Evolutionary Fuzzy ARTMAP Approach for Breast Cancer Diagnosis

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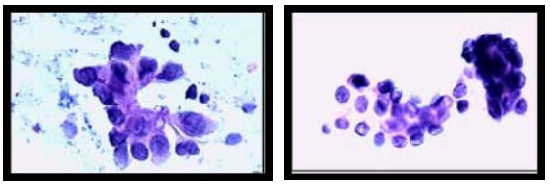
Summary
The objective of this paper is to present the strength of fuzzy artmap which is kind of neural networks in the medical field by improving its performance by genetic algorithm. Fuzzy ARTMAP is both much faster and incrementally stable than the other ordinary neural networks models like Multilayer Perceptron. Fuzzy artmap's parameters have legal range of values that should be determined in the simulation. These parameters should be adjusted and tuned many times to get the best results and optimum solution in order to generate accurate classification system. As there are large ranges of parameter's values so that lead to huge number of possible solutions. The problem is to try to find the best solution among whole possibilities in the problem search space and each point in the search space represents one feasible solution. The proposed solution to this problem is using genetic algorithms to optimize fuzzy artmap parameters and this yield to improving fuzzy artmap performance. Genetic algorithms are a part of evolutionary computing which can be used to quickly scan a vast solution set. This enhanced approached evolved fuzzy artmap will be used to generate breast cancer diagnosis system.

Keywords: *Fuzzy ARTMAP, Genetic Algorithms, Adaptive Resonance Theory, Breast Cancer, Artificial Neural Networks.*

1. Introduction

Breast cancer is the second leading cause of deaths in women today (after lung) and it is the most common cancer among women worldwide. In 2008, breast cancer caused 458,503 deaths worldwide (13.7% of cancer deaths in women) [1] [2]. In Egypt, it is the most common cancer among women, representing 18.9% of total cancer cases (35.1% in women and 2.2% in men) among the Egypt National Cancer Institute's (NCI) [2]. It appears in women in the form of lumps or tumors in the breast. Tumors can either be malignant or benign. Differentiating a malignant tumor from a benign one is a very exhausted task due to the structural similarities between the tumors as shown in (Figure 1). It is very critical mission and time consuming task for the physician to accurately identify the tumor kind. Accurate classification of tumor is substantial as the potency of the cytotoxic drugs administered during treatment can be life threatening. So it is required a diagnosis automated system with high accuracy to provide a solution to this vital issue. In this paper the proposed Evolutionary Fuzzy ARTMAP Approach is used as a classification system to diagnose the breast cancer tumor (malignant or benign).



(a) (b)
Figure 1: Fine Needle Biopsies of Breast. Malignant (a) and benign (b) breast tumors [3].

Various methods based on soft computing techniques such as neural networks and fuzzy logic systems have been proposed for diagnosis. Recently the neural networks and fuzzy logic approaches are combined to exploit the advantage of both, computational power and simple learning procedure of neural networks and high reasoning of fuzzy systems [10].
Fuzzy artmap is the most popular supervised architecture based on the adaptive resonance theory. It can learn new patterns without forgetting pervious knowledge, and without need to present previously learned pattern again. This is useful in a number of cases : if a model has to be first trained on a few available sample samples, and then improved by fresh data as they collected; if a dataset is too large and sweeping over it is computationally very costly; or if data distribution varies with time [9].
The fuzzy ARTMAP neural network architecture is capable of self-organizing stable recognition categories in response to arbitrary sequences of analog or binary input patterns. It provides a unique solution to the stability-plasticity dilemma faced by autonomous learning systems.

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Since fuzzy ARTMAP can perform fast, stable, on-line, unsupervised or supervised, incremental learning, it can learn from novel events encountered in the field, yet overcome the problem of catastrophic forgetting associated with many popular neural networks classifiers [9]. Neural network classifiers such as the Multilayer Perceptron (MLP) and Radial Basis Function (RBF) require off-line retraining on the whole data set, through a potentially lengthy iterative optimization procedure, to learn new patterns from either known or unknown recognition classes [7].

