Fuzzy ARTMAP and a Hybrid Chaos Genetic Algorithm for Medical Pattern Classification

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Abstract: In this paper, an Evolutionary Artificial Neural Network (EANN), which combines the Fuzzy ARTMAP (FAM) neural network and a hybrid Chaos Genetic Algorithm (CGA), is proposed for undertaking pattern classification tasks. The hybrid CGA is a modified version of the hybrid real-coded genetic algorithms that includes a Chaotic Mapping Operator (CMO) in its search and adaptation process. It is used to evolve the connection weights in FAM, and the resulting EANN is known as FAM-hybrid CGA. The CMO in the hybrid CGA is used to generate a group of chromosomes that incorporates the characteristics of chaos. The chromosomes are then adapted with an arbitrary small amount of variation in every generation. As the evolution procedure proceeds, chromosomes with considerable differences are produced. Such chromosomes, which are located at different regions of interest in the solution space, are able to provide good solutions to undertake search and adaptation problems. The effectiveness of the proposed FAM-hybrid CGA model is first evaluated using benchmark medical data sets from the UCI machine learning repository. Its applicability to medical decision support is then demonstrated using a real database of patient records with suspected Acute Coronary Syndrome. The results indicate that FAM-hybrid CGA is able to outperform its neural network counterpart (i.e., FAM), and it can be employed as a useful pattern classification tool for tackling medical decision support tasks.

Keywords: Fuzzy ARTMAP, hybrid chaos genetic algorithm, chaotic mapping operator, pattern classification, medical decision support

1 Introduction

The Evolutionary Artificial Neural Network (EANN) is a special group of Artificial Neural Networks (ANNs) that is produced from the combination between ANNs and Evolutionary Algorithms (EAs). The concepts of EANNs have been studied by many researchers for many years, and they found that these hybrid models exhibit a number of advantages. Apart from learning, EANNs are able to conduct a stochastic search and adaptation procedure in a dynamic environment for obtaining an optimized solution. A good literature review on using different EAs to evolve different aspects of the ANN dynamics is given in [18]. As the ANNs may not be able to learn a near-optimal set of connection weights during its phase, this limitation can be mitigated by enhancing the learning procedure of ANNs with the search and adaptation ability of EAs for optimizing the connection weights of ANNs.

One of the popular stochastic-based search algorithms in EAs is the Genetic Algorithm (GA). It is an adaptive heuristic search procedure based on the concept of survival-of-the-fittest in natural evolution [9]. The GA is an effective optimization technique to many search and optimization problems because it has the capability of evaluating many points and climbing many peaks in the search space simultaneously. The stochastic behavior of the GA allows it to explore many hills in the search space, and its search is not easily trapped in local optima. However, the GA is not efficient to exploit the search space for finding an optimized solution in the neighborhood of the optimal solution effectively. Such effort in narrowing down the search space for potential optimized solutions accounts for the long convergence speed of the GA. This means that, without the assistance of a local search technique, the GA may not be able to arrive at an optimum solution within an acceptable time.

To tackle the above problem, a hybrid GA that includes both global and local search procedures for solving non-linear constrained optimization problems is proposed in [2]. The hybrid GA operates in two phases: in the first phase a real-coded GA is deployed as a base level search procedure for finding solutions in the direction toward the optimal region; in the second phase, a Direct Search (DS) method is employed as a local refinement algorithm for fine-tuning the search by systematically reducing the size of the search region.

