

Automated Detection of Breast Cancer Using Artificial Neural Networks and Fuzzy Logic

Esraa A. AL-Dreabi^a, Mohammad M. Otoom^b*, Bareqa Salah^c, Ziad M. Hawamdeh^d, Mohammad Alshraideh^e

^{a,e}Department of Computer Science, King Abdullah II School for Information Technology, University of Jordan, Amman, Jordan

^bDepartment of Computer Science, College of Science in Zulfi, Majmaah University, Riyadh, Saudia Arabia ^cDivision of plastic and reconstructive surgery, Faculty of Medicine, University of Jordan, Amman, Jordan ^dDepartment of Rehabilitation Medicine, Faculty of Medicine, University of Jordan, Amman, Jordan

> ^{a,e}Email: mshridah@ju.edu.jo ^bEmail: m.otoom@mu.edu.sa ^cEmail: bisalah@ju.edu.jo ^dEmail: z.hawamdeh@ju.edu.jo

Abstract

Our aim was to develop a diagnostic system that could classify breast tumors as either malignant or benign to provide a faster and more reliable method for patients. In order to accomplish this, we built two systems: one is based on Artificial Neural Networks (ANN) with a resilient back propagation and the other is based on fuzzy logic. We used the dataset provided by the University of California Irvine (UCI) Machine Learning Repository: the Wisconsin Diagnostic Breast Cancer (WDBC) dataset which describes characteristics of the cell nuclei presented in the images. The dataset is composed of features computed from digitized images of a Fine Needle Aspirate (FNA) of the breast mass. The system is based on ANN and was built using a feed-forward neural network with a Resilient Back Propagation (Rprop) algorithm that used to train the network, the number of hidden layers and hidden neurons determined by performing experiments and selecting the highest architectural accuracy.

* Corresponding author.

In order to obtain general architecture and to identify the accuracy of this system, we used ten-folds cross validation. The second system is based on fuzzy logic, and we built a Fuzzy Inference System (FIS). The decision tree was used to define the membership functions and the rules. The experiments were performed on two types of FIS: Sugeno-type and Mamdani-type. For the system based on ANN, Feed-Forward Neural Network presented the highest accuracy at 97.6%. While for fuzzy system, Sugeno FIS showed the highest accuracy at 94.8%. Since breast tumors, both malignant and benign, share structural similarities, the process of their detection is extremely difficult and time consuming if it is to be manually classified. Laboratory analysis or biopsies of the tumor is a manual, time consuming process yet it is accurate system to provide a faster and more reliable method of diagnosis and prediction for patients is rising. In this paper, we developed two kinds of artificial intelligence systems that can help physicians to classify breast cancer tumors as either malignant or benign.

Keywords: Benign; Breast cancer; Fuzzy system; Malignant; Neural Networks.

1. Introduction

Medical diagnosis is an important task that should be performed as accurate and efficient as possible. Unfortunately, not all doctors are equally skilled and may lack experience, or resources. Furthermore, similar symptoms for multiple diseases may boost the chance for a medical misdiagnosis. Therefore, computerized diagnosis tools are promising for physicians to clarify the confusing data in case of imprecision and uncertainty. Computerized diagnostic knowledge can be derived from datasets of cases solved in the past. The derived classifier can then be used to assist physician in the diagnosis of new patients or to improve accuracy and diagnostic pace. It can also be used to train students or physician non-specialists to diagnose patients with special diagnostic problems [1]. Breast cancer is a type of cancer that either originates in the breast or is primarily present in the breast cells. The disease occurs mostly in women but a small population of men is also affected. Breast cancer is the most common type of cancer amongst the female population as well as the most common cause of cancer deaths after lung cancer [2]. The early detection of breast cancer can save thousands of lives each year. Since breast tumors, both malignant and benign, share structural similarities, the process of their detection is extremely difficult and time consuming if it is to be manually classified. Laboratory analysis or biopsies of the tumor is a manual, time consuming process yet it is accurate system of prediction. It is, however, prone to human errors. Consequently, a need of creating an automated system to provide a faster and more reliable method of diagnosis and prediction for patients is rising [3]. In this paper, we developed two kinds of artificial intelligence systems that can help physicians to classify breast cancer tumors as either malignant or benign. Our aim was to develop a diagnostic system that could classify lesions extracted from tumors as benign or malignant, In order to accomplish this we built two systems, one based on neural networks with a resilient back propagation and the other based on fuzzy logic. In order to get the highest accuracy possible we examined different numbers of hidden neurons and hidden layers for the neural network system. For the fuzzy logic system we tried two types of fuzzy inference systems: Sugeno and Mamdani. The models were built using MATLAB 2010a, , which was run under windows Vista Home Premium SP1 OS with an AMD Turion X2 Dual-Core processor of 2.00 GHz, and 4.00 GB of RAM.

