

# A Fuzzy-Genetic Algorithm Method for the Breast Cancer Diagnosis Problem

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**Abstract**—The computer-aided medical diagnosis of complex systems, such as breast cancer is an important medical problem. In this paper, we focus on combining two major methodologies, namely, the fuzzy-based systems and the evolutionary genetic algorithms to find a computer aided diagnosis system that will aid physicians in an early diagnosis of breast cancer in Saudi Arabia. Our results show that the fuzzy-genetics approach produces systems that attain high classification performance, with simple and well interpretive rules and a good degree of confidence.

**Keywords**—Breast cancer diagnosis problem; Fuzzy systems; Genetic algorithms; Rule-based system; Computer-aided diagnosis.

## I. INTRODUCTION

In medical science, diagnosis of a disease is a complicated problem and confirming a diagnosis is difficult even for medical experts. This has given rise to computerized aided diagnostic tools, intended to aid the physician in making primary medical decisions. A major area for such computerized tools is in the domain of breast cancer; to know early on whether the patient under examination exhibits the symptoms of a benign, or a malignant case helps to determine a suitable treatment for the cancer. The automatic diagnosis should attain the highest possible performance, which means they must correctly classify cases with a good degree of confidence. Moreover, it would be desirable for such diagnostic systems to be well interpreted by the physicians.

In this research paper, an automated diagnosis system for breast cancer is designed by combining two methodologies, namely, the fuzzy rule based systems and the genetic algorithms. Medical diagnosis is a decision-making problem that commonly has uncertainty involved; therefore, fuzzy set theory has emerged in this field. The major advantage of fuzzy systems is the simple interpretation; however, finding good fuzzy systems is a hard task. This is where the role of genetic algorithms comes up in tuning the parameters of the fuzzy systems, based on a database of training cases. There are several different examples of the application of fuzzy systems and evolutionary algorithms in the medical domain, such as applying them to the Wisconsin Breast Cancer Diagnosis Data (WBCD) in USA [4], or applying them on pathogenesis of acute sore throat conditions in humans [5], or combining with wavelets, as in [20]. In our paper, we describe the fuzzy-genetic approach, which we developed for the Saudi breast cancer data consisting of 260 patients.

In Sections II and III, we provide a brief overview of fuzzy systems and genetic algorithms respectively. Then, in Section IV, we describe the fuzzy-genetic approach, which is developed in this work for the Saudi breast cancer data discussed in Section V. In Section VI, we discuss the parameters settings in our approach and show the results of our best system evolved, and finally, we present our concluding remarks and future work in Section VII.

## II. FUZZY SYSTEMS

Fuzzy logic is a computational method manipulating information in a way that resembles human logical reasoning processes [23][24]. A fuzzy variable is characterized by its fuzzy variable  $A$  and the membership functions of these variables; with a membership value  $\mu_A(u)$ , to a given real value  $u(R)$ . A fuzzy inference system is a rule-based system that uses fuzzy logic, rather than Boolean logic [26][27]. The structure includes four main components: a fuzzifier, which translates crisp (real-valued) inputs into fuzzy values, an inference engine which applies a fuzzy reasoning mechanism to obtain a fuzzy output, a defuzzifier, that translates the output back into a crisp value, and a knowledge base, containing both an ensemble of fuzzy rules (the rule base), and a group of connection membership functions (the database); see Figure 1.