Fuzzy artmap Performance will degrade with a poor choice of user-defined hyper-parameters values so this will yield to a poor system for the classification problem [8]. To solve this drawback, genetic algorithm is proposed be used. Genetic algorithm is a search heuristic that mimics the process of natural evolution. This heuristic is routinely used to generate useful solutions to optimization and search problems. Genetic algorithms belong to the larger class of evolutionary algorithms , which generate solutions to optimization problems using techniques inspired by natural evolution, such as inheritance, mutation, selection, and crossover. Genetic algorithms are used for a number of different application areas. An example of this would be optimization problems in which the character string of the chromosome can be used to encode the values for the different parameters being optimized. According to that this paper presents hyper classification diagnose system based on the genetic algorithms and fuzzy artmap.

1.1 Paper components

This paper is organized as the following: section 2 is about breast cancer dataset description and preprocessing which describe its characteristics. Section 3 provides an overview about fuzzy artmap technique and its parameters that should be optimized to get accurate classification system. Section 4 presents short description about genetic algorithms. Section 5 discuses the proposed system for breast cancer diagnosis and describe in details its methodology. The results and performance are discussed in section 6. Conclusion is show in section 7 and finally section 8 is the paper references.

2. Dataset understanding and preprocessing

In this study the used dataset was provided by researchers at the University of Wisconsin. Dr. Wolberg, at the university of Wisconsin Hospital, first created the group of images using Fine-Needle Aspiration (FNA) biopsies of the breast. Image processing was then applied on the set of images to come up with the WDBC dataset (*Wisconsin Diagnostic Breast Cancer*). The dataset was obtained from the University of California Irvine (UCI) Machine Learning Repository, Department of Information and Computer Science [6].

The features in this dataset were computed from digitized FNA samples. A portion of the well differentiated cell was scanned using a digital camera. The researchers used an image analysis software system "*Xcyt*" to isolate the individual nuclei. An approximate boundary of each nucleus was provided as an input and taken to convergence to the exact nuclear boundary using a semi-automatic process called "*snakes*". In this process of computerized image analysis, the morphometric analysis of cell nuclei to quantify predictive features such as size, shape and texture were carried out [5].

The desired quantification of nuclear shape requires a very precise representation of boundaries. These are generated with the aid of a deformable spline technique known as a '*snake'*. The *snake* seeks to minimize an energy function defined over the arc length of the curve. The energy function is defined in such a way that the minimum value should occur when the curve accurately corresponds to the boundary of a nucleus. The second stage involves the use of these features in inductive machine learning techniques, which use cases with a known (or partially known) outcome to build a mapping from the input features to the decision variable of interest. In order to evaluate the size, shape and texture of each cell nuclei, 10 characteristics were derived namely the radius, perimeter, area, compactness, smoothness, concavity, concave points, symmetry, fractal dimension and texture [1].

(1) Radius was computed by averaging the length of radial line segments, which are lines from the center of mass of the boundary to each of the boundary points.
(2) Perimeter was measured as the sum of the distances between consecutive boundary points.
(3) Area was measured by counting the number of pixels on the interior of the boundary and adding one half of the pixels on to the perimeter to compensate for digitization error.
(4) Compactness combined the perimeter and the area to give a measure of the compactness of the cell, calculated as (Perimeter2) / area
(5) Smoothness was quantified by measuring the difference between the length of each radial line and the mean length of the two radial lines surrounding it.
(6) Concavity was captured by measuring the size of the indentations in the boundary of the cell nucleus.
(7) Concave points were similar to concavity but counted only the number of boundary points lying on the concave regions of the boundary.
(8) Symmetry was measured by finding the relative difference in length between pairs of line segments perpendicular to the major axis of the contour of the cell nucleus.

(9) *Fractal dimension* was approximated using the "coastline approximation". The perimeter of the nucleus was measured using increasingly large rulers. Plotting the values on a log-log scale and measuring the downward slope gives the negative of an approximation to the fractal dimension.
(10) *Texture* was measured by finding the variance of the gray scale intensities in the component pixels.