2. Methods

2.1. Data Preparation

In this experiment, we used the dataset provided by the University of California Irvine (UCI) Machine Learning Repository: the Wisconsin Diagnostic Breast Cancer (WDBC) which describes characteristics of the cell nuclei present in the images. The dataset is composed of features computed from digitized images of a Fine Needle Aspirate (FNA) of the breast mass. With the WDBC dataset the goal is to provide a distinction between the malignant and benign breast masses [4]. The dataset consists of 32 attributes (ID, diagnosis, 30 real-valued input features). The ID refers to a patient's number, diagnosis is the diagnosis of the patient (i.e. either malignant or benign), and ten real-valued features computed for each cell nucleus. The ten features are: (1) Radius, (2) Texture, (3) Smoothness, (4) Perimeter, (5) Area, (6) Compactness, (7) Concavity, (8) Concave points, (9) Symmetry, and (10) Fractal dimension. For each image, the mean, standard error, and "worst" or largest (mean of the three largest values) of these features were computed, resulting in 30 input features for 569 images representing 357 benign and 212 malignant cases. For the current experiment with neural networks, we took 212 benign cases to match the 212 malignant cases, resulting in a dataset of 424 records. The obtained dataset is used in all our experiments. In order to estimate the performance of the system, its accuracy and improve its generalization, a technique called cross validation was implemented, which determines accuracy by dividing the number of correct classifications by the overall number in the dataset [5]. This technique works by partitioning the dataset into training data, validation data and testing data. Training data are used to perform the analysis. Testing data are used for testing the system. Validation data are used to avoid over fitting the network. This study uses 10 folds that represented different partitions. This was done in order to improve generalization of the entire networks model. Each fold consisted of training data (80%), testing data (10%) and validation data (10%). Since the dataset consist of 424 records, it resulted in 340 training records, 42 testing records and 42 validation records for each fold. For the training data, we had 170 records that represented a benign diagnosis and 170 malignant diagnoses. For validation and testing data, we had 21 records representing a benign diagnosis and 21 a malignant diagnosis.

2.2. Using Neural Network for Breast Cancer Classification

Two architectures were created and tested in this paper: Feed-forward neural networks and cascade-forward neural networks. Feed-forward networks have weight connection from the input to each layer to the following layer. Cascade-forward networks have weight connection from the input to each layer and from each layer to the successive layers. Designing neural networks remains one of the unsolved tasks in computational research. Such a design entails selecting the appropriate network size for a given application. Network size involves the number of layers in a network and the number of nodes per layer. The quality of a solution found by a neural network depends strongly on the network size used. In general, network size affects network complexity, and learning time, but most importantly, it affects the generalization capabilities of the network; its ability to produce accurate results on testing sets. In order to determine the number of hidden layers, the following repeated steps were followed:

Step 1: start with one hidden layer, and apply Eq. (1) to find number of hidden neurons:

NumOfNeuron=(ni+no)/2....(1)

Where ni is the number of neurons of the input layer, and no is the number of neurons in the output layer. If the resulting number is fixed for example: 6 then the number of neurons are 6. If the result is not a fixed number for example 6.4, then apply cell and floor operations to get a fixed number so as the resulting numbers are 6 and 7 respectively. In order to be more precise and to increase the number of trials, we took for each result the following numbers i.e.: 6 ,the number plus one: 7 and the number minus one:5 but without any repetition in the architectures.

Step 2: add another layer: the number of neurons in this layer will be half the number of neurons in the previous layer (plus/ minus one).

Step3: repeat step 2 until the number of neurons in the layer is one.

2.2.1 Feed-Forward Neural Network

A feed-forward neural network with a Resilient Back Propagation (Rprop) algorithm has been used to build a model. The input layer had 30 neurons representing the number of feathers, and the output layer had one neuron representing the diagnosis (benign or malignant). Rprop was used as the training algorithm.

The activation function that was used in the output layer was Linear Function (LF). It was TANH and LOG-SIGMOID in the hidden layer. The results that were obtained by using these functions were compared.

