



## Article

# Application of Neural Network Methods Based on Genetic Algorithm for Breast Cancer Prediction

Rino<sup>1</sup><sup>1</sup>University of Buddhi Dharma, Information System, Banten, Indonesia**SUBMISSION TRACK**

Received: 15 Agustus 2017  
 Final Revision: 20 Agustus 2017  
 Online Available: 15 September 2017

**KEY WORDS**

*Neural Network, Genetic Algorithm,  
 Prediction, Breast Cancer*

**CORRESPONDENCE**

Telepon: 089658939791  
 E-mail: rino@ubd.ac.id

**A B S T R A C T**

Cancer is a big challenge for mankind. Cancer can affect various parts of the body. This deadly disease can be found in humans of all ages. Breast cancer is the most common cancer among women, and is the biggest cause of death also for women. In a similar study, there are several methods used but there are problems due to the formation of nonlinear cancer cells. Neural network can solve the problem, but neural network is weak in terms of parameter values, so it needs to be optimized. Genetic Algorithm is one of the best optimization methods, therefore the parameter values of neural network will be optimized by using Genetic Algorithm so as to get the best parameter value. Neural Network algorithm based on genetic algorithm has a higher accuracy value than using only Neural Network algorithm. This is evident from the increase of accuracy value for neural network algorithm model of 95.42% and the accuracy value of Neural Network algorithm based on Genetic Algorithm of 96.85% with difference of 1.43% accuracy. So it can be concluded that the application of Genetic Algorithm optimization technique can increase accuracy value on Neural Network algorithm

**INTRODUCTION**

Cancer is a big challenge for mankind, cancer can affect various parts of the body. Breast cancer is the most common cancer found among women (Dellen, Walker, & Kadam, 2005, p 2). Information about tumors from certain examinations and diagnostic tests collected determines how malignant the cancer is. By knowing the malignancies of the cancer, treatment measures can be performed better and the mortality rate can be reduced.

In this research will be applied Neural Network method optimized with Genetic Algorithm in predicting breast cancer.

**I. METHOD***a. Neural Network*

- Neural Network is a parallel distributed processor, made up of simple units, and has the ability to store experimental and ready-to-use knowledge for various purposes (Haykin, 1999, p 23). This Neural Network manipulated the human brain in term of:

- Knowledge gained by the network from the environment, through a learning process.
- The power of connection between units called synaptic weights, serves to store the knowledge that has been obtained by the network.

b. Genetic Algorithm

Optimization is about finding the optimal parameter values for an object or system that minimizes goals (costs) and functions (Shukla, 2010, p. 147). In optimization, we are given a function, known as a function of purpose. The goal is to minimize or maximize the value of the objective function by adjusting various parameters. Each combination of parameters marks solutions that may be good or bad, depending on the value of the purpose function. Soft-computing techniques produce the best set of parameters that provide the best values of the destination function in view of the constraints of the time. The genetic algorithm (GA), developed by John Holland in the 1960s and 1970s, is an attempt to mimic the computational process in which natural selection operates.

The steps in the Genetic Algorithm are as follows:

```

begin
    x ← 0;
    initialize P(x);
        evaluate P(x);
    while(not termination condition) do
        recombine P(x) to yield O(x);
        evaluate O(x);
        select P(x + ) from P(x) and O(x);
        x++;
    end
end
    
```

Ultimately, the Genetic Algorithm processes from the initial population through a series of genetic operations, such as selection, crossover and mutation, to find a better space, step by step until it reaches the optimal solution.

II. RESULTS

The purpose of this research is to develop the model that has been formed with Neural Network algorithm. Data were analyzed by doing two comparison that is using Neural Network Algorithm and Neural Network Algorithm based on Genetic Algorithm.

*Neural Network Calculation Result*

Neural network modeling will be performed on a dataset consisting of 9 attributes that are attributes of breast cancer, and a class representing benign or malignant.

