PHASE SEGMENTATION OF NOISY RESPIRATORY SOUND SIGNALS USING GENETIC APPROACH

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Abstract: In this paper, a new approach to automatically segment noisy respiratory sound signals is proposed. Segmentation is formulated as an optimization problem and the boundaries of the signal segments are detected using a genetic algorithm (GA). As the estimated number of segments present in a segmenting signal is initially obtained, a multi-population GA is employed to determine the locations of segment boundaries. The segmentation results are found through the generations of GA by introducing a new evaluation function, which is based on the sample entropy and a heterogeneity measure. Illustrative results for respiratory sound signals contaminated by loud heartbeats and other high level noises show that the proposed genetic segmentation method is quite accurate and threshold independent to find the noisy respiratory segments as well as the pause segments under different noisy conditions.

1 INTRODUCTION

Respiratory rate (RR) monitoring plays an important role in many clinical situation. Correct timing of individual respiratory phases can be useful in studying flow in the heart (Hult et al., 2000), quantifying adventitious respiratory sounds and many other situations. Different airflow measurements, such as mouthpiece pneumotachograph or chest movement measurement, are the most widely applied methods in monitoring RR and respiratory phases. However, it would be difficult to apply such methods under certain circumstances, especially when studying children with neurological impairments (Yadollahi and Moussavi, 2006). Hereby, acoustical analysis of respiratory sounds has recently provided an alternative way to detect respiratory phases and therefore RR.

Tracheal breath sound refers to respiratory sound recorded over suprasternal notch. It can be segmented into four successive phases: inspiratory phase, expiratory phase, end-inspiratory pause, expiratory phase, and end-expiratory pause. It is chosen due to its distinct phases and relatively larger amplitude compared with sounds recorded over chest, as well as its close relationship to respiratory flow. A few attempts have been done to estimate flow for segmentation through tracheal sounds in the past. Among all, one of the effective method is the signal analysis approach uses the temporal and frequency variables of tracheal sounds as well as disturbance characteristics (Hult et al., 2000). It is able to identify different respiratory phases but it requires more than one microphone to capture the ambient noise and it is sensitive to disturbance. To avoid such problems, in (Yadollahi and Moussavi, 2006), flow estimation using Shannon entropy of the bandpass filtered tracheal sounds is proposed.

Both the above mentioned methods are generally effective on preprocessed tracheal sounds which are free of heartbeats and ambient noise. However heartbeat as one of the most influential noise for respiratory sounds are usually unavoidable during signal recording. It has the frequency range of [0 300]Hz which interferes with that for respiratory sounds; and it masks the respiratory sounds because of its high intensity. When the recorded signals which are corrupted by heartbeats or other unknown types of high level noises, the segmentation becomes tough and thus it is difficult to locate the boundaries of respiratory phases accurately. To deal with this problem, a

genetic algorithm (GA) is employed for the first time to segment accurately the noisy respiratory signal.

The aim of this paper is to propose an genetic algorithm for automatic phase segmentation of respiratory sounds corrupted by heartbeats and other unknown types and levels of noises. The segmentation method described here is based on a stochastic global search method. To guide the search space of generic algorithm, an evaluation function combined sample entropy and heterogeneity measure is introduced.

2 GENETIC ALGORITHM BASED RESPIRATORY PHASE SEGMENTATION

As for our phase segmentation, the locations of the segment boundaries are detected using our genetic algorithm. Depending on the total number of segments as prior information or estimated using any existing technique(e.g. using an onset detection algorithm), an initial population is randomly generated.

To guide the search space of GA, a new evaluation function is introduced. First the irregularity in the time series (i.e. input sequence) is investigated using *sample entropy* (*SampEn*). Measuring the *homogeneity* and *heterogeneity* of the candidate segments, the fitness of the evaluation function is designed. Through the generations of GA, the locations of segment boundaries are then optimized.