The training experiments were setup in a manner that the training would be terminated in case the following conditions were satisfied: the number of epochs exceeds 1000, reaching the error goal of 1*10-8 or the number of validation checks reaches 20.

2.2.2 Cascade-Forward Neural Network

This paper also represents another model using cascade-forward neural networks which have 30 neuron in input layer, one neuron in the output layer and the output represents the diagnosis (benign or malignant). Rprop was used as the training algorithm.

The activation function that was used in the output layer is Linear Function (LF) and in the hidden layer TANH and LOG-SIGMOID. The results that were obtained by using these functions have been compared.

The training experiments were set up in a manner that the training will be terminated if the following conditions were satisfied: the number of epochs exceeds 1000, reaching the error goal of 1*10-8 or the number of validation checks reaches 50.

2.3. Fuzzy System for Breast Cancer Diagnosis

This paper represents a fuzzy system that was used to diagnose breast cancer as benign or malignant. In order to

build Fuzzy Inference System (FIS), defining a set of rules for each input membership functions (MF's) is required. The procedure can be summarized in three steps [7]: determination of the input and output variables that are used in the FIS, and the variation interval for each variable. Second, defining the set of linguistic values with MF that will map the values into fuzzy values for each variable is required. Defining a set of fuzzy inference rules between input and output that will determine the diagnosis as either benign or malignant is the third step. The MF is a curve that was used to map each point in the input space into a membership value or degree of membership. For each one of the 30 inputs, we defined the number of MF types and ranges, and then we defined a set of rules that gave us the diagnosis. This experiment used a Decision Tree (DT) to get the rules that were used to build the FIS. DTs are a method that could be used in helping to make a good choice; especially decisions that involve high costs and risks. DTs used a graphic approach to compare competing alternatives and assign values to those alternatives by combining uncertainties, costs, and payoffs into specific numerical values. This experiment represents two inference types (Mamdani and Sugeno). The results obtained from these types were compared.

2.3.1 Extracting Rules from Decision Trees

DTs are very popular classification tool as they represent rules and provide information regarding which features are the most important for classification purposes. The learning algorithms of DTs try to focus on the relevant features and ignore irrelevant ones. That happens by testing the values of certain features and then dividing training data into subsets containing a strong majority into one class [7]. This experiment used the C4.5 learning algorithm of DT. DTs take the form of a branching tree structure where each node is either a leaf node, which indicates the value of the target class (benign or malignant), or a decision node, where each node represents a single feature with two branches and each branch has a sub-tree. To get rules of classification, one moves from the root of the DT through its branches to the leaf nodes. In order to estimate the accuracy and avoid over-fitting, we used 10-folds cross validation, and the whole dataset was divided into 10 random equal size folds. Each one of the folds had 90% of the data as training data and 10% as testing data. The percentage of the training data and testing data was selected according to Hassanien [7]. By applying the DT algorithm to train data in each fold, we got 10 different DTs and the accuracy computed with the testing data was 90.8019% averaged form ten-folds. The DT learning algorithm C4.5 had an additional feature called pruning; that increased the accuracy of DT classification and improved its generalization. This is an important step and it was applied to the final results because all datasets contain a little subset of instances that are not well defined and differ from other neighborhoods. This is done to reduce classification errors caused by specialization in the training set; this is also done to make the tree more general and to avoid over-fitting, which gives an advantage to C4.5 learning algorithm [8]. By pruning all our DT's, we found that the best pruning level is level one. The DT's accuracy has increased from 90.8% to 92.22%. DT is a features selection method it selects 20 features from the total of 30 features that in the dataset. These features are mean radius, mean texture, mean smoothness, mean compactness, mean concavity, mean concavity point, mean fractal dimension, SE radius, SE area, SE smoothness, SE concavity point, SE symmetry, SE fractal dimension, largest radius, largest texture, largest parameter, largest area, largest smoothness, largest concave, and largest concave point. The total number of extracted rules from the DTs was 130 rules. An Example of one of the DTs is shown in figure 1.



Figure 1: Example of one of the decision trees

In figure 1, feature 23, which refers to the largest parameter, appears in the tree (as X23). This feature has two MFs: one is with range less than 105.15 and the other is greater than or equal to 105.15, X27. It refers to feature 27 (largest concave) and it also has two MFs: one is with range less than 0.21805 and one is greater than or equal to 0.21805. Since X2 (meaning texture) appears three times in the tree, it will have 6 MFs: the first is less than 19.86, the second is greater than or equal to 19.86, the third is less than 15.535, the forth is greater than or equal to 15.535, the fifth is less than 16.605 and the sixth MF is greater than or equal to 16.605. Feature 25 (largest smoothness) has two MF: one is with range less than 0.1003 and the other is greater or equal to 0.1003.

