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Fuzzy Relational Model and Genetic Algorithms for Early Detection and Diagnosis of Breast Cancer in Saudi Arabia

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Abstract. Breast Cancer (BC) is considered as the most implacable malignancy and the leading cause of mortality among women in general and in Saudi Arabia specially. Most of the previous work in Saudi Arabia on this subject was on epidemiology, knowledge of (BC) and practice of breast self-examination (BSE), etiological factors, metastases and rate of survival. Early detection and diagnosis of Breast Cancer (BC) is an important, real-world medical problem. In this paper, we propose a soft computing methodology to build a Breast Cancer (BC) diagnosis system with high capabilities as described by Andres et al. [4] but on the Saudi Arabian breast cancer dataset and using a simplified fitness function. We focus on combining fuzzy concepts and genetic algorithms so as to automatically produce diagnostic systems to support and assist the expert to understand and evaluate its results with high classification performance.

1. Introduction

Fuzzy logic was invented by Zadeh [25] in 1965 for handling uncertain and imprecise knowledge in real world applications. It has proved to be a powerful tool for decision-making, and to handle and manipulate imprecise and noisy data [19–25]. A fuzzy system is characterized by a set of linguistic statements based on expert knowledge. 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 [4]. In such a case, evolution has to deal with the simultaneous design of rules [10], 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 modeling are viewed as rule base learning processes with different levels of complexity. In the evolutionary algorithm applications, the main approaches for evolving such rule systems are the Michigan approach, the Pittsburgh approach and the iterative rule learning approach [8]. In the Michigan approach, each individual represents a single rule, and the entire population represents the fuzzy inference system. Since several rules participate in the inference process, the rules are in constant competition for the best action to be proposed, and cooperate to form an efficient fuzzy system. In the Pittsburgh approach, the evolutionary algorithm maintains a population of candidate fuzzy

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systems, each individual representing an entire fuzzy system [6]. Selection and genetic operators produce new generations of fuzzy systems. This approach allows including additional optimization criteria in the fitness function, thus affording the implementation of multi-objective optimization. The main disadvantage of this approach is its computational cost, since a population of a complete fuzzy system has to be evaluated each generation.

2. Breast Cancer Database

The medical diagnosis data of breast cancer used in this study is from patients in Saudi Arabia [7]. The database is similar to the Wisconsin Breast Cancer Diagnosis Data (WBCD) of the University of Wisconsin Hospital[12, 14], where diagnosis of breast masses is based solely on an FNA test [13]. Nine visually assessed characteristics of an FNA sample considered relevant for diagnosis are identified, and 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, $[v_1, v_2, v_3, ..., v_9]$). 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. Diagnostic: *Benign* or *Malignant*. Note that diagnostics do not provide any information about the degree of *benignity* or *malignancy*. There are several studies based on WBCD database. Bennet and Mangasarin [1, 12, 13] used linear programming techniques, obtaining 99.6% classification rate on 699 cases similar to results in Andres [4]. Other recent research papers applied the fuzzy-genetic approach on pathogenesis of acute sore throat conditions in humans [5] or combining fuzzy relations with wavelets [15]. 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*.

The evolutionary algorithm then fine-tunes the membership functions, *i.e.* the P and d values defining *Low* and *High*. The genetic algorithm 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 behavior. One of the major disadvantages of knowledge tuning is its dependency on the initial setting of the knowledge base. Further, as the number of variables and membership functions increases, large dimensionality decreases the systems performance since the genetic algorithm encoding will involve large dimension arrays and will need many generations to converge. Evolutionary structure learning 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 we must set some preliminary parameters in the fuzzy system itself and in the genetic algorithm encoding which will be discussed in the next sections.

