

Genetic algorithm based independent component analysis to separate noise from Electrocardiogram signals

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Abstract – A technique is proposed to reduce additive noise from biomedical signals that have high kurtosis values using genetic algorithm (GA). The technique is applied to reduce multiple linear additive noises from electrocardiogram (ECG) signals, which have high kurtosis values due to the presence of R peaks. This GA method uses the basic principles of Independent Component Analysis (ICA) and could also be used to reduce additive noise from other signals that have high kurtosis values. The method is simpler compared to neural learning algorithms and does not require any prior statistical knowledge of the signals. An additional advantage of the method compared to other ICA methods is that only the ECG signal will be extracted thus avoiding extraction of all independent components and manual inspection to determine the ECG signal.

I. INTRODUCTION

In this study, the aim is to reduce linear additive noise from electrocardiogram (ECG) signals, which is important for accurate detection of irregular ECG rhythms. Accurate detection of irregular ECG rhythms is important because they signify problems with the heart like the detection of ectopic beats [1]. However, most ECG signals are buried in noises like powerline interference, baseline, random, and other biological signals like electroencephalogram (EEG) and electromyogram (EMG). There are many techniques to reduce noise like adaptive filtering, ICA, wavelets and Principal Component Analysis (PCA). ICA is somewhat the most successful of these methods. However, most of the existing ICA methods use neural learning algorithms [2,3], which are complex and the performance highly variable with the update formula for the separating matrix. Furthermore, different independent components are obtained each time the methods are used, i.e. they are not unique. Also, the learning algorithm has to be chosen based on some prior knowledge of the signal, which may not be possible all the time [4].

Here, an alternative method to reduce noise from ECG signals is proposed using genetic algorithm (GA) that maximizes the kurtosis of the extracted independent components. Kurtosis maximization is one of the common techniques used in ICA [2].

The use of GA with kurtosis maximization has been proposed in [4] but never applied for any application. Other functions like Kullback-Leibler (KL) divergence [3] or mutual information (MI) minimization [5] has also been proposed as

fitness functions but the use of kurtosis function is more suitable for ECG signals due to the presence of R peaks. In addition, computation of kurtosis is simpler and faster than KL or MI.

The method proposed here automatically extracts ECG only, i.e. it avoids the extraction of all independent components and avoids the manual identification of the ECG signal, which would be the situation if neural learning ICA methods were to be used.

II. METHODOLOGY

It is well known in the field of ICA that a mixed signal will have more gaussian behaviour than its independent components [2, 3]. Therefore, by using kurtosis as a measure of gaussianity, we could separate the mixed signals into the independent components. Here, the mixing matrix is iteratively improved for source separation using increments in kurtosis as a measure of non-gaussian behaviour using GA. That is the kurtosis is used as the fitness function to be maximized by the GA. The method will work as long as one of the signals is non-gaussian [2].

The mixing matrix is represented by binary chromosomes converted to real-value that iterates through the GA operators: selection, crossover, mutation and inversion [6], to maximize the fitness function given by the kurtosis of the independent components.

Kurtosis is given by

$$\left[\frac{n(n+1)}{(n-1)(n-2)(n-3)} \sum \left(\frac{x_j - \tilde{x}}{s} \right)^4 \right] - \frac{3(n-1)^2}{(n-2)(n-3)}, \quad (1)$$

where n is the number of data, x_j is the data at point j , while \tilde{x} is the mean of the data.

The method is particularly suitable for ECG signals due to the presence of R peaks that give super-gaussian behavior (i.e. very high kurtosis). The method relies only on GA, which is simple as compared to existing ICA techniques that use complicated neural learning algorithms.

Consider the noise corrupted ECG signal to be represented in matrix form as

$$[Y]=[A][X], \quad (2)$$

where $[A]$ is the arbitrary noise mixing matrix, $[X]$ is the matrix containing ECG plus noise signals, while $[Y]$ is the matrix of the observed signals.

In ICA methods, the task is to obtain the inverse of matrix $[A]$ to reconstruct the original matrix $[X]$. In this proposed method, instead of the entire matrix $[X]$, only one signal that represent ECG in matrix $[X]$ will be extracted (reconstructed)¹ as GA iterates to give the signal with the highest kurtosis, which will be the ECG signal. In other words, GA will iterate such that only one output signal will be obtained, which will be ECG. This is an advantage as compared to using other existing ICA methods as it avoids the extraction of all independent components, and then to manually identify the ECG signal.

