ECG Signal Classification using Block-based Neural Networks

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Abstract – **This paper investigates the application of evolvable block-based neural networks (BbNNs) to ECG signal classification. A BbNN consists of a two-dimensional (2-D) array of modular basic blocks that can be easily implemented using reconfigurable digital hardware. BbNNs are evolved for each patient in order to provide personalized health monitoring. A genetic algorithm evolves the internal structure and associated weights of a BbNN using training patterns that consist of morphological and temporal features extracted from the ECG signal of a patient. The remaining part of the ECG record serves as the test signal. The BbNN was tested for ten records collected from different patients provided by the MIT-BIH Arrhythmia database. The evolved BbNNs produced higher than 90% classification accuracies.**

I. INTRODUCTION

The electrocardiogram (ECG) makes a useful diagnostic technique for monitoring heart activities. Analysis of heartbeat patterns extracted from the ECG signal may reflect the symptoms indicating that the heart needs immediate attention. Several methods have been proposed to classify ECG heartbeat patterns. Various features are obtained from the ECG signal such as morphological features [1], heartbeat temporal intervals [2], frequency domain features [3], and wavelet transform coefficients [4]. Classification techniques of ECG patterns include linear discriminant analysis [1], support vector machines [5], and artificial neural network [6]. Unsupervised clustering of ECG complexes using self-organizing maps has been studied [7].

ECG signal patterns vary greatly for different individuals. Even for the same individual, heartbeat patterns significantly change with the time of day and under different situations. Abnormal patterns result from a wide variety of heart problems. As a consequence, a certain classification method that works well for a given dataset may produce inconsistent results on different datasets. A fixed-structure classifier trained with a limited number of data may not be able to track the time-varying nature of ECG signals.

Evolvable classifiers change the structure and configurations as well as internal parameters to cope with dynamic environments. Block-based neural network (BbNN)

[8] models incorporate modular neural networks and evolutionary algorithms. BbNNs offer simultaneous optimization of structure and weight with a genetic algorithm (GA). The modular structure of BbNNs enables easy expansion in size by adding more blocks. BbNNs can be implemented by use of reconfigurable digital electronic hardware such as FPGAs that allow on-line partial reorganization of internal structures. BbNNs have been applied to the problems such as mobile robot navigation [8], pattern recognition [9], and time series prediction [10].

This paper presents evolvable BbNNs for the classification of abnormal heartbeat patterns from the ECG signal. The internal structure and associated weights of a BbNN are evolved to classify heartbeat patterns of each individual for personalized health monitoring. The BbNNs use both morphological and temporal features extracted from the ECG signal. The evolved BbNN produced an average of 98% classification accuracy of the ECG signals from the MIT-BIH Arrhythmia database [15].