Table 1. Dataset Of Breast Cancer

Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
5	3	3	3	2	3	4	4	1	Benign
5	4	4	5	7	10	3	2	1	Malignant
10	7	7	6	4	10	4	1	2	Benign
8	10	10	8	7	10	9	7	1	Benign
4	1	1	3	2	1	3	1	1	Malignant

From that data, the hidden layer will be calculated by the calculation with (number of attributes + results) / 2 + 1 is 7 hidden layers, the weights for the hidden layer are initially

randomly assigned, the models with randomly assigned weights can be seen in Figure 1 Model will be formed with momentum of 0.1 and learning rate 0.3.

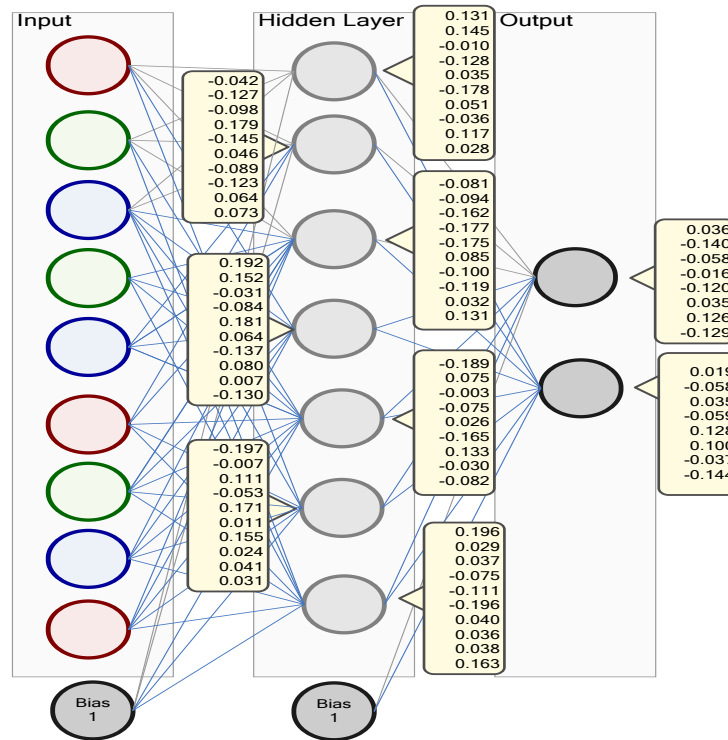


Figure 1. Initial Model of Neural Network

$$y_{hidden1} = f(0.028 + (5 * 0.131) + (3 * 0.145) + (3 * -0.010) + (3 * -0.128) + (2 * 0.035) + (3 * -0.178) + (4 * 0.051) + (4 * -0.036) + (1 * 0.117)) = 0.414$$

$$y_{hidden1} = \frac{1}{1 + e^{-(0.414)}} = 0.602$$

$$y_{hidden2} = f(0.073 + (5 * -0.042) + (3 * -0.127) + (3 * -0.098) + (3 * 0.179) + (2 * -0.145) + (3 * 0.046) + (4 * -0.089) + (4 * -0.123) + (1 * 0.064)) = -1.221$$

$$y_{hidden2} = \frac{1}{1 + e^{-(-1.221)}} = 0.227$$

The value for the output is calculated based on the weight of the output node with the value of the hidden layer. Calculations can be seen in the following:

$$\begin{aligned}
 y_{output1} = & f(-0.129 + (0.0364 * 0.602) \\
 & + (-0.140 * 0.227) \\
 & + (-0.058 * 0.074) \\
 & + (-0.016 * 0.781) \\
 & + (-0.120 * 0.249) \\
 & + (0.035 * 0.583) \\
 & + (0.126 * 0.657)) = -0.082
 \end{aligned}$$

$$y_{output1} = \frac{1}{1 + e^{-(-0.082)}} = 0.479$$

$$\begin{aligned}
 y_{output2} = & f(-0.144 + (0.019 * 0.602) \\
 & + (-0.058 * 0.227) \\
 & + (0.035 * 0.074) \\
 & + (-0.059 * 0.781) \\
 & + (0.128 * 0.249) \\
 & + (0.100 * 0.583) \\
 & + (-0.037 * 0.657)) = -0.124
 \end{aligned}$$