How this works could be understood with the following example. Assume

$$[Y] = \begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \end{bmatrix}, [X] = \begin{bmatrix} \text{noise1} \\ \text{ECG} \\ \text{noise2} \\ \text{noise3} \end{bmatrix}, \text{inv}[A] = \begin{bmatrix} a_{11} & a_{12} & a_{13} & a_{14} \\ a_{21} & a_{22} & a_{23} & a_{24} \\ a_{31} & a_{32} & a_{33} & a_{34} \\ a_{41} & a_{42} & a_{43} & a_{44} \end{bmatrix}, \quad (3)$$

Then

$$X_{ECG} = a_{21}y_1 + a_{22}y_2 + a_{23}y_3 + a_{24}y_4. \quad (4)$$

As could be seen from (4), GA will iterate to give only the coefficients a_{21} , a_{22} , a_{23} and a_{24} to reconstruct the ECG signal.

GA is a computational model inspired by evolution and is based on genetic processes of biological organisms. It is an adaptive method, which may be used to solve search and optimization problems. Over many generations, natural populations evolve according to the principles of natural selection and “survival of the fittest” [7]. GA requires fitness or objective function, which provide a measure of performance of the population individuals.

The use of GA will now be explained using the example discussed with eqs. (3) and (4). GA operates on the coding of parameters rather than the parameter itself. These parameters or genes, which are known as chromosomes, are a string of values representing potential solutions to a problem. Binary coding is used here for convenience but in future studies, it is planned to migrate the method to real-values (continuous) coding.

These certain number of genes (bits) will be used to represent each of the coefficients in $\text{inv}[A]$ as in (4). Assuming that 4 signals are observed as in (3) and 6 bits² are used for each coefficient, then each chromosome will have 24 bits. A population will consist of a certain number of these chromosomes, say 20. This is shown in Figure 1.

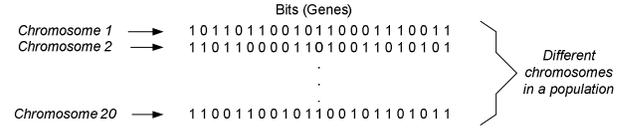


Fig. 1. Genes and chromosomes in a population.

The genes values in the chromosomes of the initial population will be set randomly. These bit valued genes will be converted to real-valued in the range of $[0,1]$ ³. Next, these 4 real-valued gene values are used in (4) to generate 20 independent signals and the kurtosis of each signal is computed. The fitness of each of the 20 chromosomes will be set to these kurtosis values.

Selection (reproduction) operator is performed next based on these fitness values. During this reproductive phase of the GA, chromosomes are selected from the population and recombined, producing offspring chromosomes that will comprise the population for next generation. GA starts with an initial population and selection is applied randomly from the initial population using a scheme that favors the more fit individuals (evaluated using the fitness function) to create the intermediate population. Good individuals will probably be selected several times in a generation while the poor ones may not be selected at all.

There are a number of ways of performing the parent selection process. The common methods are roulette wheel selection and rank based methods such as tournament selection. Both these selection operators are used here.

In tournament selection, certain number of chromosomes is picked randomly (in this case, 5) and the best chromosome (i.e. with the highest fitness) is stored. Since 50% of the new population will be selected here using this method, this procedure is repeated for 10 times (with the entire population) to obtain 10 chromosomes, where there maybe more than one similar chromosome.

The rest half of the new population will be selected using the roulette-wheel method. In this method, the fitness values of each chromosome are cumulatively added into a roulette wheel and when the wheel spins, there are higher chances for the higher fitness chromosomes to be selected. Here, a number is randomly generated to represent the wheel spin and the particular chromosome with the cumulative fitness range denoted by the number will be selected. This is repeated 10 times to add to the existing 10 chromosomes from tournament selection.

Despite the effectiveness of reproduction in increasing the percentage of better fitness chromosomes, the procedure is essentially sterile; it cannot create new and better chromosomes. This function is left over to crossover and to a lesser but critical extent, to mutation and inversion. Crossover process is intended to simulate the exchange of genetic material that occurs during biological reproduction. Here, pairs in the

¹ With different scale factors.

² Higher number of bits will be more accurate but will increase the computation time.

³ This range is suitable since the extracted signals of all ECG methods are likely to be scaled anyway.

breeding population are mated randomly with a crossover rate. There are a few popular types of crossover techniques like one point, two points and uniform crossover. In this work, uniform crossover is used.

The uniform crossover scheme works as follows. A randomly generated bit string called the crossover mask is used to generalize the process. A bit value of 1 in this bit string indicates that corresponding bits in the parents are to be exchanged while a 0 bit indicates no bit interchange. Here, uniform crossover is applied to two randomly chosen chromosomes to produce two new offsprings. This is repeated (with the exclusion of used parent chromosomes) for 5 times (since the crossover rate is 0.5). The parent chromosomes that have not been used are kept intact in the population.

