

# Breast Cancer Prediction

Muhammad Abdul-Mahdi Al-Khalidi, Mohammed Abdul Hay Abu Bakr, Haitham Maher Al-Attar, Nader Kamal Mahra

Department of Information Technology,  
Faculty of Engineering and Information Technology,  
Al-Azhar University, Gaza, Palestine

**Abstract-** Breast Cancer is mostly identified amongst women and is a main reason for increasing the rate of mortality amongst women. Diagnosis of breast cancer takes time and due to the importance of the topic, it is necessary to develop a system that can automatically diagnose breast cancer in its early stages. Many Machine Learning Algorithms have been used for the detection breast cancer. The Wisconsin Breast Cancer Dataset has been used which contains 699 samples and 10 features. The paper proposes an Artificial Neural Network model that is implemented using Just Neural Networks (JNN) using the dataset which is collected from UCI machine learning repository. The proposed model has been trained and validated. The accuracy rate obtained from the proposed ANN model was 99.57%.

**Keywords:** Prediction, JNN, ANN, Breast Cancer

## 1. Introduction

Breast Cancer is the second most dangerous cancer after Lung Cancer which is classified to the number one dangerous cancer. Breast cancer constitutes 12% of new cancer cases approximately out of which close to 25% are women [1]. People visit an oncologist, in case of any sign or symptom of cancer. The oncologist can diagnose and detect breast cancer through Mammograms, Magnetic resonance imaging (MRI) of breast, ultrasound of X-ray of the breast, tissue biopsy etc[2]. Once breast cancer is confirmed, sentinel node biopsy of the patient is done regularly which helps to detect cancerous cells in lymph nodes. Machine Learning techniques are also used for the classification of benign and malignant tumors. The early detection of Breast Cancer can enhance the prediction and survival rate of the patients [3]. This will help the patients to take necessary treatments at the right time [4]. For benign tumors the patients can avoid unnecessary treatments. Artificial Neural Networks technique when applied in the medical field can help in prediction of various outcomes, cost minimization and upgrade the healthcare value to rescue lives of people. The process of classifying tumors can be done by Artificial Neural Networks technique.

In information technology (IT), an artificial neural network (ANN) is a system of hardware and/or software patterned after the operation of neurons in the human brain. ANNs -- also called, simply, neural networks -- are a variety of deep learning technology, which also falls under the umbrella of artificial intelligence (AI)[5].

Commercial applications of these technologies generally focus on solving complex signal processing or pattern recognition problems. Examples of significant commercial applications since 2000 include handwriting recognition for check processing, speech-to-text transcription, oil-exploration data analysis, weather prediction and facial recognition [7].

An ANN usually involves a large number of processors operating in parallel and arranged in tiers. The first tier receives the raw input information -- analogous to optic nerves in human visual processing. Each successive tier receives the output from the tier preceding it, rather than from the raw input -- in the same way neurons further from the optic nerve receive signals from those closer to it. The last tier produces the output of the system[98].

Each processing node has its own small sphere of knowledge, including what it has seen and any rules it was originally programmed with or developed for itself. The tiers are highly interconnected, which means each node in tier  $n$  will be connected to many nodes in tier  $n-1$  -- its inputs -- and in tier  $n+1$ , which provides input data for those nodes. There may be one or multiple nodes in the output layer, from which the answer it produces can be read [8].

Artificial neural networks are notable for being adaptive, which means they modify themselves as they learn from initial training and subsequent runs provide more information about the world. The most basic learning model is centered on weighting the input streams, which is how each node weights the importance of input data from each of its predecessors. Inputs that contribute to getting right answers are weighted higher [12-14].

Typically, an ANN is initially trained or fed large amounts of data [15-17]. Training consists of providing input and telling the network what the output should be. For example, to build a network that identifies the faces of actors, the initial training might be a series of pictures, including actors, non-actors, masks, statuary and animal faces. Each input is accompanied by the matching identification, such as actors' names, "not actor" or "not human" information. Providing the answers allows the model to adjust its internal weightings to learn how to do its job better [18-21].