$$y_{output2} = \frac{1}{1 + e^{-(-0.124)}} = 0.469$$

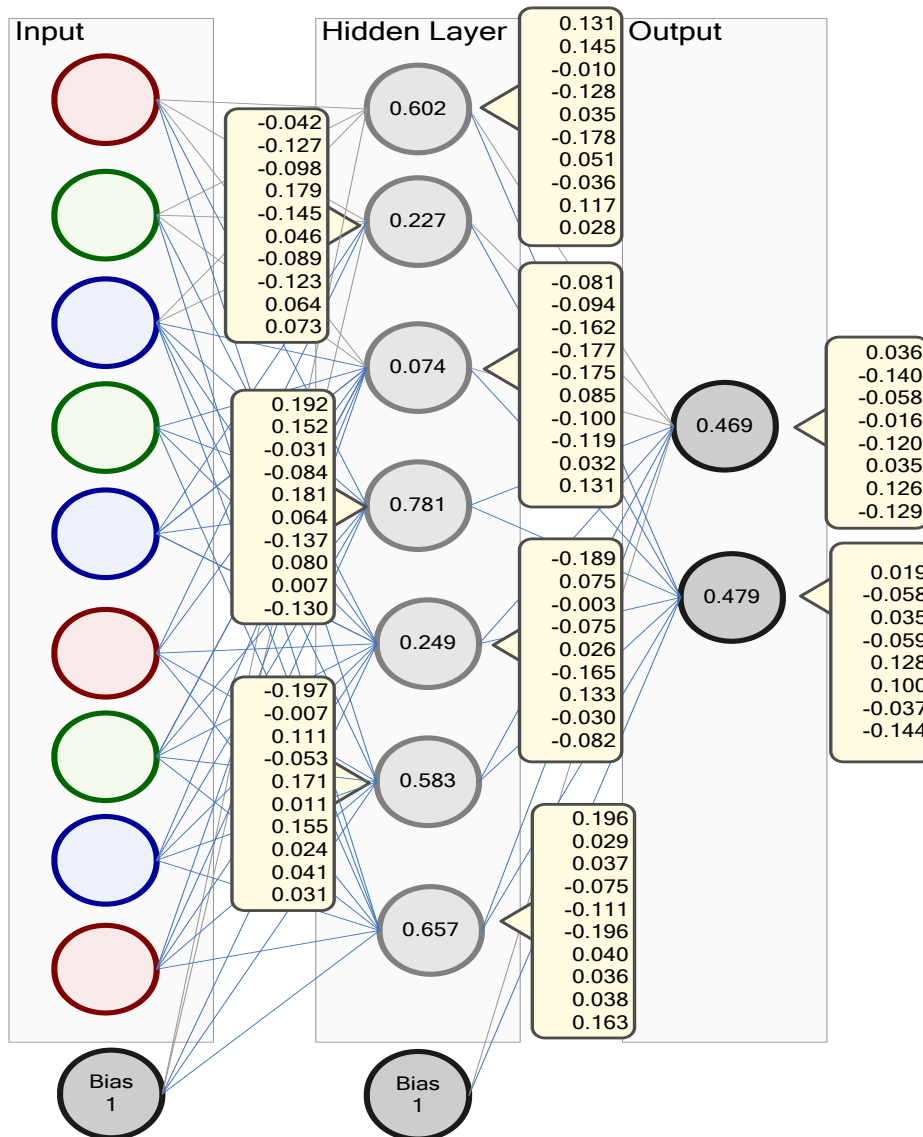


Figure 2. Processing Value In Hidden Layer and Output Layer

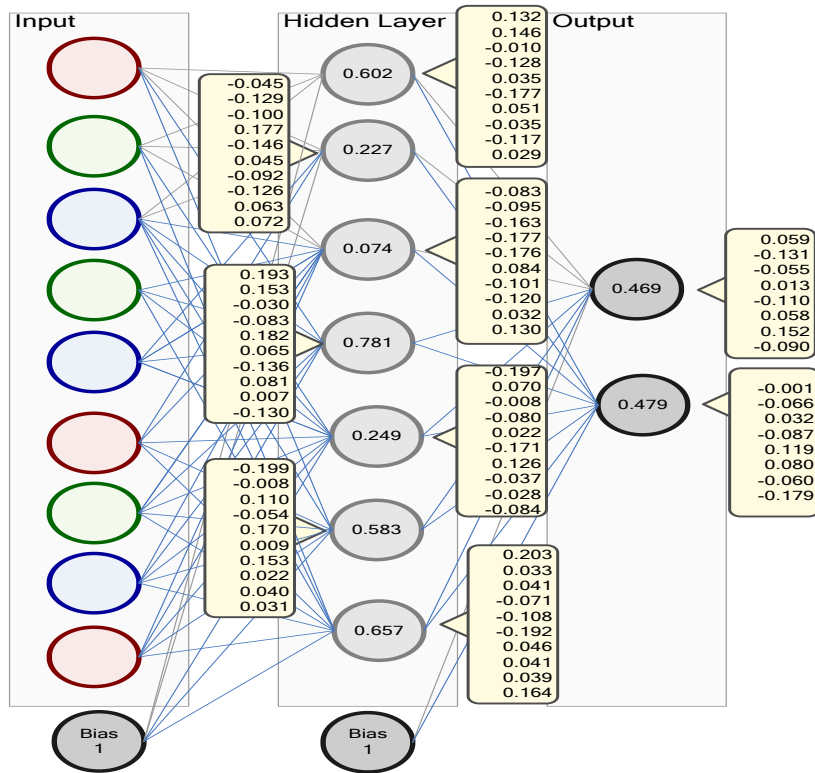


Figure 3. Value Image of New Weight Change

The calculation continued by applying the model that has been adjusted to the second data. The second data is entered into the input variable, then