2.1. Fuzzy system parameters

All previous knowledge about the problem and about the rule-based models gives us valuable information for our choices of fuzzy parameters. It has been shown in previous work that systems with no more than four rules obtain high performance with Small number of variables and the higher-valued variables are associated with malignancy [16–18]. Moreover, each variable should have semantic meaning and the fuzzy set should clearly define a range that describes it. Any value belongs to at least one fuzzy set *(Low, High, or both)*; no value lies outside the range of all sets. Since all labels have semantic meaning, then for each label, at least one element of the space should have a membership value equal to one. Note that both *Low* and *High* have elements with membership value equal to 1 and for each element the sum of all its membership values should be equal to one. Therefore, the fuzzy system setup consists of:

(a) Logical parameters: According to the analysis in [3] the situation with fuzzy operations: maximum (*max*) and minimum (*min*) is the following. They have been used to define the union and the intersection of fuzzy sets [9, 25]. Bellman and Giertz [2] found that they are the only choices consistent with the standard set theoretical axioms. Also Zimmermann and Zysno [26] deduced that the combination of *max* and *min* in a convex way fits the empirical data much better after analyzing human responses with respect to the questions involving fuzzy sets intersection. The concepts of triangular norms (*t-norms*) and conorms (*t-conorms*) have been introduced to fuzzy set theory from the area of statistical metric spaces. Usually, *t-norms* and *t-conorms* represent respectively the intersection and the union of fuzzy sets and the complement is represented by the standard negation [3]. In our work, we did not conduct any studies to justify the use of *min* and *max* operators for breast cancer diagnosis. We plan to do it in the future to finish this preliminary study.

We use in our mechanism a singleton-type fuzzy system (i.e. output membership functions are real values, fuzzy operators: *min* and *max*, Input membership function type: *orthogonal*, *trapezoidal* and defuzzification method: *weighted average*).

(b) Structural parameters: Relevant variables: specified by the genetic algorithm, number of input membership functions: two, denoted *Low* and *High*. Number of output membership functions: two singletons for the benign and malignant diagnostic cases. Number of rules: specified by the user between 1 and 4, and the rules are to be found by the genetic algorithm. Antecedents of rules: found by the genetic algorithm, and consequent of rules: the algorithm finds rules for the benign diagnostic; so that the malignant diagnostic is an else condition. Rule weights: active rules have a weigh of value I, and the else condition has a weight of 0.25. Input membership function values: found by the genetic algorithm, and output membership function values: following the database, 2 for benign and 4 for malignant.

2.2. Genetic algorithm system parameters

We applied the Pittsburgh-style-structure learning, using a genetic algorithm to search for three parameters, the genome (encoding relevant variables), input membership function values, and antecedents of rules:

(a) Membership function parameters: Nine variables ($v_1, ...v_9$) each with two parameters P and d, defining the start point and the length of the membership function, respectively.

(b) Antecedents. The *i-th* rule has the form: *if* (v_1 *is* M_1^i) *and ...and* (v_2 *is* M_9^i) *then (output is benign)*, where M_j^i represents the membership function. M_j^i which can take on the values: 1 for Low, 2 for High, or 0 for Other.

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 and will not show up in the rule. For example, the rule *if* (v_1 is *High*) and (v_5 is *Low*) and (v_8 is *Low*) then (output is *benign*) is coded with $v_1 = 2$, $v_5 = 1$, $v_8 = 1$, and $v_2 = v_3 = v_4 = v_6 = v_7 = v_9 = 0$.

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, G_{max} 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 2×10^{-6}. Our fitness function F is set to depend mainly on the classification performance, computed as the percentage of cases correctly classified cases out of the 260 cases given in the database, and that is a simplified version of the fitness function used by Andres et al. [4] which used a penalty parameter for low confidence in the value of the diagnosis.

Crossover is done at a single point randomly chosen with probability 0.8, the selection operator is set to the stochastic uniform selection and mutation probability 0.01. Table 1, shows the parameters encoding, forming a single individuals genome. Example 1, shows a sample genome structure with its interpretation from a single rule fuzzy system, with 27 parameters: where $P_1 = 1, d_1 = 5, P_2 = 2, d_2 = 3, P_9 = 1, d_9 = 4$, and membership functions: ${M_1}^1 = 1, {M_2}^1 = 0, {M_3}^1 = 1, {M_4}^1 = 0, {M_5}^1 = 2, {M_6}^1 = 0, {M_7}^1 = 0, {M_8}^1 = 0, {M_9}^1 = 0$.