On the other hand, the Chaos Genetic Algorithm (CGA) is introduced in [17]. The CGA is a variant of the GA that possesses chaotic variables, i.e. pseudo-randomness, ergodicity and irregularity. These chaotic chromosomes are distributed across the whole search place. According to the chaos principle [1], an evolving system with minute changes in its initial condition can lead to a radically different final one in the long run. Likewise, the chaotic chromosomes in the CGA, which are adapted with an arbitrary small amount of variation in every generation, are able to, as evolution proceeds, generate considerable differences among the chromosomes. Such chromosomes, which are located at different regions of interest of the solution space, provide good solutions for
the search and adaptation problems under scrutiny. Normally, an inherent feature of the linear crossover operation in the GA is that the individual generations are scattered around the main distribution of the individuals in solution space. As claimed in [17], the use of a Chaotic Mapping Operator (CMO) in its search and adaptation process in the CGA is able to overcome the scattering phenomenon. By chaotically mapping the parameters forward and backward, and distribution of individuals can finally be scattered over the whole solution space. Hence, the CGA has a higher chance of arriving at the global optimal region of the solution space.

In this paper, a hybrid CGA, which follows the way the hybrid GA performs search and the chaotic characteristics in adaptation, is proposed. The hybrid CGA model performs search and adaptation in two phases: in the first phase, the CGA is used to induce a population of chaotic chromosomes with disordered variations that are randomly distributed over arbitrary regions of interest in the search space; in the second phase, the DS procedure as in a hybrid GA is employed to refine the solution that has been found in the first phase. This hybrid CGA combines the advantages of the characteristics of chaotic variables, GA, and DS, in its model. In this regard, the chaotic chromosomes, which are distributed over the whole search space, help improve the convergence rate of the GA. In addition, the DS procedure accelerates the convergence rate of search and adaptation by turning global search to local search. The proposed hybrid CGA model is used to evolve the connection weights of ANNs to formulate EANNs.

The main focus of this research work is to use the hybrid CGA to evolve the connection weights of the Fuzzy ARTMAP (FAM) [4] neural network, in an attempt to improve the classification performance of FAM. FAM is a supervised variant of the Adaptive Resonance Theory (ART) family of ANNs [3]. The ART-based ANNs have a distinct feature for overcoming the stability-plasticity dilemma [3]. FAM utilizes two fuzzy ART models to conduct supervised learning. It can process both analog and binary inputs. In pattern classification, the performance of FAM is governed by its connection weights that encode information directly from the training data set used during the learning process. So, searching and adapting a “better” set of the connection weights is the main research focus of this work, and the hybrid CGA is employed to serve this purpose.

This paper is organized as follows. In section 2, FAM, hybrid GA and CGA are described. In section 3, a detailed explanation on the hybrid CGA model and its integration with FAM for constructing the proposed FAM-hybrid CGA is provided. In section 4, the effectiveness of FAM-hybrid CGA is evaluated by using benchmark data sets. The proposed model is also applied to classifying a medical data set pertaining to a heart disease problem. In section 5, a summary of the work accomplished in this research and suggestions for further work is provided.

2 Fuzzy ARTMAP and Chaos-Genetic Algorithms

In this section, an explanation on FAM [4], the hybrid GA [2], and CGA [17] is presented. Further details of these models can be obtained in the relevant references.

2.1 Fuzzy ARTMAP (FAM)

The FAM network incorporates two fuzzy ART modules: ART$_a$ for receiving input patterns and ART$_b$ for receiving output patterns. These two fuzzy ART modules are linked together through a map field, $F^{ab}$. Each fuzzy ART module consists of three layers: the $F_0$ layer, which is a preprocessing layer that transforms the input pattern via the complement-coding technique [4]; the $F_1$ layer, which receives both bottom-up input pattern prototypes from $F_0$ and top-down prototype weight patterns from $F_2$; the $F_2$ layer, which is category representation layer where new category nodes are formed dynamically. Figure 1 depicts the architecture of FAM.

