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# Embedded Development System Based Blind Signal Separation of Multi-channel Eeg Analyzer

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**Abstract:** The EEG (electroencephalogram) signal is a whole express way to show it's complicated electronic composition signal. It is a generally-accepted test method of epilepsy. An analysis algorithm of 24 lead EEG signal and it's embedded development system circuit method is discussed in the article. The method is based on genetic algorithms and fast ICA (FICA). And here a novel GA process is designed to realize a high-speed and automatic estimation. The comparative experiments show the whole solution is a robust, effective and superior method to solve the EEG blind signal separation problem.

**Key words:** Embedded development, EEG, FICA, genetic algorithms

## INTRODUCTION

Epilepsy is a disorder of the nervous system diseases, the incidence in the population is about 0.5 to 2%. the disease to a large group of brain cells caused by repeated episodes of super-synchronous discharge resistance, sudden, transient cerebral dysfunction as features. Electroencephalogram (EEG) examination is the clinical diagnosis of epilepsy and lesion localization techniques commonly used by EEG epilepsy. EEG signals high temporal resolution and in millisecond level accurately reflects the brain's time-varying characteristics. However, due to time-varying sensitivity of EEG itself may also be subject to some unrelated electrophysiological signal interference, the clinical point of collection to the brain signals often contain EOG artifacts (ocular artifacts), EMG artifact (muscle artifacts) and ECG artifact and so on. Therefore artifact removal method is currently a hot research.

## DATA PREPROCESSING

30 inpatients' EEG signals and long-term video, monitoring come from Beijing EEG Epilepsy Center of a hospital, the hospital uses Nicolet 24-32 leads system, the sampling frequency is 500Hz. Fig.1 shows Mr. Han's Fp1 signal about 2 seconds collected in April 2012, we can see in the raw data there is a clear 50Hz industrial frequency noise interference. The current international new study suggests that interictal high-frequency oscillations may exist in the slow wave, therefore, keep the original signal of other band is very important. through a 50Hz band-stop
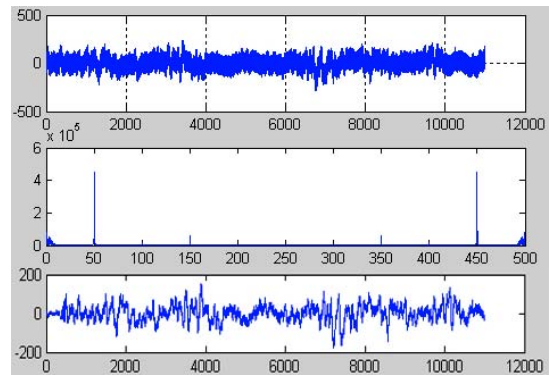


Fig. 1: UP: The original Fp1 signal, showed obvious industrial frequency noise Middle: Original Fp1 signal spectrum, Bottom: Filtered Fp1 signal
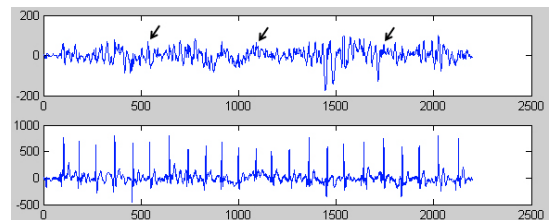


Fig. 2: UP: Fp1 signal , Bottom: reference ECG signal Alpha

filter can accurately remove the industrial frequency noise, the filtered data is shown in Fig.1.

To comparison with reference ECG signal, there was obvious ECG interference in most leads (Fig. 2).

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## FAST INDEPENDENT COMPONENT ANALYSIS (FICA)

ICA method is a powerful signal processing and data analysis tool to solve the blind source separation and gradually developed in recent years (De al Torre and Black, 2001; Hyvarinen and Oja, 1996). In many ICA algorithms the fixed point algorithm (also known FICA) is widely used in the field of signal processing and analysis by its fast convergence and good separation. The algorithm can estimate statistically independent signal from the observed signal which is mixed by unknown factors (Delfosse and Loubaton, 1995).The algorithm is proposed by Aapo Hyvarinen of the University of Helsinki, Finland. Based on the fixed-point recursive algorithm, applicable for any type of data . FICA algorithm is essentially a component of minimizing estimated mutual information method, using the maximum entropy principle to approximate the negative entropy and a suitable nonlinear function optimal. Fig. 3 is Principle diagram of FICA algorithm.