The evolutionary experiments performed this into three learning categories, in accordance with the data partitioning into two distinct sets: training set and testing set. The three experimental categories are:

1. Training set contains all 260 cases of the database, while the testing set is empty;
2. Training set contains 75% of the data cases, and the testing set contains the remaining 25% of the cases;
3. Training set contains 50% of the database cases and the testing set contains the remaining 50%

Parameters	*Values*	*Bits*	*Total bits*
P	*1-8*	*3*	*27*
d	*1-8*	*3*	*27*
M	0-2	2	18*number of rules

Table 1: Parameter encoding of genome

Database

	v1	*v2*	*v3*	*v4*	*v5*	*v6*	*v7*	*v8*	*v9*
P	*1*	*2*	*1*	*4*	*6*	*2*	*2*	*3*	*1*
d	*5*	*3*	*2*	*7*	*7*	*4*	*8*	*1*	*4*

Rule 1: *if (v1 is low) and (v3 is low) and (v5 is High) then (output is benign) Default else (output is malignant).*

Example 1: *A genome structure and interpretation for a single rule evolved system.*

3. Fuzzy-Genetic algorithm results

- Example 2, consists of the best diagnostic system with three rules (45 parameters). Taking into account the performance classification rate this system 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%.
- Table 2, presents the average performance obtained by the genetic algorithm with this system over all 50 evolutionary runs, divided according to the three experimental categories. The performance value denotes the percentage of cases correctly classified. Three such performance values are shown: the performance over the training set; the performance over the test set; and the overall performance on the entire database.
- Figure 2, shows the plots of the best fitness value over the generations and the average distance between individuals for the evolved fuzzy three rule diagnostic system
- Example 3, shows a diagnostic system with two rules which obtained 97% correct classification rate over the benign cases, 97.06% correct classification rate over the malignant cases, and an overall classification rate of 97.03%.
- Figure 3, shows the plot of the best fitness value over the generations and the current best individual of all 36 variables in a two rule fuzzy diagnostic system.

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 1 : if (v_3 is Low) and (v_7 is Low) and (v_8 is Low) and (v_9 is Low) then

Rule 2: if (v_1 is Low) and (v_2 is Low) and (v4 is Low) and (v5 is High) and (v9 is Low) then (output is benign)

Rule 3 : if (v1 is Low) and (v4 is Low) and (v6 is Low) and (v8 is Low) then (output is benign) else (output is malignant)

Example 2: Consists of the best diagnostic system with three and an overall classification rate of 97.33%.

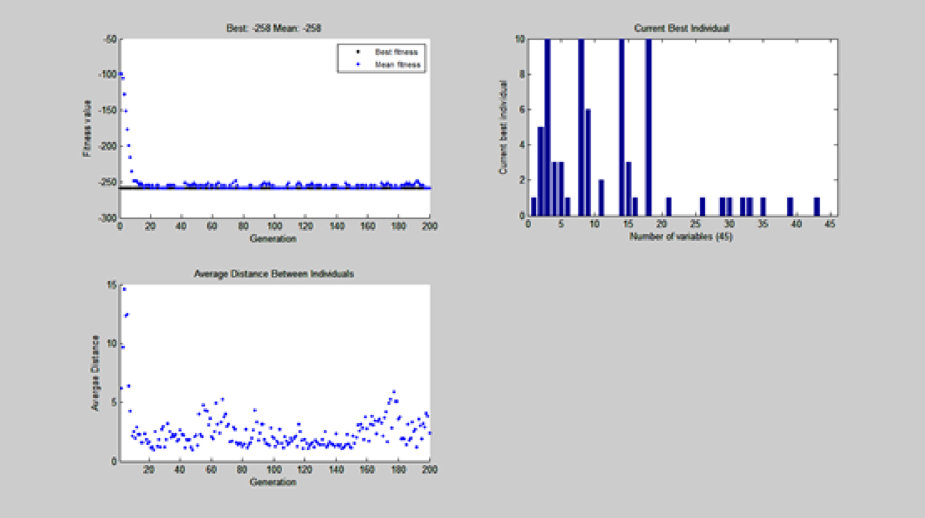

Figure 2: Plots of the best fitness value over the generations, average distance between individuals and current best individual for the evolved fuzzy three rule diagnostic system.