Feature 28 (largest concave point) also has two MFs: one is less than 0.13385 and the other greater than or equal to 0.13385. Feature 19 (SE symmetry) has 2MFs: one is less than 0.009266 and the other is greater than or equal to 0.009266. Feature 11 (SE radius) has 2 MFs: one is less than 0.6431 and one greater or equal to 0.6431, while feature 22 (largest texture) have 4 MFs: one is less than 30.145, one greater or equal to 30.145, one less than 24.785 and one greater or equal to 24.785. Feature 10 (meaning fractal dimension) has two MFs: one is less than 0.056075 and one that is greater or equal to 0.056075. Finally, feature 15 (SE smoothness) has two MFs: one is less than 0.007444 and the other is larger than or equal to 0.007444. As an example, the extracted rules are provided (shown in bold): If input23 < 105.15, input28 \geq 0.13385 and input22 < 24.785 \rightarrow Benign.

2.3.2 Building Breast Cancer Fuzzy Inference Systems

This experiment represents two types of FISs: Mamdani-type and Sugeno-type (zero-order Sugeno fuzzy model). Mamdani FIS is a method that interprets the values in the input vector and it is based on user defined rules and assigned values to the output vector. The FIS was created by using MATLAB® version 2010a. The steps of FIS for the two types are the same except for the last step. The steps of building the Breast Cancer FIS are as follows: The first step is fuzzification. This step is taken to take the crisp inputs (20 features) and

determine the degree to which these inputs belong to each of the appropriate fuzzy set. The crisp inputs were limited to the universes of discourse (that were defined with the help of experts). The purpose of fuzzification is to map input values into the range [0, 1] by using a set of input MFs. In this paper, we used two types of MFs: Triangular and Trapezoidal. The second step is rule evaluation to take the fuzzified inputs, and to apply them to the antecedents of the fuzzy rules. If the fuzzy rules have multiple antecedents, the fuzzy operator (AND or OR) will be used to get a single number that represents the result of the antecedent evaluation. This number is in Mamdani-type and then it is applied to the consequent membership function. While in Sugeno-type, the output of each rule is crisp number. We extracted these rules from DTs.

In our FIS, all the rules have at least two antecedents and all our rules were defined by AND-operator. The third step is Aggregation of the rule outputs. In this step, all the membership functions of rules consequent were previously clipped, scaled and combined into one fuzzy set. The input of the aggregation process is the list of clipped or scaled consequent membership functions. And the output in the Mamdani-type is one fuzzy set for each output variable, and in the Sugeno-type, it is crisp output.

The diagnosis is based on testing all the rules in the FIS. Thus, the rules must be combined in order to make a decision. Aggregation is the process that is used to combine the fuzzy sets of all rules outputs into a single fuzzy set (for Mamdani) and crisp number (for Sugeno). The forth step is Defuzzification (For Mamdani-type). The input for the defuzzification process is the aggregate output fuzzy set and the output is a single number. There is a set of parameter used to define the FIS, and we defined the type of AND-method, Aggregation type, and Defuzzification method. The parameter of the Mamdani model is shown in Table 1.

Method	Value
AND method	Min
Aggregation	Sum
Defuzzification	Centroid

Table 1: Mamdani model parameter

The Sugeno model had the parameters that are shown in Table 2. The product was selected as the AND operation and for Defuzzification Wtaver (weighted average).

Table 2:	Sugeno	model	parameter
----------	--------	-------	-----------

Method	Value
And method	Prod
Defuzzification	Wtaver

3. Results

At First, we presented results for feed-forward neural networks. This paper represents different architectures for feed-forward neural networks. Table 3 summarizes the best results we obtained from different architectures.

