

A Genetic Algorithm for Blind Source Separation Based on Independent Component Analysis

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Abstract— This paper presents the implementation of genetic algorithm (GA) to a simple blind source separation(BSS) problem using independent component analysis(ICA). The process did not include pre-processing of mixture signals such as centering and whitening like most of ICA algorithms. The GA directly guesses the coefficients of the separating matrix given the mixture signals as inputs using maximization of kurtosis and minimization of mutual information as fitness function. Only one fitness function was defined to account the fitness for kurtosis and mutual information. Two sets of simulations were performed: two mixtures and three mixtures with two and three independent sources, respectively. Synthetic signals of 500 samples were used. It was found out that the GA for BSS indeed separates the independent sources. The signal with the highest value of kurtosis got the best estimate

Index Terms— blind source separation, BSS, independent component analysis, ICA, genetic algorithm, GA

I. INTRODUCTION

Blind source separation (BSS) is an advanced signal processing technique which aims to recover source signals from a received mixture without any information about the independent sources and how the signals were mixed. It has been considered in many research fields such as speech processing [1], image [2] [3], communications [4], and bio-medicine [5]. One can think of a BSS system as a black box with inputs as mixtures of independent sources and the outputs are the estimate of the independent sources. BSS algorithms are used to adjust the parameters of the black box in order to obtain the independence of its output [6]. The process involves minimization and/or maximization of one or more objective functions.

One of the techniques used for BSS is independent component analysis (ICA). It is a technique based on statistics. It assumes that independent sources are non-

gaussian signals and that they are mutually independent. Typical optimization criteria used in ICA are kurtosis, mutual information and negentropy. Various algorithms have been developed for ICA and one of the most popular is fastICA[7]. FastICA and most of the ICA algorithms do pre-processing of mixture signals to simplify the analysis such as centering and whitening. Centering is the process of removing the mean from the mixture but this mean is added back to the estimated signal after estimating the mixing matrix, and whitening is the process of transforming the mixture signals such that the new signals are uncorrelated.

This paper presents the genetic algorithm (GA) as it applies to a simple BSS problem using ICA. The process did not include pre-processing of mixture signals such as centering and whitening like most of ICA algorithms. GA is a well-known technique for optimization. The GA directly estimates the coefficient of the separating matrix and uses kurtosis and mutual information as fitness function.

Solving BSS using ICA and GA is an active research area. There are many literatures that explore ICA and GA for BSS, [8-16]. Mostly, they differ in the architecture of GA and the optimization criteria used.

This paper is organized as follows: Section 2 presents the fundamental concepts of BSS and ICA; Section 3, the details of genetic algorithm in solving BSS. Sections 4,5,6,7 present the simulation, results, conclusion, and recommendation, respectively.

II. BLIND SOURCE SEPARATION

A. Mathematical model of BSS

Let the independent sources $s_1(t)$ $s_2(t)$, ... , $s_n(t)$ be represented as vector $s(t) = [s_1(t) \ s_2(t) \ \dots \ s_n(t)]^T$ and the observed linear mixtures of independent components are $x_1(t)$, $x_2(t)$, ..., $x_n(t)$ represented as $x(t)$ vector, $x(t) = [x_1(t) \ x_2(t) \ \dots \ x_n(t)]^T$. The relationship of $s(t)$ and $x(t)$ is

$$x(t) = A s(t) \quad (1)$$

where A is called a mixing matrix. The task of BSS is to find the separating matrix B such that

$$y(t) = B x(t) \quad (2)$$

where $y(t) = [y_1(t) y_2(t) \dots y_n(t)]^T$. If $B = A^{-1}$, then $y(t)$ is exactly $s(t)$. One requirement of BSS is that the number of mixtures should be greater than or equal to the number of independent sources. For simplicity, it is considered in this research that the number of independent sources is equal to the number of mixtures.

B. Independent Component Analysis

The idea of most BSS algorithms is based on ICA. It is a subcategory of BSS which attempts to separate the independent sources based only on their statistical characteristics. It assumes that the independent sources are non-gaussian signals. Information bearing signals such as speech are non-gaussian [17]. Also, it assumes that the sources are independent statistically. The following items are two of the typical optimization criteria applied to ICA.