The mean value, standard error, and the extreme value of each characteristic were computed for each image, resulting in 30 features of 569 images representing 357 benign and 212 malignant cases. Of the 30 features, the mean and worst case values of Radius, Texture, Parameter, Area, Standard Error of Area, were large-valued [1].

2.1 Data Preprocessing

The data was rescaled to the range [0-1] because of preventing the data in the greater numeric range dominating those in the smaller range and the data should be normalized before entered to fuzzy ARTMAP classifier

3. Fuzzy ARTMAP

A short description of main fuzzy artmap algorithm will be presented as described in Carpenter's *et al.* article [17]. A FAM consists of a pair of fuzzy ART modules, ART_a and ART_b connected by an inter-ART module called Mapfield. ART_a and ART_b are used for coding the input and output patterns, respectively, and Mapfield allows mapping between inputs and outputs. The ART_a module contains the input layer F_1^a and the competitive layer F_2^b.

A preprocessing layer F_0^a is also added before. Analogous layers appear in ART_b. Fuzzy artmap architecture is shown in figure (3).

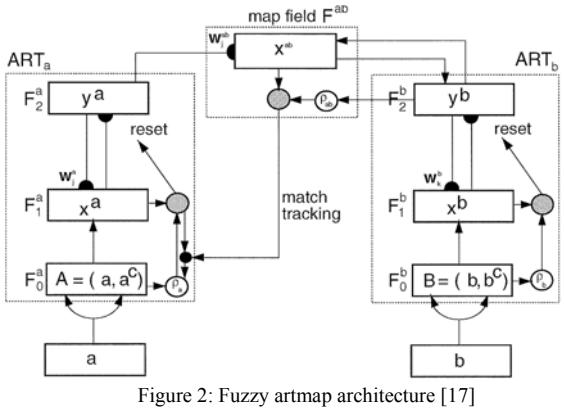

Figure 2: Fuzzy artmap architecture [17]

The initial input vectors have the form: a = (a1, . . . , an) $\in [0, 1]^n$. A data preprocessing technique called *complement coding* is performed in the two fuzzy art module by the F_0^a (and F_0^b respectively) layer in order to avoid proliferation of nodes. Each input vector a produces the normalized vector A = (a, 1 − a) whose L1 norm is constant: |A| = n.

Let M_a be the number of nodes in F_1^a and N_a be the number of nodes in F_2^b. Due to the preprocessing step, M_a = 2n. W^a is the weight vector between F_1^a and w_j^{ab}. Each F_2^a node represents a class of inputs grouped together, denoted as a "category". Each F_2^a category has its own set of adaptive weights stored in the form of a vector w_j^a, j = 1,……, N_a whose geometrical interpretation is a hyper-rectangle inside the unit box. Similar notations and affirmations are valid for ART_b that receives m-dimensional input vectors. For a classification problem, the class index is the same as the category number in F_2^b, thus ART_b can be simply substitute an N_b−dimensional vector.

The Mapfield module allows fuzzy artmap to perform heteroassociative tasks, establishing many-to-one links between various categories from ART_a and ARTb, respectively. The number of nodes in Mapfield is equal to the number of nodes in F_2^b. Each node j from F_2^a is linked to every node from F_2^b via a weight vector w_j^{ab}.

The learning algorithm is sketched below. Training pattern, the vigilance parameter factor is set equal to its baseline value, and all nodes are not inhibited. For each (preprocessed) input A, a fuzzy choice function is used to get the response for each F_2^b category:

$$T_j(A) = \frac{|A \wedge w_j^a|}{\alpha_a + w_j^a}, \quad j = 1,\ldots\ldots, N_a \qquad (1)$$

Let J be the node with the highest value computed as in (1). If the resonance condition from eq. 2 is not fulfilled, then the Jth node is inhibited such that it will not participate to further competitions for this pattern and a new search for a resonant category is performed. This might lead to creation of a new category in ART_a.

$$\rho(A, w_j^a) = \frac{|A \wedge w_j^a|}{|A|} \geq \rho_a \qquad (2)$$

A similar process occurs in ART_b and let K be the winning node from ART_b. The F_2^b output vector is set to:

$$y_k^b = \begin{cases} 1, & if \ k = K \\ 0, & otherwisw \end{cases} \quad k= 1,\ldots,\ N_b \quad (3)$$

