as a true valley preceding a breathing peak (VD = true) if the following are met: if a valley was not detected previously (VD = false), value at current sample is less than the baseline (y_i < BL), depth of the current valley is greater than 10% of the mean depth of the previous 100 valleys (valley $depth_i$ > DT) and the Mahalonobis distance of the current valley depth to the distribution of past 100 valley depths is less than 20. When a peak is detected it is flagged as a true breathing peak (PD = true) if the following are met: if a peak was not detected previously (PD = false), but a valley was (VD = true), value at current sample is greater than the baseline (y_i > BL), height of the current valley is greater than 10% of the mean height of the previous 100 peaks (peak $height_i$ > HT), and the Mahalonobis distance of the current peak height to the distribution of past 100 peak heights is less than 20. If the current sample is neither a peak nor a valley, the sample is added to the baseline vector (b). Whenever a true peak is detected the height threshold (HT) is updated with the current peak height, and similarly when a true valley is detected the depth threshold (DT) is updated with detected valley depth. If the baseline vector contains samples for a time longer than 5s, the vector is reset and the algorithm is set to initial conditions as that indicates the signal segment is a noisy period or a flat line. The algorithm was implemented in MATLAB 2014b (The Mathworks, Inc., Natick, MA).

3. Experimental Methods

The algorithm was tested on respiration signals measured using a resistive band placed around the thorax (fs=1,000 Hz, PowerLab; AD Instruments, Castle Hill, Australia) in a conscious ovine hemorrhage model (N=9) obtained from a previously reported experiment [6,7]. The hemorrhage experiment started with a 7min baseline period followed by 25ml/kg blood removal over 15min, post-hemorrhage period up to 15min and reinfusion period that included closed-loop fluid resuscitation to restore blood pressure. The total combined length of respiration signals across all hemorrhage experiments was 11.0h with breathing rate varying from 15 to 160 breaths/min. Breathing peaks on the respiration signals were annotated by a human expert.

The algorithm was applied to the annotated respiration signals. A true positive was declared if a beat was detected within 200ms of a reference annotation. The result of applying the algorithm on the validation set was assessed by calculating sensitivity and precision. Sensitivity was defined as TP/TP+FN while precision as TP/TP+FP, where TP (true positive) is the number of peaks the algorithm correctly identified which are also members of the expert annotated breathing peak set, FP (false positive) is the number of peaks the algorithm incorrectly identified which are not members of the expert annotated breathing peak set, and FN (false negative) is expert annotated breathing peaks the algorithm failed to identify.

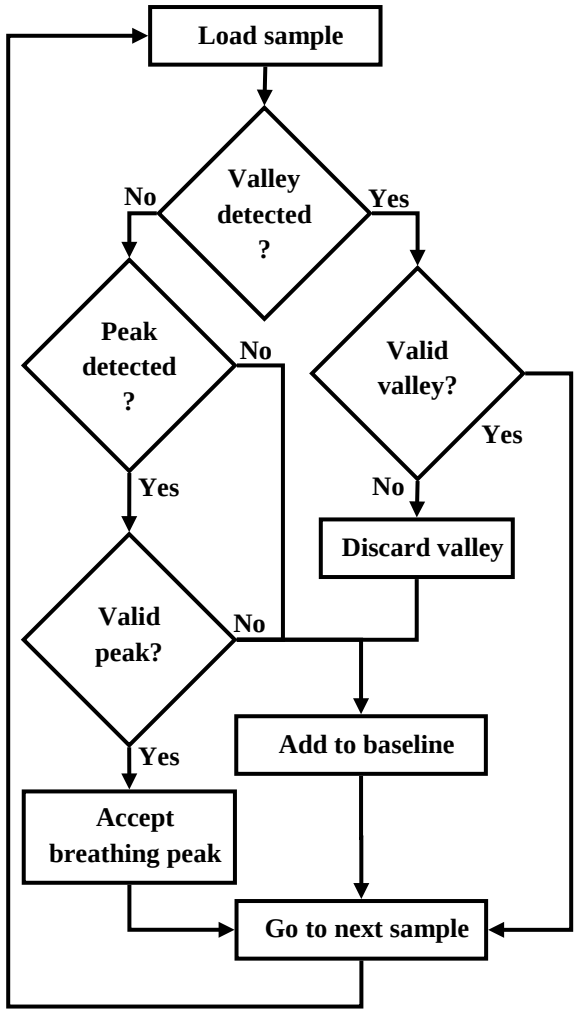

Fig.1: Flow diagram of breath detection algorithm. The input is the i^{th} sample from a 10s low pass filtered and baseline wander corrected segment.

