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Standard 12-lead ECG Synthesis Using a GA Optimized BP Neural Network

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***Abstract*—This paper presents a method to reconstruct the standard 12-lead ECG from a 3-lead subset (I, II and *V*2) by optimizing the back propagation neural network with genetic algorithm (GA-BP). The non-linear method BP network is more suitable for ECG signal processing and GA is utilized to optimize the initial settings of the weights and biases in the BP network. Based on the results experimented on the study population of 39 subjects randomly selected from the PTB diagnostic ECG database, the proposed GA-BP method is proved to achieve accurate synthesis of the standard 12-lead ECGs, showing significant improvements over the common BP network ($p \leq 0.001$) and linear transformation method ($p \leq 0.001$) in terms of correlation coefficient values and root-mean-square errors.**

I. Introduction

RECENTLY, people's interest in self-care has been growing with the increasingly common cardiac diseases. Patients want to stay at home to be monitored all the time while some healthy people such as the old hope to receive an early warning before diseases strikes them. In most cases, doctors tend to know the patients' physical information as much as possible and the conventional 12-lead ECG appears to be the best choice and the gold standard in cardiology [1]. However, the standard 12-lead ECG is usually inconvenient to directly obtained especially in home care or remote monitoring environments because it needs 10 electrodes pasted on people's skin to simultaneously record the standard 12-lead ECG. So it's unpractical for most people to collect the whole standard 12-lead ECG signals by themselves without staying at the hospital. Fortunately, however, leads of the 12-lead ECG system are not independent of each other [2], i.e. there exists information redundancy between the 12-lead ECGs, which makes it possible for us to reconstruct the whole standard 12-lead ECG system from a subset of leads called "reduced-lead sets"[3], or other special leads.

The most common strategy for the 12-lead ECG synthesis is to construct a linear transformation which relies on the assumption that the heart-torso electrical system is linear and quasi-static [4]. But Atoui et al.[5] analyzed the noise and uncertainty of linear approach and pointed out nonlinear methods such as the artificial neural network (ANN) could accomplish the improvement of synthesis accuracy and hinder the weakness of linear transformation.

Atoui et al.[6] proved the superiority of the ANN model based on back propagation (BP) over the linear regression based method, but the weakness of the ANN architecture also limited the performance. On the one hand, it's well known that the BP network is based on the gradient information and has a slow convergence, which also will easily result in local minima and missing the global optimum [7]. On the other hand, the random selection of the initial settings of the weights and biases of the BP network will lead to a quite wide fluctuation of the synthesis performance.

This paper proposes a method to enhance the accuracy of reconstructing the standard 12-lead ECGs from a person-specific 3-lead subset (I, II, *V*2) with the GA optimized BP neural network. We take advantage of GA's strong ability to execute a global search and the superiority of the non-linear method BP network to process biomedical signals.

The remainder of the paper is organized as follows: Section II briefly reviews the main existing synthesis methods, followed by the detailed introduction of our proposed GA-BP synthesis method in Section III. The experiment settings, results as well as discussion are shown in Section IV. The last Section V concludes the paper and involves the future work.

II. Related Work

Based on the 3-lead subset I, II and *V*2, the other limb leads III, *aVR*, *aVL* and *aVF* can be easily calculated from the Eq. 1~4 directly. Therefore, how to derive the precordial leads *V*1, *V*3, *V*4, *V*5 and *V*6 from the 3-lead subset is the main research target of the standard 12-lead ECG synthesis. In this section, we review two state-of-the-art synthesis methods as follows.

$$\mathrm{III} = \mathrm{II} - \mathrm{I} \tag{1}$$

$$aVR = -(\mathrm{I} + \mathrm{II})/2 \tag{2}$$

$$aVL = \mathrm{I} - \mathrm{II}/2 \tag{3}$$

$$aVF = \mathrm{II} - \mathrm{I}/2 \tag{4}$$

A. Linear Transformation

Linear transformation is the most popular method to conduct the standard 12-lead synthesis. As early as 1964, Dower [8] made use of the linear transformation to reconstruct the 12-lead ECGs from a Frank system. After that,

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Nelwan et al.[9] attempted to find the best subset of the precordial leads to reconstruct the 12-lead ECGs; Finlay et al.[10] reconstructed the 12-lead ECGs from a 3-bipolar leads subset "Eigenleads", and Trobec et al.[1] used 3 pairs of differential leads for the ECG synthesis. All these 12-lead ECG synthesis system employed a linear transformation to do the research.