adjusted the weights until it becomes output, then calculated the error value,

and obtained the value of delta for output, then the delta value is adjusted to the hidden layer node and then calculated the new weight. The following model is formed with 2 hidden layer as in Figure 4

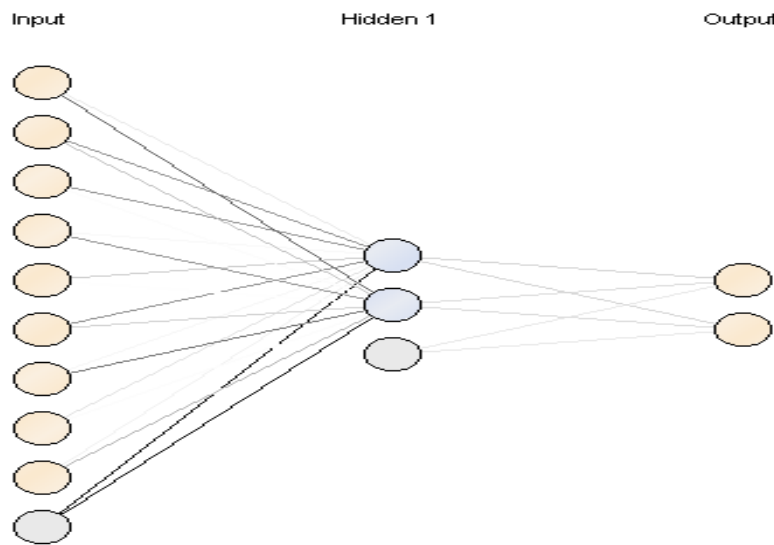


Figure 4. Model With 2 Hidden Layer

Continue up to 9 hidden layers.