4. Results

Table 1 summarizes sensitivity and precision of the algorithm applied to respiration signals from each animal. The third column in Table 1 includes the minimum and maximum breathing rates during the recording period for

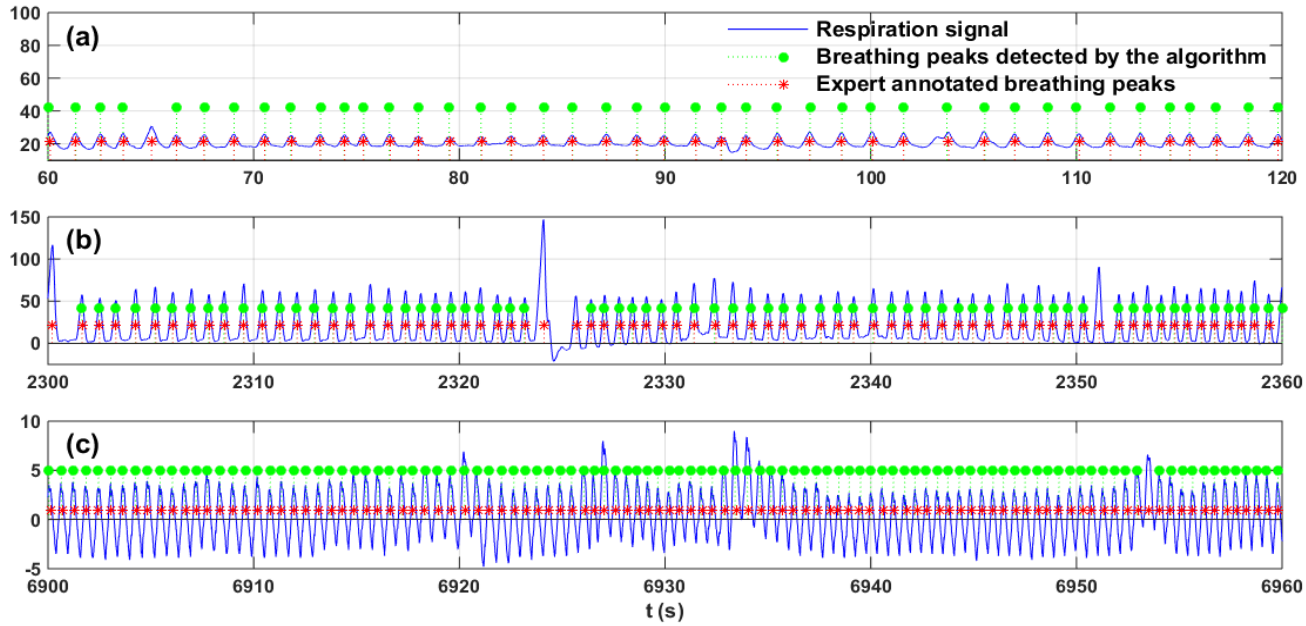

Fig.2: Examples of breathing peak detection on signal segments of varying breathing rates; (a) 45, (b) 75, and (c) 120 breaths/min.

each animal. Average sensitivity of the algorithm across animals was 93.7% with a precision of 94.5%. Fig. 2 demonstrate examples of breathing peak detection on signal segments of varying breathing rates, 45, 75, and 120 breaths/min respectively.

Animal	Length (h)	Breathing Rate Range (breaths/min)	Se. (%)	P (%)
1	0.7	60 - 120	94.8	95.9
2	1.1	40 - 100	93.5	92.7
3	1.2	55 - 100	82.4	80.5
4	2.1	35 - 100	91.2	92.5
5	1.1	40 - 140	93.4	98.4
6	0.9	30 - 40	99.1	99.2
7	1.1	40 - 70	95.4	97.1
8	1.0	15 - 70	96.4	96.3
9	1.8	20 - 160	97.0	98.2

Table.1: Sensitivity (Se) and precision (P) of the algorithm at each respiration signal.