1. Kurtosis

Kurtosis is used as a measure of non-gaussianity. It describes the “spikeness” of the signal. A Gaussian probability function has a zero kurtosis. Those random variables with positive kurtosis are called super-gaussian and those with negative kurtosis are called sub Gaussian. The higher the value of kurtosis, the more the signal is away from Gaussian. The kurtosis of the estimated signals is defined as

$$J_{kurt}(y) = \sum_{i=1}^N |kurt(y_i)| \\ = \sum_{i=1}^N |E[y_i^4] - 3(E[y_i^2])^2| \quad (3)$$

One task of BSS is to find W that can maximize (3). Kurtosis shows the independency of the components of the source signals, but kurtosis alone is not sufficient to separate independent signals from the mixture [19]. Usually it is combined with other criteria such as negentropy, entropy, diagonalization of the correlation matrix, mutual information.

2. Mutual information

A measure of how much common information between two random variables X and Y is called mutual information (MI). MI is always non-negative and identically zero if the two random variables are statistically independent. The mutual information of two random variables X and Y is mathematically defined as

$$I(X;Y) \triangleq E \left\{ \log \frac{p(X,Y)}{p(X)p(Y)} \right\} \\ = E\{\log p(X,Y)\} - E\{\log p(X)\} - E\{\log p(Y)\} \quad (4)$$

3. Negentropy

The negentropy $J(y)$ of a random variable y is defined as

$$J(y) \triangleq H(Y_{gauss}) - H(Y) \quad (5)$$

It is a measure of the difference in entropy of a given distribution and Gaussian distribution with the same mean and variance. Negentropy is non-negative and identically zero if and only if Y has a Gaussian distribution.

III. GENETIC ALGORITHM FOR BLIND SOURCE SEPARATION

GA is a biologically inspired computational model based on Darwin’s theory of evolution for function optimization. The following are the steps of GA in solving BSS based on ICA. The flowchart is shown in Figure 1.

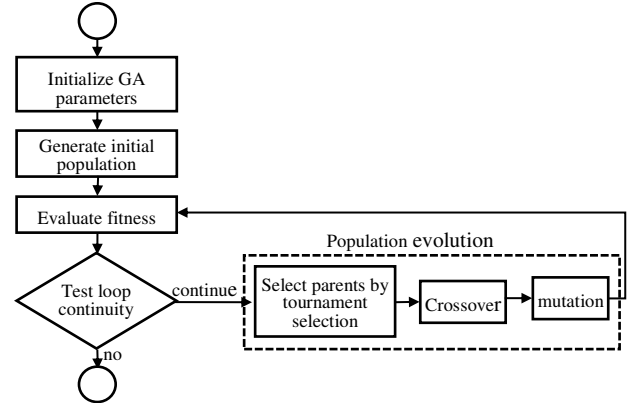


Figure 1. Flowchart of GA for BSS

1. Chromosome encoding

Encoding is the process of identifying the possible solution of the optimization problem and represents it as a vector or a string. Each element in a vector defines a particular parameter in the solution and it could be represented as binary or real value number. The number of elements of a vector depends on the number of unknown parameters. This vector or string is referred to as chromosome. Each element of the chromosome is called a gene.

The chromosome of individuals used for BSS consists of the elements of the separating matrix. Its size depends on the number of unknown independent sources. If there are n independent sources, then the size of the separating matrix is $n \times n$. The elements are arranged from the first element of the first row to the last element of the last row. Each element w_{ij} , which is referred to as a gene is represented as double precision floating number and the value is

constrained from -5.0 to + 5.0. Figure 2 shows the chromosome structure.

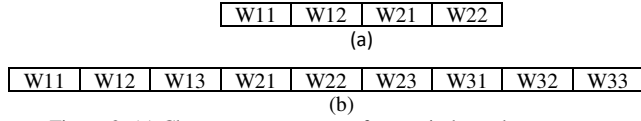


Figure 2. (a) Chromosome structure for two independent sources
(b) Chromosome structure for three independent sources

2. Generate the initial population

The number of individuals in the population is called the population size. Basically, it is a predefined constant. An individual is characterized by its chromosome. Each individual is a candidate to the solution of the problem. Usually, the individuals in the initial population are generated with random elements of chromosome constrained to some value as defined in Step 1.