Based on the assumption of the linear heart-torso electrical system in the linear transformation method, lead V_k can be expressed in a linear transformation with the synthesis leads I, II and $V2$ as follows:

$$V_k = a_k + b_k \mathrm{I} + c_k \mathrm{II} + d_k V2 \quad (5)$$

where the coefficients of a_k, b_k, c_k and d_k are derived from the training sets. A least square method is used to accurately calculate a_k, b_k, c_k and d_k for the missing five leads $V1$, $V3$, $V4$, $V5$ and $V6$.

B. BP Neural Network

The non-linear approach to reconstruct the standard 12-lead ECGs was first proposed in [5]. Atoui et al. described how to reconstruct the missing precordial leads from the original 12-lead ECG subset by means of a supervised BP algorithm in the ANN. Compared to the linear method, the BP neural network was proved to be more accurate for the 12-lead ECG synthesis.

The BP network is set up as shown in Fig. 1. Each individual BP network consists of one input layer with 3 neurons (I, II and $V2$), one output layer with 5 neurons ($V1$, $V3$, $V4$, $V5$ and $V6$), and one hidden layer. The initial weighs and biases of the network are randomly generated. To overcome the performance limitations caused by the random selection of the initial BP network settings, they built up BP network committees of 50 individual BP network of the Fig. 1 type, and averaged the 50 outputs of each derived lead.

III. Proposed GA-BP Method

As a kind of classic algorithm which is based on biological principles (selection, crossover and mutation), GA is routinely used to generate useful solutions to optimization and search problems [11]. To overcome the performance limitations of the common BP network described above and improve the synthesis accuracy, this paper proposes a new method GA-BP to reconstruct the standard 12-lead ECGs. GA is utilized to optimize the initial settings of weights and biases of the BP network, and the BP network starts to train with the optimized settings of weights and biases. This method combines the GA's strength of the strong ability to conduct a global search and the superiority of BP network for the biomedical signal processing. The method consists of following two parts.

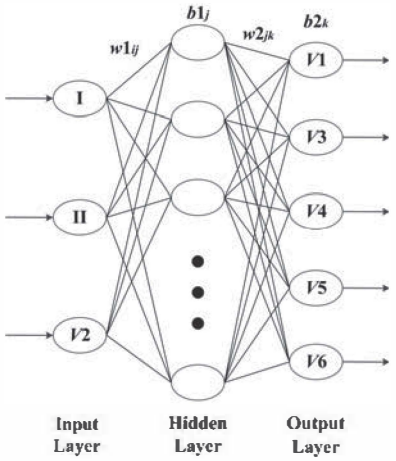

Fig. 1. Synthesis of the standard 12-lead ECG from I, II and $V2$ using a BP architecture. The set of weighs and biases of the network is expressed as $C = (w1ij, b1j, w2jk, b2k)$, where $w1ij$ is the weight of ith input neuron to jth hidden neuron, $b1j$ is the bias of jth hidden neuron, $w2jk$ is the weight of jth hidden neuron to kth output neuron and $b2k$ is the bias of kth output neuron.

A. GA Optimization

The target of the GA optimization is to find the optimal chromosome which contains the settings of weights and biases of the BP network. Algorithm 1 describes the process of the GA optimization as follows.

1) Initialization: One group of the weights and biases of the BP network is modeled as a chromosome based on real number encoding. The chromosomes of the first generation are randomly generated in the range of ±1 and processed by a simple linear interpolation method. The size of chromosome population and the evolution generations are also defined as P and Q, respectively. The pth chromosome of the population in qth evolution generation can be expressed as C_{pq}, $p \in (1,2,...,P)$, $q \in (1,2,...Q)$.