FAM is a supervised ANN. During supervised learning, the input pattern vector, $a$, is fed to ART$_a$ whereas the target class vector, $b$, is fed to ART$_b$. These vectors are then classified independently in the respective ART modules. When both ART modules are active, the map field ($F^{ab}$) becomes active to adaptively associate prototype patterns in ART$_a$ with their respective target classes in ART$_b$. The fuzzy set theory employed in FAM enables it to learn using both analog and binary inputs. Moreover, the input pattern vector is complement-coded so as to avoid the category proliferation problem [4]. Given an input pattern, the category node in $F_2$ that has the highest value of the choice function is selected as the winning node to go through a vigilance test against a vigilance parameter, $\rho$. If the vigilance test fails, a mismatch reset is exercised to prohibit the current winning node from re-selection. This procedure allows another category node that has the next highest value of its choice function to be selected. If the selected node in an ART module satisfies the vigilance test, resonance is said to occur. Note that a high value of $\rho$ leads to the formation of fine categories, and vice versa. After resonance has occurred in ART$_a$ and ART$_b$, the map field receives a predictive signal from the winning node in ART$_a$. If the prediction is confirmed by the target class in ART$_b$, the match tracking mechanism is executed to increase $\rho_a$ until a mismatch reset has occurred in ART$_a$. Subsequently, a new cycle of search for a better category node for resonance takes place in ART$_a$. For a successful match at the map field, the weight vectors of the winning nodes in ART$_a$ and ART$_b$ are updated according to the learning rule, either in a fast learning mode or a fast-commit-slow-recoding learning mode. Extra category nodes can be added to $F_2$ when necessary. Readers can refer to [4] for a full description of the dynamics of FAM.
2.2 The Hybrid Genetic Algorithm

The hybrid GA is a search algorithm for finding an optimal solution in two phases. In the first phase, a real-coded GA is used to conduct a search towards the optimal region quickly. The solution found in the first phase is then refined using DS in the second phase. DS performs local optimization by systematically reducing the size of the search region based on the solution found by global search. Hence, a near-optimum solution can be found by conducting a search at the surrounding regions of the GA solution. The hybrid GA employs a roulette wheel-based selection scheme to choose chromosomes (solutions) for mating. The chromosomes with a higher fitness value are more likely to be selected for producing offspring in the next generation. It adopts the arithmetic crossover and dynamic mutation as the genetic operators. On the other hand, DS used in the second phase is a local search method on a solution acceleration technique [2] for refining the solution in its space. In this regard, a multiplication factor (i.e., RMD) is defined to generate a set of solutions which is in the range within the best GA solution found in the first phase. Such set of solutions can be refined by systematically reducing the size of the search space from the location of the GA solution where it resides. Details of the hybrid GA can be found in [2].

2.3 The Chaos Genetic Algorithm (CGA)

The chromosome populations of the CGA exhibit the characteristic of a chaotic variable, which include pseudo-randomness, ergodicity, and irregularity [17]. The chromosomes evolve with minute changes in the initial population, and, subsequently, they develop into substantially different individuals as evolution proceeds. Therefore, the distributions of these chaotic chromosomes can be placed egordically over the solution space. This helps increase the chances of arriving at a successful search for finding the global or near-global optimum region. The chaotic properties are provided by CMO [17], and its procedure is as follows.

Step 1: The working parameters $x^{(k)}$ (i.e.,
\[ x^{(k)} = [x_1^{(k)}, x_2^{(k)}, \ldots, x_n^{(k)}] \]) are linearly mapped from the solution space, $S_0$, to a normalized chaotic space, $CS_0$, by using the linear mapping operator to obtained $c x^{(l)}$. The linear mapping operator is:
\[ cx_i^{(k)} = \frac{1}{b_i - a_i} \left( x_i^{(k)} - a_i \right) \] (1)
where $cx_i \in (0,1)$ denotes the $i$-chaotic variable; $a_i$ and $b_i$ are respectively the lower and upper limits of the $i$-dimensional region ($i \in \{1,2,\ldots,n\}$) in $S_0$; $k$ denotes the number of iteration.

Step 2: The next iteration of chaotic variables $cx^{(l+1)}$ are produced according to the iteration operator:
\[ cx_i^{(k+l)} = \mu cx_i^{(k)} \left( 1 - cx_i^{(k)} \right) \] (2)
where $\mu$ is a control parameter normally set as 4. In order to assure the evolution can go on smoothly, $cx_i \not\in [0.25, 0.5, 0.75]$.