**Result of model optimization calculation with Genetic Algorithm**

1. Determine the initial population

$$C1 \rightarrow [0.3\_0.1\_3] = 95.14\%$$

$$C2 \rightarrow [0.2\_0.4\_8] = 96\%$$

$$C3 \rightarrow [0.5\_0.9\_4] = 96.57\%$$

$$C4 \rightarrow [0.1\_0.2\_5] = 96\%$$

$$C5 \rightarrow [0.02\_0.08\_9] = 96.57\%$$

2. Evaluation of fitness values

$$\begin{aligned} \text{Fitness } C1 &= 1 / (1 + |95.14 - 100|) \\ &= 1 / 5.86 \\ &= 0.170648 \end{aligned}$$

$$\begin{aligned} \text{Fitness } C2 &= 1 / (1 + |96 - 100|) \\ &= 1 / 5 \\ &= 0.2 \end{aligned}$$

$$\begin{aligned} \text{Fitness } C3 &= 1 / (1 + |96.57 - 100|) \\ &= 1 / 4.43 \\ &= 0.225734 \end{aligned}$$

$$\begin{aligned} \text{Fitness } C4 &= 1 / (1 + |96 - 100|) \\ &= 1 / 5 \\ &= 0.2 \end{aligned}$$

$$\begin{aligned} \text{Fitness } C5 &= 1 / (1 + |96.57 - 100|) \\ &= 1 / 4.43 \\ &= 0.225734 \end{aligned}$$

$$\begin{aligned} \text{Total fitness} &= 0.170648 + 0.2 + 0.225734 + 0.2 \\ &+ 0.225734 = 1.022116 \end{aligned}$$

The probability of each chromosome becomes:

$$P[C1] = 0.170648 / 1.022116 = 0.166956$$

$$P[C2] = 0.195672507$$

$$P[C3] = 0.220849688$$

$$P[C4] = 0.195672507$$

$$P[C5] = 0.220849688$$

3. Selection of the parent Chromosome

For the selection process used Roullete Wheel, for it required the cumulative value of probability of each chromosome, namely as follows:

$$C1 = 0.166956$$

$$C2 = 0.166956 + 0.195672507 = 0.362628117$$

$$\begin{aligned} C3 &= 0.166956 + 0.195672507 + 0.220849688 \\ &= 0.583477805 \end{aligned}$$

$$\begin{aligned} C4 &= 0.166956 + 0.195672507 + 0.220849688 \\ &+ 0.195672507 = 0.779150312 \end{aligned}$$

$$\begin{aligned} C5 &= 0.166956 + 0.195672507 + 0.220849688 \\ &+ 0.195672507 + 0.220849688 = 1 \end{aligned}$$

The next step is to use a random number R between 0 until 1. Random numbers are used as many as chromosomes, for example as follows:

$$R1 = 0.227186742$$

$$R2 = 0.221614966$$

$$R3 = 0.857372275$$

$$R4 = 0.649737022$$

$$R5 = 0.799273008$$

Choosing chromosome to x as Parent. The result of Roulette Wheel selection in this population for crossover becomes:

$$P1 \rightarrow C2 \rightarrow 0.2\_0.4\_8$$

P2 -> C2 -> 0.2\_0.4\_8 -> because the same then repeated

$$P2 \rightarrow C5 \rightarrow 0.02\_0.08\_9$$

Both parent to be taken are C2 and C, then the child that produced by the parent chromosome will replace the existing chromosome, then taken R value randomly again

$$R1 = 0.849110706$$

$$R2 = 0.300092891$$

$$R3 = 0.002780315$$

$$R4 = 0.305677568$$

$$R5 = 0.306442102$$

4. Conducting crossovers (cross-breeding)

With a crossover probability value of 0.5, only chromosomes whose R value is less than 0.5 will mutate. then in addition to C1 all will be replaced with chromosomes of marriage results, C3 and C5 values have the highest fitness value, so C3 and C5 pass the selection process. Only C2 and C4 that need to be replaced by crossover marriage process

is done by taking a random value of a number of attributes that is 1- 3.

