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A Genetic-Neural System Diagnosing Hepatitis B

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Abstract

Hepatitis B is a life threaten disease and if not diagnose early can lead to death of the infected patient. In this paper a genetic neural system for diagnosing hepatitis B was designed. The system was designed to diagnose HBV using clinical symptoms. The dataset used in training the system was gotten from UCI repository. The system incorporated both genetic algorithm and neural network. The genetic algorithm was used to optimize the dataset used in training the neural network. The neural network was trained for 300 iterations and the system had a prediction accuracy of 99.14

Index terms— genetic algorithm, hepatitis B, neural network.

1 Introduction

he human body is made up of various organs and of these organs the liver is the largest. The liver performs various functions in the human body. It produces bile which aids the breaking down of fat, it breaks down alcohol and toxic waste in the blood stream and passes them out of the body as either stool or urine and it absorbs glucose from the blood and stores them in form of glycogen for subsequent use by the body (WHO, 2014). Some diseases are known to affect the liver are they include Hepatitis A, Hepatitis B, Hepatitis C, Hepatitis D and Hepatitis E to mention but a few **??**Ghumbre et al, 2009). Hepatitis B is an infectious viral disease caused by the Hepatitis B virus (HBV).

According to WHO about one-third of the entire world population has been infected with HBV at one point in their lives and 750,000 people die each year of the disease (WHO, 2014). In 2013 it was estimated 129 million person where infected with HBV and the number of infected individual is predicted to rise each year by 2.5% (WHO, 2014). Hepatitis B is prevalent in East Asia and Sub Saharan Africa where about 5-10% is chronically affected while in Europe and North America the prevalence rate of HBV is less than 1% (WHO, 2014). HBV is transmitted by exposure to infected blood or body fluid or sexual intercourse with an infected person or by birth from mother to child (Chen et al, 2005). Symptoms of Hepatitis B includes jaundices (yellowish eye and skin), fatigue, dark urine nausea, vomiting, skin rash, polyarteritis and in some cases abdominal pain (Shepard et al, 2006, Chen et al, 2005 **??**nd Schroth et al, 2004). These symptoms might last for several weeks. The gold standard for diagnosing HBV is by laboratory test. Although accurate, laboratory test are quite expensive and the infected patient need to wait for at least 30 days before the HBV virus can be detected in the blood. Hence, there is a need for other technique for diagnosing HBV. In recent past, machine learning techniques have been applied in diagnosing hepatitis B virus (Chen et al, 2005, Riudiger, 2001 **??** Ghumbre et al, 2009). These techniques have provided a non-invasive means for diagnosing Hepatitis B virus and most importantly in a timely manner. Most machine learning techniques utilized by various researchers in diagnosing HBV were neural network, Fuzzy Logic, Neuro-fuzzy system and Support Vector Machine (SVM). The fundamental weakness of these approaches used by these researchers is that no attention was paid to optimal selection and extraction of the dataset used in training their systems. To this, we propose a genetic neural system for diagnosing Hepatitis B virus. The system will comprise of two components genetic algorithm and neural network. Genetic Algorithm (GA) is a strong machine learning tool which is capable of performing feature selection and extraction. On the other hand Neural Network is also a machine learning technique that is capable recognizing patterns based on input fed into it. Combining these two excellent machine learning technique to diagnose HBV will create a system with higher prediction accuracy.