Training/test Performance			
Ratio (%)	Training set (%) (%)	Test set (%)	Overall
100/0		-	- 97.33
75/25	98.30	96.21	97.25
50/50	97.50	96.61	97.05

Table 2, Average performance obtained by the genetic algorithm with the three rule system over all 50 evolutionary runs, divided according to the three experimental categories.

Database

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

Rule 1 : if (v2 is Low) and (v3 is low) then (output is beningn)

Rule 2: if (v2 is low) and (v5 is low) and (v6 is low) and (v8 is low) then (output is benign) else (output is malignant)

Example 3, the best fuzzy diagnostic system with two rules. It exhibits an overall classification rate of 97.03

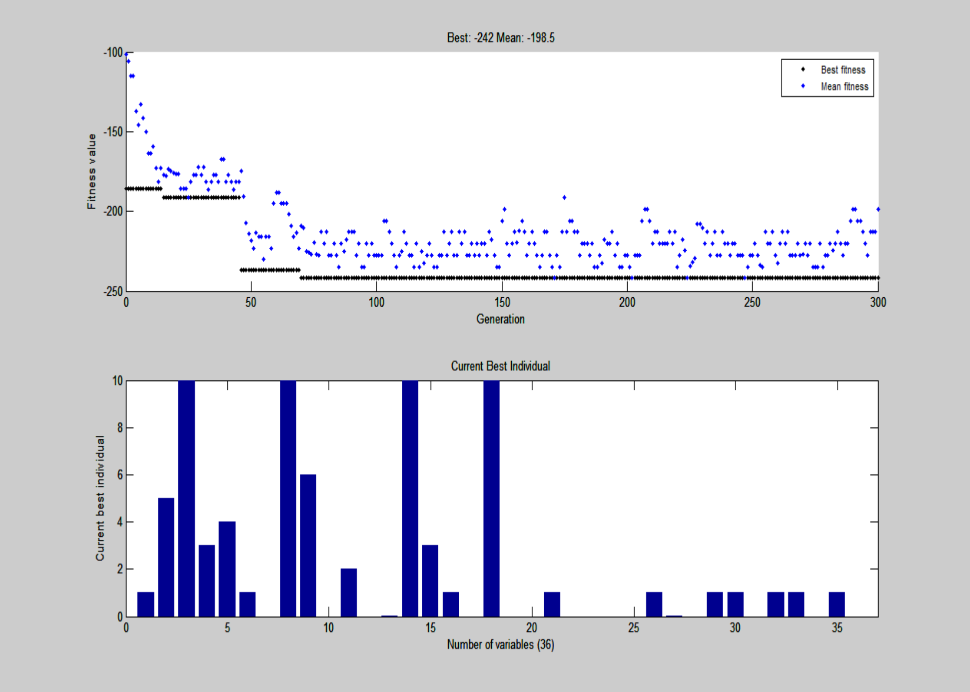

Figure 3: Plots of the best fitness value over the generations and the current best individual of all 36 variables in a two rule fuzzy diagnostic system.

Database

	v_1	v_2	v_3	v_4	v_5	v_6	v_7	v_8	v_9
P	4	2	5	6	6	2	٤	3	6
d	3	5	3	1	2	3	3	1	5

Rule 1: if (v3 is Low) and (v7 is Low) and (v8 is Low) and (v9 is Low) then (output is benign)

Rule 2 : if (v1 is Low) and (v2 is Low) and (v4 is High) and (v5 is High) and (v9 is Low) then (output is benign)

Rule3 : if (v1 is Low) and (v7 is Low) and (v6 is Low) and (v8 is Low) then (output is benign)

Rule 4:if (v3 is Low) and (v2 is Low) and (v4 is High) and (v9 is Low) then (output is benign) else (output is malignant)

Example 4: The best evolved fuzzy diagnostic system with four rule. It exhibits an overall classification rate of 96.19%.