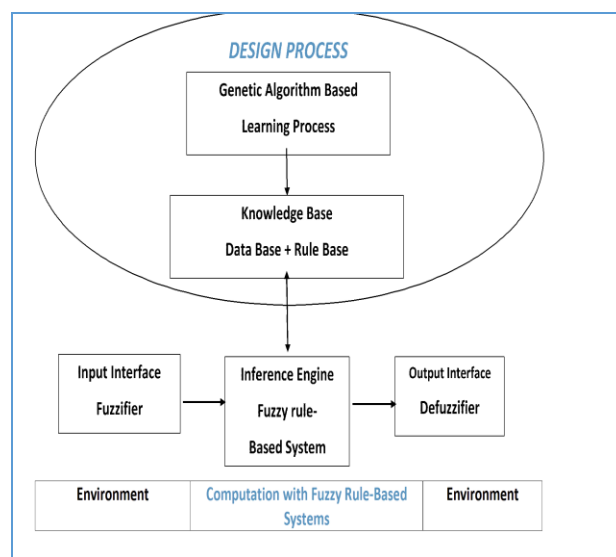


Figure 1. Basic structure of a fuzzy-Genetic system

Moreover, the decision-making process is performed in the inference engine using the rules contained in the rule base. A fuzzy rule has the form “IF antecedent THEN consequent”, where the antecedent is a fuzzy-logic expression composed of one or more simple fuzzy expressions connected by fuzzy operators, and the consequent is an expression that assigns fuzzy values to the output variables. The inference engine performs the learning phase, where it evaluates all the rules in the rule base and combines the weighted consequents of all relevant rules into a single fuzzy set using the aggregation operation [16][28]. An example of a fuzzy rule in our case would be: if ( $v_1$  is Low) and ( $v_2$  is Low) then (output is benign), where  $v_1$  and  $v_2$  are variables given in the data set.

Using the direct fuzzy model with knowledge from a human expert, the fuzzy simulation identifies the parameters of a fuzzy inference system, so that a desired decision can be made. This task is difficult when the problem space is complex and very large; thus, motivating us to use genetic algorithms to produce fuzzy models. In the literature, there are several approaches to fuzzy modelling based on neural networks [10][12], genetic algorithms [1][6][8], and other hybrid methods [25]. Selection of relevant variables and adequate rules is critical for obtaining a good accurate classification system. One of the major problems in fuzzy simulation is that the amount of computation grows exponentially with the number of variables.

### III. GENETIC ALGORITHM

A Genetic Algorithm (GA) is a search heuristic that mimics the process of natural selection. Genetic algorithms are used to generate solutions to optimization and search problems. They belong to the larger class of evolutionary algorithms, used to generate solutions to optimization problems using techniques inspired by natural evolution, such as inheritance, mutation, selection based on a relative fitness, and crossover [13]. Genetic algorithms are usually applied to spaces which are too large to be exhaustively searched and have applications in bioinformatics, industry, medical, science, engineering, chemistry, computational mathematics [3], and many other fields.

The genetic algorithm method is an iterative procedure that involves a population representing the search space for solutions to the problem, as individuals, each one represented by a finite string of symbols, called the genome. The basic procedure proceeds as follows: an initial population of individuals is generated at random or heuristically. In every evolutionary step (generation), the individuals in the current population are decoded and evaluated according to a fitness function that describes the optimization problem in the search space. To form a new population (the next generation), individuals are selected according to their fitness, a fitness function is a particular type of objective function that is used to measure how close the given individual is to achieving the set aims of the problem [18]. Many selection procedures are available, one of the simplest being fitness-proportionate selection, where individuals are selected with a probability proportional to their relative fitness. This ensures that the expected number

of times an individual is chosen is approximately proportional to its relative performance in the population. Thus, high-fitness individuals stand a better chance to reproduce and bring new individuals to the population, while low-fitness will not. Genetic algorithms are stochastic iterative processes, which are not necessarily guaranteed to converge, and the stopping condition may be specified as a maximal number of generations or a chosen level of the fitness.