Where, S is independent source signal, X is the observed signal can be collected (mixed signal) which can be regarded as produce of independent of the source signal and mixing the product of matrix A. FICA is to find an Unmixing matrix W, so that, mixed signals transferred into separation signals Y, Y can be as close as S. Because ICA can not distinguish between noise and independent source signals it is necessary to make signals zero-mean

and whitening to simplify the FICA algorithm and after this two pretreatment, optimization iteration time would be more superior.

The flow of the algorithm is shown in Fig. 4:

**Made the observed signal zero-mean:** First, standardized the observed signal (mixed-signal) $X = [x_1(t), x_2(t), \dots, x_n(t)]$ by $X = (X-m_j)/S_j$ . where $m_{j \text{ and }} S_j$ separately for mean and standard deviation. Subtracting the mean vector from the observed signal to get zero mean vector signal. The pretreatment only to simplify the ICA algorithm.

**Whitening:** For any multi-dimensional signal by applying a linear transformation to make it into a white signal process is called whitening and the corresponding transformation matrix called whitening matrix, after whitening each component is independence and has a unit variance.

Let Q be a whitening matrix of X, so cov $(QX) = I$ Use $X = AS$ substituted into the formula and let $H = QA$, then $\overline{x}(t) = QAs(t) = Hs(t)$.

Because $\overline{x}(t)$ and $s(t)$ are two white random vector connected by linear transformation H, thus the matrix H must be an orthogonal matrix. Whitening make the original
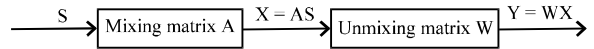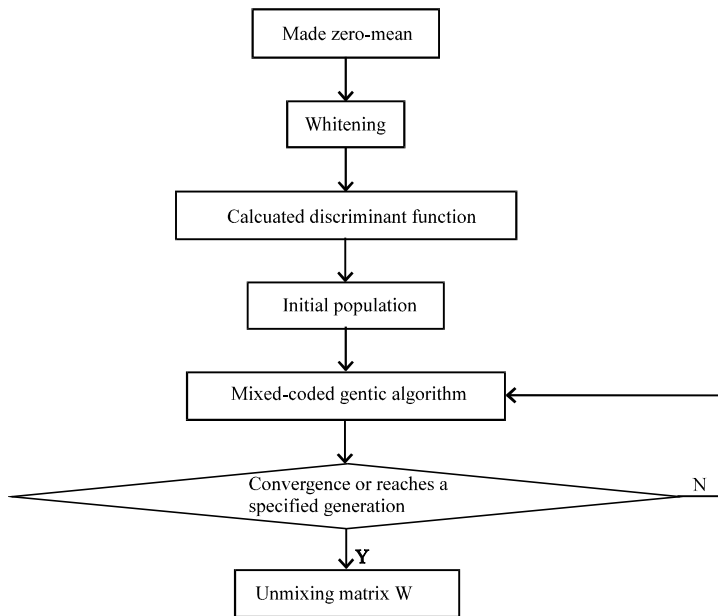


Fig.3: Principle diagram of FICA



Fig.4: flowchart of FICA

Table 1: Item selection of real coding-term

| Initial solution group | Translation parameter | Genetic operator | Crossover strategy | Mutation strategy |
|---|---|---|---|---|
| Flow No. ranging in a fixed area | -0.08~0.08 | Window rolling selection | Partly arithmetic crossover | Uniform mutation |

mixing matrix A reduced to an orthogonal matrix H to reduce the complexity of the problem effectively.

**Optimization algorithm:** FICA's basic goal is to find a linear transformation W (unmixing matrix). The problem can be decomposed into two basic issues: Optimization criterion (objective function) and optimization algorithms. Genetic Algorithm (GA) (Hill *et al.,* 2 005; To and Vohradsky, 2007) is a simulation of natural biological evolution and mechanisms for solving a class of extremal problems self-organizing, adaptive artificial intelligence techniques. It is also more suitable for parallel computation, easy hardware implementation. In this study, negative entropy was used as a optimization criterion, with the real number coding and Gray code encoding hybrid genetic algorithm to optimize and determine the matrix W.