II. BLOCK-BASED NEURAL NETWORKS

A. Network Structures

A BbNN can be represented by a two-dimensional (2-D) array of blocks. Each block is a basic processing element that corresponds to a feedforward neural network with four variable input/output nodes. A block is connected to its four neighboring blocks with signal flow represented by an arrow between the blocks. Leftmost and rightmost blocks are laterally interconnected. Signal flow uniquely specifies the internal configurations of a block as well as the overall network structure. Figure 1 illustrates the network structure of an $m \times n$ BbNN of m rows and n columns of blocks labeled as B_{ij}. The first row of blocks B_{11}, B_{12}, …, B_{1n} is an input stage and the blocks B_{m1}, B_{m2}, …, B_{mn} form an output stage. BbNNs with n columns can have up to n inputs and n outputs.
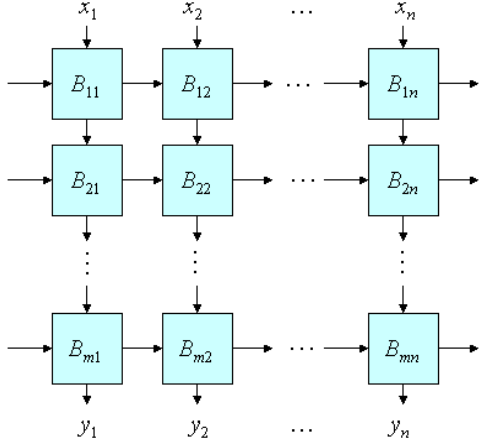
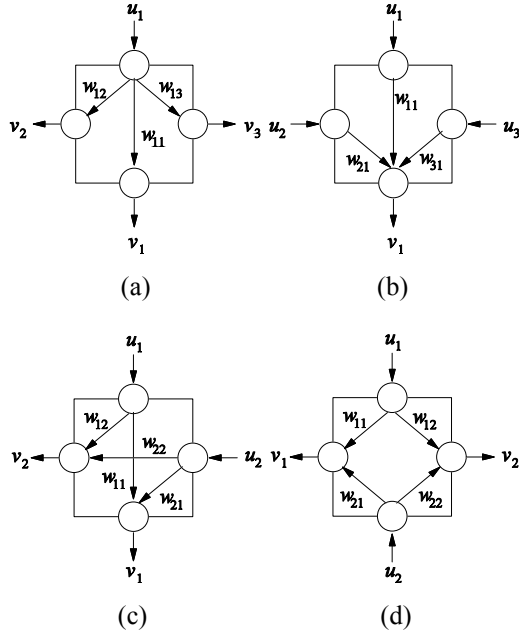Figure 1: Structure of block-based neural networks

Figure 2: Four possible internal configuration types of a block. (a) One input and three outputs (1/3), (b) Three inputs and one output (3/1), (c) Two inputs and two outputs (2/2), (d) A different arrangement of 2/2

Internal configuration is characterized by the input-output connections of the nodes. A node can be either an input or an output according to the internal configuration determined by the signal flow. An incoming arrow to a block specifies the node as an input, and output nodes are associated with outgoing arrows. Generalization capability emerges through various internal configurations of a block. A block can be represented by one of the four different types of internal configurations. Figure 2(a) shows a block with one input and three outputs (1/3). A block in (b) has three inputs and an output (3/1). Both Figure 2(c) and (d) correspond to the type

of two inputs and two outputs (2/2), but with different placement of the nodes. The cases of all input nodes (4/0) or all output nodes (0/4) are considered as invalid configurations and therefore are not allowed.

The four nodes inside a block are connected with each other with the weights. The signal u_j denotes the input and v_k indicates the output of the block. A weight w_{jk} denotes a connection between the jth input node u_j and the kth output node v_k. A block can have up to six connection weights including the bias. For the case of two inputs and two outputs (2/2), there are four weights and two biases. The 1/3 case has three weights and three biases, and the 3/1 configuration has three weights and one bias. An output node produces an output v_k with an activation function $g(\cdot)$:

$$v_k = g\left(w_{0k} + \sum_{j=1}^{J} w_{jk} u_j \right), \; k = 1, 2, \cdots, K \quad (1)$$

where J and K denote the number of input and output nodes of the block. For the type 1/3 basic block, $J = 1$ and $K = 3$. For blocks of the type 3/1, $J = 3$ and $K = 1$. Type 2/2 blocks have $J = 2$ and $K = 2$. The term w_{0k} is called a bias, or the weight corresponding to a constant input $u_0 = 1$. A bipolar logistic sigmoid function in the range [-1,1] is chosen as an activation function:

$$g(u) = \frac{2}{1 + e^{-u}} - 1 \quad (2)$$

Other popular choices of the activation function include saturated linear or logistic sigmoid functions.

B. Evolutionary Optimization of BbNN

Network structure and connection weights of an individual BbNN are encoded to form a chromosome for optimization using the GA. The overall structure of a BbNN can be effectively encoded with binary directions of signal flow. Signal flow provides an integrated representation of BbNN structure and internal configurations. The signal flow determines the structure and the internal configuration of a BbNN using a sequence of binary numbers. Any connection between the blocks is represented with either 0 or 1. Bit 0 denotes down ($\downarrow$) and left ($\leftarrow$), and bit 1 indicates up ($\uparrow$) and right ($\rightarrow$) signal flows. The signal flow bits associated with the blocks in the input and output stages are all zeros and therefore are not included in structure encoding.