Neural network architecture	Number of hidden layer(s)	Accuracy
[30 16 1]	1	97.14%
[30 16 7 1], [30 14 7 1], [30 15 8 1] and [30 16 7 1]	2	97.38%
[30 15 8 3 1]	3	97.62%
[30 17 9 5 3 1]	4	97.14%
[30 16 8 4 2 1 1]	5	96.90%

Table 3: Summery of highest accuracy architecture

The architecture differs in the number of hidden layers and activation functions. We have started with one hidden layer and increased the number to five hidden layers. The highest accuracy achieved was 97.61% by the architecture [30 15 8 3 1] that had 3 hidden layers; the highest accuracy using one hidden layer was 97.14%. By adding a second hidden layer, the accuracy increased to 97.38%. It also increased by adding a third hidden layer to 97.62%. However, the accuracy decreased with a fourth hidden layer to 97.14% and witnessed further decrease with the addition of a fifth hidden layer to 96.90%. An explanation for the results could be that using small numbers of hidden layers (1 and 2) gives high training errors and high generalization errors due to underfitting according to Xu and Chen [6] and by using too many hidden layers (4 and 5), you may get low training errors but still have high generalization errors due to over-fitting according to Xu and Chen [6]. The experiments are the only way to determine the best neural network architecture for solving a specific problem, as the results represent in the experiment that we performed. In this experiment, the architecture with three hidden layers [30 15 8 3 1] yielded the highest accuracy. Second, the results of the Cascade-Forward Neural Network experiment are shown in (Table 4) and the highest accuracy was 97.3% by the architecture [30 16 8 4 3 2 1]. However, we obtained higher accuracy by using feed-forward.

Table 4: Summary of highest accuracy architecture

Neural network architecture	Number of hidden layers	Accuracy
[30 14 1]	1	97.14%.
[30 17 7 1]	2	96.90%
[30 17 7 2 1], [30 15 8 5 1] and [30 16 8 3 1]	3	96.43%
[30 17 9 5 1 1]	4	97.14%
[30 16 8 4 3 2 1]	5	97.3%

Third, the results of fuzzy logic systems are as follow: the results obtained from the Mamdani-type are shown in (Table 5) the highest accuracy was 90.8% and the results from the Sugeno-type are shown in (Table 6) with the highest accuracy at 94.81%.

MF type	Accuracy
Triangular	90.8%
Trapezoidal	90.8%

Table 6: Results of the Sugeno model

MF type	Accuracy
Triangular	94.34%
Trapezoidal	94.81%

4. Discussion

Early diagnosis and treatment of breast cancer play a critical role in increasing the chance of survival. The characterization of benign and malignant lesions represents a very complex problem even for an experienced radiologist. In the literature, several techniques have been proposed to detect the presence of cancers using various methodologies. This paper proposed two artificial intelligence systems: one is based on Artificial Neural Networks (ANN) and the other is based on fuzzy logic.

This section first shows the comparison of the results that we obtained from all the models that were built in these experiments then comparing them to other authors' study results.

This paper shows two models based on Neural Networks: one is in feed-forward architecture and the other one is in Cascade-forward architecture and two FISs: one is based on the Mamdani-type model and the other is based on the Sugeno-type model. All four models were tested using the same dataset, WDBC. (Figure 2) shows the percentage of correct diagnosis of the models applied to the test datasets. All models had high accuracy percentages, but models based on neural networks were more accurate. Furthermore, the experiments showed that feed-forward was more accurate than cascade-forward.

For neural network models, they can be compared on the basis of their performance, which translates into the lower the percentage the better (less training time and memory consumption) the performance of feed-forward and cascade-forward models shown in (Figure 3).



Figure 2: Accuracy percentages of all built models



Figure 3: Neural networks models performance

The performance of neural networks has been computed according to training time and memory consumption. As (Figure 3) shows, cascade-forward has better performance, which is referred to the architecture of cascade-forward which has additional weight connections from the input to each layer and from each layer to the successive layers, unlike feed-forward that has weight connections from each layer to the successive layer only. These additional connections might improve the speed at which the network learns the desired relationship [9]. Cascade-neural networks may have better performance, but the accuracy of feed-forward is higher. For application to breast cancer diagnosis, accuracy is the most important factor.

In the literature, several techniques have been proposed to detect the presence of breast cancers using various methodologies. The accuracy achieved was 97.62% which was higher than the study proposed by Mashor and Esugasini [12]. They used MLP which accuracy was 92.78%, and for RBF, 83.31%, but less than HMLP 100%. The accuracy was also less than the findings of the study proposed by Hassanien [7] which used decision tree analysis; as the feature selection method for neural networks and used WPBC as the dataset, with accuracy for the test data at 99.55%. Likewise, our accuracy was less than Liu and Deng [10] who used a neural network based on an adaptive genetic algorithm using the WPBC dataset, with an accuracy of 98.9%. The study proposed by Anagnostopoulos and Maglogiannis [11] also applied neural networks using the WPBC and WDBC datasets, and their accuracy using PNN on the WDBC dataset was 97.9% which was better than our accuracy, but on the WPBC dataset it was less at (94.6%). Our results were also less than Parthiban and

Subramanian's [13] who built a neuro-fuzzy inference system to diagnose breast cancer, using the WPBC dataset, with accuracy at 98.82%.