An output vector X^{ab} is formed in Mapfield: $X^{ab} = y^b \wedge w_j^{ab}$. A Mapfield vigilance test controls the match between the predicted vector X^{ab} and the target vector y^b :

$$\frac{|X^{ab}|}{|y^b|} \geq \rho_{ab} \quad (4)$$

Where $\rho_{ab} \in [0, 1]$ is a Mapfield vigilance parameter. If the test from (4) is not passed, then a sequence of steps called match tracking is initiated (the vigilance parameter ρ a is increased and a new resonant category will be sought for ART_a); otherwise learning occurs in ART_a, ART_b and
Mapfield:

$$w_j^{a(new)} = \beta_a (A \wedge w_j^{a(old)}) + (1 - \beta_a) w_j^{a(old)} \quad (5)$$

3.1 Fuzzy artmap parameters

Vigilance values ρ represent the degree of belonging and its range in the interval [0, 1]. It establishes a network matching criterion that if not met leads to category reset and research [18]. By increasing ρ the number of created prototypes will increase. This can improve recognition rate on noisy data but on the other hand will decrease both training and online operation speed [19]. So, it's necessary to optimize ρ to overcome the problems which result inadequate choice.
The choice parameter α is used to control the learning process and should be tuned carefully because larger values will increase the number of prototypes and small value of α forces the network pick on larger classes and their prototypes in case when more than one of them is close to input pattern [20].
The learning factor parameter β controls the application speed and has two modes, fast mode when β =1 and slow mode when β < 1. In slow learning mode more prototypes will be created which sometimes prevent the network to learn all training patterns [19].
The match tracking parameter ε causes the network to automatically adjust the selected value of the ρ parameter of classification errors which are found in training. In case of large value of ε could trigger a false data mismatch alarm, by causing the value of the ρ to go beyond 1. In the case of some real data mismatch exist; larger value of ε will increase the error [19]. Fuzzy artmap parameters can be summarized in table 1.

Table (1): fuzzy artmap parameters and their values

parameter	***Range***	***Default value***
Baseline vigilance Training ρ	[0 – 1]	0.0
Baseline vigilance Test $\overline{\rho}$	[0 – 1]	0.0
choice parameter α	[0 – 1]	0.01
Learning factor β	[0 – 1]	1.0
Match tracking parameter ε	[-1 – 1]	-0.001

4. Genetic Algorithms

Genetic algorithms are inspired by Darwin's theory about evolution. Solution to a problem solved by genetic algorithms is evolved. Algorithm is started with a set of solutions each solution is represented by a chromosome to form population. Solutions from one population are taken and used to form a new population. This is motivated by a hope, that the new population will be better than the old one. Solutions which are selected to form new solutions (offspring) are selected according to their fitness - the more suitable they are the more chances they have to reproduce. The algorithm terminate due to a maximum number of generations, a satisfactory solution may or may not have been reached [11].
Genetic algorithm requires a genetic representation of the solution domain and a fitness function to evaluate the solution domain. A standard representation of the solution is as an array of bits. Arrays of other types and structures can be used in essentially the same way. The main property that makes these genetic representations convenient is that their parts are easily aligned due to their fixed size, which facilitates simple crossover operations. The fitness function is defined over the genetic representation and measures the quality of the represented solution. The fitness function is always problem dependent. It is a particular type of objective function that prescribes the optimality of a solution (that is, a chromosome) in a genetic algorithm so that that particular chromosome may be ranked against all the other chromosomes. Optimal chromosomes, or at least chromosomes which are more optimal, are allowed to

breed and mix their datasets by any of several techniques, producing a new generation that will (hopefully) be even better [13].
Once we have the genetic representation and the fitness function defined, GA proceeds to initialize a population of solutions randomly, and then improve it through repetitive application of mutation, crossover, and selection operators.