$$R[C2] = 2$$

$$R[C4] = 3$$

Results of crossover

$$C2 = 0.2\_0.4\_8 \gg 0.02\_0.08\_9 \\ \Rightarrow 0.2\_0.08\_8$$

$$C4 = 0.2\_0.4\_8 \gg 0.02\_0.08\_9 \\ \Rightarrow 0.2\_0.4\_9$$

New populations are formed with crossover results that have occurred to be:

$$C1 \rightarrow [0.3\_0.1\_3] = 95.14\%$$

$$C2 \rightarrow [0.2\_0.08\_8] = ?$$

$$C3 \rightarrow [0.5\_0.9\_4] = 96.57\%$$

$$C4 \rightarrow [0.2\_0.4\_9] = ?$$

$$C5 \rightarrow [0.02\_0.08\_9] = 96.57\%$$

### 5. Chromosome Mutations

The number of chromosomes undergoing mutase in one population is determined by the percentage of p mutation. The mutation process is performed by substituting one randomly selected gene with a new value obtained randomly.

Total gen = (gene in chromosome) \* number of chromosomes

$$= 3 * 5$$

$$= 15$$

In determining the position of the mutated gene is done by using a random number between 1 to total genes, ie between 1 to 15. Suppose we determine 10% then the number of genes that have mutations is 10% of 15 that is 1.5 or 1 gene. Then using a random number and the selected gen position 12 that mutated. Thus the mutation will be the 3rd chromosome of the number 8 gene. Then the gene value in that position we replace with a

random number 0-1 (Momentum). Suppose that the random number used is 0.3, the 8th chromosome changes to [0.5\_0.3\_4]. The population in the first generation becomes:

$$C1 \rightarrow [0.3\_0.1\_3] = 95.14\%$$

$$C2 \rightarrow [0.2\_0.08\_8] = 95.71\%$$

$$C3 \rightarrow [0.5\_0.3\_4] = 95.42\%$$

$$C4 \rightarrow [0.2\_0.4\_9] = 96.57\%$$

$$C5 \rightarrow [0.02\_0.08\_9] = 96.57\%$$

## III. DISCUSSION

### Testing Results with Confusion Matrix

Evaluation Model with Confusion Matrix, confusion matrix model will form a matrix consisting of true positive or positive tuple and true negative or negative tuples, then input the test data that has been prepared into confusion matrix so that the results obtained in Table 2 as below:

**Table 2. Result of Confusion Matrix With 2 Hidden Layer**

	true benign	true Malignant	Class precision
Benign Prediction	440	12	97.35%
Malignant Prediction	18	229	92.71%
Class Recall	96.07%	95.02%	
Accuracy	95.71%		

In Table 2 the accuracy of 95.71% and for the number of True Positive (TP) is 229, for False Negative (FN) is 440, for False Positive (FP) is 12, and for True Negative (TN) is 18. Confusion Matrix in continue until with 9 hidden layers.

### Testing Results With ROC Curve (AUC)

In Figure 6 shows the ROC graph with the value of AUC (Area Under Curve) of 0.994.



Figure 5. The value of AUC in ROC Curve With 2 Hidden Layer

ROC is continued up to 9 hidden layers.

1.1.1. Determination of parameter values

The result of model testing conducted in chapter three is the determination of parameter value with Neural Network algorithm and Neural Network algorithm based on Genetic Algorithm to determine parameter value. The results obtained from the parameter values determined by the Genetic Algorithm tested on

the Neural Network method will result in accuracy and AUC.

Seeking to result of test of parameter value determination by Genetic Algorithm got best result for parameter value of Learning Rate is equal to 0.562070136566738 and Momentum parameter value is 0.9366372796859641 with 4 Hidden Layer. Comparison of results can be seen in table 3 below.