Step 3: The chaotic variables $cx^{(l+1)}$ are linearly mapped from $CS_0$ to $S_0$ by using the back-mapping operator to produce $x^{(k+1)}$
\[ x_i^{(k+1)} = a_i + cx_i^{(k+1)} (b_i - a_i) \] (3)
Steps 1 to 3 are repeated to map the working variables forward and backward with the chaotic variables in an arbitrary number of iteration before a final set of working parameters is obtained.

3 Integration of FAM and the hybrid Chaos Genetic Algorithm

In this section, the proposed hybrid CGA model is first described. Then, integration of FAM and hybrid CGA to form a new FAM-hybrid CGA model is explained.

3.1 The Hybrid CGA

The operations of hybrid CGA and hybrid GA are similar as both of them conduct an evolutionary procedure consisting of global and local searches in two separate phases. However, hybrid CGA is different from hybrid GA in which the former includes a chaotic search in addition to a global search by the GA the first phase. Both hybrid CGA and hybrid GA use the DS method to fine-tune the chromosomes that have been found through the global search in the first phase in an attempt to find an improved solution. The algorithm of Hybrid CGA is as follows.
Phase – 1 of Hybrid CGA

Step 1: Define \( n_p \) (number of population), \( p_c \) (probability of crossover), \( p_m \) (Probability of mutation) and the maximum number of generation, \( t_m \).

Step 2: The first generation of \( n_p \) chromosome, \( X^{(1)} = \{x_1(t), x_2(t), ..., x_{n_p}(t)\} \), is initialized.

Step 3: The chaotic chromosome, \( X^{(2)} = \{x_1(t)^2, x_2(t)^2, ..., x_{n_p}(t)^2\} \), is generated by CMO from \( X^{(1)} \).

Step 4: By using the roulette wheel-based selection method, select \( n_p \) chromosomes from the set consisting of \( X^{(1)} \) and \( X^{(2)} \) to form a reproduction set \( X^{(0)} \).

Step 5: Produce the new population \( X^{(3)} \) from \( X^{(0)} \) through the arithmetic crossover operator.

Step 6: Produce the new population \( X^{(3)} \) from \( X^{(0)} \) through the dynamic mutation operator.

Repeat Steps 3 to 7 until the termination criterion, i.e., either 100% accuracy or the number of generations \( t_m \), is achieved.

Phase – 2 of Hybrid CGA

The best chromosome \( x_{best} \) from phase-1 is chosen for evolution in phase-2. The DS algorithm is used, as follows

Step 1: Define the range multiplication factor, \( RMF \), and the maximum number of generation, \( t_m \). Let \( t = 0 \), and the \( x(t) \) is equal to the best solution, \( x_{best} \).

Step 2: Initialize an initial range vector, \( R(t) \) using \( R(t) = RMF \times \text{Range} \).

Step 3: Generate \( n_p \) trail solution vectors \( \{ X_i, i \in \{1, 2, ..., n_p\} \} \) around the solution vectors, \( x(t) \), i.e., \( X_i = x(t) + R(t) \times \text{rand}(1, n) \).

Where \( \text{rand}(1, n) \) is a random vector generated from a normal distribution from -0.5 to 0.5.

Step 4: For each feasible trail solution vector, find the best solution, \( x_{best} \), from the solution vectors.

Step 5: Set \( t = t + 1 \), and let \( x(t) \) is set to the best solution from \( X \).

Step 6: Reduce the range by using \( R(t) = R(t) \times (1 - \epsilon) \).

Repeat Steps 2 to 6 until the termination criterion, either 100% accuracy or the maximum number of generations, \( t_m \), is achieved.