Mutation randomly perturbs the population's characteristics, thereby preventing evolutionary dead ends. Most mutations are damaging rather than beneficial; mutation rate must be low to avoid the destruction of species. It works by randomly selecting a bit with a certain mutation rate in the string and reversing its value. Here, mutation is applied to the randomly chosen bit in a randomly chosen chromosome. Since the rate is 0.01, the mutation is repeated for $0.01 \times 24 \text{ bits} \times 20 \text{ chromosomes} \approx 5$ times or 5 bits.

Inversion works by reversing the bits with a certain inversion rate between two randomly chosen points in a randomly chosen chromosome. Here, inversion is applied to the bits between two randomly chosen points in a randomly chosen chromosome. Since the rate is 0.01, the inversion is repeated for $0.01 \times 24 \text{ bits} \times 20 \text{ chromosomes} \approx 5$ bits⁴.

Figure 2 shows a block diagram on the use of GA here.

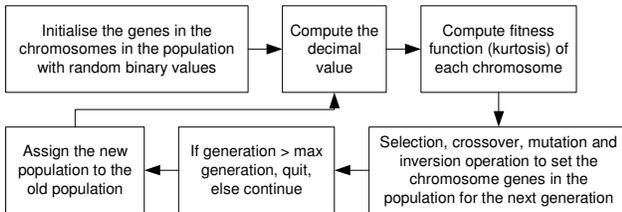


Fig. 2. Block diagram on the use of GA here.

III. EXPERIMENT, RESULTS AND DISCUSSIONS

To show the effectiveness of the proposed method, two simulations were conducted. Table 1 summarizes the used GA parameters. In the first simulation study, different noises (random, baseline, powerline, EEG and EMG) were created and added to a clean ECG signal obtained from an ECG emulator. Figure 3 shows the clean ECG signal and the two biological noises: EEG and EMG.

Figure 4 shows the random, baseline and powerline noises. Random noise was created using a random function generator to generate the noise, while the powerline was created using a

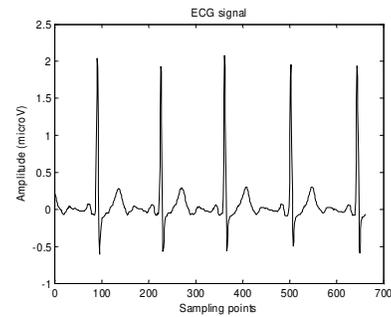
sine wave with frequency at 50 Hz. Baseline noise was created using the following function [8]:

$$Baseline_{noise}(n) = A \cos((2/N)\pi) - B + m \quad (5)$$

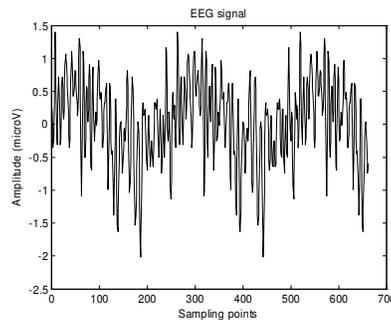
where $A=0.01$, $m=0.001$, and $B=-0.1$ were fixed based on studies in [8]. N was fixed at 662 since it was the length of the ECG signal used here. The values in the mixing matrix were randomly set in the range $[0,1]$.

TABLE I
GENETIC ALGORITHM PARAMETERS

Coding of genes	Binary coding converted to real value [1,0] for fitness computation
Fitness function	Kurtosis (4th order moment of the signal)
Population size	20
No. of genes	6 bits for each gene
Reproduction (selection)	Roulette wheel (50% of population) and tournament selection (50% of population)
Crossover type and rate	Uniform crossover, 0.5
Mutation type and rate	Mutate randomly selected bits, 0.01
Inversion type and rate	Inversion between 2 randomly selected points, 0.01
Convergence	Maximum 100 generations
Repetition	GA simulation is repeated 3 times and the best chromosome is selected

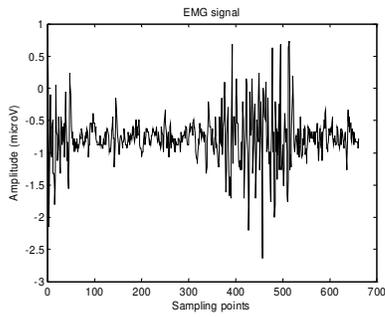


(a)



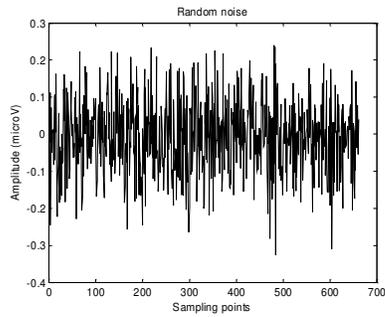
(b)

⁴ It could be that inversion is applied only once or several times, the criterion is that 5 bits will be inverted.