### IV. FUZZY-GENETIC ALGORITHMS

Since GAs are used to search large complex search spaces and are able to give optimal and near-optimal solutions on numerous problems; therefore, fuzzy-genetic algorithms can be considered as an optimization process where the parameters of a fuzzy system constitute the search space. Many researchers investigated the application of evolutionary techniques in the domain of fuzzy modelling [1][5][4], where the tuning of fuzzy inference systems involved in control tasks were done by genetic algorithms. Fuzzy-genetic modelling has been applied to many domains [6][8][11][19], branching into many areas as electric engineering, chemistry, telecommunications, biology, geophysics and medicine. The GA can be used to tune the knowledge contained in the fuzzy system by finding membership function values. An initial fuzzy system is defined by an expert; then, the membership function values are encoded in a genome, and a genetic algorithm is used to find systems with high performance. GAs often overcome the local-minima problem seen in other gradient descent-based optimization methods [18]. GAs can be applied in different stages of the fuzzy system parameters search depending on several conditions, like the availability of a priori knowledge, the size of the parameter, and the availability and completeness of input/output data. The fuzzy parameters used to define targets for genetic fuzzy modelling are: structural parameters, connective parameters, and operational parameters.

In many cases, the available information about the system is composed almost exclusively of input/output data, and specific knowledge make up the system structure. In such a system, evolution has to deal with the simultaneous design of rules, membership functions, and structural parameters. Structure learning permits to specify other criteria related to the interpretability of the system, such as the number of membership functions and the number of rules, while, the strong interdependency among the parameters involved in this form of learning may slow down the convergence of the genetic algorithm. Both connective and structural parameters simulation [1][11] are viewed as rule base learning processes with different levels of complexity. In most GA applications, the main approaches for evolving such rule systems are the Michigan approach [1], the Pittsburgh approach [13] and the iterative rule learning approach [11].

## V. BREAST CANCER DATA BASE

Breast cancer is known as one of the most common cancers type affecting the female population. It is one of the major causes of death among women and a true emergency for health care systems of industrialized countries. One of the epidemiological studies conducted by AlDiab et al. [2] reported that the incidence of breast cancer in Saudi Arabia was 19.8% of all the female cancers detected in Saudi Arabia. Researchers in the field [7][21] have shown that breast cancer is the second most common malignancy for women in Saudi Arabia. Nevertheless, there is a paucity of detailed published epidemiologic data. An earlier report according to Saudi National Cancer Registry, mentioned an increasing proportion of breast cancer among women of different ages from 10.2% in 2000 to 24.3% in 2005 [7]. The presence of a breast mass is an alert, but it does not always indicate a malignant cancer. Fine needle aspiration (FNA)<sup>2</sup> of breast masses is a cost-effective, non-traumatic, and mostly non-invasive diagnostic test that obtains information needed to evaluate malignancy. The medical diagnosis data of breast cancer used in this study is from patients in Saudi Arabia. The database is similar to the WBCD dataset of the University of Wisconsin Hospital [17], where diagnosis of breast masses is based solely on an FNA test [15]. Nine visually assessed characteristics of an FNA sample considered relevant for diagnosis are identified, and were assigned an integer value between 1 and 10. The diagnostics in the database were done by specialists in the field, and the database itself consists of 260 cases, with each entry representing the classification for a certain ensemble of measured values, (Case number, [ $v_1, v_2, v_3, \dots, v_9$ , Diagnostic: Benign or Malignant]). The measured variables are as follows:  $v_1$  is clump thickness,  $v_2$  is uniformity of cell size,  $v_3$  is uniformity of cell shape,  $v_4$  is marginal adhesion,  $v_5$  is single epithelial cell size,  $v_6$  is Bare nuclei,  $v_7$  is bland chromatin,  $v_8$  is normal nucleoli and  $v_9$  is mitosis.