3.2 The FAM-hybrid CGA Model

FAM-hybrid CGA is an EANN model integrating the proposed hybrid CGA algorithm for evolving the connection weights of FAM. The FAM-hybrid CGA model performs adaptation in two modes: a supervised learning of FAM followed by an evolutionary search on the connection weights for improving the classification performance of FAM. The connection weights of the ART\(_1\) module are chosen for evolution because they represent prototype categories of the problem. It is believed that a further evolutionary search and adaptation on such connection weights can help FAM to form a more accurate knowledge base that encodes the problem at hand; hence, a better classification performance. The procedure of FAM-hybrid CGA is as follows.

1. The FAM is trained according to its supervised learning algorithm. FAM learns the input patterns and their corresponding output classes from the training data set. In this regard, FAM self-organizes information from the data set by adjusting the connection weight vectors of both fuzzy ART modules and establishing linkages between the two modules through the map field. The weight vectors, \( w_{\alpha} \), from ART\(_\alpha\) is extracted for further search and adaptation using hybrid CGA.

2. The first chromosome is generated by concatenating the weight vectors \( w_{\alpha} \). Applying Eq. (2), another \( (n_p - 1) \) number of chromosomes are generated. To measure the fitness of the chromosomes in the population, each chromosome is converted back as the weights of ART\(_\alpha\) and the FAM performance in terms of classification accuracy of the training data set is computed.

3. All chromosomes in a population represent the candidate solutions to the problem under scrutiny. The chromosomes go through a global search and adaptation procedure governed by the chaotic and genetic operators (selection, crossover, and mutation) in phase-1, and a local search by DS for fine-tuning the candidate solution in phase-2.

4. Upon completion of two phases of search, the chromosome that has the highest fitness value is decoded back as the weight vectors of ART\(_\alpha\). The classification performance of FAM is evaluated using the test data set.

A flow chart of the FAM-hybrid CGA procedure is shown in Appendix.

4 Experimental Results and Discussion

In this section, the effectiveness of the proposed FAM-hybrid CGA model is evaluated. The comparison between FAM and FAM-hybrid CGA is first made by using two medical benchmark data sets. Besides that, the applicability of the proposed FAM-hybrid CGA model is demonstrated using a real set of patient records with suspected Acute Coronary Syndrome. The results are analyzed and discussed.

4.1 Benchmark Medical Problems

Two medical benchmark data sets, i.e., Pima Indian Diabetes (PID) and Heart (HEA) from the UCI machine learning repository [1], are first used to evaluate the classification performances of FAM-hybrid CGA. They are binary classification problems consisting of 768 and 270 samples, and with 8 and 13 input attributes, respectively.
For each experiment, the data samples were randomized and divided equally into two subsets: the training set and the test set. In order to measure the stability of the classification results, eight experimental runs were conducted, each with a different sequence of the training data samples, and the average test accuracy rates were computed with the bootstrap method [7, 5] at 95% confidence intervals. Note that the 95% confidence interval is a less stringent setting for performance indication. This setting was chosen because it has been widely used, and it was pointed out in [8] that this setting is a customary standard for estimating the statistical interval of a parameter (e.g. mean). Nevertheless, other tighter confidence interval settings, e.g. 99%, are possible under different circumstances [6].

All FAM-based classifiers were coded in MATLAB. Each experiment was conducted using a computer with an Intel Pentium Duo CPU T2310 @ 1.46GHz and 1.47GHz, and with RAM 2038MB. Since FAM-hybrid CGA is an integration of FAM and hybrid CGA, it was trained with the parameters of the two constituents. FAM-hybrid CGA was trained at the first epoch with the default parameter setting of FAM: choice parameter, \( \alpha = 0.001 \); fast learning rate, \( \beta = 1 \); and the baseline vigilance parameter of the ART\(_4\) module, \( \beta_a = 0.01 \). During the evolutionary procedure, FAM-hybrid CGA was trained with the parameter setting of hybrid CGA: the number of population, \( n_p = 10 \); the crossover rate=0.5, the mutation rate=0.3, and the maximum number of generation, \( t_m = 10 \). Table I shows the classification results.