3. Calculate the fitness

The fitness of an individual in the population is calculated based on the so called fitness function. This function is dependent on the problem to be optimized. This is a function that tests how far or near the individual is to the solution of the problem. The nearer the individual to the solution of the optimization problem, the more fit is the individual. It could also be possible that the solution is found at this stage. If that is the case, then go to Step 7.

The function used to evaluate the fitness of each individual to separate the independent components is maximization of the sum kurtosis (3) and minimization of mutual information (4). In order to combine the minimization of mutual information and maximization of kurtosis as one fitness function, the authors used exponential decay function of mutual information, the lower the value of mutual information, the higher the value is added to the fitness. Mutual information is accounted to the fitness if the mutual information between two signals is less than 0.2. That is, if the mutual information $I(Y_i; Y_j)$ (4) where $i \neq j$ represented as m_{ij} is less than 0.2 then a value of $100e^{-10m_{ij}}$ is added to the sum kurtosis. The overall fitness function, $J_o(y)$, then is

$$J_o(y) = \sum_{i=1}^N |kurt(y_i)| + \sum_{i=1, j=1, i \neq j}^N 100e^{-10m_{ij}}, \forall m_{ij} < 0.2 \quad (6)$$

The flowchart evaluating fitness is shown in Figure 3.

4. Reproduction process

The basic operation in reproduction process is selection, crossover and mutation. In this stage, two individuals which shall serve as parents are selected by tournament selection. Tournament selection involves creating a small size population defined by tournament size

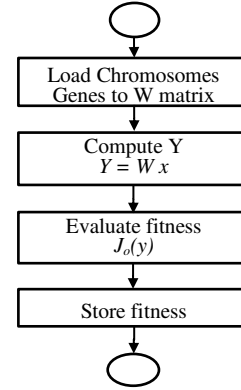


Figure 3. Flow chart of fitness evaluation

and the fittest individual is selected. This population is filled with randomly chosen individuals from the pool of parents. The selected parents undergo mating or crossover in GA terms and produce an offspring. In this step, only one offspring is used although it is common in the literature, [19] that the crossover operation produces two offspring. Crossover can be single point, two-point or multipoint. Multipoint is used. Which genes would take by an offspring is determine by the constant called *crossover rate*, that is 0.5. For a particular gene of an offspring a random number is generated, if it is less than 0.5 the offspring will get the gene of parent 1 otherwise the offspring will get the gene of parent 2. An offspring then undergoes mutation, which gene will mutate is determined by the constant called mutation rate. The gene will mutate if the randomly generated number is less than *mutation rate*. Reproduction process is repeated until the number of offspring is equal to *population size*. The generated offspring will serve as the parents for the next generation. They will serve as individuals of the new population.

5. Do step 3 for the new population.

6. Test for loop condition. If satisfied then go to next step or else proceed to Step 4.

7. Stop.

IV. SIMULATION

Three synthetic signals of 500 samples were used in simulations. Figure 4 shows the first 100 samples of these signals. The kurtosis value of these sources is shown in Table 1.

Table 1. Kurtosis of synthetic signals

Signal	Kurtosis
Signal 1	-1.4984
Signal 2	2.4775
Signal 3	-1.1994

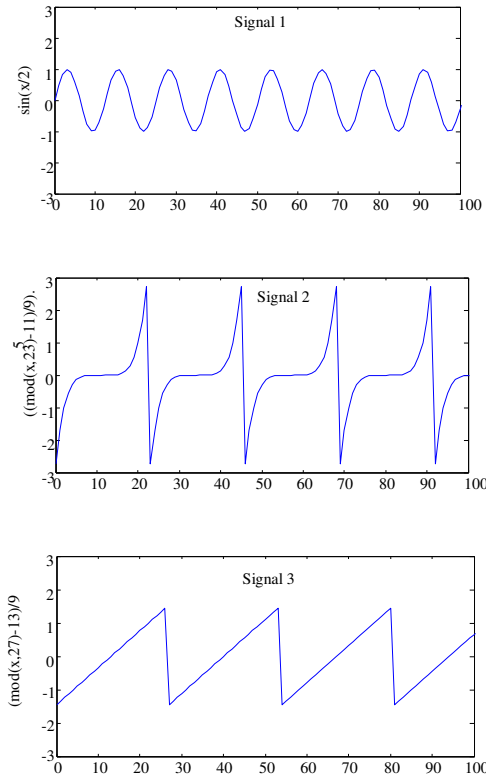


Figure 4. Synthetic signals

The first simulation uses the mixture of the first two signals in Figure 4 with the following mixing matrix