2.1 Sample Entropy

In this GA based segmentation method, a similarity measure of times series (sample entropy) is employed to determine the boundaries of respiratory segments. Sample entropy (*SampEn*) is applied here to measure the complexity and regularity of time series signals' similarities. $SampEn(m,r,N)$ is chosen as it does not count self-matches of the time series. This ensures the consistency of the measurement and reduces the dependency on the signal length. It is defined in (Richman and Moorman, 2000) as the negative natural logarithm of the conditional probability that a data set of length N, having repeated itself within a tolerance r for m points, will also repeat itself for $m+1$ points, without allowing self-matches.

For an input signal u of length N, $\{u(j) : 1 \le j \le N\}$ forms the $N - m + 1$ vectors $x_m(i)$ for $\{i | 1 \le i \le N - m + 1\}$, where $x_m(i) = \{u(i+k) : 0 \le k \le m-1\}$ is the vector of m data points from $u(i)$ to $u(i+m-1)$. In this context, only the first $N - m$ vectors of length m are considered to ensure that, $x_m(i)$ and $x_{m+1}(i)$ are

defined for $1 \le i \le N - m$. Let $B^m(r)$ is the probability that two sequences will match for m points and $A^m(r)$ is the probability that two sequences will match for $m+1$ points. $B_i^m(r)$ is defined as $(N - m - 1)^{-1}$ times the numbers of vectors $x_m(j)$ within r of $x_m(i)$, where $1 \le j \le N - m$, and $j \ne i$ to exclude self-matches. Then $B^m(r)$ is defined as

$$B^m(r) = (N-m)^{-1} \sum_{i=1}^{N-1} B_i^m(r) \qquad (1)$$

Similarly, $A_i^m(r)$ is defined as $(N - m - 1)^{-1}$ times the numbers of vectors $x_{m+1}(j)$ within r of $x_{m+1}(i)$, where $1 \le j \le N - m$ and $j \ne i$. Then set $A^m(r)$ as

$$A^m(r) = (N-m)^{-1} \sum_{i=1}^{N-1} A_i^m(r) \qquad (2)$$

Finally, sample entropy (*SampEn*) is calculated by

$$SampEn(m,r,N) = -\ln \frac{A^m(r)}{B^m(r)} \qquad (3)$$

SampEn measures the regularity of data sequence. A low value of *SampEn* reflects a high degree of self-similarity in time series. With increasing irregularity, a larger value of *SampEn* is obtained. The *SampEn* increases for respiratory segments and decreases during the appearance of pause segments. Hence, the dynamics of segmenting respiratory signal can be investigated through the sample entropy sequence. And sample entropy can be applied as a useful tool to determine the locations of the respiratory segments as well as pause segments for a noisy respiratory sound signal.

2.2 Genetic Algorithm

GAs are numerical optimization algorithms inspired by both natural selection and natural genetics (Coley, 2001). GAs operate on a population of strings, that is, a group of potential solutions of a problem. To measure how good or bad the solutions within the population, fitness of each string is calculated in decoded form (solution vector) applying an evaluation function. At each generation, a new set of solutions are produced by selecting the fittest strings in the problem domain and through the application of the genetic operators such as crossover and mutation. A review for the fundamental operations of a simple GA can be found in (Tang et al., 1996). The procedure of a simple GA can be described as follows, where the population of candidate solutions at time t is represented by P(t):

```
begin
        t = 0;
        initialize P(t);
        while not termination criteria do
        begin
                t = t + 1;
                select P(t) from P(t-1);
                reproduce pairs in P(t);
                evaluate P(t);
        end
end
```

2.2.1 Initial Population

In order to detect both start and end locations of each segment, a population of GA is generated with strings whose length is two times the total number of segments as obtained earlier. A string is a real-valued string representing the locations of the candidate segment boundaries in increasing order. Although the binary-coded GAs are the most commonly used representation, a more natural real-valued representation is used in this system to increase the efficiency of GA. Using the real-valued strings, there is no need to convert strings to solution vectors to evaluate their fitness. Thus it would be faster in computation.