2) Evolution: The purpose of evolution is to generate new population with better chromosomes. In each generation, the process of evolution is executed by following steps.

Algorithm 1: Process of the GA Optimization

P: the number of chromosomes in the population
Q: the number of evolution generations
C_{pq}: the pth chromosome of the population in the qth generation
C_{best}: the best chromosome with the largest fitness

Process:

- Initialize the population of first generation with P chromosomes
- **for** q=1:Q
  - **-for** p=1:P
    - ✧ Setup a new BP network with C_{pq} as its initial settings
    - ✧ Train N
    - ✧ Calculate each fitness C_{pq} from training error *mse* according to Eq. 6
  - **-end for**
  - -Select
  - -Crossover
  - -Mutation
  - -Generate a new population for next generation
- **end for**
- Pick up the C_{best} as the result

a) Fitness evolution: To calculate the fitness of each

chromosome, a new BP network whose weights and biases come from C_{pq} is setup and trained. The BP network here is just for fitness calculation and the architecture of the network is the same as what described in Section II-B. To avoid over training, the training iterations here are set to a relatively small fixed number 100. 80% data of our training sets is used to train the network while the other 20% is for validation. When the training of each BP network is completed, the average mean-square-errors (*mse*) of the validation results of 5 outputs is used as the error measure and the fitness of the chromosome C_{pq} was calculated as 1/*mse*, as follows:

$$fitness = 1/mse = 1/\sqrt{\frac{\sum_{m=1}^{N}\sum_{n=1}^{5}\left(D_{mn}-O_{mn}\right)^2}{N}} \quad (6)$$

where D_{mn} and O_{mn} are the *m*th sample values of *n*th lead from derived and original ECG signals, respectively, and N is the total number of the sample points of each ECG signal. In our approach, $N = 10s * 1000 sample/s = 10000$.

b) Selection: Roulette wheel selection is used by assigning higher reproduction probability for chromosomes with better fitness and lower probability for chromosomes with worse fitness in the population.

c) Crossover: Single-point crossover strategy is chosen in our method and its probability is *Pm*.

d) Mutation: For the mutation operator, a value randomly generated between (-1, 1) will be added to each mutation point and the mutation probability is *Pc*.

After that, a new population with better chromosomes is generated. This population will continue the evolution of the next generation and this process ends in *Q*th generation.

3) *Result*: When the evolution is completed, we pick up the best chromosome C_{best} with the largest fitness from the final population as the optimization result.

B. BP Training and Application

After we get the best chromosome C_{best} with the largest fitness from the GA optimization result, the corresponding weights and biases of C_{best} will be sent to the BP network as the initial settings. The architecture of the BP network here is the same as what described in Section II-B and the difference between them is that the initial weights and biases of the BP neural network here is optimized by GA. The BP network is person-specific and the network of each individual should be trained with his particular training sets.

When the training is completed, 3-lead subset I, II and *V*2 can be input into the trained BP network, and its outputs are the derived ECG leads *V*1, *V*3, *V*4, *V*5 and *V*6.

IV. Experiments and Results

A. Study Population

The PTB diagnostic ECG database [12], which contains 549 standard 12-lead ECG records of 268 subjects with healthy controls and some common cardiac diseases such as myocardial infarction (MI), cardiomyopathy, dysrhythmia etc., is chosen to set up our study population. The ECG signals of this database were sampled at 1000 Hz with 16-bit resolution over a ±16 mV range.

Our study population P1 consists of a series of 78 pairs of digital standard 12-lead ECGs from 39 subjects (25 male, 14 female; mean age 51 ± SD = 15 years) which are randomly selected from the database. Each record is cut to a 10-s-duration one. Since each individual has two pairs of ECGs recorded in average at 20 (range: 1-77) days, we divide the study population into two datasets S1 and S2. S1 is used for training and S2 is the test sets. The diagnostic classes of the 39 subjects are summarized as shown in Table I.

Each pair of ECGs was preprocessed by removing the baseline wandering and noises.