5. Discussion

Detecting breathing peaks in respiratory waveform data is important to accurately monitor breathing and assess coupling between the respiratory and cardiovascular systems; however, it can be erroneous in long term measurements from spontaneous breathing subjects due to noise, varying breathing rates over time, and motion artifacts. The algorithm presented in the paper indicates that by using an automated adaptive approach, it is possible to detect breathing peaks precisely over a wide range of breathing rates.

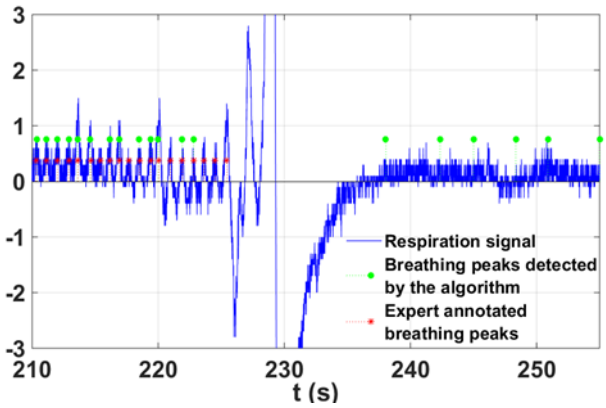

Fig.3: False positives due to noisy segments in the respiration signal for animal 3.

As shown on Table 1, the proposed algorithm performed comparatively poorly for animal 3. This is due to the large noisy segments in this respiration signal as shown in Fig.3. Possible improvement to avoid this occurrence would be to include rules based on the distribution of inter-breath-interval to determine valid peaks and valleys to improve the sensitivity and precision of the algorithm. As shown in Fig.3 the false positive detections have larger inter-breath-interval compared to the true positives and this feature can be used to remove false positive detections which occur due to noise. Distribution of inter-breath-interval can also be used to reduce false negatives which occur due a large breath amidst a sequence of smaller breaths as seen on Fig.2

while disqualifying noisy peaks which has the same characteristic.

Overall the developed algorithm presents a promising approach to detect breathing peaks in respiration signals from spontaneously breathing subjects. The algorithm was able to identify breathing peaks consistently while the breathing rate varied from 15 to 160 breaths/min and also in presence of noise and motion artifacts. The wide range of breathing rates in this study represents a physiological response to hemorrhage in the conscious ovine model. The most critical monitoring times may be during acute events when vital signs are highly dynamic, and physiological monitoring algorithms in these scenarios need to adapt to continuously changing conditions to provide accurate measurements. The presented algorithm accomplishes this by performing a series of checks on each potential peak or valley and updating thresholds based on the current signal state.

One limitation to the set of data used to test the algorithm here is that low breathing rates (6-15 breaths/min) that may occur in humans were not encountered in the conscious ovine model. Future studies will focus on validating the algorithm in human data using capnography as reference.

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References

[1] Fieselmann, J., et al., Respiratory rate predicts cardiopulmonary arrest for internal medicine inpatients. Journal of General Internal Medicine, 1993; 8(7): 354-60.

[2] Barthel, P., et al., Respiratory rate predicts outcome after acute myocardial infarction: a prospective cohort study. European Heart Journal, 2013; 34: 1644-50.

[3] Folke, M., et al., Critical review of non-invasive respiratory monitoring in medical care. Medical and Biological Engineering and Computing, 2003; 41(4): 377-83.

[4] Wilson, A.J., C.I. Franks, and I.L. Freeston, Algorithms for the detection of breaths from respiratory waveform recordings of infants. Medical and Biological Engineering and Computing, 1982; 20(3): 286-92.

[5] Cohen, K.P., et al., Comparison of impedance and inductance ventilation sensors on adults during breathing, motion, and simulated airway obstruction. Biomedical Engineering, IEEE Transactions on, 1997; 44(7): 555-66.

[6] Scully, C.G., et al., Evaluation of heart rate and blood pressure variability as indicators of physiological compensation to hemorrhage before shock. Shock, 2015; 43(5): 463-469.

[7] Ying H., et al., Closed-loop fuzzy control of resuscitation of hemorrhagic shock in sheep. 24th Annual Conference and the Annual Fall Meeting of the Biomedical Engineering Society EMBS/BMES Conference 2002; 1572: 1575-6.

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