$$A = \begin{bmatrix} 1.25 & 0.75 \\ 1.50 & 2.0 \end{bmatrix}.$$

The first 100 samples of the mixtures are shown in Figure 5. The second simulation uses the mixture of all three signals with mixing matrix,

$$A = \begin{bmatrix} 0.2142 & 0.1786 & -0.125 \\ 0.5000 & -0.250 & -0.250 \\ -0.0714 & 0.1071 & 0.250 \end{bmatrix}.$$

The mixtures are shown in Figure 6.

The GA parameters were adjusted until useful results were obtained. These parameters are *population size*, *crossover probability*, *mutation probability*, *tournament size*, and *number of generations*.

The performance of the estimates is measured using mean square error (*MSE*) defined as

$$MSE = \frac{\sum_{i=1}^n (s_i(t) - y_i(t))^2}{n} \quad (7)$$

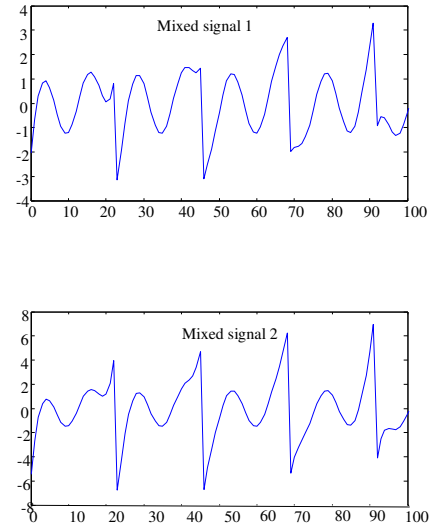


Figure 5. Mixtures for Simulation 1

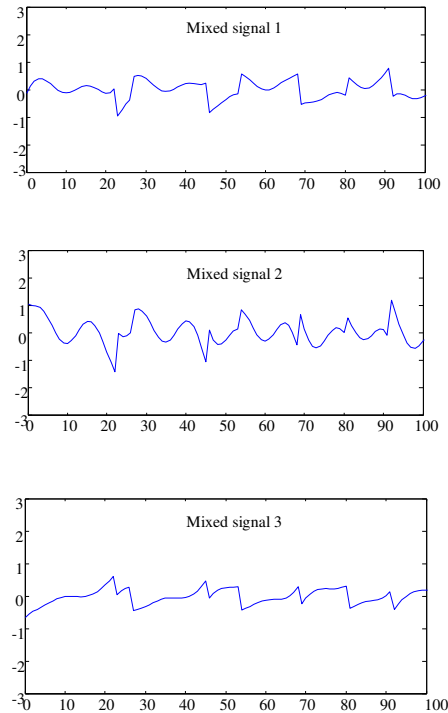


Figure 6. Mixtures for Simulation 2

V. RESULTS

The useful results of the simulations were obtained using the GA parameters shown in Table 2.

Table 2. GA parameters used in simulations

GA parameters	Simulation 1 (two signals)	Simulation 2 (three signals)
<i>population size</i>	50	100
<i>tournament size</i>	10	10
<i>crossover probability</i>	0.5	0.5
<i>mutation probability</i>	0.25	0.25
<i>number of generations</i>	190	218

The best fitness of an individual in each generation for one chosen run of the first simulation is shown in Figure 7. A good estimate was obtained at 190th generations or iterations. The estimated signals at this generation are shown in Figure 8 and the mean square error at this generation is shown in Table 3. It can be observed that the estimated signal has no order. The first estimated signal corresponds to Signal 2 and the second estimated signal corresponds to Signal 1. Also, the best estimate was obtained by the signal with the highest value of kurtosis as shown in Table 1.