TABLE I
Study Population P1

Diagnostic class	Number of subjects
Myocardial infarction	21
Cardiomyopathy	3
Bundle branch block	2
Dysrhythmia	2
Myocardial hypertrophy	1
Myocarditis	1
Miscellaneous	1
Healthy controls	8
Total	39

B. Experiment Settings

1) BP Network Settings: According to [6], a linear activation function for the output neurons is selected in the BP network of MATLAB Toolbox, and we configured 15 neurons and a *tansig* transfer function for the hidden layer.

Since it is difficult to decide when to stop the process of training, we use a fixed number of iterations K to train the BP networks. To determine the optimal *K*, first we train the BP network of each subject using five different numbers of iterations 200, 400, 600, 800 and 1000 respectively, and find the optimal number of iterations K_i among the five numbers that results in best synthesis performance for *i*th subject. After the 39 subjects of the study population are all experimented in this way, a set of $\{K_1, K_2, ..., K_{39}\}$ is obtained. A histogram as shown in Fig. 2 is set up to display the subject number with each specific optimal number of iterations 200, 400, 600, 800 and 1000. It's easy to judge that the optimal number of iterations is around 600 for the BP network training of the whole study population. We further average $\{K_1, K_2, ..., K_{39}\}$ and determine the result *K*=605 as the optimal number of iterations in the BP network training for the future ECG synthesis.

2) GA Settings: As the number of input neurons, hidden neurons and output neurons is 3, 15 and 5 respectively, in GA-BP, one chromosome consists of 140 (3*15+15+15*5+5) weights and biases. The size of the chromosome population in GA is *P*=10, and the crossover probability is 50% while the mutation probability is 10%. The number of generation *Q* is determined by observing the fitness change trend of the

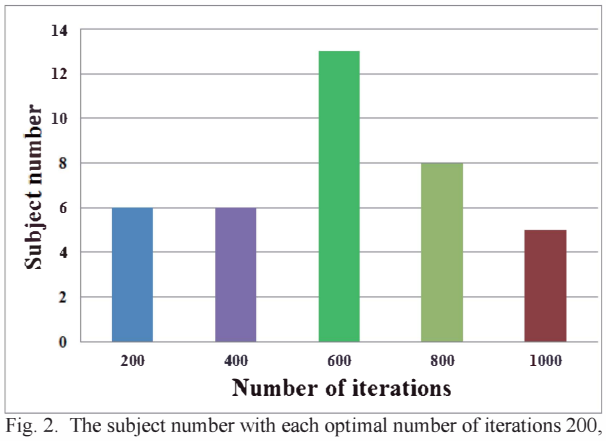

Fig. 2. The subject number with each optimal number of iterations 200, 400, 600, 800 and 1000.

chromosomes of each subject. For the jth subject, we pick up the best chromosome and observe the fitness change of the best chromosome in each generation. When the fitness of the best chromosome in the population has no longer increased since Q_jth generation, we record Q_j to a further calculation. After 39 subjects are all tested, we get the set of $\{Q_1,Q_2,...,Q_{39}\}$ and the largest number in the set of $\{Q_1,Q_2,...,Q_{39}\}$ is determined as the generation number Q=33.

C. *Experiment Results*

This section shows the synthesis results of our experiments on study population P1 for the linear transformation method, common BP model and our proposed GA-BP method, respectively. In common BP method, the initial weighs and biases are randomly created while in GA-BP, they are optimized by GA.

Fig. 3 shows the signal comparison between the original and derived ECGs of lead *V*1, *V*3, *V*4, *V*5 and *V*6 as a result of GA-BP method. Note that we deliberately separate the original and reconstructed waveforms for a display purpose and the difference between the two corresponding waveforms are too small to be discernible.

The results of the comparison between the three methods are illustrated in Fig. 4, where the error bars representing the average values and standard deviations of correlation coefficient (CC) values and root-mean-square errors (RMSEs) of the 39 subjects are plotted.