Basically, an initial fuzzy rule base is defined by an expert, for example a fuzzy rule in this case would be: if [ $v_1$  is Low] and [ $v_7$  is Low] then (output is benign). Therefore, each of the nine variables ( $v_1$ - $v_9$ ) has two parameters P and d, defining the start point and the length of the membership function, respectively. Then, the GA fine-tunes the membership functions. Also for the antecedents: the  $i^{\text{th}}$  rule has the form if ( $v_1$  is  $M_1^i$ ) and ( $v_7$  is  $M_7^i$ ) then (output is benign), Where  $M_j^i$  represents the membership function applicable to variable  $v_j$ ,  $M_j^i$  can take on the values: 1 (Low), 2 (High). The GA is also used to find either the rule consequents, or other subset rules to be included in the rule base. As the membership functions are fixed this approach lacks the flexibility to modify substantially the system behaviour. One of the major disadvantages of knowledge tuning is its dependency on the initial setting of the knowledge base. Furthermore, as the number of variables and membership functions increases, large dimensionality decreases the system's performance. Evolutionary structure modelling is done by encoding within the genome an entire fuzzy system using the Pittsburgh approach. The fuzzy

system computes a continuous appraisal value of the malignancy of a case, based on the input values. According to the fuzzy system's output the threshold unit then outputs a benign or malignant diagnostic. In order to evolve the fuzzy model, as seen in Figure 2, we must set some preliminary parameters in the fuzzy-genetic system itself encoding.

## VI. FUZZY-GENETIC PARAMETERS

All previous knowledge about the problem and about the existent rule-based models gives us valuable information for our choices of fuzzy parameters. Since all the labels have semantic meaning, for each label, at least one element of the space should have a membership value equal to one. Hence, a Low membership value of 0.8 entails a High membership value of 0.2, and for each element the sum of all its membership values should be equal to one. The parameter settings are set as in the following.

### A. The Fuzzy-Genetic System Parameter Settings

- Number of input membership functions: is set to two, (Low and High).
- Number of output membership functions: is two singletons for the benign and malignant diagnostic cases.
- Number of rules: is fixed to three.
- Antecedents of rules: is found by the genetic algorithm.
- Consequent of rules: the algorithm finds rules for the benign diagnostic; the malignant diagnostic is an else condition.
- Rule weights: the learning is done by letting active rules have a weigh of value 1, and the else condition has a weight of 0.25.
- Input membership function values: is found by the genetic algorithm.
- Output membership function values: following the database, we used a value of 2 for benign and 4 for malignant.

We applied the Pittsburgh-style-structure learning, using a genetic algorithm to search for three parameters, namely, the genome (encoding relevant variables), input membership function values, and antecedents of rules: Relevant variables are searched for implicitly by letting the algorithm choose non-existent membership functions as valid antecedents; in such a case the respective variable is considered irrelevant. To evolve the fuzzy inference system, we used a genetic algorithm with a fixed population size of 50 individuals. The algorithm terminates when the maximum number of generations is reached at 300, or when the increase in fitness of the best individual over five successive generations falls below a certain threshold, set at  $2 \times 10^{-6}$ . Our fitness function F is set to the classification performance, computed as the percentage of cases correctly classified, given by

$$F = Fr - \alpha Fc \quad (1)$$

where  $\alpha = 0.1$ ,  $Fr$ , the ratio of correctly diagnosed cases, which is the most important measure of performance, and  $Fc$  measures the confidence, penalizing systems with large number of low appraisal value cases i.e., cases that are diagnosed with low confidence. The crossover between the

two chosen parents genome is done at a single point randomly chosen with probability 0.8 to produce the new generation offspring. The selection operator of parent's genome is set to the stochastic uniform selection method, and the mutation done on the new offspring has probability 0.01. Hence, the experiment starts by finding from a population of 50 genomes of length 45, where the first 18 bits represent the parameters of the membership functions ( $P_i, d_i$ ) of each  $v_i$  and the remaining 27 bits are the output function  $M_j^i$  for each  $v_i$  in the three rule base system showing Low or High or irrelevant. Table I shows the parameters encoding to form a single individual's genome. The GA runs throughout the generations to find the best genome in this population. The best genome is the one which classifies correctly the largest number of the 260 cases given in the data set. After all 300 generations (repeated 50 times), the genetic algorithm found the optimum genome; hence, it found the best diagnostic system with three rules given in Figure 2.