**Optimization criterion:** It is known that the Gaussian variable has maximum entropy. Thus we can use the entropy to measure non-Gaussian. Negative entropy, modified form of entropy, is always use as a measure of zero Gaussian distribution with non-negative, non-Gaussian. The entropy is:

$$H(Y) = -\int p_Y(y) \lg P_Y(y) dy \qquad (1)$$

where, p (Y) is probability density function of random variable Y. Its negative entropy is defined as:

$$J(Y) = H(Y_{gauss}) - H(Y) \qquad (2)$$

Which $Y_{gauss}$ is composed of n Gaussian random vector and have the same mean and covariance matrix with Y. So negative entropy always non-negative. Negative entropy can measure the independence between the signals:

$$
\begin{aligned}
J(Y) &= \int p(Y) \log p(Y) dY - \int p_{gauss}(Y) \log p_{gauss}(Y) dY \\
&= \begin{aligned}[t] &\int p(Y) \log p(Y) dY - \int p(Y) \log p_{gauss}(Y) dY \\ &+ \int p(Y) \log p_{gauss}(Y) dY - \int p_{gauss}(Y) \log p_{gauss}(Y) dY \end{aligned} \\
&= \int p(Y) \log(\frac{p(Y)}{p_{gauss}(Y)}) dY \\
&\quad + \int (p(Y) - p_{gauss}(Y)) \log p_{gauss}(Y) dY
\end{aligned}
\qquad (3)
$$

The mutual information can be expressed by negative entropy:

$$I(Y) = J(Y) - \sum_{i=1}^{n} J(Y_i) \qquad (4)$$

Mutual information ninimization is equivalent to negative entropy maximization. Thus based on negative entropy maximizing optimization criterion is:

$$\phi_{NM}(W) = -\log|\det W| - \sum_{i=1}^{n} J(Y_i) + H_{gauss}(Y) - H(X) \qquad (5)$$

**Genetic algorithms (GA):** Theoretically GA shows superior performance but in practice it is easy to fall into local extremum. The most critical step in GA is coding, different coding method in evolutionary algorithm complexity and efficiency of a huge difference. the real coded GA with the ability of searching large space (results in high scanning speed and an overall observation) could give a overshoot result during a small-space-scan and the Gray coding has a strong adjusting ability in small space, though, a slow speed in the initial term, here a combination-scan is composed. This means that in the initial term the Real-code method is used, after obtaining a good convergence the Gray-scan method is used to perform a local fine turning, thus reach a high speed and accurate optimal scan. the encoding method has been tested on many occasions and proved very effective. This phased coded genetic algorithm used in this article to optimize W.

The first phase-the real coding-term is composed as shown in Table 1

Facing different application problems there are a variety of operator forms. In the period of real code, Window-Rotation-Selection method is used and its cross- and strange-changing operator is described as following. Making cross-operation on selected individuals $x_1$, $x_2$, according to probability $P_c$, new individuals are produced as $x_1$, $x_2$ by equation 6, Where, i: Randomly selected cross-point; k: pre-given real number, $0<l<1, 0<l, 0<k<1$; l length of chromosome.

$$
\begin{aligned}
x_1 &= K \times x_{1i} + (1-k) \times x_{2i} \\
x_2 &= (1-k) \times x_{1i} + k \times x_{2i}
\end{aligned}
\qquad (6)
$$

After finishing cross-operation and producing new class-group, select the strange-changing-joining individuals to execute the changing operation as described in equation 7 Where, $x_m$s: Selected individual; var: Randomly produced random numbers ranging within the weight-area:

$$x''m = x'_m + var \qquad (7)$$

The second phase-the Gray-code method is composed as the following:

- Translation parameters are mininum:-0.01, maximum: 0.01, digit number:10, Chromosome number:50, cross probability:0.8, mutation probability:0.01

In the period of Gray-code, the window-rotation method is used, the cross-operator is classical 2-point-cross-operator, and the strange-changing-strategy is 1-bit-random-changing.

**Detailed steps of GA based FICA:**

- Pretreatment of the observed data, i.e. made zero-mean and whitening
- Randomly generate the initial population of matrix W
- Calculate the initial population optimization criterion-negative entropy
- By the optimization criterion value sorted, use crossover and mutation operations and make the population into the next generation
- To reach the specified hereditary algebra or a negative change in entropy threshold is reached, stop the GA
- Obtain the best $W = [w_1, w_2,...wn]^T$

This algorithm is implemented in EL-DSP/ARM-IV hardware which will discussed in another paper.