In this study, the performance of FAM-hybrid CGA is compared with its counterparts of ANN and EANN models, as follows: (i) FAM: an ANN which is trained in single and multiple epochs; (ii) FAM-GA [15]: an EANN version of FAM which performs a GA search; (iii) FAM-HGA [15]: an enhanced FAM-GA model which incorporates a local search for refining the global solutions.

On one hand, FAM-hybrid CGA and FAM-HGA conduct both global and local searches whereby the former is enriched with an additional CMO; FAM-GA, on the other hand, uses the GA without local search in its evolutionary process. From Table I, it is clear that the proposed FAM-hybrid CGA model is able to give higher accuracy rates than those from other FAM-based models. To further compare the performance of FAM-hybrid CGA from the statistical viewpoint, the bootstrap hypothesis test [7] was carried out. The bootstrap method was employed because of it is not necessary that the data samples must follow a normal distribution. In the hypothesis test, the null hypothesis states no difference between the performances of two classifiers, whereas the alternative hypothesis claims that the performance of classifier 1 is lower than that of classifier 2. When the \( p \)-value from a hypothesis test is above the significance level, we accept the null hypothesis; otherwise, we reject the null hypothesis and accept the alternative hypothesis. Table II lists the \( p \)-values for each hypothesis test of accuracy result between the FAM-based classifiers.

Table II. Test accuracy rate comparisons by using the bootstrapped hypothesis test at 95% confidence interval. The \( p \)-values are computed from the bootstrap method to compare the average test accuracy rates of two classifiers. The null hypothesis states that the average test accuracy rates are the same between the two classifiers, while alternative hypothesis claims that the average test accuracy rate of classifier 1 is lower than that of classifier 2.

As can be seen from Table II, all \( p \)-values are smaller than 0.05. This means that classification performances of FAM-hybrid-CGA are statistically (at the 95% confidence level) better than other FAM-based models in these two problems.

The training times of FAM-hybrid CGA and other FAM-based models were also compared. For this, all FAM-based models were trained in one epoch with \( t_m = 1 \). The average training times of eight runs of FAM (single-epoch), FAM-GA, FAM-HGA and FAM-hybrid CGA were 0.16s, 1.39s, 1.64s, and 1.92s for HEA, and 0.36s, 3.67s, 4.39s, and 5.31s for PID, respectively. The increase in training time from the basic FAM model to another improved FAM-based model, and subsequently to FAM-hybrid CGA is within expectation. This is because additional time is required by the respective improved FAM-based model to refine its network adaptation capability in an attempt to improve classification accuracy.
learning algorithm) [12]; (iii) LFOIL (linguistic first-order inductive learning) [11], which is a knowledge-based model constructed from the linguistic rule induction algorithm; (iv) FNB (Fuzzy Naïve Bayes) [14], which learns and searches for a set of linguistic rules (based on label semantics) and utilizes the “mass assignment” of the labels to perform classification in a probabilistic approach. Table III shows the performance comparison. Note that the results of C4.5, FNB, LID3, and LFOIL are those reported in [11].

FAM-hybrid CGA achieves the highest accuracy rates as compared with those from the knowledge-based models (i.e., C4.5, LID3 and LFOIL) and the probabilistic linguistic classifier (FNB) in the HEA problem. For the PID problem its performance is inferior to LID3. These results indicate that the classification performance of FAM-hybrid CGA is problem dependent. Such observation is in line with the “No Free Lunch Theorem for search” [16] as it is impossible to have a single search algorithm (in this case, the CGA in FAM) to give the best result for all problems.

Comparing the results in Tables I and III, other FAM-based models perform poorly as compared with the knowledge-based models and the probabilistic linguistic classifier, except FAM-HGA which is better than LFOIL for the HEA problem. Improvement in classification accuracy is achieved by FAM-hybrid CGA. This clearly shows the benefit of integrating the hybrid CGA into FAM in order to enhance the performance of FAM for pattern classification problems.