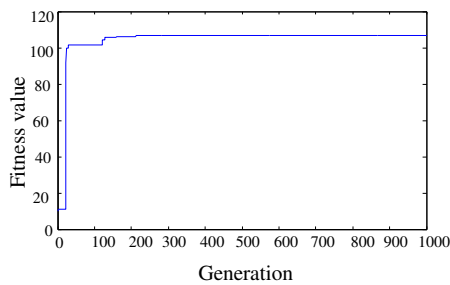


Figure 7. Best fitness of Simulation 1

Table 3. Mean square error of Simulation 1

Signal	MSE
Signal 1	0.0317
Signal 2	0.0130

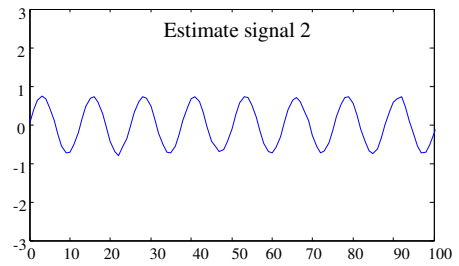
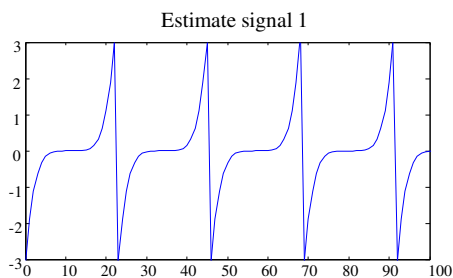


Figure 8. Estimated signal in Simulation 1 at 190th generation

For the second simulation consisting of three mixtures, the best fitness of one randomly chosen output is shown in Figure 9. A good estimate starts at generation 218. The estimated signals at this generation are shown in Figure 10 and mean square error of the estimated signals is shown in Table 2. As with the first simulation, the signal that gets the best estimate is the signal with the highest value of kurtosis.

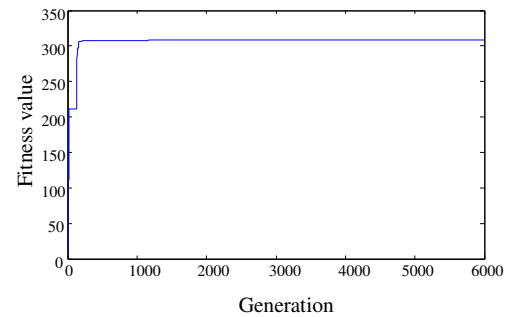
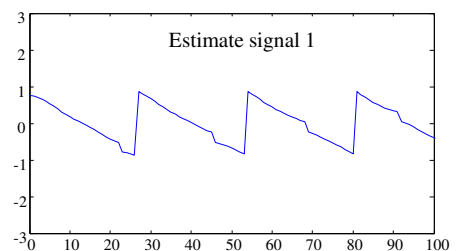


Figure 9. Best fitness of Simulation 2.

Table 3. Mean square error of Simulation 2

Signal	MSE
Signal 1	0.1191
Signal 2	0.0047
Signal 3	1.8044



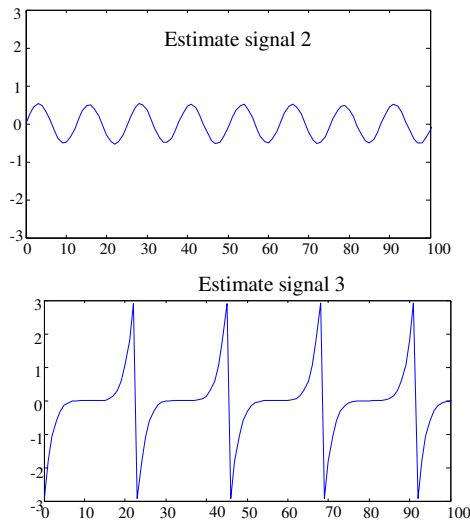


Figure 10. Estimated signals in Simulation 2.

VI. CONCLUSION

The genetic algorithm for BSS was successfully implemented. Although only few runs were performed in the simulation consisting of two and three mixtures, the results show that the algorithm developed by the authors that utilizes genetic algorithm with kurtosis and mutual information as fitness function in solving blind source separation indeed separates the independent sources.