2.2.2 Evaluation Function

In GAs, an evaluation function or fitness function is usually used to evaluate the performance of the strings in the problem domain. In order to obtain accurate boundaries of each segment, an evaluation function is designed using the heterogeneity measure and sample entropy. This function simultaneously maximize the homogeneity within the segments and heterogeneity among different segments using sample entropy.

In this context, *SampEn* of the original segmenting signal is calculated first to investigate the dynamics. To prevent the requirement of large computational time (to obtain the feasible computation time and to make the proposed algorithm to be tractable), *SampEn* is calculated on each data set of length 100 (i.e. $N=100$) within a tolerance r of $0.15 \times SD$ for 1 point (i.e. $m=1$). Here, SD is the standard deviation of the data set. Let H_w be the total within-segment homogeneity and H_b denotes the total between-segment heterogeneity, a segmentation evaluation function is defined as

$$H = \frac{H_b + 1}{H_b + H_w + 1} \qquad (4)$$

where total within-heterogeneity H_w is defined as

$$H_w = \frac{\sum_{i=1}^{S} L_i \sigma_i^2}{L} \qquad (5)$$

where L is the total length of the segmented signal, L_i is the length of i-th segment, σ_i^2 is the variance of the sample entropy of the i-th segment and S is the number of segments in the segmented signal. The between-segment heterogeneity, H_b, is defined as the average Euclidean distance between the mean value of the sample entropy of any two adjacent segments.

$$H_b = \frac{\sum_{(i,j)\in adjacent, i \neq j} \|\mu_i - \mu_j\|^2}{ns} \qquad (6)$$

where ns is the total number of the adjacent segments in the segmented signal, μ_i and μ_j are the mean value of the sample entropy of the i-th and j-th segments. H becomes one when the internals of all segmented respiratory signals are completely homogeneous.

2.2.3 Evolution Procedure

In order to effectively search the solution space, and to take advantage of the parallelism of GAs, the proposed algorithm applies the multiple subpopulations approach provided by (Chipperfield et al., 1995) for the evolutionary process. Using multiple populations the quality of the results obtained can be improved compared to GAs with single population. This approach divides the population into a subpopulations where each of them can evolve independently using parallel processing technique. It can search in parallel different subspaces of the search space, thus making it less likely to become trapped by low-quality subspaces. Multiple populations GA is a widely used parallel GA model where multiple subpopulations evolve independently toward different optima. More diverse subpopulations can be maintained by exchanging genetic materials between subpopulations. The premature convergence effect of simple GA can then be mitigated by this approach. To reduce the required computational time, it is implemented through the use of high-level genetic operator functions and exchanging individuals between subpopulations.

Over generations, each subpopulation is evolved as in traditional simple genetic algorithm (SGA) using the basic operators: *crossover* and *mutation*. Depending on the migration interval (i.e. the number of generations between successive migration) and the migration rate (i.e. the number of individuals to be migrated from one subpopulation to another), individuals from one subpopulation migrate to another from time to time. The initial population is created using 8 subpopulations containing 20 individuals each. At each generation, 90% of the individuals with higher fitness values within each subpopulation are selected for breeding using a *stochastic universal sampling*

function which has minimum spread and zero bias.

In GAs, the recombination operator is usually used to produce the new offsprings. By applying *discrete recombination crossover*, a uniform crossover for real-valued representation, the new offsprings within each subpopulation are produced. Normally, offsprings are mutated after recombination to prevent the population from converging to local minima. And the new possible solutions can be introduced to the population by mutating the offsprings. In this system, a mutation rate of $1/nvar$ is used, where *nvar* is the length of an individual.

When the offsprings produced are less than the size of the original population, the new offsprings have to be reinserted into the population to maintain the size of the original population. Similarly, when not all the offsprings are to be used at each generation, or if the offsprings produced are more than necessary, a reinsertion scheme must be used. This scheme determines which individuals should be replaced by the offsprings produced and which individuals should be inserted into the new population.