In defining the rules and making determinations -- that is, the decision of each node on what to send to the next tier based on inputs from the previous tier -- neural networks use several principles. These include gradient-based training, fuzzy logic, genetic

algorithms and Bayesian methods. They may be given some basic rules about object relationships in the space being modeled [22-25].

Further, the assumptions people make when training algorithms causes neural networks to amplify cultural biases. Biased data sets are an ongoing challenge in training systems that find answers on their own by recognizing patterns in data. If the data feeding the algorithm isn't neutral -- and almost no data is -- the machine propagates bias [26-29].

Neural networks are sometimes described in terms of their depth, including how many layers they have between input and output, or the model's so-called hidden layers [30-34]. This is why the term neural network is used almost synonymously with deep learning. They can also be described by the number of hidden nodes the model has or in terms of how many inputs and outputs each node has. Variations on the classic neural network design allow various forms of forward and backward propagation of information among tiers [35-38].

Specific types of artificial neural networks include [39-40]:

- Feed-forward neural networks
- Recurrent neural networks
- Convolutional neural networks
- De-convolutional neural networks
- Modular neural networks

**Feed-forward neural networks** are one of the simplest variants of neural networks. They pass information in one direction, through various input nodes, until it makes it to the output node. The network may or may not have hidden node layers, making their functioning more interpretable. It is prepared to process large amounts of noise. This type of ANN computational model is used in technologies such as facial recognition and computer vision [41-43].

**Recurrent neural networks (RNN)** are more complex [44]. They save the output of processing nodes and feed the result back into the model. This is how the model is said to learn to predict the outcome of a layer. Each node in the RNN model acts as a memory cell, continuing the computation and implementation of operations. This neural network starts with the same front propagation as a feed-forward network, but then goes on to remember all processed information in order to reuse it in the future. If the network's prediction is incorrect, then the system self-learns and continues working towards the correct prediction during backpropagation. This type of ANN is frequently used in text-to-speech conversions [45,46].

**Convolutional neural networks (CNN)** are one of the most popular models used today. This neural network computational model uses a variation of multilayer perceptrons and contains one or more convolutional layers that can be either entirely connected or pooled[47]. These convolutional layers create feature maps that record a region of image which is ultimately broken into rectangles and sent out for nonlinear processing [48]. The CNN model is particularly popular in the realm of image recognition; it has been used in many of the most advanced applications of AI, including facial recognition, text digitization and natural language processing. Other uses include paraphrase detection, signal processing and image classification [49,50].

**De-convolutional neural networks** utilize a reversed CNN model process. They aim to find lost features or signals that may have originally been considered unimportant to the CNN system's task. This network model can be used in image synthesis and analysis [51,52].

**Modular neural networks** contain multiple neural networks working separately from one another[52,53]. The networks do not communicate or interfere with each other's activities during the computation process. Consequently, complex or big computational processes can be performed more efficiently [54].

Advantages of artificial neural networks include [55]:

- Parallel processing abilities mean the network can perform more than one job at a time.
- Information is stored on an entire network, not just a database.
- The ability to learn and model nonlinear, complex relationships helps model the real life relationships between input and output.
- Fault tolerance means the corruption of one or more cells of the ANN will not stop the generation of output.
- Gradual corruption means the network will slowly degrade over time, instead of a problem destroying the network instantly.
- The ability to produce output with incomplete knowledge with the loss of performance being based on how important the missing information is.
- No restrictions are placed on the input variables, such as how they should be distributed.
- Machine learning means the ANN can learn from events and make decisions based on the observations.

- The ability to learn hidden relationships in the data without commanding any fixed relationship means an ANN can better model highly volatile data and non-constant variance.
- The ability to generalize and infer unseen relationships on unseen data means ANNs can predict the output of unseen data.