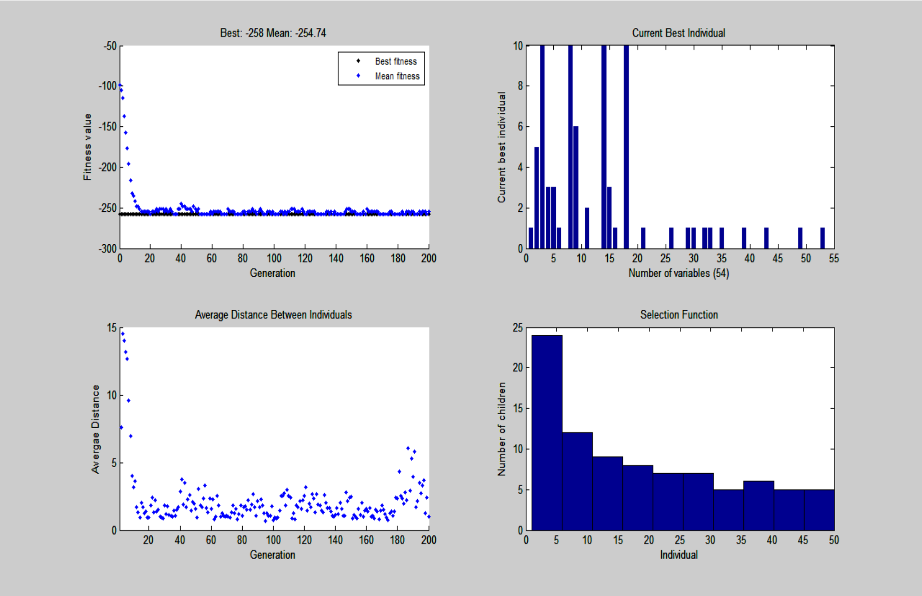

Figure. 4: Plots of the best fitness value over the generations and the current best individual, average distance between individuals and the selection function for best parent in all 54 variables in a four rule fuzzy diagnostic system.

Database

	v_1	v_2	v_3	v_4	v_5	v_6	v_7	v_8	v_9
P	1	7		6	3	6	8	3	
d	5	2		1	2	0	1	1	

Rule 1: if (v2 is Low) and (v5 is Low) and (v6 is Low) and (v8 is Low) then (output is benign) else (output is malignant)

Example 5: The best evolved fuzzy diagnostic system with one rule. It exhibits an overall classification rate of 96.19%.

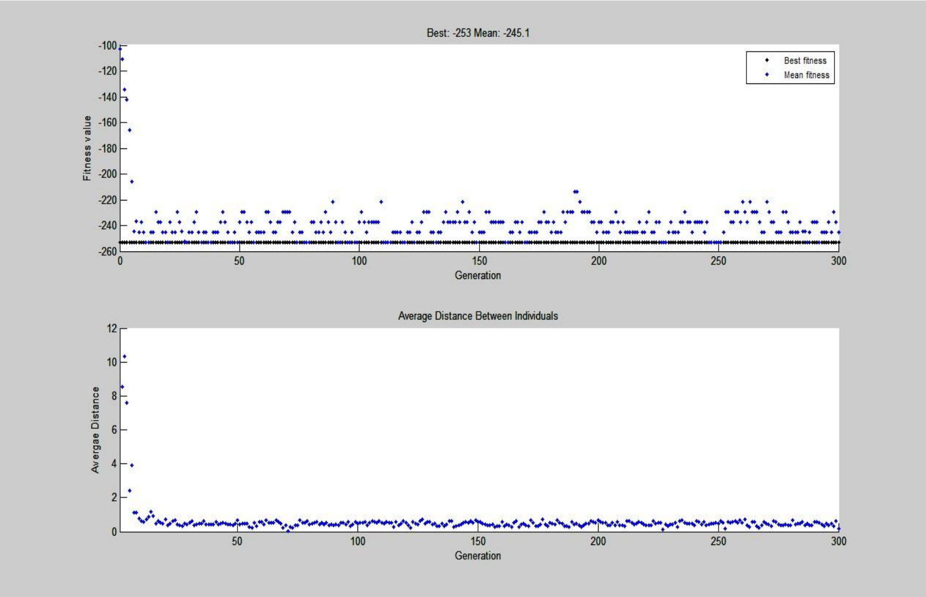

Figure 5: Plots of the best fitness value over the generations, and average distance between individuals for the evolved fuzzy one rule diagnostic system.