The resulting separated signals have no order and the best estimate was obtained by the most non-Gaussian signal, the signal with the highest value of kurtosis.

VI. RECOMMENDATION

In order to observe the stability of the algorithm, the computer program should be run several times for two and three mixtures. Better or efficient GA parameters may be obtained from these observations. Using these parameters, the program can be run using the speech recorded signals or tests real time in order to determine the suitability of the algorithm in real time speech signals for a particular environment.

ACKNOWLEDGMENT

The authors would like to acknowledge the financial support extended by Mindanao State University-General Santos City, De La Salle University and Commission on Higher Education (CHED).

REFERENCES

- [1] B. Rivet, L. Girin, C. Jutten, J. Schwartz, "Using audiovisual speech processing to improve the robustness of the separation of convolutive speech mixtures," 6th IEEE Workshop on Multimedia Signal Processing, pp. 47-50, Oct. 2004.
- [2] Y. Hujun, I. Hussain, "Blind Source Separation and Genetic Algorithm for Image Restoration," International Conference on Advances in Space Technologies, pp.167-172, Sept. 2006.
- [3] E. Karray, M.A. Loghmari, M.S. Naceur, "Blind source separation of hyperspectral images in DCT-domain," 5th Advanced satellite multimedia systems conference and the 11th signal processing for space communications workshop, pp.381-388, Sept. 2010.
- [4] A.K. Kattapur, F. Sattar, C. See, "Doppler aided blind source separation of communication signals," 10th International Conference on Information Sciences Signal Processing and their Applications (ISSPA), pp.526-529, May 2010.
- [5] A. Kachenoura, L. Albera, L. Senhadji, P. Comon, "ICA: A Potential Tool for BCI Systems," IEEE Signal Processing Magazine. 2008.
- [6] Y. Tan, J. Wang, "Nonlinear blind source separation using higher order statistics and a genetic algorithm," IEEE Transactions on Evolutionary Computation, vol.5, no.6, pp.600-612, Dec 2001.
- [7] A. Hyvarinen and E. Oja (2000) Independent Component Analysis: Algorithms and Applications, Neural Networks, 13(4-5), pp.411-430, 2000
- [8] X. Zeng, Y. Chen, Z. Nakao and G. Yamashita, "Signal separation by independent component analysis based on a genetic algorithm," Proceeding of ICSP. 2000
- [9] Y. Tan, J. Wang, "Nonlinear Blind Source Separation Using Higher Order Statistics and a Genetic Algorithm"
- [10] Y. Huang, S. Lou, "Genetic Algorithm Applied to ICA Feature Selection" IEEE 2003
- [11] N. L. Peng, D. H. Zhao, "Independent Component Analysis Based on Improved Quantum Genetic Algorithm: Application in Hyperspectral Images" 2005
- [12] S. Kai, W. Qi and D. Mingli, "Approach to Nonlinear Blind Source Separation Based on Niche Genetic Algorithm" 2006
- [13] K. Wang, W. Zhang, "Blind Source Separation Based on Chaotic Immune Genetic Algorithm with High-order Cumulate" 2006
- [14] D.P. Archaya, G. Panda, Y. Lakshmi, "Constrained Genetic Algorithm Based Independent Component", Congre 2007
- [15] Xiang-Yan Zeng, Yen-Wei Chen, Zensho Nakao and Gtsumi Yamashita, "Signal separation by independent component analysis based on a genetic algorithm". Proceedings of ICSP.2000
- [16] S. Kai, W. Qi, D. Mingli, "Approach to Nonlinear Blind Source Separation Based on Niche Genetic Algorithm," Sixth International Conference on Intelligent Systems Design and Applications, 2006. ISDA '06., vol.1, no., pp.441-445, Oct. 2006
- [17] M. Wolfel, J. McDonough, Distance Speech Recognition, John Wiley & Sons, 2009.
- [18] A.Ebrahimzadeh, S.Mavaddati, "A novel technique for blind source separation using beescolonyalgorithm an defficient cost functions". Elsevier. Swarm and Evolutionary Computation.2013
- [19] Elmer P. Dadios and Jamshaid Ashraf, Genetic Algorithm with Adaptive and Dynamic Penalty functions for Constrained