TABLE I. PARAMETER ENCODING IN A GENOME

Parameter	values	Total number of bits (45)
P	1-8	9
d	1-8	9
M	0-2	27

Database									
	$v_1$	$v_2$	$v_3$	$v_4$	$v_5$	$v_6$	$v_7$	$v_8$	$v_9$
P	2	5	8	4	6	3	4	5	4
d	5	3	1	2	1	6	3	2	1

Rule base
<i>Rule 1 : if (<math>v_3</math> is Low) and (<math>v_7</math> is Low) and (<math>v_8</math> is Low) and (<math>v_9</math> is Low) then (output is benign)</i>
<i>Rule 2 : if (<math>v_1</math> is Low) and (<math>v_2</math> is Low) and (<math>v_4</math> is Low) and (<math>v_5</math> is High) and (<math>v_9</math> is Low) then (output is benign)</i>
<i>Rule 3 : if (<math>v_1</math> is Low) and (<math>v_4</math> is Low) and (<math>v_6</math> is Low) and (<math>v_8</math> is Low) then (output is benign) else (output is malignant)</i>

Figure 2. The best evolved fuzzy-genetic diagnostic system with three rules which exhibits an overall classification rate of 97.33%.

**B. Results**

The solution scheme we present for the Saudi breast cancer diagnosis problem consists of a fuzzy system model and a threshold unit. The fuzzy system computes a continuous appraisal value of the malignancy of a case, based on the input values. The threshold unit then outputs a benign or malignant diagnostic according to the fuzzy system's output. In order to evolve the fuzzy model, we must set the fuzzy system parameters and the genetic

algorithm encoding according to the previous discussion in part A. The evolutionary performed experiments fall into a learning category, in accordance with the data partitioning into two distinct sets: training set and testing set, Training set contains 50% of the database cases and the testing set contains the remaining 50% of the cases. Fifty evolutionary runs were performed, all of which found systems whose classification performance exceeds 95%. MATLAB Genetic Toolbox [29] was modified to implement the fuzzy-genetic algorithm and to generate the results. Taking into account the performance classification rate, the best diagnostic system with three rules stated in details in Figure 2 is the top one over all 50 evolutionary runs. It obtained 98.3% correct classification rate over the benign cases, 96.2% correct classification rate over the malignant cases, and an overall classification rate of 97.33%. The performance value denotes the percentage of cases correctly classified. Three such performance values are shown in Table II: the performance over the training set, the performance over the test set, and the overall performance on the entire database. Figure 3 shows a close up of the plot of the best fitness value over the generations, which scored on average 254 cases accurate out of the 260 data cases. Figure 4 shows the best individual (45 parameters) for the evolved fuzzy three rule diagnostic system described in Figure 2. In Figure 5, we can see the average distances between individuals for the evolved fuzzy three-rule system throughout the generations. Figure 6 shows the best, worst, and mean fitness scores reached by the evolved fuzzy three-rule system during the procedure.

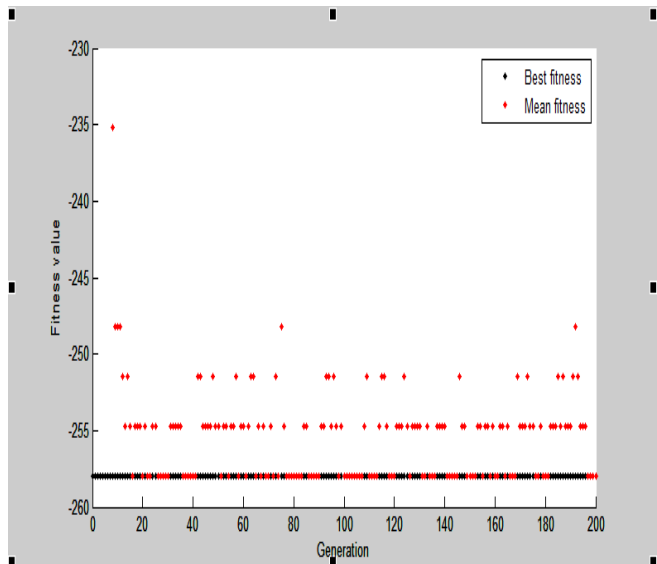


Figure 3 The best fitness value for the evolved three rule fuzzy-genetic system.