2 II.

3 Related Work

Several researchers have tried to improve the accuracy of HBV diagnosis and have applied various machine learning techniques in diagnosing HBV. In 2006 Plot and Günes, used a hybrid method comprising of Feature Selection (FS) and Artificial Immune Recognition System (AIRS) with fuzzy resource allocation mechanism in predicting Hepatitis. The system had an average prediction accuracy rate of 92.59% in classifying HBV. In 2011 Chen et al proposed a hybrid method which combined Local Fisher Discriminant Analysis (LFDA) and SVM in diagnosing Hepatitis. The dataset used in the study was gotten from the UCI repository. The Local Fisher Discriminant Analysis was used to perform feature extraction and SVM was using in classifying the data algorithm. The result obtained show that the system had an average prediction accuracy rate of 96.59% in classifying HBV. Also in a similar study conducted by Calisir and Dogantekin, they used Principle Component Analysis (PCA) and Least Square Support Vector Machine SVM (LSSVM) in diagnosing HBV. The dataset used in the study was gotten from the UCI repository. The Principle Component Analysis (PCA) was used to perform feature extraction and while Least Square Support Vector Machine SVM (LSSVM) was used to classify the Hepatitis datasets. The result obtained show that the system had an average prediction accuracy rate of 95% in classifying HBV. In 2011 Sartakhti et al, combined Support Vector Machine with Simulated Annealing (SA) to diagnose HBV. The dataset used in the study was gotten from the UCI repository. The result obtained show that the system had an average prediction accuracy rate of 96.25% in classifying HBV. In 2012 Bascil et al used a Probabilistic Neural Network structure to diagnose HBV. The result obtained show that the system had an average prediction accuracy rate of 91.25% in classifying HBV. In 2013 Mahesh et al, used Artificial Neural Network (ANN) to diagnose HBV. In their study 300 cases was used to train the ANN. The HBV dataset was divided into four categories (Normal, light, Severe and Hyper Severe) which indicated the severity of HBV. The ANN used markers in diagnosing each case. The marker were Hepatitis B surface Antigen, anti VHC and anti-VHD. The ANN had a prediction of accuracy of 87% and 89% on acute and chronic HBV respectively. Also in a similar study conducted by Mehdi et al, (2009), they designed a fuzzy expert system and an Adaptive neural Network fuzzy system to diagnose and compare their intensity rate. The dataset used in their study contained 300 diagnosed cases of HBV. The dataset was collected from Imam Reza hospital in Mashad, India. A triangular membership function was used to map the values in the dataset into each membership set for the fuzzy system and the bell membership function for the Adaptive neural Network fuzzy system. Both system had 54 rules. The Adaptive neural Network fuzzy system was trained 100 epoch with an error tolerance of 0. Upon completion of the training the system had an accuracy of 94.24% on HBV intensity. In a similar study conducted by Pushpalatha et al, (2016). They designed a framework comprising of neural network, Naïve bayes and Support Vector machine in diagnosing HBV. In their work 155 cases of HBV diagnosed patients was used. The dataset has 11 input and an output which indicated the status of HBV. The dataset was used to train the 3 techniques and it had an accuracy of 98.07, 82.58 and 84.52 for neural network, Naïve Bayes and SVM respectively. In 2019 Gulzar et al proposed an automated diagnostic system for predicting Hepatitis B using Multilayer Mamdani Fuzzy inference logic. The system has two layers. In the first layer has two inputs (Alanine Aminotransferase (ALT) and Aspartate Aminotransferase (AST)) the output of this layer is fed into the second layer. The second layer has8 inputs which are the output from layer 1, HBsAg, Anti-HBsAg, Anti-HBcAg, Anti-HBcAg-IgM, HBeAg, Anti-HBeAg and HBV-DNA. The system had an overall classification accuracy of 92.2% in classifying HBV. In 2018 Rahmon et al, proposed an Adaptive Neuro-Fuzzy Inference System for diagnosing HBV. The dataset used to train their system was obtained from Carnegie-Mellon University database, Yugoslavia. It contained 155 HBV cases. Five symptom attribute were used as inputs in training the system they are; Albumin, Ascites, Alk-Phosphate, Bilirubin, and SGOT. The output of the system graded HBV as either mild or severe. The system had a Mean Square Error (MSE) of 0.11768, Root Mean Square Error (RMSE) of 0.34305, Error Mean of -3.143e-005, Error St.D of 0.34567 and an overall prediction accuracy of 90.2%. In 2013, Mohammed et al, used Support vector Machine in classifying Hepatitis Disease. The dtaset used in their study was gotten from UCI machine learning repository. The datset contained 155 HBV cases. The result obtained from the study showed that 3SVM had a prediction accuracy of 93.2%. In 2017, Ogah et al, proposed a Generalized Regression Neural Network for diagnosing HBV. The dataset used in the study was collected through filed study and observation. The ANN was trained for 50 iterations and it had a prediction accuracy of 87 on classifying HBV%. In 2014, Khosro et al, used Support Vector Machine (SVM) and Fuzzy Cluster Mean (FCM) in diagnosing Hepatitis B. The datset used in the study was gotten from Vasei Hospital in Sabzevar, Iran. The dataset was normalized and SVM was used to classify the dataset. The classified dataset was fed into the FCM to determine the severity of HBV. The system had an accuracy of 94.09%. In 2016, Ruijing et al, compared and evaluated the prediction of Hepatitis in Guangxi Province, China using three neural networks models; back propagation neural networks based genetic algorithm (BPNN-GA), generalized regression neural networks (GRNN), and wavelet neural networks (WNN). The incidence of hepatitis data used in their study was gotten from Chinese National Surveillance System and the Guangxi Health Information Network. The result obtained from the study showed that back propagation neural networks based genetic algorithm (BPNN-GA) was better and forecasted Hepatitis better than the generalized regression neural networks (GRNN), and wavelet neural networks (WNN). Although from the above reviewed literature these techniques generated excellent results, but it is obvious that no attention was paid to feature selection and extraction on the dataset used in training these models.