Each generation of the GA process involves the three stages: fitness evaluation, selection, and genetic operation. The current population of BbNNs are evaluated and ranked in terms of fitness value. The population goes through the selection and the genetic operation until the maximum fitness reaches the desired value.

The selection schemes used in this paper are elitist method, binary tournament with disruptive pressure. Popular

selection methods such as roulette-wheel often show premature convergence in early phases of evolution or genetic drift in later phases. Elitist methods ensure that the best individuals pass their traits to the next generation in order to reduce a genetic drift. The individual with the highest fitness value in the previous generation is preserved in the next generation. The elitist method increases selection pressure by preventing the loss of important genes. Elitist methods can also speed up the convergence. In the elitist method, individuals with the lowest and the highest fitness values are exchanged only when the individual with the highest fitness value in the previous generation does not exist in the current generation. Tournament selection [11][12] has the same effects as both fitness proportional sampling and selection probability adjustment [13][14]. The binary tournament scheme finds one of the two individuals selected by a fitness comparison. The tournament size can adjust the selection pressure to reduce disruptive effect of uniform crossover. A larger tournament size usually increases the selection pressure.

Crossover and mutation serve as basic genetic operators used to evolve the structure and weights of the BbNN. Connection weights and biases are represented with real-valued numbers. For a crossover operation of a pair of BbNNs, a group of signal flow bits are selected with a crossover probability. The selected signal flow bits are exchanged. After the exchange, the internal structure of a block is reconfigured according to the new signal flow bits. Corresponding weights will be updated by a weighted combination of the two weights.

$$
\begin{aligned}
w_j^* &= \alpha w_j + (1-\alpha) w_k \\
w_k^* &= (1-\alpha) w_j + \alpha w_k
\end{aligned}
\tag{3}
$$

where α denotes a uniform random number in [0, 1]. New connection weights generated accordingly are initialized with random numbers, and unconnected weights are removed.

Mutation operator randomly adds a perturbation in an individual according to the mutation probability. A BbNN can have different probabilities for the mutation of structure and weight bit strings. When signal flow is reversed after mutation, all the irrelevant weights are removed and created with a random value on a proper direction. A weight selected for mutation will be updated with:

$$
w_k^* = w_k + r \tag{4}
$$

where r denotes a zero mean, unit variance Gaussian random variable. Mutation probabilities for weight and structure were 0.005 and 0.001 in the experiments.

III. ECG SIGNAL CLASSIFICATION

A. Dataset

The MIT-BIH Arrhythmia Database [15] provides the ECG signals used in the experiment. The database contains 48 records obtained from 47 different individuals (Two records came from the same patient). Each record contains 2-channel ECG signals measured for 30 minutes. Twenty-three records serve as representative samples of routine clinical recordings. The remaining 25 records include heartbeat waveforms such as complex ventricular, junctional, and supra-ventricular arrhythmias. Continuous ECG signals were filtered using a bandpass filter with a passband from 0.1 to 100 Hz. Filtered signals were then digitized at 360 Hz. The beat locations are automatically labeled at first and verified later by independent experts to reach consensus. The whole database contains more than 109,000 annotations of normal and 14 different types of abnormal heartbeats. Four records containing paced heartbeats were excluded in this study according to Association for the Advancement of Medical Instrumentation recommended practices [16]. Several noisy records were also excluded. Channel 1 signals of the 10 records (100, 106, 119, 202, 205, 209, 210, 212, 213, and 215) were chosen from the dataset for experiment.