Rules-per system	Best system (%)	Average (%)
1	96.19	96.8
2	97.03	96.7
3	97.33	97.0
4	96.67	96.7

Table 3, presents the results of overall classification performance for all fuzzy diagnostic systems with rules from one to four.

- Example 4, gives the diagnostic system with four rules. It obtains 96.55% correct classification rate the benign cases, 96.8% correct classification rate over the malignant cases and an overall classification rate of 96.67%.
- Figure 4, Plots of the best fitness value over the generations and the current best individual, average distance between individuals and the selection function for best parent in all 54 variables in a four rule fuzzy diagnostic system.
- Example 5 delineates the best one-rule system found through our evolutionary approach. It obtains 96.17% correct classification rate the benign cases, 96.22% correct classification rate over the malignant cases and an overall classification rate of 96.19%.
- Figure 5, shows the best fitness and distance between individuals with this system. We have performed a total of 40 evolutionary runs in every system, the results of which are summarized in Table 3.

Following these steps and obtaining the results completes the fuzzification phase. For the inference engine to compute the truth value of each rule it applies the fuzzy and operator to combine the antecedent clauses in a fuzzy manner. These results in the output truth value, which is a continuous value which represents the rules degree of activation. Thus, a rule is not merely either activated or not, but in fact is activated to a 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 truth value. The defuzzifier then works to produce the final continuous value of the fuzzy inference system; this latter value is the value that is passed on to the threshold unit. For our best three rule fuzzy system given in Example 2, we calculate the membership values for each of the 260 patients and 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*. Thus, if a case in the database scores a value of 2.6 and that is classified as *benign*, but since it is close to the threshold 3 so its confidence will be *low*. This demonstrates a prime advantage of fuzzy systems which is the ability to give a diagnostic output not only a binary: *benign* and *malignant* classification, but also a measure representing the systems confidence in its output either as *low* or *high* confidence. Also A machine learning method expresses patterns as relations in first order logic and assigns probabilities to rules generated by composing patterns [11]. Our three-rule system computes intermediate values between $[2.5, 3.5]$ for only 23 cases out of the 260 in the Saudi Database; and these are the cases for which this system is less confident about the output. Our proposed fuzzy system described in this paper performs very well and reached comparable results similar to work done on the WBCD data by Reyes[16] and Setiono [17] in terms of both performance and simplicity of rules and we reached similar results in terms of accuracy and in time efficiency. It is worth noting that [4, 16] had 699 cases in the WBCD dataset from patients in USA and they used a different fitness function denoted $F = F_c - 0.05F_v - 0.01F_e$ where F_c computes the number of correctly diagnosed cases, F_v measures the linguistic integrity (interpretability) and F_e adds selection pressure towards systems with low quadratic error. Moreover, Setiono [17] they used an application of neural networks that involves Boolean rule bases extracted from trained neural networks.

4. Conclusion

In this paper, we use a relational fuzzy model and a genetic algorithm approach to the Saudi breast cancer diagnosis database. Our evolved systems exhibit both high classification performance with the possibility of attributing a confidence measure to the output diagnosis; with a few simple rules and are therefore interpretable, *i.e.* when a patient case is presented to the three rule diagnostic system the output will be given in two aspects: the first one is diagnosis: malignant(benign) and the second one is a confidence value. low(high). Our results suggests that the fuzzy-genetic approach is highly effective on early medical diagnosis and can help reduce the high cost of medical treatments of breast cancer. Our future work will involve applying our approach to other complex real-world diagnosis problems. We will also try alternative fuzzy logic approaches such as Neuro-Fuzzy networks or Fuzzy Petri with demonic relational methods

[19, 20]. Since neural networks has shown capabilities in rule and feature extracting, we can combine adaptive fuzzy inference systems and principle component analysis neural networks, to introduce a new computerized diagnostic tool and give similar accurate diagnostic results. Also, we plan to conduct some studies to justify the use of *min* and *max* operators for breast cancer diagnosis.

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