As shown in Fig. 4(a), compared with the common BP model and linear regression based method, the proposed GA-BP achieves a quite significant superiority in terms of the CC values. The average CC values of all the five derived leads of the GA-BP method is 0.948, versus 0.929 of common BP and 0.904 of regression-based method. The differences are both significant (p≤0.001).

Moreover, lead *V*1, *V*4 and *V*5 are more accurately reconstructed by the GA-BP method with the average CC values of 0.979, 0.932 and 0.912, than the common BP method with the average CC values of 0.967, 0.902 and 0.88, respectively. The differences are all significant (p≤0.001). The average CC values of *V*3 (0.973) and *V*6 (0.94) of the GA-BP method are both larger than that of common BP (0.969 and 0.93), but the differences are not significant (p=0.284 and p=0.395, respectively). And in the *V*1, *V*4, *V*5 and *V*6 synthesis, the GA-BP method outperforms the linear regression method whose CC values are 0.964, 0.892, 0.831 and 0.866 respectively by a significant margin (p≤0.001). However, the CC value of *V*3 for the linear regression is 0.966, and the difference between GA-BP and linear method is not significant (p=0.09) in *V*3 synthesis.

Fig. 4(b) shows the RMSEs of the three methods. In contrary to the common BP and linear regression methods, the proposed GA-BP method also achieves a pronounced superiority. The average RMSE of all the five derived leads of the GA-BP method is 54.4μV, versus 59.2 of common BP and 68.2μV of regression-based method. The differences are both significant (p≤0.001).

Besides, lead *V*4, *V*5 and *V*6 are more accurately reconstructed for the GA-BP method with average RMSEs of 75.5μV, 54.7μV and 43.3μV, respectively, than the common BP method with average RMSEs of 82.1μV, 62.1μV and 50.4μV, respectively. The differences are all significant (p≤0.001). Although the average RMSEs of *V*1 (36μV) and *V*3 (62.6μV) of the GA-BP method are both smaller than that

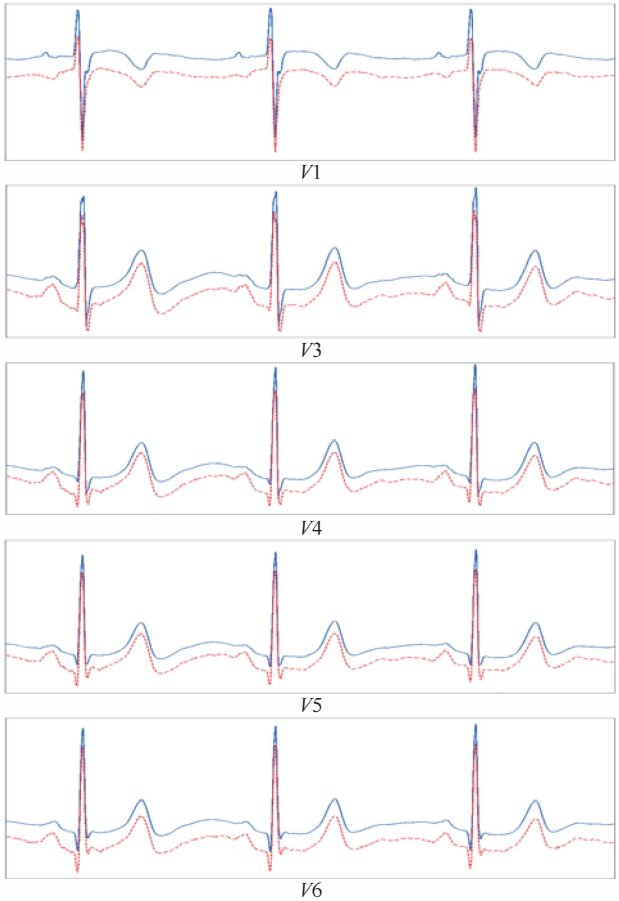

Fig. 3. Typical *V*1, *V*3, *V*4, *V*5 and *V*6 ECG segments of original (upper solid line) and reconstructed (below dashed line) signals with GA-BP method.