B. Feature Extraction

A heartbeat template defines a partial waveform of an ECG signal that includes an R-peak [6]. Figure 3 shows heartbeat templates H_{k-1}, H_k, and H_{k+1}. Let T_k and T_{k+1} denote the time intervals between the neighboring R-peaks of the current heartbeat template H_k. The template H_k includes all the samples in the interval $[t-T_k/2, t+T_{k+1}/2]$. The intervals range from 132 to 819 ms in the selected MIT-BIH database. Heartbeat templates are then normalized to have an equal number of samples. In each heartbeat template, the R peak is shifted to the center and then linearly interpolated to have a uniform number of samples among all the heartbeat templates of a record.
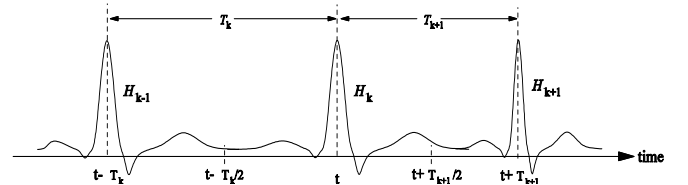

Figure 3: Definition of an ECG heartbeat template

Heartbeat templates are processed by a dimensionality reduction technique to reduce the amount of data to be processed each time. Principal components analysis (PCA) finds a projection that best represents the data in a least mean-squared error sense for feature dimensionality reduction [17]. The PCA reduces the original dimensions of

heartbeat templates (greater than 150) to three principal components as the morphological features of the heartbeat template. The time interval T_k between neighboring R peaks gives useful information for the classification of abnormal heartbeat patterns. A feature vector is composed of three principal components (x_1, x_2, x_3) as morphological features and the time interval T_k (x_4) between the R peaks as a temporal feature. The 4-dimensional features serve as the input to the BbNN for the classification of ECG heartbeat patterns after proper normalization.

C. Evolution of BbNN

For the BbNN training patterns we use the heartbeat templates corresponding to the first five minutes of a record. The remaining templates of the record are used for test patterns.

A 2×4 BbNN was chosen for classification of ECG heartbeat patterns. The GA optimizes network structure and connection weights by maximizing the fitness function given by:

$$\text{Fitness} = \frac{p_1 p_2}{1 + \frac{1}{N} \sum_{j=1}^{N} \sum_{k=1}^{n_0} \left(d_{jk} - y_{jk} \right)^2} \qquad (5)$$

where N denotes the number of training data, n_0 is the number of actual output nodes. d_{jk} and y_{jk} are desired and actual outputs of the kth output block referred to jth pattern. The term p_1 prevents an invalid internal block configuration with all input nodes (4/0) or all output nodes (0/4), while p_2 excludes invalid structures that all the outputs of a middle stage are composed of only upward signal flow. Both terms are initially set to 1. An invalid configuration results in a smaller value of 0.9. Table 1 lists detailed parameter settings used in the GA evolution.

TABLE 1: PARAMETERS FOR GA EVOLUTION

| Parameter	Value
Population	100
Crossover Probability	0.30
Mutation for Weight	0.005
Mutation for Structure	0.001
Max. Fitness Value	0.999
Max. Generations	50

IV. EXPERIMENT RESULTS

Six different types of abnormalities are considered: atrial premature, premature ventricular contraction, aberrated atrial

premature, ventricular escape, right bundle branch block, and the fusion of ventricular and normal beats. Figure 4 shows example waveforms of normal and two abnormal heartbeats (atrial premature and premature ventricular contraction). There exists a morphological similarity between the normal and atrial premature pattern. The temporal feature gives higher discrimination of atrial premature pattern since the time interval (652.8 ms) is smaller than that of normal pattern (813.9 ms). For a premature ventricular contraction pattern, the time intervals of both patterns are similar (644.4 ms), while the shapes are quite different. A combined use of morphological and temporal features provides successful classification of abnormal heartbeat patterns.
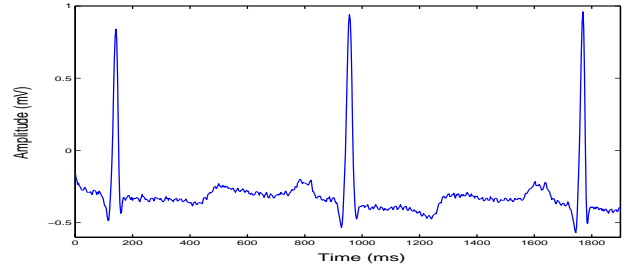
(a)
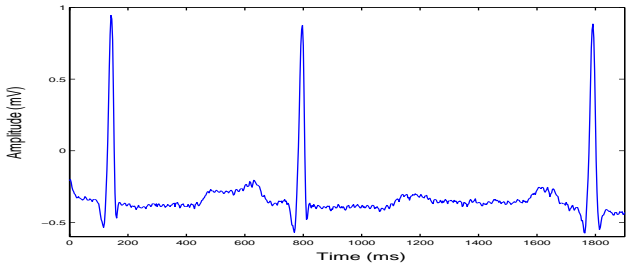
(b)
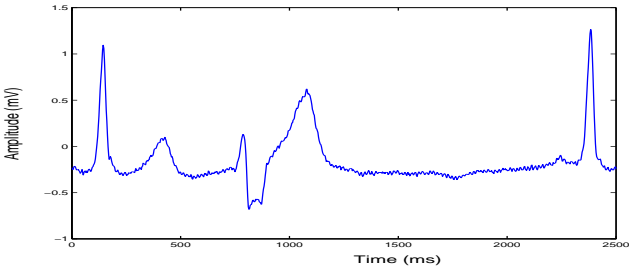
(c)