Initialization

Initially many individual solutions are randomly generated to form an initial population. The population size depends on the nature of the problem, but typically contains several hundreds or thousands of possible solutions. Traditionally, the population is generated randomly, covering the entire range of possible solutions (the *search space*). Occasionally, the solutions may be "seeded" in areas where optimal solutions are likely to be found.

Selection

During each successive generation, a proportion of the existing population is selected to breed a new generation. Individual solutions are selected through a fitness-based process, where fitter solutions (as measured by a fitness function) are typically more likely to be selected. Certain selection methods rate the fitness of each solution and preferentially select the best solutions. Other methods rate only a random sample of the population, as this process may be very time-consuming [14] [15].

Crossover

For each new solution to be produced, a pair of "parent" solutions is selected for breeding from the pool selected previously. a new solution is created which typically shares many of the characteristics of its "parents". New parents are selected for each new child, and the process continues until a new population of solutions of appropriate size is generated [14] [15].

Mutation

After a crossover is performed, mutation takes place. This is to prevent falling all solutions in population into a local optimum of solved problem. Mutation changes randomly the new offspring. For binary encoding we can switch a few randomly chosen bits from 1 to 0 or from 0 to 1 [16].

Termination

This generational process is repeated until a termination condition has been reached. Common terminating conditions are a solution is found that satisfies minimum criteria or fixed number of generations reached [13]. Genetic algorithm processes and step can be shown clearly and summarized in figure (3):

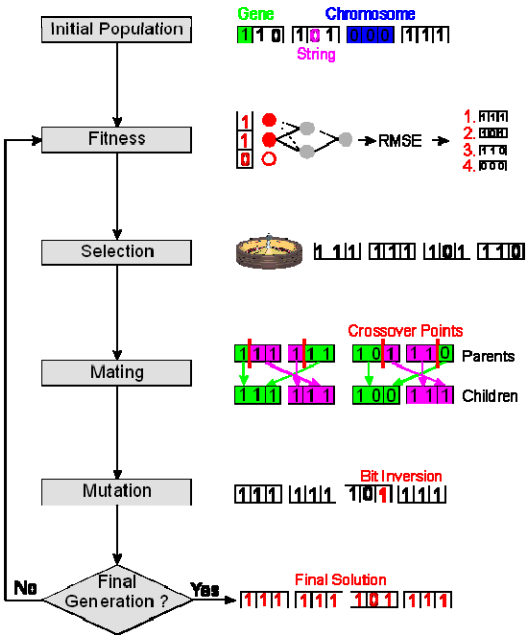

Figure (3): Simplified flow chart of a Genetic Algorithm [12].

5. Proposed system

Genetic algorithm can be used to solve many problems in an effective way. Many benefits can be gained from Genetic Algorithms once encode solutions of a given problem to chromosomes in GA, and compare the relative performance (fitness) of solutions. An effective GA representation and meaningful fitness evaluation are the keys of the success in applying genetic algorithm. The appeal of GAs comes from their simplicity and elegance as robust search algorithms as well as from their power to discover good solutions rapidly for difficult high-dimensional problems. GAs are useful and efficient when the search space is large, complex or poorly understood as in our cause the values of fuzzy artmap parameters have large ranges from 0 to 1.
GAs can be applied in wide variety of optimization tasks, including numerical optimization, and combinatorial optimization problems, so genetic algorithms in this paper is used to tune fuzzy artmap parameters to enhance its performance. We are going to apply genetic algorithms on fuzzy artmap algorithm by determining three elements:

1. Define a representation.
2. Define the objective function.

3. Define the genetic operators.

When using a genetic algorithm to solve fuzzy artmap optimization problem, it must be able to represent each single solution to the problem in a single data structure which referred as a chromosome as shown in figure (4).

ρ	$\overline{\rho}$	α	β	ε

Figure (4): fuzzy artmap chromosome

The genetic algorithm will create an initial population of solutions (chromosomes) based on a sample data structure of provided chromosome. To evaluate the fitness of each individual solution (chromosome) in the population the fuzzy artmap algorithm is used as an objective function to determine how fit each chromosome is for survival. Then genetic operators such as selection, crossover and mutation are applied on the population to generate new generation. The genetic algorithm replaces the initial population with the new generation to evolve the best solution and so on until finishing. This approach will work until get the satisfied solution or reach the maximum number of the predetermined generation the proposed system is shown in figure (5).