## 2. Literature Review

Lots of breast cancer research has been reported in the literature of medical data analysis, and most of them turn up with good classification accuracies. Author in [56] proposed LS-SVM classifier algorithm for the diagnosis of breast cancer and achieved the classification accuracy of 98.53% using 10-fold cross validation. Author in [57] proposed a new method for the breast cancer diagnosis using support vector classification algorithm on the most predictive features and obtain the classification accuracies of 99.02% without cross-validation. Author in [58] presented an innovative technique for breast cancer detection, by using statistical methods in combination with swarm optimization and reported the accuracy of 98.71%. Authors in [59] proposed a new method AMMLP for the classification of breast cancer datasets by using an Artificial Neural Network over the biological met plasticity property and acquire classification accuracy of 99.26. Authors in [60] discussed the use of available technological advancements to develop prediction models for breast cancer. The manuscript used Naïve Bayes, RBF Network and J48 to develop prediction model by 10 fold cross-validation method for measuring the unbiased estimate of these models for performance comparison. Author in [61] used five classification algorithms Naïve bayes, SMO, REP Tree, J48 and MLP upon two data sets which are breast cancer and diabetes respectively, from the UCI machine learning repository. Author in [62] used C4.5 decision tree for classification with a success of 94.74% was achieved. Author in [63] used fuzzy genetic algorithm with a success of 97.36% was obtained. Author in [64] achieved a 95% success using blurred neurons. Author in [65] used feedforward neural networks with a success of 98.1%. Author in [66] used perceptron neural network method and a success rate of 98.8% was obtained. Author in [67] used fuzzy clustering method with a success of 95.57% was achieved. Author in [68] used generalized regression neural networks and achieved a success of 98.8%. Authors in [69] used multilayer perceptron neural network, combined neural network (CNN), probabilistic neural network, recurrent neural network and support vector machine. The highest success was obtained using support vector machines with 99.54%. Authors in [70] achieved a success rate of 99.50% using the filter and wrapper methods. Author in [71] performed using support vector machines, a diagnostic success of 97.71% were obtained.

## 3. Methodology

After getting the Breast Cancer Wisconsin dataset from “the Center for Machine Learning and Intelligent Systems, University of California, Irvine”[73], we identified the input variables, output variables, upload the dataset, divided it to training and validating sets, determined the proper hidden layers. Then we trained and validated the sets to get the best accuracy.

### 3.1 The Input Variables

The input variables selected are those which can easily be obtained from Breast Cancer Wisconsin Database. The input variables are: Sample code number, Clump Thickness, Uniformity of Cell Size, Uniformity of Cell Shape, Marginal Adhesion, Single Epithelial Cell Size, Bare Nuclei, Bland Chromatin, Normal Nucleoli, Mitoses, and Class. These factors were transformed into a format suitable for neural network analysis. The domain of the input variables used in this study shown in Table1.

Table 1 : Input and out attributes

| S.N. | Attribute name              | Domain of Attribute             | Attribute type |
|------|-----------------------------|---------------------------------|----------------|
| 1    | Sample code number          | id number                       | Input          |
| 2    | Clump Thickness             | 1 - 10                          | Input          |
| 3    | Uniformity of Cell Size     | 1 - 10                          | Input          |
| 4    | Uniformity of Cell Shape    | 1 - 10                          | Input          |
| 5    | Marginal Adhesion           | 1 - 10                          | Input          |
| 6    | Single Epithelial Cell Size | 1 - 10                          | Input          |
| 7    | Bare Nuclei                 | 1 - 10                          | Input          |
| 8    | Bland Chromatin             | 1 - 10                          | Input          |
| 9    | Normal Nucleoli             | 1 - 10                          | Input          |
| 10   | Mitoses                     | 1 - 10                          | Input          |
| 11   | Class                       | (2 for benign, 4 for malignant) | Output         |

### 3.2 Output variable

The output variable is the class whether the breast cancer is benign or malignant.