Figure 4: Sample ECG heartbeats, (a) Normal , (b) Atrial premature, and (c) Premature ventricular contraction

Figure 5 shows a scatter plot of normal and abnormal heartbeats in terms of the first principal component (x_1) and the time interval (x_4). The temporal feature increases the separability of normal and abnormal patterns.
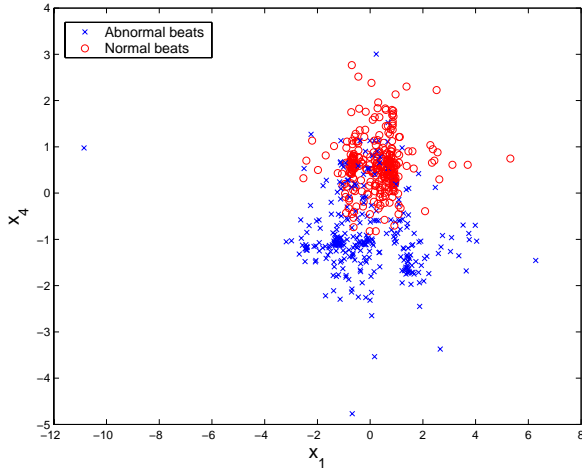
Figure 5: Scatter plot of normal and abnormal heartbeats in terms of the first principal component (x_1) and the time interval (x_4)

Figure 6 displays a typical evolution trend of BbNNs for ECG heartbeat classification. The solid line indicates the maximum fitness trend and dotted line shows the average fitness values. Evolution stops if the maximum fitness value does not reach the limit of 0.999 in 50 generations.
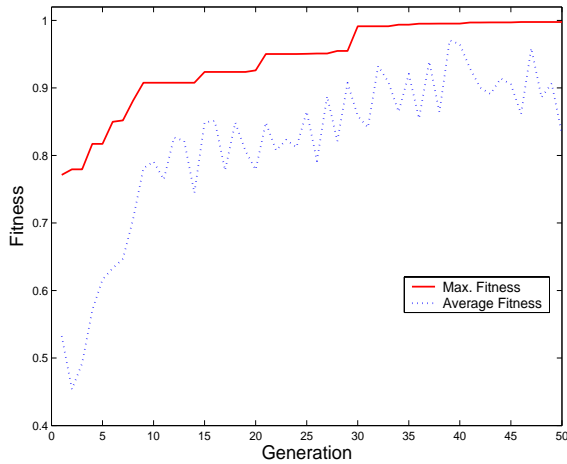