The proposed fuzzy system described in this paper performs very well and reached comparable results similar to work done on the WBCD data by Andres et al. [4], and Setiono [22] in terms of both performance and simplicity of rules as seen in Table III. It is worth noting that [4] had 699

cases in the WBCD dataset from patients in USA and they used a different fitness function denoted  $F = Fc - 0.05Fv - 0.01Fe$ , such that  $Fc$ , the number of correctly diagnosed cases,  $Fv$  measures the linguistic integrity (interpretability), and  $Fe$  adds selection pressure towards systems with low quadratic error. Moreover, Setiono [22] used an application of neural networks that involves Boolean rule bases extracted from trained neural networks. Table III shows the classification performance values obtained by these different approaches, looking very close in terms of accuracy and in time efficiency.

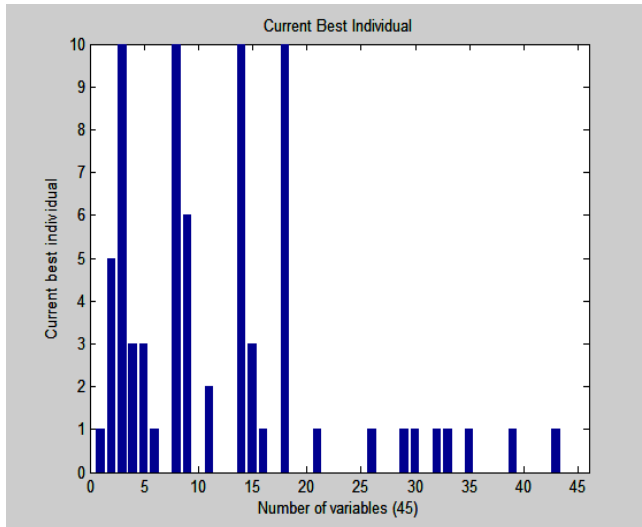


Figure 4. Current best individual in the three rule fuzzy-genetic system.

Following these steps and obtaining the results complete the fuzzification phase; it is time for the inference engine to compute the truth value of each rule, by applying the fuzzy ‘and’ operator to combine the antecedent clauses in a fuzzy manner. This results in the output truth value, which is a continuous value which represents the rule’s degree of activation inference. Thus, a rule is not merely either activated or not, but in fact is activated to a certain degree represented by a value between 0 and 1. The inference engine now goes on to apply the aggregation operator and combining the continuous rule activation values to produce a fuzzy output with a certain truth. Then, the defuzzifier works to produce the final continuous value of the fuzzy system; this latter value is the value that is passed on to the threshold unit. For our best three rule fuzzy system we calculate the membership values for each 260 patients and with the “and” function we get the appraisal value in the range [3,5]. We chose to place the threshold value at 3, with inferior values classified as benign, and superior values classified as malignant. Hence, a value of 2.42 is classified as benign, which is correct; but, it is among the closest to the threshold value, and its confidence is low. Most other cases result in an appraisal value that lies close to one of the extremes (i.e., close to either 2 or 4). Thus, in a sense, we can say that we are somewhat less confident where this case is concerned, with respect to most other entries in the

database. Moreover, the appraisal value can accompany the final output of the diagnostic system, serving as a confidence measure. This demonstrates a prime advantage of fuzzy systems, namely, the ability to output not only a (binary) classification, but also a measure representing the system’s confidence in its output. For our best three rule system presented here, only 13 cases out of 260 were diagnosed with low confidence.