### 3.3 Neural Network

The neural network topology was built based on the Multilayer Perceptron with one input layer, one hidden layer (4 nodes) and one output layer as shown in Figure 2.

### 3.4 Evaluation of the study

First of all, for the evaluation of our study, we used a sample of 699 of Breast Cancer Wisconsin representing benign or malignant cancer. We developed a model able to differentiate between benign or malignant cancer. Our model uses a neural network with one input layer, one hidden layers and one output layer. As input data for predicting the Validity of breast cancer we used attribute as shown in Figure 1.

Our task was to predict the result based on the 10 input variables. We conducted a series of tests in order to establish the number of hidden layers and the number of neurons in each hidden layer. Our tests give us that the best results are obtained with one hidden layer. We used a sample of (699 records): 469 training samples and 230 validating samples. The network structure was found on a trial and error basis (as seen in Figure 2). We started with a small network and gradually increased its size. Finally, we found that the best results are obtained for a network with the following structure: 10I-1H-1O, i.e. 10 input neurons, 1 hidden layers with (4) neurons, and an output layer with 1 neuron. For this study we used Just Neural Network (JNN)[74]. We trained the network for 8830 epochs (as shown in Figure 3) on a regular computer with 4 GB of RAM memory under the Windows 10 operating system. We got an accuracy of 99.57%. Figure 4 shows Parameters of the proposed ANN model. Figure 5 shows the factors, their importance and relative importance that affect the breast cancer artificial Neural Model using Just NN environment. Figure 6 outlines the detail of the proposed ANN model.



| Sample ID | Conc   | Clump | Thickness | Uniformity | Cellularity | Bare Nuclei | Mitoses | Normal Nuclei | Class |
|-----------|--------|-------|-----------|------------|-------------|-------------|---------|---------------|-------|
| 0100225   | 0.4444 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0002945   | 0.4444 | 0     | 0         | 0          | 0           | 0.4444      | 1       | 0.2222        | 0     |
| 0105425   | 0.2222 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0014277   | 0.8888 | 1     | 1         | 0          | 0           | 0.2222      | 0       | 0.2222        | 1     |
| 0017422   | 0.2222 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0017422   | 0.7777 | 1     | 1         | 1          | 1           | 0.4444      | 1       | 0.4444        | 1     |
| 0022888   | 0.0000 | 0     | 0         | 0          | 0           | 0.1111      | 1       | 0.2222        | 0     |
| 0022888   | 0.1111 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0033888   | 0.1111 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.5555        | 0     |
| 0033888   | 0.5555 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.1111        | 0     |
| 0039288   | 0.0000 | 0     | 0         | 0          | 0           | 0.8888      | 0       | 0.2222        | 1     |
| 0050272   | 0.1111 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.1111        | 0     |
| 0043931   | 0.4444 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.3333        | 0     |
| 0043931   | 0.0000 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0044872   | 0.7777 | 1     | 0         | 1          | 1           | 0.4444      | 1       | 0.4444        | 1     |
| 0047630   | 0.4444 | 0     | 1         | 0          | 0           | 0.5555      | 0       | 0.3333        | 0     |
| 0048672   | 0.3333 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.1111        | 0     |
| 0048672   | 0.3333 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0048672   | 0.0000 | 1     | 1         | 1          | 1           | 0.2222      | 1       | 0.3333        | 0     |
| 0048672   | 0.8888 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0048672   | 0.0000 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.4444        | 1     |
| 0048672   | 0.0000 | 0     | 0         | 0          | 0           | 0.8888      | 1       | 0.4444        | 1     |
| 0048672   | 0.2222 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.1111        | 0     |
| 0048672   | 0.7777 | 0     | 0         | 0          | 0           | 0.1111      | 1       | 0.4444        | 1     |
| 0048672   | 0.0000 | 0     | 0         | 0          | 0           | 0.1111      | 0       | 0.2222        | 0     |
| 0048672   | 0.4444 | 0     | 0         | 0          | 0           | 0.1111      | 1       | 0.2222        | 1     |
| 0048672   | 0.2222 | 0     | 0         | 0          | 0           | 0.8888      | 0       | 0.1111        | 0     |