Figure 6: Evolution trend of BbNNs

A near-optimal BbNN structure is found during the evolution process. In Figure 7, a BbNN with near-optimal structure survives the competition. The number of BbNNs with a near-optimal structure increases, while the number of all the other structures gradually decreases during the evolution. The solid line indicates the near-optimal structure and the dotted lines represent five non-optimal structures. Finally all the BbNN individuals are evolved to the near-optimal structure.
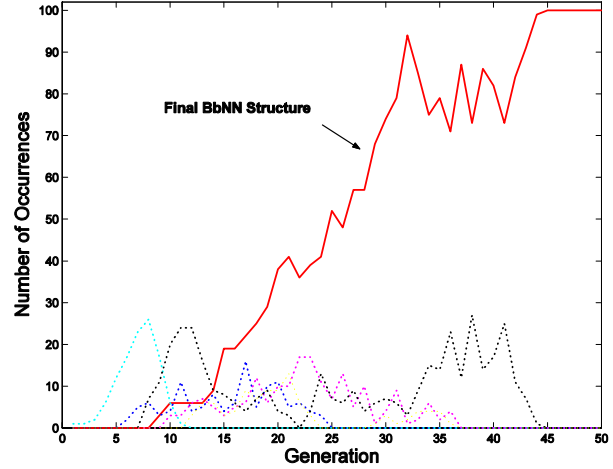

Figure 7: A structure evolution trend

Figure 8 shows the structure and weights of the evolved BbNN for classification of ECG heartbeat classification. The last output block was chosen as the output y. All the other redundant output nodes marked as * are ignored. Inputs $x_1,\ldots, x_4$ to the BbNN correspond to the three morphological features and the temporal feature. The output indicates either a normal or an abnormal heartbeat class.
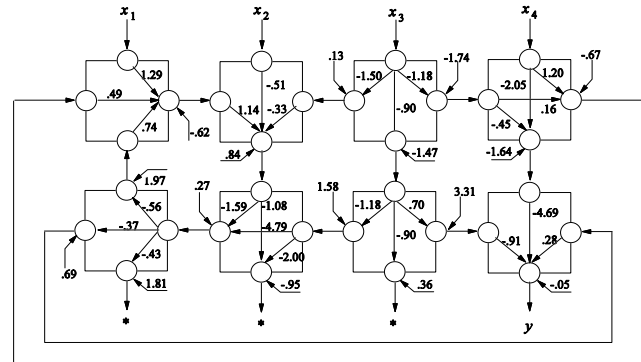

Figure 8: Evolved BbNN for ECG signal classification after 50 generations

Classification of ECG heartbeat patterns using the BbNN is summarized in Table 2. True positive (TP) and true negative (TN) indicate the correct classification of normal and abnormal patterns. False negative (FN) refers to misclassification of normal patterns as abnormality and false positive (FP) defines misclassification of abnormal patterns into normality. Classification accuracy is then defined as the ratio of the number of correctly classified patterns (TP and TN) and the total number of patterns. Each experiment was averaged over five repeated trials. An average classification rate obtained by the evolved BbNNs was approximately 98%. A two-layer multiplayer neural network of the size 51-25-2 reported an average accuracy of 90% [6]. Although a direct comparison of the results is not possible because of

the difference in the datasets selected, the evolved BbNN demonstrates its potential for ECG signal classification.

TABLE 2: SUMMARY OF CLASSIFICATION ACCURACIES

Record	TP	TN	FP	FN	Accuracy (%)
100	1799	30	0	72	96.21
106	1234	460	0	1	99.94
119	1296	364	0	0	100.00
202	1789	25	46	10	97.01
205	2120	54	24	2	98.82
209	2100	348	25	45	97.22
210	2001	174	20	8	98.73
212	787	1482	9	6	99.34
213	2135	405	86	73	94.11
215	2661	131	2	0	99.93
Total	17922	3473	212	217	98.03

V. CONCLUSION

This paper presents ECG signal classification with evolvable block-based neural network. Heartbeat signals vary significantly depending on many factors such as individual differences and time. A variety of heart problems are responsible for abnormal heartbeat signals. Block-based neural networks offer an evolvable ECG signal classifier that can change structure and internal parameters for personalized health monitoring system. The internal structure and associated weights are optimized simultaneously with the GA. A 2×4 BbNN evolved with a subset of ECG signals produced an average of 98% classification accuracy for the ECG signals from the MIT-BIH database.

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