In this segmentation method, offsprings are inserted into the appropriate subpopulations depending on *fitness-based reinsertion* with a rate of 0.9. In this multi-population GAs, migration of individuals between subpopulations is performed at every 20 generations with a migration rate of 0.2. After GA iterates for *maxgen* times (here *maxgen*=80), the evolution of this GA stops. The best individual with the maximum fitness value presents the optimized solution for the boundaries of the segments of the segmented signal.

3 SIMULATION RESULTS

In this section, performance of the method is presented for the noisy respiratory sound signals. Both the standard preprocessed normal tracheal breath sound from (Lehrer, 2002; Tilkian and Conover, 2001; R. L. Wilkins and Lopez, 2004) and normal recorded data as corrupted with heartbeats(Phonocardiogram, PCG) and ambient noise, are used to test the segmentation method.

3.1 Acquisition of Respiratory Sounds

The recording environment and equipments are chosen based on the standard given by (Rossi et al., 2000). Short-term recordings have been done in sitting position in audio laboratory which provides a quiet environment. One electret condenser microphone (ECM-77, Sony, Inc., Tokyo, Japan) has inserted into a hemispherical rubber chamber 2cm in diameter, and placed at suprasternal notch of the test subjects to record the tracheal breath sounds. Recording software WAVEPAD (V3.05, NCH Swift Sound Software) has been used and the signal clips have been recorded and saved as mono-channel *.wav file at sampling frequency of 8 kHz. Test subjects have been asked to breath normally, and 20s recording are saved each time.

3.2 Test Respiratory Data

Tracheal breath sounds signals from 10 healthy students of Nanyang Technological University have been used as the dataset of the performance test. The sample size of 10 consists of 6 females and 4 males, each producing two clips of 20s recording. All clips have been testified to be normal tracheal breath by Dr. Daniel Goh from National University Hospital of Singapore.

3.3 Results

This section presents the simulation results using noisy respiratory sound signals. Four different examples regarding segmentation of normal noisy breath sounds are given below. The sampling frequency used is 8 kHz.

Example 1: In this example, the segmentation results for a normal infant tracheal sound from the standard data set, are demonstrated. In contrary to the existing phase segmentation methods, the proposed method is able to function with the presence of heartbeats and provides accurate segmentation results at different levels of PCG (varying with a scaling factor of α)(See Fig. 1). Fig. 1(a) shows the segmentation result for 3 cycles of infant tracheal breath, whereas Figs. 1(b)-(c) show the results with the superimposed PCG. Comparing the results in Fig. 1, it is found that the present method performs well irrespective of PCG level without using any threshold parameter.

Example 2: In this example, segmentation results for the recorded adult normal tracheal breath sound are shown. Both the original signal and the noisy recorded signal interfered with heartbeats, are considered here for illustration. Unlike the infant breath (Fig. 2(a)), the adult breath in Fig. 2(a) has different time evolution (i.e. slower respiration rate) and shallow. The segmentation results in the presence of heartbeats are still found effective like the previous case.