Figure 1: Imported dataset in JNN environment

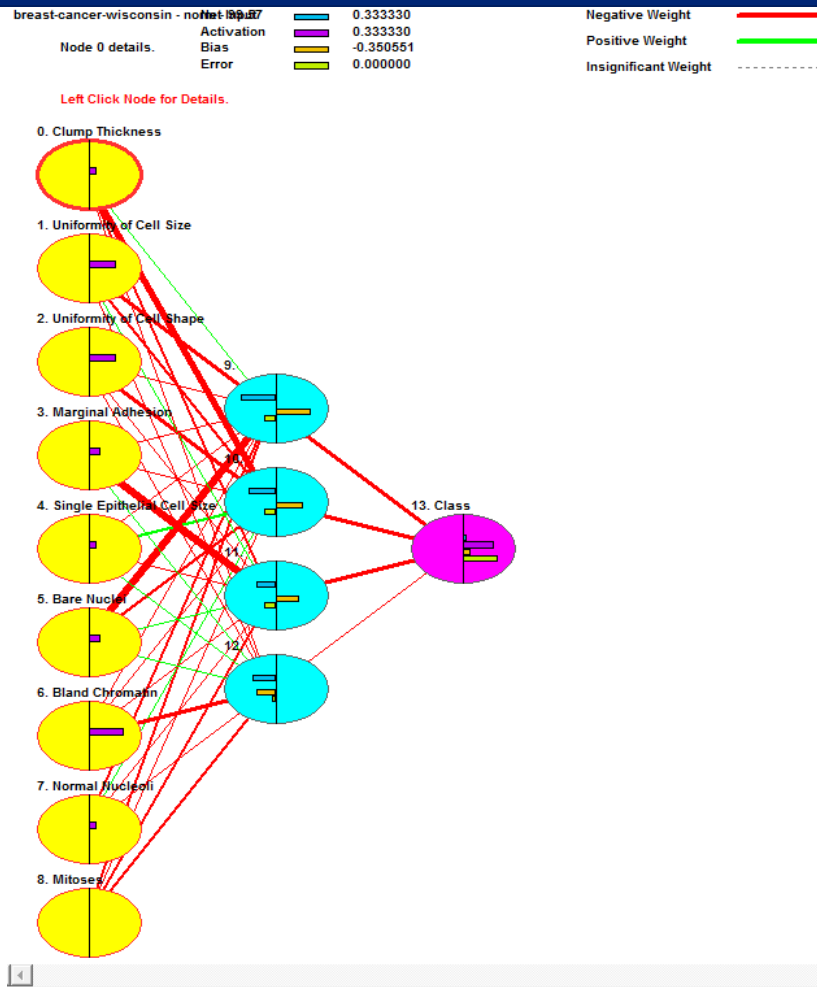


Figure 2: Structure of the proposed ANN model

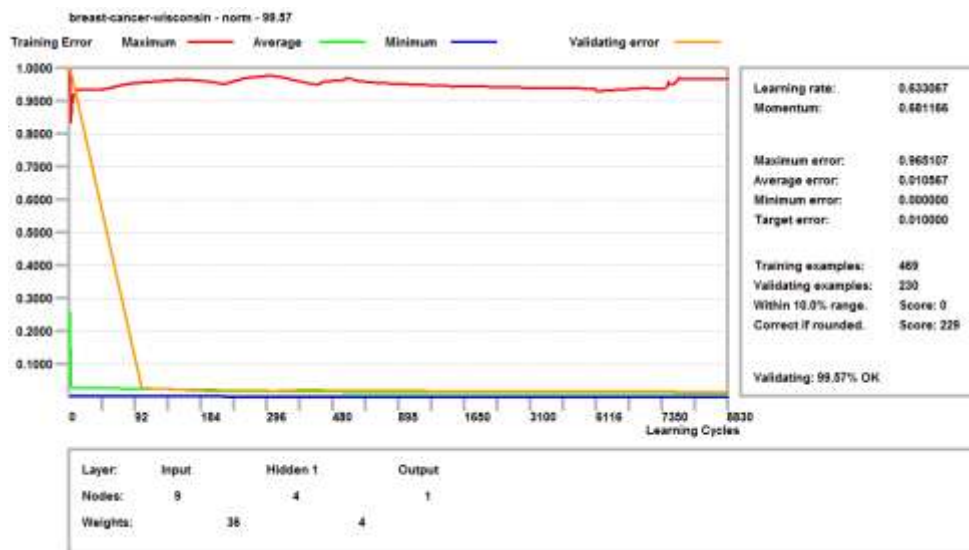


Figure 3: Training and validating the ANN model