### 4.2 Diagnosis of Acute Coronary Syndrome

Acute Coronary Syndrome (ACS) is a type of heart disease which is complex and difficult to diagnose. As such, computerized intelligent systems can be deployed as a useful decision support tool to assist the diagnosis of ACS. The decision support system can provide a prompt prediction for suspected ACS patients so that an earlier medical treatment can be made.

The ACS data set was collected from Penang Hospital, Malaysia. The data set consisted of 118 real patient records. Each data sample contained 16 input attributes and a binary output (ACS or non-ACS identified after consultation with medical specialists). The input attributes comprised medical background of patients, physical examination, ECG, and cardiac enzymes, and the target output was either ACS or non-ACS. For the experimental study, the data samples were randomly divided into a training set (79 samples) and a test set (39 samples). The same experimental procedure as in the benchmark studies was followed, except that the experiment was repeated for twenty runs. Table IV presents the overall results of the ACS diagnosis using different FAM-based models. Table V lists the p-values from the bootstrap hypothesis tests.

<table>
<thead>
<tr>
<th>Model</th>
<th>Acc. (%)</th>
<th>Size (units)</th>
<th>Time (s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>FAM (single-epoch)</td>
<td>70.19</td>
<td>4.9</td>
<td>0.3</td>
</tr>
<tr>
<td>FAM (multi-epoch)</td>
<td>71.92</td>
<td>9.2</td>
<td>1.9</td>
</tr>
<tr>
<td>FAM-GA</td>
<td>75.90</td>
<td>4.9</td>
<td>3.1</td>
</tr>
<tr>
<td>FAM-HGA</td>
<td>82.31</td>
<td>4.9</td>
<td>3.7</td>
</tr>
<tr>
<td>FAM-hybrid CGA</td>
<td>84.32</td>
<td>4.9</td>
<td>4.7</td>
</tr>
</tbody>
</table>

**Table IV. Classification results of the ACS problem.**

<table>
<thead>
<tr>
<th>Classifier 1</th>
<th>Classifier 2</th>
<th>Acc.</th>
<th>Size</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>FAM (single-epoch)</td>
<td>FAM-hybrid CGA</td>
<td>0.000</td>
<td>0.469</td>
<td>0.000</td>
</tr>
<tr>
<td>FAM (multi-epoch)</td>
<td>FAM-hybrid CGA</td>
<td>0.000</td>
<td>1.000</td>
<td>0.000</td>
</tr>
<tr>
<td>FAM-GA</td>
<td>FAM-hybrid CGA</td>
<td>0.001</td>
<td>0.474</td>
<td>0.000</td>
</tr>
<tr>
<td>FAM-HGA</td>
<td>FAM-hybrid CGA</td>
<td>0.047</td>
<td>0.469</td>
<td>0.001</td>
</tr>
</tbody>
</table>

**Table V. The estimated p-values from the bootstrap hypothesis test for performance comparison.**

By analyzing the results in Tables IV and V, one can observe that FAM-hybrid CGA gives significantly higher accuracy rates as compared with other FAM-based models in classifying the unseen test data samples. All FAM-based models also exhibit a similar complexity in terms of network size. On the other hand, the training time of FAM-hybrid CGA is the longest. This is because FAM-hybrid CGA needs to search for a global or near-global optimum solution in its solution space. In other words, while FAM-hybrid CGA is structurally similar to its ANN or EANN counterparts, it requires additional computational time in conducting a series of searches for improving its solutions. The processing time may be shortened with advancements in computing technologies. Nevertheless, one major interest of research in new classification methods is to strive for improved performances in undertaking classification problems. In this study, FAM-hybrid CGA is able to exhibit better diagnostic accuracy than its counterparts, and the potential of deploying FAM-hybrid CGA as a useful decision support tool for ACS diagnosis is also demonstrated.