Table 3. Parameter Value Determination Results (Learning Rate, Momentum, Hidden Layer)

Learning Rate	Momentum	Hidden Layer	Accuracy	AUC
0.20328958812	0.975066453274	5	96.2	0.9
0.11866	8256	5	9%	89
0.14253444065	0.060348510904	6	96.1	0.9
61286	87091	6	4%	92
0.16984871625	0.071171563014	7	94.5	0.9
963385	32243	7	6%	91
0.57660285292	0.936731569017	8	96.7	0.9
56312	8865	8	1%	87
0.62049898445	0.873177214729	9	96.5	0.9
11428	6034	9	7%	87
0.562070136566738	0.9366372796859641	4	96.8	0.9
			5%	93

Comparison Results Using Neural Network with Neural Network Based Genetic Algorithm

- a. Evaluation Model With Confusion Matrix

The confusion matrix model will form a matrix consisting of either positive or positive tuples and true negative or negative tuples, then input

the test data that has been prepared into the confusion matrix.

In Table 4-11 the accuracy of 95.42% and for the number of True Positive (TP) is 225, for False Negative (FN) is 442, for False Positive (FP) is 16, and for True Negative (TN) is 16.



**Table 4. Result of Confusion Matrix NN**

	true Benign	true malignant	Class precision
Benign Prediction	442	16	96.51%
Malignant Prediction	16	225	93.36%
Class Recall	96.51%	93.36%	
Accuracy	95.42%		

After optimizing the visible increase as shown in Table 4-12 with 96.85% accuracy and for the number of True Positive (TP) is 234, for False Negative (FN) is 443, for False Positive (FP) is 7, and for True Negative (TN ) is 15 with the number of Hidden Layer 4.

**Table 5. Result of Confusion Matrix NN+GA**

	true Benign	true malignant	Class precision
Benign Prediction	443	7	98.44%
Malignant Prediction	15	234	93.96%
Class Recall	96.72 %	97.10%	

Accuracy	96.85%
----------	--------

b. Evaluation with *ROC Curve*

Accuracy has a diagnosis level that is (Gorunescu, 2011):

1. Accuracy Value 0.90 – 1.00 = *Excellent classification*
2. Accuracy Value 0.80 – 0.90 = *Good classification*
3. Accuracy Value 0.70 – 0.80 = *Fair classification*
4. Accuracy Value 0.60 – 0.70 = *Poor classification*
5. Accuracy Value 0.50 – 0.60 = *Failure*

In Figure 6 shows the ROC graph with the AUC (Area Under Curve) value of 0.984 with the Excellent classification diagnostic level.



**Figure 6. Values Of AUC NN Inside ROC Curve**

After optimized the increase as shown in Figure 4-22 shows the ROC graph with the value of

AUC (Area Under Curve) of 0.993 with the diagnosis level Excellent classification.



Figure 7. Values of AUC Neural Network+GA inside ROC Curve

The result of the experiment is to get accuracy value, and the value of AUC (Area Under Curve) using parameter value that has been determined to get the best result as Table 4-13 as follows:

Table 6. Neural Network Testing and Neural Network Based genetic Algorithm

	Accuracy	AUC
Neural Network	95.42%	0.984
Neural Network Based GA	96.85%	0.993

The best neural network architecture obtained from the experiment can be seen in Figure 8 below:

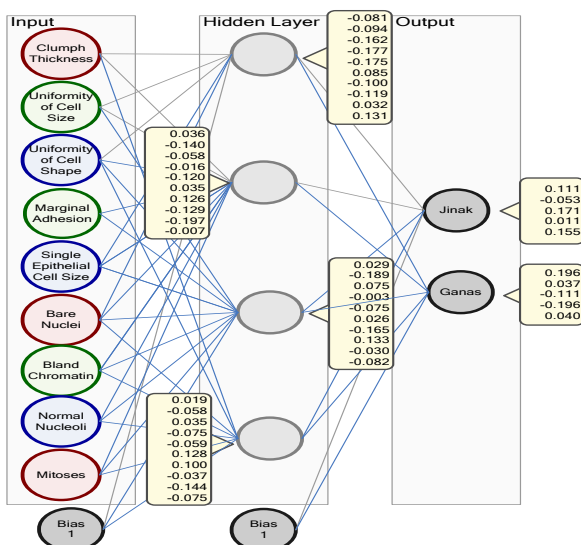


Figure 8. Best Neural Network Architecture from Experiment Results

The model test to determine the parameter values on the neural network is done using 10 folds cross validation which will randomly take 10% of the training data for as data testing. Then this process is done in rapid miner with initial test which then parameter value in adjusted and optimized so as to increase accuracy value.