4 III.

5 Experiment and Simulation

The proposed model for diagnosing HBV seeks to eliminate the challenges faced with the current system. It uses a hybrid system comprising of Genetic Algorithm (GA) and Neural Network (NN). The Genetic algorithm will perform feature selection and extraction on the dataset before it is used to train the neural network. The GA component will optimize the clinical dataset by performing feature extraction and selection. It will utilize the value encoding method where each gene in a chromosomes is value between the lower and upper range of the in each column in the dataset. The GA component will include the fitness function component, selector, crossover, mutation and acceptance component.

6 a) Objective function of the Genetic Algorithm

The objective function is the function that determines the diagnosis. The Objective function will be a mathematical model used to represent the diagnostic process of HBV. The objective function was arrived at after several consultation with several medical doctor.Objective function = ? Symptom i Weight n i

Where n= total number of symptoms, i=1, 2, 3 ? n Fitness Function: The fitness function should be able to measure how fit a given chromosome is. The fitness for the proposed model is given below Where n= total number of symptoms i=1,2,3 ? n Selection: The idea of selection phase is to select the fittest individuals and let them pass their genes to the next generation. Two pairs of individuals (parents) are selected based on their fitness scores. Individuals with high fitness have more chance to be selected for reproduction. The roulette selector will be employed in selecting chromosome because study has shown that it provides more optimal solution and has better convergence speed than the simple genetic algorithm (Yadav et al, 2017).

Crossover: Crossover is the most significant phase in a genetic algorithm. For each pair of parents to be mated, a crossover point is chosen at random from within the genes. Offspring are created by exchanging the genes of parents among themselves until the crossover point is reached. The new offspring are added to the population. The One point mutation operator will be used because study has shown it generates the best results (Jorge, 2013).

7 Mutation:

In certain new offspring formed, some of their genes can be subjected to a mutation with a low random probability.

Mutation occurs to maintain diversity within the population and prevent premature convergence. The power mutation operator will be employed because it performs better than other mutation techniques (Siew et al, 2017).

The multilayer perceptron neural network was used to train the model. This is a type of the feed forward neural network. The multi-layer perceptron neural network is very powerful because it utilizes nonlinear activation functions. In this model the sigmoid pole activation function was utilized. Equation **??**.1 shows the mathematical representation of the sigmoid transfer function. The output of the hidden layer are computed using the equation stated in 3.2y j (p) = f?? x jk (p). w ij ? 0 j m i=1 ? (3.2)

Where n is the number of inputs for the neuron j from the hidden layer, and f is the sigmoid activation function. The outcome is then sent to the output layer to generate the final output of the system. The output layer using the equation stated in 3.3 V.

8 Conclusion

The accuracy of medical diagnosis has lately been attributed to the advancement in technology and with the advent of machine learning tools such as Artificial Neural Networks, Genetic Algorithm and Support Vector Machines medical diagnosis became easier. Hepatitis B is a life threaten disease and if not diagnose early can lead to death of the infected patient. In this project work a genetic neural system was designed to diagnoses Hepatitis B virus. The system had a prediction accuracy of 99.14% on predicting Hepatitis B. [1]