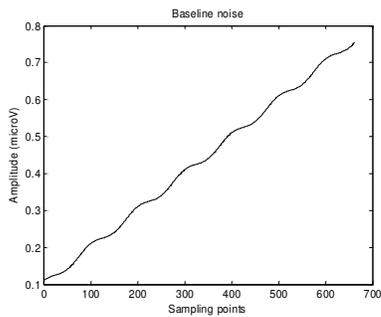


(c)

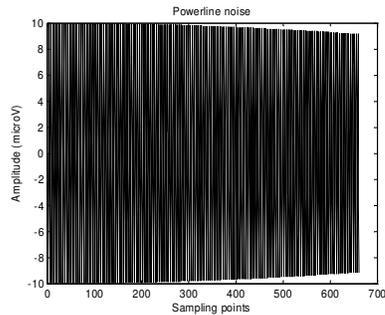
Fig. 3. Signals used in computer simulations: (a) the clean ECG signal, (b) the EEG noise signal, and (c) the EMG noise signal.



(a)



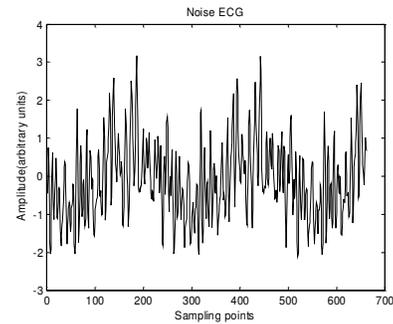
(b)



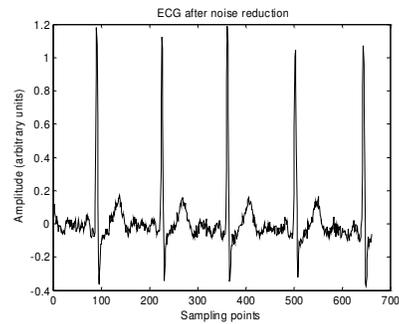
(c)

Fig. 4. Signals used in computer simulations: (a) random, (b) baseline and, (c) powerline noises.

Figure 5 shows the noise corrupted ECG signal and the noise reduced ECG signal. After applying the proposed method, the SNR improvement was from 0.0055 dB to 53.4119 dB, which shows that the proposed method has reduced noise from the ECG signal.



(a)



(b)

Fig. 5. Signals used in computer simulations: (a) noisy ECG signal, and (b) noise reduced ECG signal.

In the next simulation study, the proposed method was applied to reduce noise from real ECG signal obtained from the Massachusetts General Hospital/Marquette Foundation (MGH/MF) database (simulation done with 3 recordings of lead I ECG signals at different time intervals). From Figure 6, it could be seen that the proposed method also reduced noise from ECG signal obtained from MGH/MF database. It must be noted that the reconstructed signal will be scaled or inverted (just like in other ICA methods). This would be due to the negative/positive coefficients of the inverse of matrix $[A]$ given by GA.

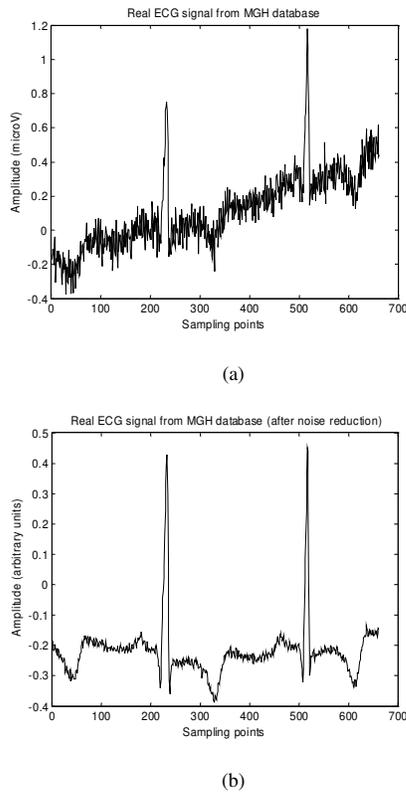


Fig. 6. Signals used in computer simulations: (a) lead I ECG signal from MGH/MF, and (b) noise reduced ECG signal.

IV. CONCLUSION

In the simulation study, the method successfully separated a mixed signal consisting of ECG and multiple noises like random noise, powerline interference, EEG, muscle artifacts (EMG) and baseline. To validate the method further, the experiment was conducted with ECG signal from MGH/MF database, which also gave good results. Since the method does not assume any property of noise, it could be applied to reduce

any type of linear additive noise from ECG signals or any other signal with high kurtosis value. For future work, chromosomes with continuous values will be explored instead of binary chromosome converted to real-values as done here.

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