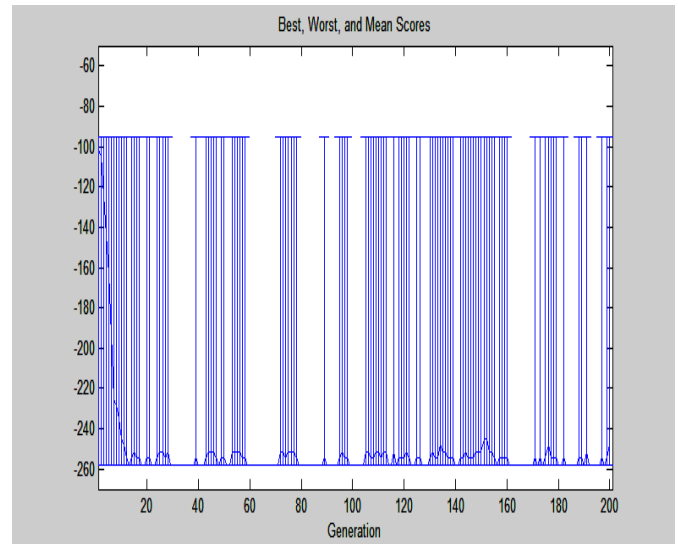


Figure 5. The best, worst and mean fitness scores for the three rule fuzzy-genetic system.

TABLE II. RESULTS OF 50 EVOLUTIONARY RUNS, DIVIDED ACCORDING TO THE THREE CATEGORIES

Training/test 50/50	Performance		
	Training set	Test set	Overall
	97.70 %	96.91%	97.33%

TABLE III. COMPARING OUR RESULTS FOR A THREE RULE BASE SYSTEM WITH OTHER APPROACHES

This work	Andres, Pena and Sipper [4]	Setiono [22]
97.33 %	97.80 %	97.14 %

### VII. CONCLUSION AND FUTURE WORK

In this paper, we applied a combined fuzzy-genetic approach to the Saudi breast cancer diagnosis database. Our evolved three rules system exhibits both high classification performance and a good confidence measure. Our results suggest that the fuzzy-genetic approach could be highly effective on medical diagnosis problems and may help in designing computer-aided software to obtain an early diagnosis and reduce treatment expenses, which are considered to be among the highest sanitary priorities in many countries. Our future work will involve finding more rule bases and making comparisons. We also plan to apply

the fuzzy-genetic approach to other complex real-world diagnosis problems and extend our work to data from all over the Middle East. We will also try alternative fuzzy logic approaches, such as neuro-fuzzy networks or fuzzy-Petri with the evolutionary genetic algorithm method. In addition, we will explore another promising area combining genetic algorithm with neural networks such as adaptive neuro-fuzzy inference systems.

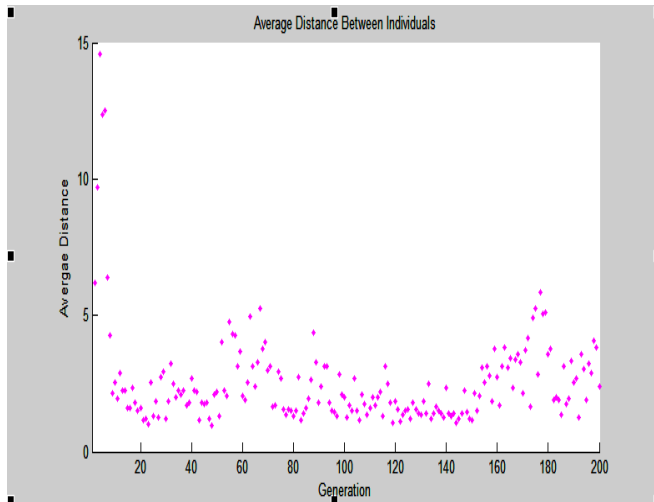


Figure 6. The average distance between individuals for the best three rule fuzzy-genetic system.

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