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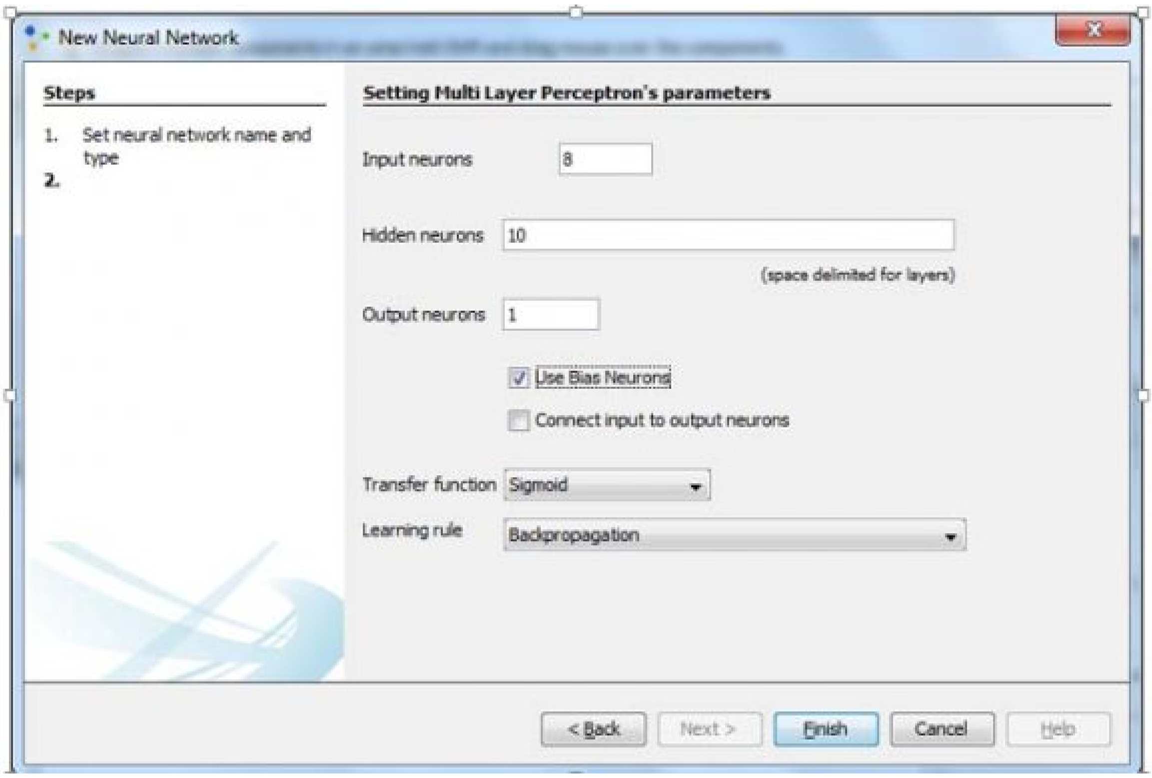
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Figure 1:

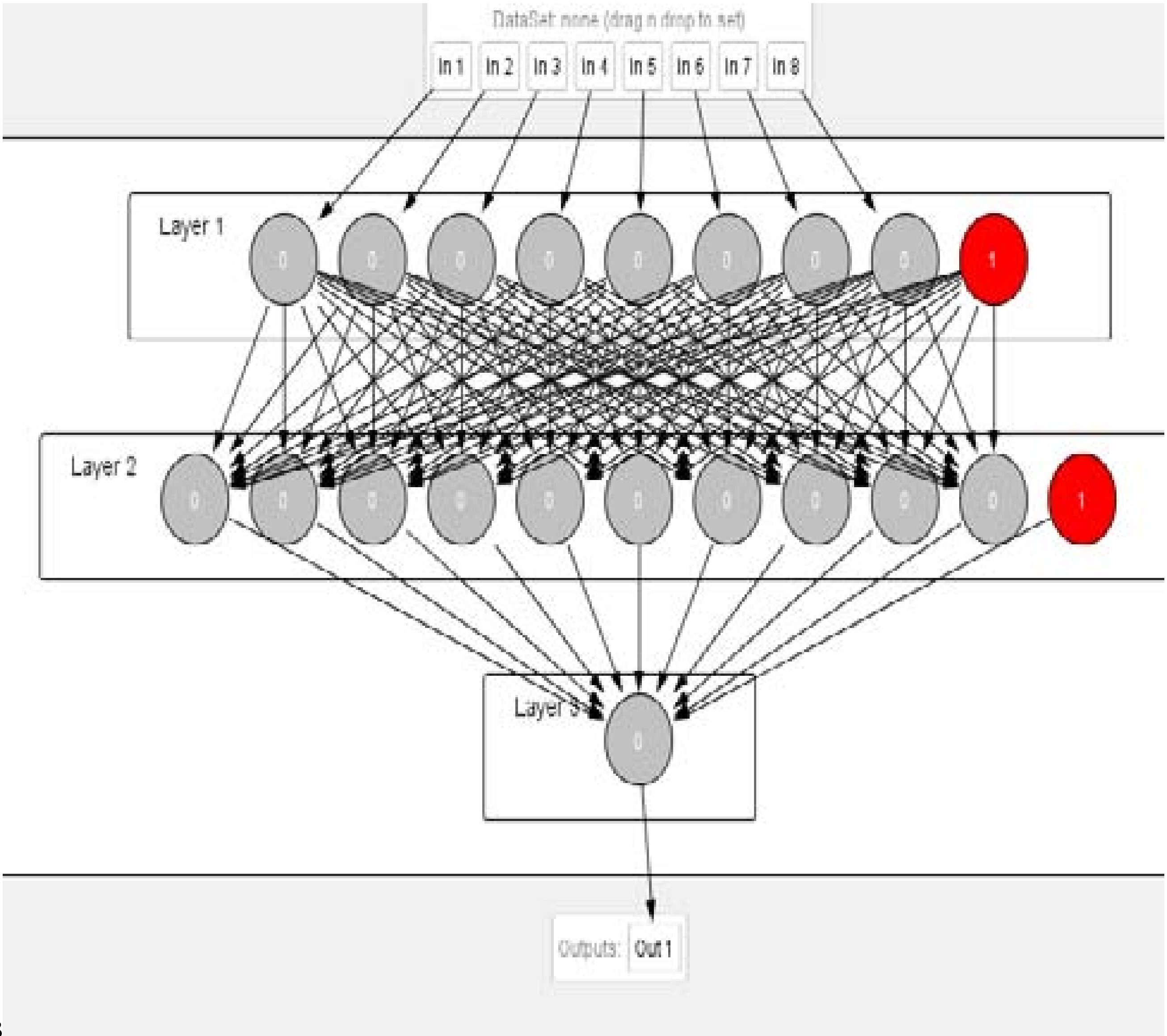

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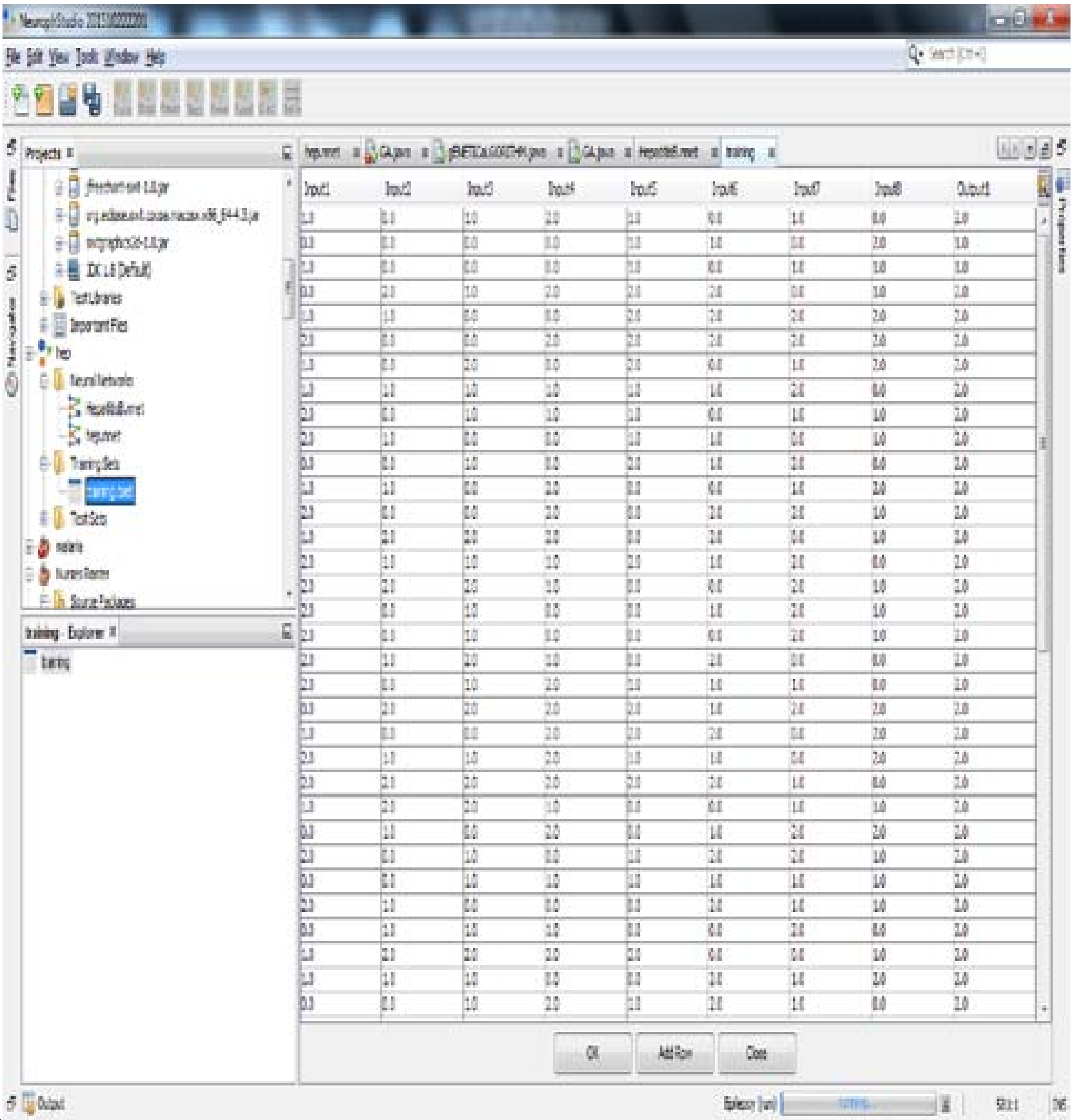
Figure 2: ? (3 . 3)