Example 3: In this example, segmentation results are shown for a signal of noisy recorded respiratory sound due to background White Noise (WN) of varying noise variance as ambient noise (see Fig. 3(a)-
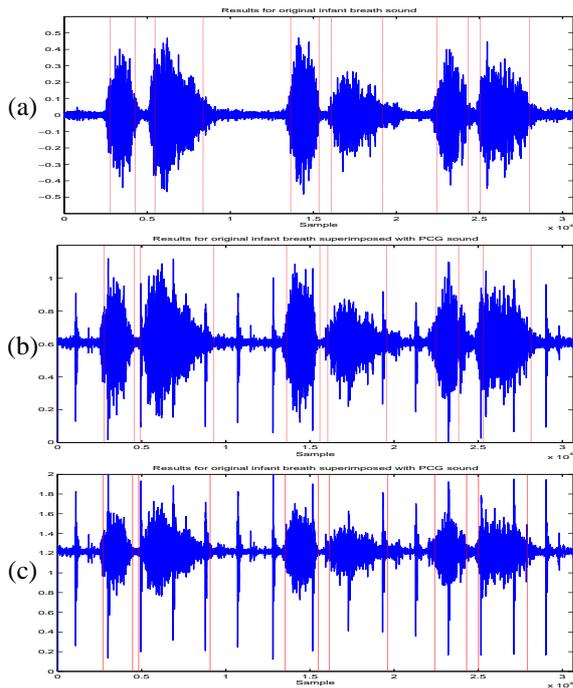
Figure 1: Segmentation results of the standard infant tracheal breath sound: (a) without PCG sound; (b)-(c) with PCG sound added with scaling factor α=1 and 2, respectively.
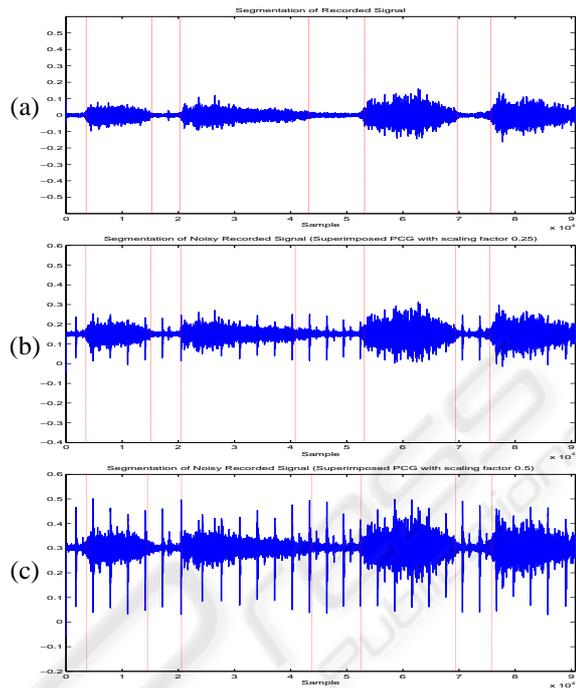

Figure 2: Segmentation results of: (a) preprocessed recorded tracheal breath sound; (b) original recorded tracheal breath sound with heartbeats; (c) recorded tracheal breath sound with superimposed PCG for scaling factor α=0.5.

(b)). Also, simulation result in the presence of both white noise and PCG (heartbeats) is illustrated in Fig. 3(c). As it is seen in Fig. 3 that the segmenation method provides good results for white background noise and heartbeats.

Example 4: In this example, segmentation results are presented, Fig. 4(a)-(b), for the noisy recorded signal corrupted by background Colored Noise (CN) with varying noise level. Also, a simulation example for both ambient colored noise and PCG interference is shown in Fig. 4(c). The colored noise is realized as EEG noise, $v(n)$, which is simulated by an ARMA process described as $v(n) = \frac{C(z^{-1})}{A(z^{-1})}e(n)$ where $e(n)$ is the zero-mean white Gaussian noise and $C(z^{-1})$ and $A(z^{-1})$ are third-order polynomials in the backward shifting operator z^{-1}. The coeffects of $C(z^{-1})$ and $A(z^{-1})$ are chosen in a way that makes the spectrum of the ARMA precess approximates the EEG process.

The estimation error is defined as

$$\varepsilon = \frac{1}{N}\sum_{n=1}^{N} \left| \frac{P_{est}^n - P_{ref}^n}{P_{ref}^n} \right| \qquad (7)$$

where P_{est}^n is the starting/ end position of the nth segment for a noisy signal and P_{ref}^n is that for a preprocessed signal without white noise, colored noise, and

PCG. For performance of segmentation method on real Recorded Tracheal Sound (RTS) with different types of noises imposed onto it as indicated in Figs. 2-4, the error is calculated for each subject using Eq. 7 and then averaged between the subjects.