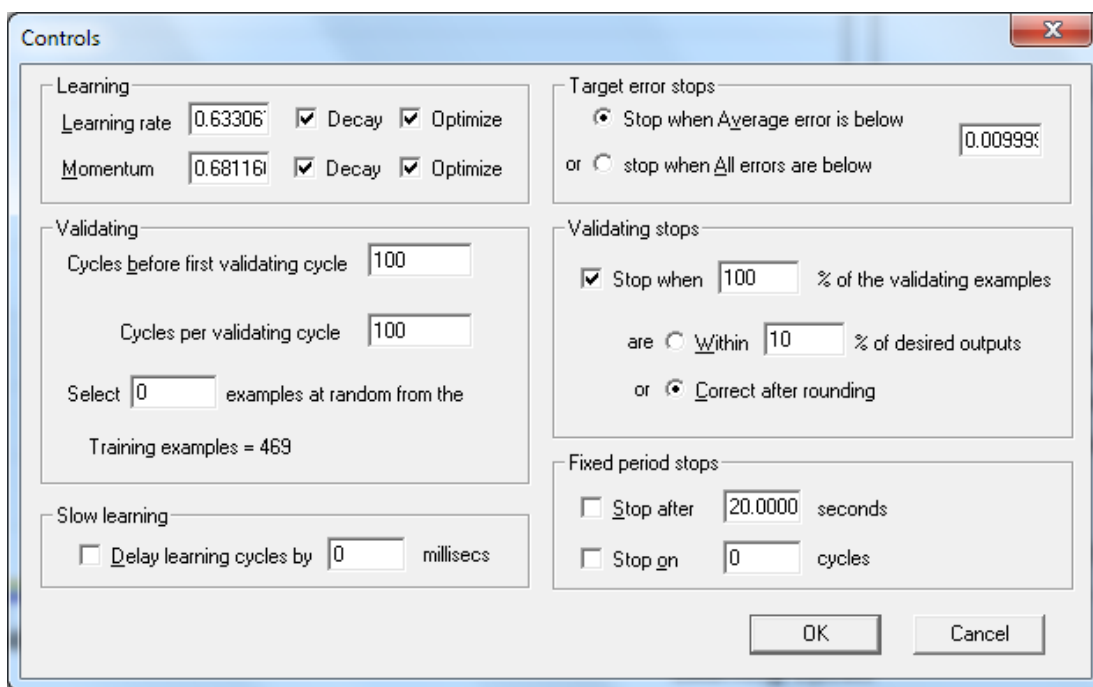


Figure 4: Parameters of the proposed ANN model

breast-cancer-wisconsin - norm - 99.57 8830 cycles. Target error 0.0100 Average training error 0.010567  
 The first 9 of 9 Inputs in descending order.