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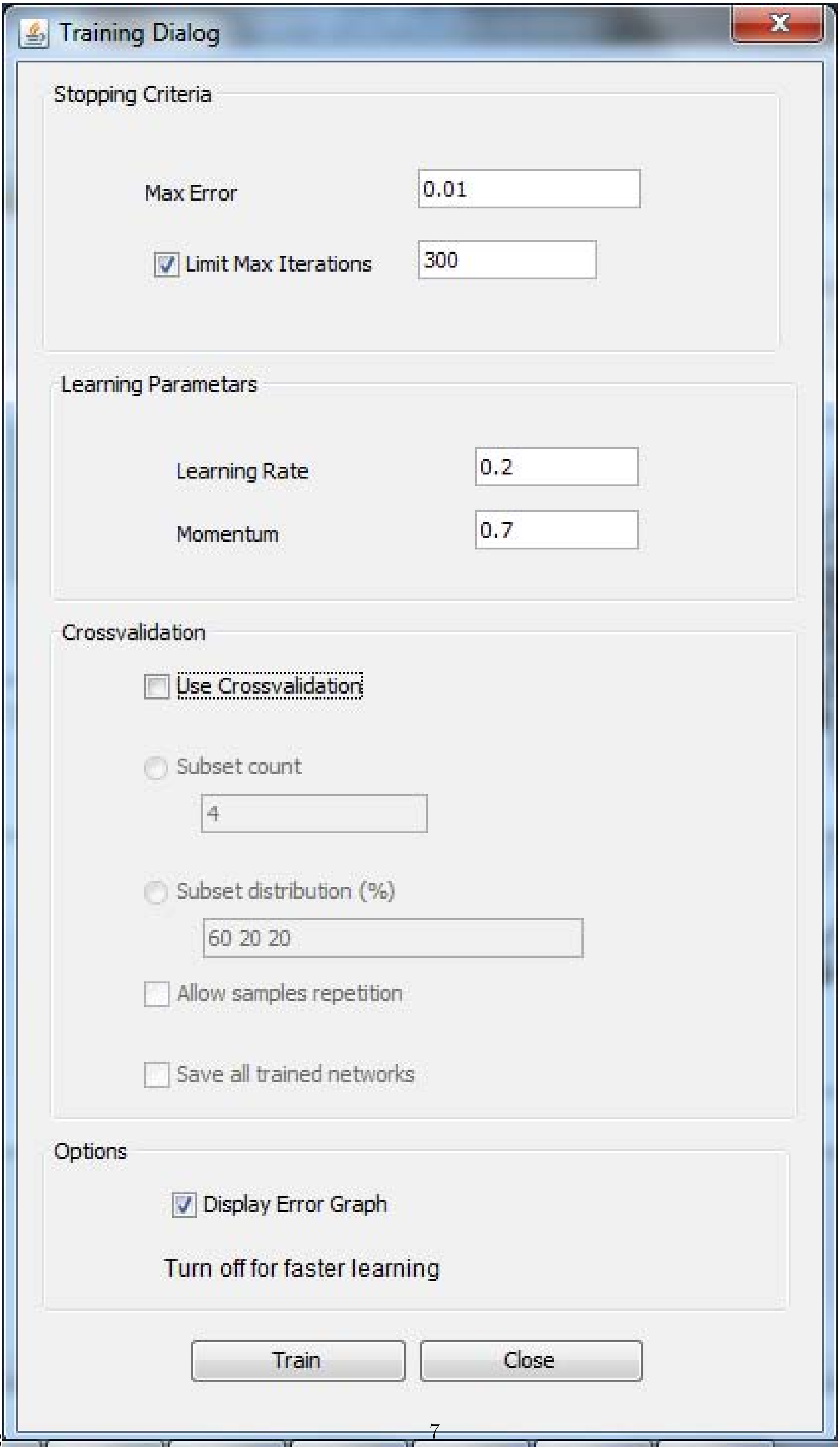