Table 1: The estimation errors of the segmentation method for different types of noisy signals.

Type of Signal	Segmentation Error
RTS (Fig. 2(b))	0.014 ± 0.011
RTS with PCG (Fig. 2(c))	0.016 ± 0.010
RTS with WN (Fig. 3(a))	0.016 ± 0.013
RTS with WN & PCG (Fig. 3(c))	0.015 ± 0.009
RTS with CN (Fig. 4(a))	0.013 ± 0.009
RTS with WN & PCG (Fig. 4(c))	0.018 ± 0.018

4 CONCLUSIONS

In this paper, effective segmentation of noisy respiratory sound signals is introduced based on genetic (GA) approach. Using sample entropy, a regularity measure of the time sequence and heterogeneity measure, the evaluation function of GA is designed.
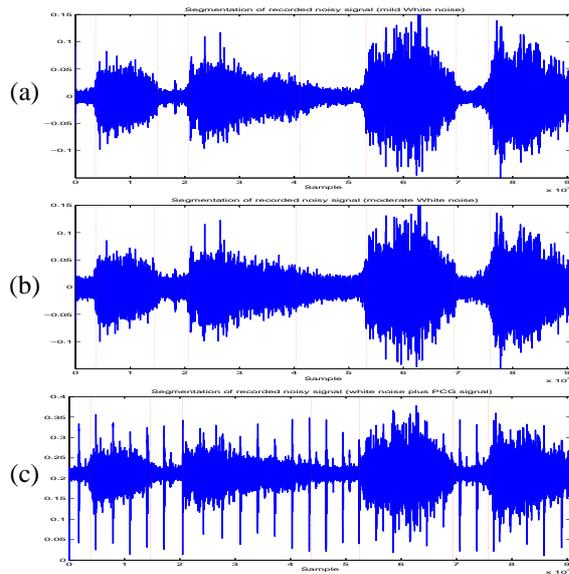
Figure 3: Segmentation results of the noisy recorded breath signal together with (a)-(b) varying white noise;(c) white noise and PCG.
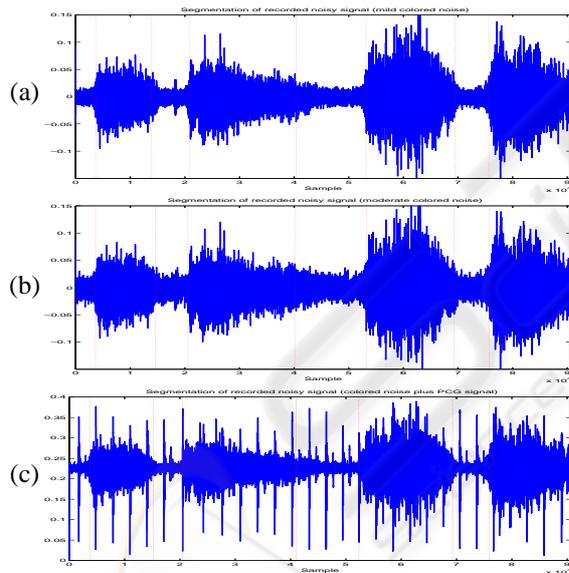

Figure 4: Segmentation results of the noisy recorded breath signal together with (a)-(b) varying colored noise;(c) colored noise and PCG.

The segmentation results for normal tracheal breath sounds corrupted with heartbeats and ambient noise are found quite accurate, especially when the existing methods only perform well on the processed signals without these noise. The method is found effective in the presence of various types and levels of noise.

Furthermore, many approaches for initial segment number estimation (e.g. onset or other detection tech-niques) are suitable for the proposed segmentation method. As the performance of the proposed method does not depend heavily on the accuracy of the total segment number estimated, only a rough estimation by using any detection technique is required. More-over, the independency on threshold values makes the method very robust and suitable for segmentation of recorded respiratory sound signals.

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