A. Starting fuzzy artmap algorithm with default parameters values.

If classification rate of fuzzy artmap is satisfied then END.

Else

Go to the next step

B. Initialization:

Determine population size

Initialize population randomly

Maximum number of generation

Crossover rate

Mutation rate

C. For I = 1 to max no. of generation do

Begin

Evaluate the fitness of each individual in the population by fuzzy artmap.

If classification rate = satisfied rate then END

Else

Go to the next step

Generate new generation:

Select chromosomes for reproduction

Crossover

Mutation

Replace old population with the new population

END.

Figure (5): Evolutionary Fuzzy ARTMAP Approach

6. Results

The following open source tools GAlib library and classer toolkit were used in the proposed system (Evolutionary Fuzzy ARTMAP) implementation. GAlib is C++ Library of Genetic Algorithm Components devolved by Matthew Wall in Mechanical Engineering Department at Massachusetts Institute of Technology. Classer toolkit is used for applying machine learning classifier models for ARTMAP neural networks implementations. It has been developed by Siegfried Martens in the Department of Cognitive and Neural Systems at Boston University.
First experiment, fuzzy artmap with default parameters were used for breast cancer diagnoses to determine which tumor is Malignant or benign. Cross-validation protocol is used for training and testing in all experiments which allows avoiding bias in the selection of training and test sets, and maximizing use of the dataset. Table (2) shows the result of fuzzy artmap with the default parameters values.

Table (2): Fuzzy artmap performance with default parameters values

Dataset	Default parameters values (ρ - $\overline{\rho}$ - α - β - ε)	No .of samples	Cross-validation	Classification Rate
Breast Cancer WDBC	0.0 , 0.0 , 0.01 , 1.0, -0.001	569	Five-fold	89%

Second experiment, for enhancing the performance of fuzzy artmap algorithm , evolutionary fuzzy artmap

approach is used. According to the algorithm in figure (5), initialization step is set as the following :-
Population size = 100, initializing population randomly, Maximum number of generation =100, Crossover rate = 0.9 and Mutation rate = 0.01
Then the algorithm works until finishing or satisfied solution is obtained. The result of evolutionary fuzzy artmap approach is shown in table (3).

Table (3): Evolutionary fuzzy artmap performance.

Dataset	optimized parameters values (ρ _ $\overline{\rho}$ _ α - β - ε)	No .of samples	Cross-validation	Classification Rate
Breast Cancer	0.731629, 0.143389 ,0.110107 , 0.333668 , 0.320947	569	Five-fold	97.2%

According to the results of experiments as shown in table 2 and 3, it is yield that evolutionary fuzzy artmap algorithm has enhanced the classification ratio rather than the ordinary fuzzy artmap with the default parameters values. The classification ratio of breast cancer diagnoses is improved from 89% to 97.2% by the proposed system.

7. Conclusion

In this paper the major point is to enhance the performance of fuzzy artmap algorithm by optimizing its parameters values. Fuzzy artmap parameters have large ranges of values as shown in table (1) previously, these parameters should be assigned by the user and this may lead to assign values which affect the final result of algorithm. If fuzzy artmap algorithm is applied to solve any critical problems with poor values this may yield to terrible solutions. This drawback isn't the user's responsibility but it is according to the sensitivity of fuzzy artmap algorithm and to the large ranges of the values. According to these ranges, the search space becomes large so that fuzzy artmap algorithm needs to be optimized.
Genetic algorithm is used to optimize fuzzy artmap algorithm parameters. This proposed system determines and optimizes the values of fuzzy artmap algorithm parameters automatically without any interference from the user.
Diagnosis of breast cancer is one of critical mission to physician to identify the tumor kind accurately, so after applying the evolutionary fuzzy artmap algorithm on Breast Cancer (WDBC) dataset, it yields to high classification rate. The main conclusion of this solution is that it could be applied on any problem, give high accurate classification result and solve drawback of user tuning for fuzzy artmap parameters.

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