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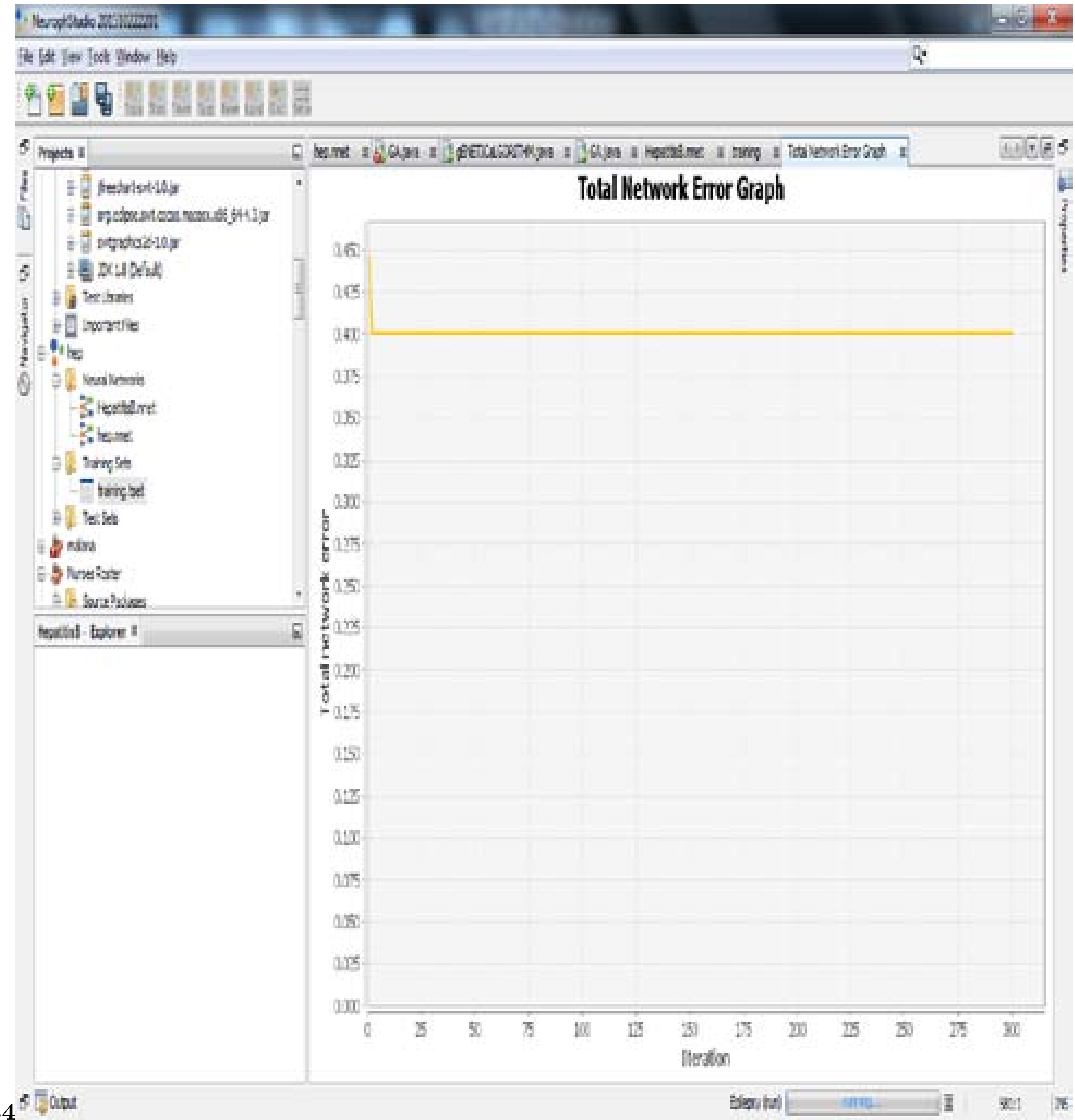