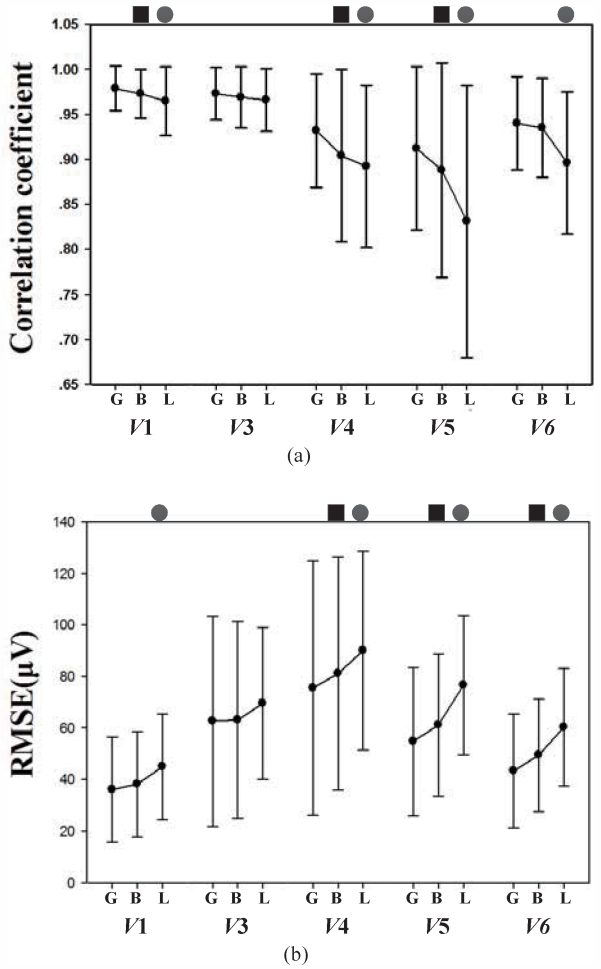

Fig. 4. Error bars of (a) CC, and (b) RMSE between the original and reconstructed leads for G (GA-BP method), B (BP method) and L (linear regression method). A square indicates that the particular lead is more accurately reconstructed with the GA-BP method than the linear regression by a significant margin. Leads that are marked by a circle are more accurately reconstructed with the GA-BP than the BP method by a significant margin. No mark means the difference is not significant. The confidence is 0.95. The folding line is used to help the values comparison between the three methods.

of common BP (38.1μV and 63.1μV), the differences are not significant (p=0.479 and p=0.469, respectively). And in the $V1$, $V4$, $V5$ and $V6$ synthesis, the GA-BP method outperforms the linear regression method whose RMSEs are 44.9μV, 90μV, 76.6μV and 60.2μV respectively by a significant margin ($p \leq 0.001$). However, the RMSE of $V3$ synthesis for the linear regression is 69.5μV, and the difference between GA-BP method and linear-based method is not significant (p=0.06).

D. Discussion

The experiment results verify that the proposed GA-BP method performs much better than the common BP and linear regression in standard 12-lead ECG synthesis according to the CC values and RMSEs.

However, when reconstructing some leads such as $V1$ and $V3$, the proposed GA-BP method doesn't have much advantage over the other two methods. The reason probably is that our 3-lead subset used for synthesis contains $V2$, the physical position of which is very close to $V1$ and $V3$. The adjacent leads share much physical information so the methods like common BP and linear regression are also able to reconstruct the leads effectively.

V. Conclusion

In this study, we propose a new method GA-BP to reconstruct the standard 12-lead ECGs from a 3-lead subset I, II and $V2$. Based on the GA optimization of the initial weights and biases in the BP neural network, this method significantly enhances the performance of the ECG synthesis compared with other two common methods the BP neural network and linear regression in terms of the mathematical analyses of CC and RMSE. The future work will focus on studying the medical meanings of ECG features, and further optimization of the synthesis algorithm aiming to reconstruct the ECG signals containing the medical information as much as possible. Besides the pure mathematical calculation of CC and RMSE, new evaluation criteria based on feature extraction are also worth to be explored.

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