#### IV. CONCLUSION

Genetic Algorithms have been shown to improve prediction accuracy in breast cancer. The model formed by a neural network based on Genetic Algorithm produces better accuracy than a neural network without optimization.

The increase can be seen from the increase of accuracy value for neural network algorithm model 95.42%, after optimized the accuracy value of algorithm of Neural Network based on Genetic Algorithm equal to 96.85% with difference of 1.43% accuracy. For evaluation using ROC curve so as to generate the value of AUC (Area Under Curve) for model Neural Network algorithm yield value 0.984, while for Neural Network algorithm based on Genetic Algorithm yield value 0,993 with value of diagnosis Excelent Classification, with difference of both value equal to 0.009.

As for the model that is formed, later can be developed or implemented into an application. so it can help and facilitate for health practitioners in diagnosing breast cancer, and the diagnosis can be more accurate and reliable.

### REFERENCE

- Abbas, H. A. (2002). An Evolutionary Artificial Neural Networks Approach For Breast Cancer Diagnosis. *Artificial Intelligence in Medicine*, vol.25, no.3, 1-30.
- Adam, A., & Omar, K. (2006). Computerized Breast Cancer Diagnosis with Genetic Algorithms and Neural Network. *Department of System and Management Sciences, Faculty of Technology and Information Sciences*, 183-188.
- Bellachia, A. (2000). Predicting Breast Cancer Survivability Using Data Mining Techniques. *Ninth Workshop on Mining Scientific and Engineering Datasets in conjunction with the Sixth SIAM International Conference on Data Mining (SDM 2006), Saturday, April 22, 2006.* .
- Calle, J. (2004). *Breast cancer facts and figures 2003—2004*. American Cancer Society. p. 1—27. Retrieved from (<http://www.cancer.org/>).
- Dellen, D., Walker, G., & Kadam, A. (2005). Predicting Breast Cancer Survivability: A Comparison of Three Data Mining Methods. *Artificial intelligence in medicine, Elsevier*, 27-113.
- Gorunescu, F. (2011). *Data Mining Concepts, Models and Techniques*. Springer; 1st Edition. edition (June 24, 2011).
- Han, J., & Kamber, M. (2007). *Data Mining: Concepts and Techniques 2nd Edition*. Morgan Kaufmann Publishers is an imprint of Elsevier.
- Haykin, S. (1999). *Neural Networks: A Comprehensive Foundation.*: Prentice Hall.
- K. Hornik, M. Stinchcombe, H. White. (1989). Multilayer Feedforward Networks are Universal Approximators. *Journal Neural Networks Volume 2 Issue 5, 1989*, 359-366.
- Larose, D. T. (2005). *Discovering Knowledge In Data An Introduction to Data Mining*. A John Wiley & Sons, Inc., Publication.
- Lundin, M., & Burke, H. B. (1999). Artificial Neural Networks Applied to Survival Prediction in Breast Cancer. *Journal Artificial Intelligence in Medicine Volume 34 Issue 2, June, 2005*, 281-286.
- Shukla. (2010). *Real Life Application of Soft Computing*. Taylor and Francis Group, LLC.
- Wu, G. (2009). Research on Parameter Optimization of Neural Network. *International Journal of Hybrid Information Technology Vol. 2, No. 1, January, 2009*, 81.
- Zhang, Q., & Wang, C. (2008). Using Genetic Algorithm to optimize Artificial Neural

### BIOGRAPHY

**Rino** Graduated in Informatics Engineering Study Program (S1) in Networking, 2008, Informatics Engineering (S2) Program in Software Engineering. Currently as A Permanent Lecturer in Information Systems Studies Program, Buddhi Dharma University.