### 5 Summary

In this paper, a novel hybrid EANN that integrates FAM and the hybrid CGA for pattern classification has been described. The hybrid CGA is a variant of hybrid GA
that initiates a global search and a local search in succession for optimizing its solution. The proposed hybrid CGA uses the CGA in its global search for generating and evolving chaotic chromosomes that are distributed ergodically in the solution space. It then applies DS for refining the solution that has been found by the global search. In other words, DS systematically reduces the search space from the target solution in an attempt to arrive at the global or near-global optimum solution.

A series of experiments using benchmark as well as real medical data sets has been conducted. From the benchmark problems, FAM-hybrid CGA consistently outperforms FAM to provide better classification results. It also demonstrates comparable performances in comparison with the results from other classifiers published in the literature. The advantage of FAM-hybrid CGA is to its chaotic characteristics in nature where the ART module is selected from a group of chaotic individuals that are, after going through a series of search, distributed ergodically in the solution space. In addition, the applicability of FAM-hybrid CGA has been evaluated using a real set of medical records. The empirical results have revealed that FAM-hybrid CGA is able to identify and diagnose ACS patients with a high accuracy rate (84%). Such finding indicates the potential of deploying FAM-hybrid CGA as a useful intelligent decision support system for medical diagnosis problems.

As for future work, more experimental studies to evaluate the effectiveness of FAM-hybrid CGA in other application domains can be conducted. The success of the proposed EANN model is dependent on the global search. In this case, it is worth investigating how to initiate the global search in a more effective way before embarking on the local search. On the other hand, new variants of FAM-based EANN can be developed, e.g. by combining other FAM-based models with hybrid EAs. Besides, the hybrid CGA can be applied to evolve other ANN-based classifiers. It is envisaged that new classification algorithms with better performances can be realized for solving a broad range of real-world problems.

**References**


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Appendix : Flow chart of FAM-hybrid CGA

1. **Start**
2. Train FAM using the training data set.
3. Define all necessary parameters and represent the trained weight vectors of ART\(_a\) into a chromosome, \(x(t)\)
4. Generated \((n_p-1)\) population of chromosomes by using \(X_i = x(t) + R(t) \times \text{rand}(1,n)\)
5. **Phase-1**
   - Termination criterion satisfied?
     - No
     - **Phase-2**
       - Termination criterion satisfied?
         - No
         - **End**
         - Choose the chromosome with the best fitness value and decode it back as the weight vectors of ART\(_a\)
9. **End**
Phase-1

Define all parameters and initialize the first population of chromosomes, $X_t^{(1)}$.

Generate a chaotic chromosome population, $X_t^{(2)}$ from $X_t^{(1)}$ by using the chaotic mapping operator.

Form a new reproduction set of chromosomes, $X_t^{(r)}$, from $X_t^{(1)}$ and $X_t^{(2)}$.

Use the roulette wheel selection method to select a pair of chromosome

- Apply the arithmetic crossover operator
- Apply the dynamic mutation operator

Insert the mutated offspring into the new population, $X_t^{(3)}$.

Size of $X_t^{(3)} = \text{number of population}$?

- No
- Yes: Increase the number of generation by 1 and let $X_t^{(1)} = X_t^{(3)}$.

Termination criterion satisfied?

- No
- Yes: End
Define all parameters \( t = 0 \) and start at the initial starting point, \( x(t) \).

Initialize a range vector by using \( R(t) = RMF \times Range \).

Generate a trail solution vector by using \( X_j = x(t) + R(t) \times \text{rand}(1,n) \).

Evaluate the fitness value for each trail solution and find the best solution, \( x_{\text{best}} \).

Increase \( t \) by 1 and set \( x(t) = x_{\text{best}} \).

Reduce the range vector by an amount given by \( R(t) = R(t) \times (1 - \varepsilon) \).

Termination criterion satisfied? 

No 

Yes 

End