The Sugeno-type FIS accuracy was 94.8% which was better than the study at [14] which had accuracy 87% on a fuzzy system.

This paper proposed two artificial intelligence systems: one is based on Artificial Neural Networks (ANN) and the other is based on fuzzy logic. For ANN, we used feed-forward neural networks trained with the Rprop training algorithm, and the architecture we used to build the network consisted of 30 input features and 3 hidden layers: 15 neurons in the first hidden layer, 8 in the second, 3 in the third, and one neuron in the output layer. The output was either malignant or benign. Moreover, a ten-fold cross validation was used to access the generalization of the proposed system, the accuracy achieved was 97.62%. Our second system was based on fuzzy logic. Fuzzy Inference Systems (FIS) need a defined Membership Function (MF) for each input and a set of rules. In this study, we used a Decision Tree (DT) to extract rules and range of MF; DTs are very popular tool for classification because DTs generate rules and provide information about which features are the most important to classification. The Sugeno-type FIS accuracy was 94.8%. Although our proposed two artificial intelligence systems will never replace human experts, it can help physicians to determine breast cancer tumors as either malignant or benign faster and in a more reliable manner.

References

- [1] Kononenko I. Machine learning for medical diagnosis: history, state of the art and perspective, Artificial Intelligence in Medicine. Slovenia: Ljubljana; 2001. p. 89-109.
- [2] American Cancer Society, Breast Cancer Overview. USA: 2010.p. 1-58.
- [3] Frank A, and Asuncion A. UCI Machine Learning Repository, Irvine, CA: University of California, School of Information and Computer Science http://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Diagnostic%29, Accessed: July 16th, 2011
- [4] Sewak M, Vaidya P, Chung Chan C, and Duan Z. SVM Approach to Breast Cancer Classification, IMSCCS '07 Proceedings of the Second International Multi-Symposiums on Computer and Computational Sciences. 2007; 94.
- [5] Yan H, Jiang Y, Zheng J, Peng C, and Li Q, A Multilayer Perceptron-Based Medical Decision Support System for Heart Disease Diagnosis, Expert Systems with Applications. 2006; 30: 272-281.
- [6] Xu S, and Chen L. A Novel Approach for Determining the Optimal Number of Hidden Layer Neurons for FNN"s and Its Application in Data Mining, In the 5th International Conference on Information Technology and Applications, Cairns, Australia. 2008; 683-686.
- [7] Hassanien A. Classification and feature selection of breast cancer Data based on Decision Tree Algorithm, International Journal of Studies in Informatics and Control Journal. 2003;12:33-39.
- [8] Korting T. C4.5 algorithm and Multivariate Decision Trees, Multivariate decision trees, Machine Learning, 2006; 19:45–77.
- [9] Demuth H, Beale M, and Hagan M, Math Works, Neural Network Toolbox[™] 6 User's Guide, 2010.

- [10] Liu L, and Deng M. An Evolutionary Artificial Neural Network Approach for Breast Cancer Diagnosis, Third International Conference on Knowledge Discovery and Data Mining, 2010.
- [11] Anagnostopoulos I, and Maglogiannis I. Neural network-based diagnostic and prognostic estimations in breast cancer microscopic instances, International Federation for Medical and Biological Engineering. 2006; 44:773–784.
- [12] Mashor M, Esugasini S, Isa N and Othman N. Classification of Breast Lesions Using Artificial Neural Network, Biomed 06, IFMBE Proceedings. 2007; 15: 45-49.
- [13] Parthiban L, and Subramanian R, CANFIS—a computer aided diagnostic tool for cancer detection, J. Biomedical Science and Engineering.2009; 2:323-335.
- [14] Balanica V, Dumitrache L, Caramihai M, Rae W, and Herbst C. Evaluation Of Breast Cancer Risk By Using Fuzzy Logic, U.P.B. Sci. Bull, Series C. 2011;73: 402-4014.