| Column | Input Name              | Importance | Relative Importance |
|--------|-------------------------|------------|---------------------|
| 6      | Bare Nuclei             | 55.8217    |                     |
| 4      | Marginal Adhesion       | 52.0087    |                     |
| 9      | Mitoses                 | 48.5929    |                     |
| 1      | Clump Thickness         | 48.0378    |                     |
| 7      | Bland Chromatin         | 38.7285    |                     |
| 2      | Uniformity of Cell Size | 36.9008    |                     |
| 5      | Single Epithelial Cell+ | 35.3891    |                     |
| 3      | Uniformity of Cell Sha+ | 29.5640    |                     |
| 8      | Normal Nucleoli         | 28.6905    |                     |

Figure 5: Most influential features in the dataset

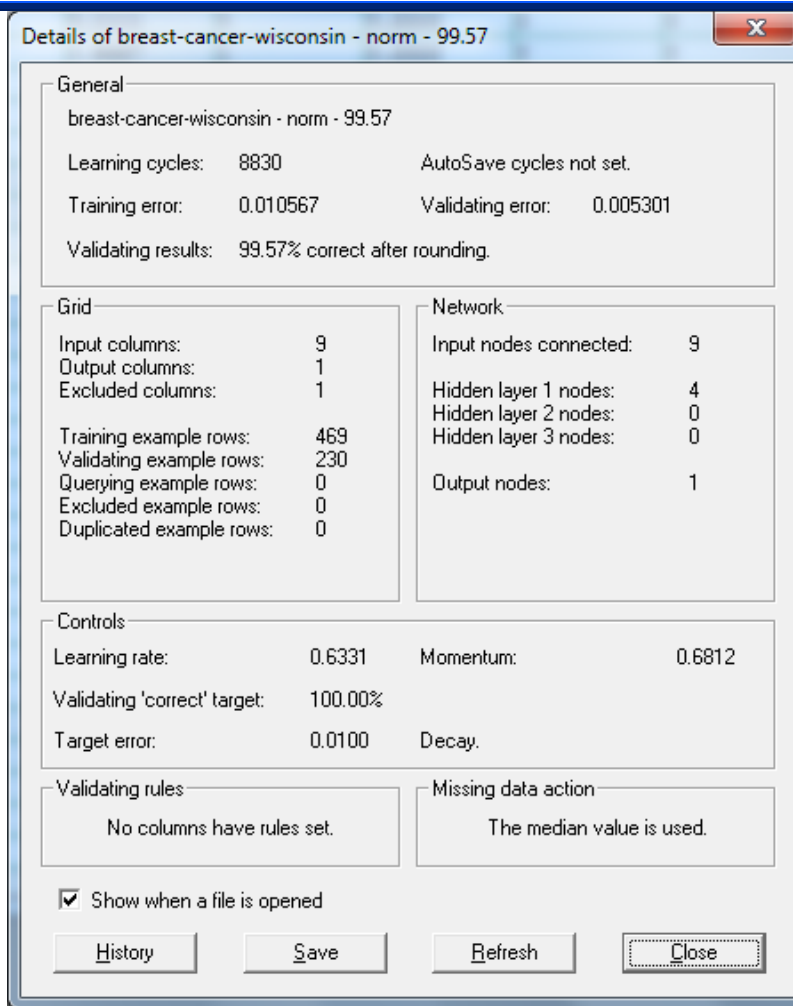


Figure 6: Details of the proposed ANN model

#### 4. Conclusion

In This paper, we used the prediction power of a neural network to classify whether Breast Cancer is benign or malignant cancer. Our network achieved an accuracy of 99.57%. We used the JustNN environment for building the network that was a feed forward Multi-Layer Perceptron with one input layer, one hidden layer and one output layer. The average predictability rate was 99.57% for prediction of whether Breast Cancer is benign or malignant cancer.

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