## RESULT

To facilitate the display, only six leads signal of actual clinical 24 lead and the results were showed in the Fig. 5 to 8.
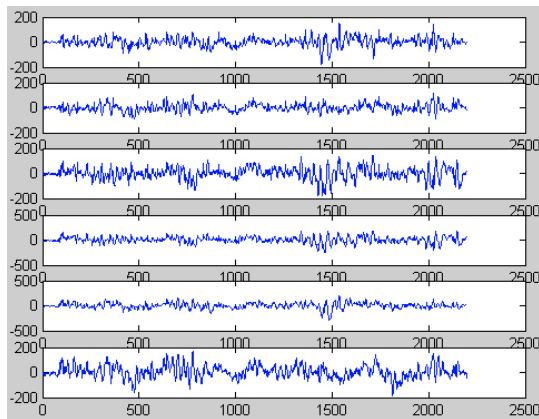
Fig. 5: A clinical EEG signals in 6-lead, ECG artifact visible

## SUMMARY

In this article, we use a GA combined FICA algorithm to compute unmixing matrix W of the clinic EEG signals and the result shows that the whole algorithm is effective and robust. The algorithm can seamlessly migrate to DSP/ARM hardware e architecture
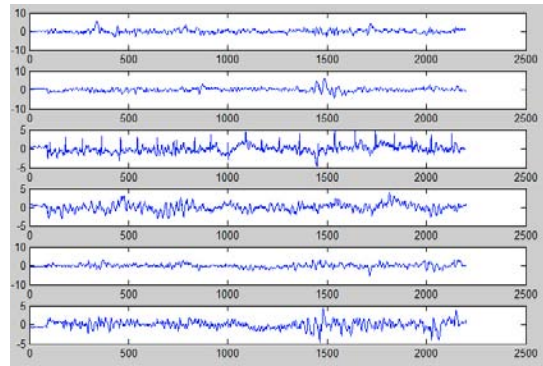
Fig. 6: After FICA solution, where the third channel signals reflect more realistic ECG R spikes
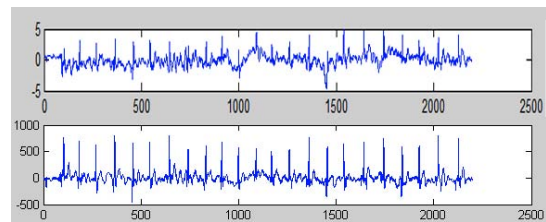
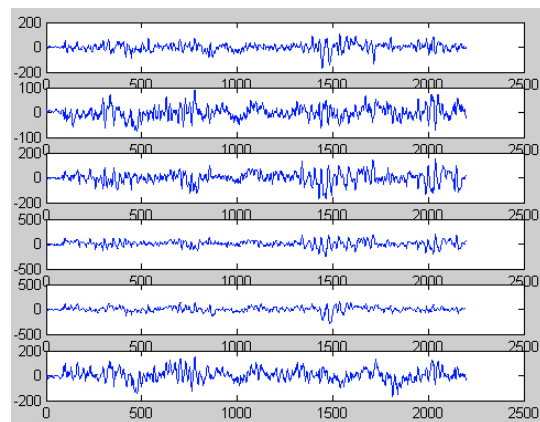Fig. 7: Extraction third lead signal comparison with ECG signal

Fig. 8: Delete the third channel signal, the remaining signal is re-mixed to obtain a recovery signal, where the basic ECG artifact disappeared

which can used in real-time analysis of EEG and we will discuss this in another article.

Currently, the FICA algorithms are more limited on the software part, mainly due to its huge amount of calculation. The next step of our research is focus on developing specific method for retrospective prediction of Epilepsy signal.

## ACKNOWLEDGMENT

## REFERENCE

De al Torre, F. and M. Black, 2001. Robust principal component analysis for computer vision. Proceedings of the International Conference on Computer Vision, July 2001, Vancouver, Canada, pp: 362-369.

Delfosse, N. and P. Loubaton, 1995. Adaptive blind separation of independent sources. Signal Proc., 45: 59-83.

Hill, T., A. Lundgren, R. Fredriksson and H.B. Schioth, 2005. Genetic algorithm for large-scale maximum parsimony phylogenetic analysis of proteins. Biochim. Biophys Acta, 1725: 19-29.

Hyvarinen, A. and E. Oja, 1996. Simple neuron models for independent component analysis. Int. J. Neural Syst., 7: 671-687.

To, C.C. and J. Vohradsky, 2007. A parallel genetic algorithm for single class pattern classification and its application for gene expression profiling in *Streptomyces coelicolor* . BMC Genomics, Vol. 8. 10.1186/1471-2164-8-49