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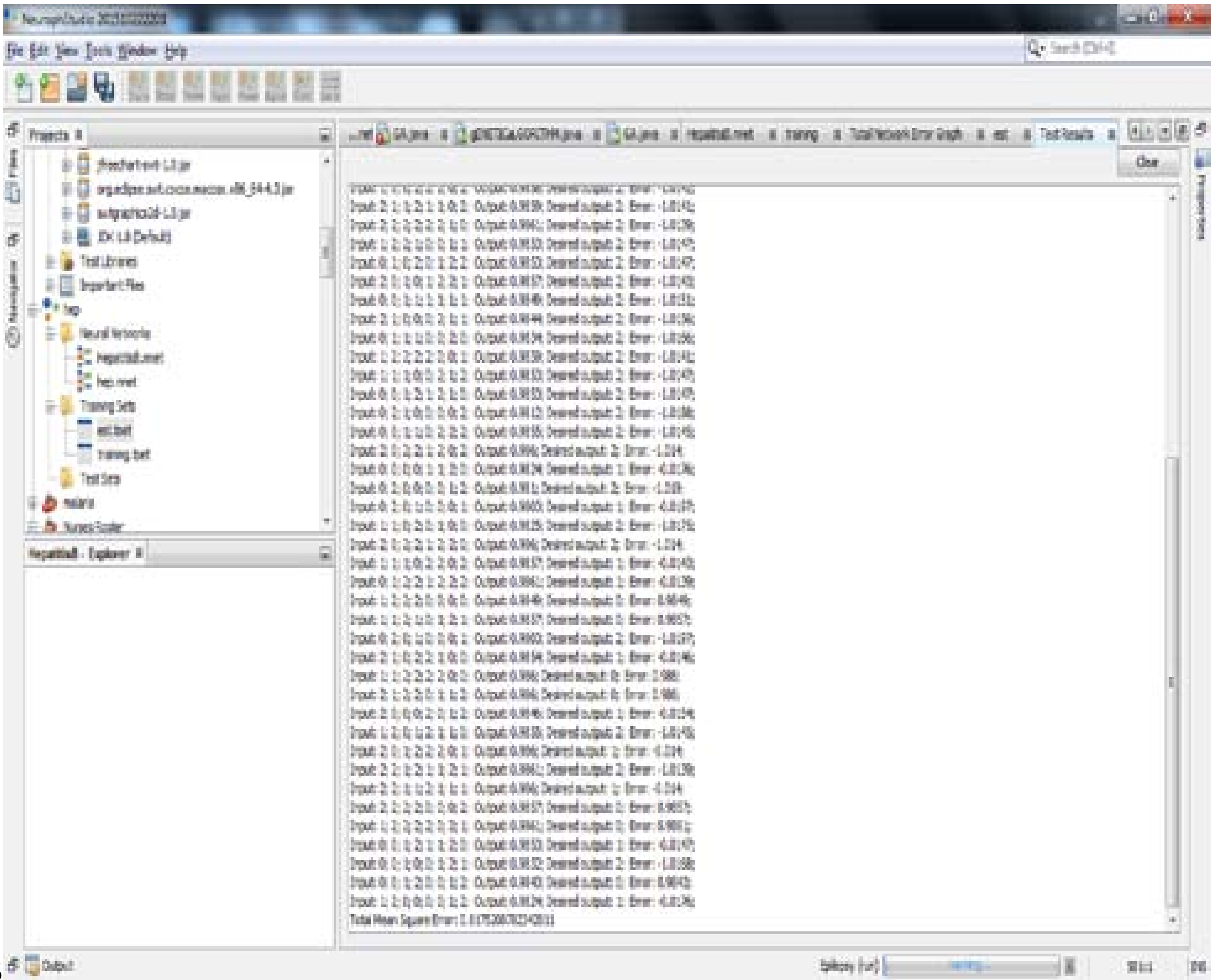

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Figure 6: Figure 5 :

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