

Input Feature Selection using Hybrid Neuro-Genetic Approach in the Diagnosis of Stroke Disease

D.Shanthi¹, Dr.G.Sahoo², Dr.N.Saravanan¹

¹Department of Computer Science and Engineering, Birla Institute of Technology, Kingdom of Bahrain.

²Department of Computer Science and Engineering, Birla Institute of Technology, India.

Summary

The Application of Artificial Neural Network (ANN) can be time-consuming due to the selection of input features for the Multi Layer Perceptron (MLP). The number of layers, number of neurons in each layer is also determined by the input attributes. Reducing the dimensionality, or selecting a good subset of features, without sacrificing accuracy, is of great importance for neural networks to be successfully applied to the area. In this paper, we propose a neuro-genetic approach to feature selection in disease classification. Candidate feature subsets are evaluated by using three-layer feed forward neural networks. A MLP whose inputs are automatically selected using a Genetic Algorithm (GA) is developed for the diagnosis of Stroke disease and experimental results show that the classification accuracy is better with the fewer input features.

Keywords: Artificial Neural Network, Genetic Algorithm, Neuro-Genetic Approach, Stroke disease.

1. Introduction

In medical diagnosis, the information provided by the patients may include redundant and interrelated symptoms and signs especially when the patients suffer from more than one type of disease of same category. The physicians may not be able to diagnose it correctly. So it is necessary to identify the important diagnostic features of a disease and this may facilitate the physicians to diagnose the disease early and correctly. Stroke is a life-threatening event in which part of the brain is not getting enough oxygen. There are different types of stroke namely Brain Attack, Embolic Stroke, Thrombotic Stroke, Ischemic Stroke, Cerebrovascular Accident (CVA). Medical personnel treating a stroke are challenged to treat the patient as quickly as possible to avoid permanent tissue damage or death. Strokes were responsible for more deaths and nearly half of those deaths occurred outside of a

hospital. Stroke is the third leading cause of death, behind heart disease and cancer. Most recovery occurs during the first few months following a stroke. According to the National Institute of Health, the risk of stroke is greater – and the recovery process is slower. Thrombo embolic strokes are caused by fatty deposits (plaques) that have built up in the arteries carrying blood to the brain. This slows blood flow and can cause clots to form on the plaques that narrow or block the flow of oxygen and nutrients to the brain. It is also caused by a blood clot formed in another part of the body that breaks loose, travels through the bloodstream, and blocks an artery carrying oxygen and nutrients to the brain. When travelling through the body the blood clot is called an embolus [20]. A hemorrhagic stroke is caused when an artery supplying blood bleeds into the brain. The broken blood vessel prevents needed oxygen and nutrients from reaching brain cells. One type of hemorrhagic stroke is caused when an artery that has weakened over time bulges (called an aneurysm) and suddenly bursts [2]. Thrombo-embolic Stroke can be classified as Transient Ischemic attacks (TIA), Evolving Stroke, Completed Stroke, Residual Stroke, Classical Stroke, Inappropriate Stroke, Anterior Cerebral Territory Stroke, Posterior Cerebral Stroke, Middle Cerebral Territory Stroke. Hemorrhagic Stroke can be classified as Cerebellar stroke, Thalamic Stroke and Cortical Stroke.

The main goal of this work is to establish either the category of a stroke disease, which is defined by some attributes or clinical variables. Nevertheless, not all those attributes give the same quality and quantity of information when the classification is performed. Sometimes, too much information can cause deteriorating the performance of the classification. The problem of variable selection involves choosing a subgroup of variables from an overall set of them that might carry out the finest classification. The advantages of selection process are cost reduction for data acquisition, Increased efficiency of classifier system, improved understanding of classification model, Efficacy improvement. [22]. In this paper, we have proposed a neuro-genetic approach to select input features for the diagnosis of Stroke disease. The rest of

the paper discusses about related studies, the proposed model, results and discussion along with conclusion.

2. Related Studies

Genetic algorithms [10] are optimization procedures that maintain candidate solutions encoded as strings (or chromosomes). A fitness function is defined that can assess the quality of a solution represented by some chromosome. A genetic algorithm iteratively selects best chromosomes (i.e., those of highest fitness) for reproduction, and applies crossover and mutation operators to search in the problem space. Most often, genetic algorithms are used in combination with some classifier induction technique or some schema for classification rules in order to optimize their performance in terms of accuracy and complexity [7, 15]. They can also be used alone, e.g., for the estimation of Doppler signals [11] or for multi-disorder diagnosis [24]. Genetic algorithms have been used together with neural networks in a variety of ways. One such way is to use genetic algorithms for the pre processing of neural network data, usually using the genetic algorithm to perform feature selection [4, 8]. GAs are used to optimize the ANN architecture prior to learning of the weights. For a typical example of the use of GAs in developing ANN architecture refer to [16]. Another hybrid approach is to use both GAs and a back-propagation neural network to solve the same optimization problem. Since GAs have a better chance of getting to the global optimum and ANNs are faster, we can combine the best of both worlds by first getting close to the global optimum using the GA and then using the ANN to improve our result [13]. A method proposed by [14] consists of M genes (where M is a user-specified parameter), where each gene can contain either the index (id) of an attribute or a flag denoting no attribute. GAs that perform attribute selection for the clustering task can be found [18, 25].

3. Neural Networks

The design and implementation of intelligent systems with human capabilities is the starting point to design Artificial Neural Networks (ANNs). The original idea takes after neuroscience theory on how neurons in the human brain cooperate to learn from a set of input signals to produce an answer. Because the power of the brain comes from the number of neurons and the multiple connections between them, the basic idea is that connecting a large number of simple elements in a specific way can form an intelligent system. ANN have been successfully used to solve classification problems in several domains, specifically the Backpropagation algorithm is very often the favorite to train feedforward neural networks. An ANN is composed

by a number of interconnected artificial neurons that process information using a computational model inspired in the human brain behavior. Figure 1 shows schematically a typical representation of a MLP with nine input neurons, four hidden neurons, and one output neuron. Each of the input neurons connects to each of the hidden neurons, and each of the hidden neurons connects to the output neuron.

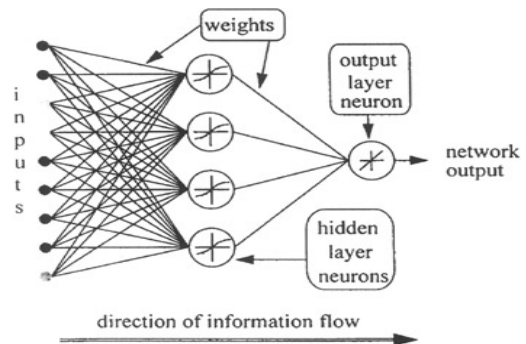


Figure 1: Architecture of MLP

ANN is a network of many simple processors called *units*, linked to certain neighbors with varying coefficients of connectivity (called *weights*) that represent the strength of these connections. The basic unit of ANNs, called an *artificial neuron*, simulates the basic functions of natural neurons: it receives inputs, processes them by simple combination and threshold operations, and outputs a final result. ANNs often employ supervised learning in which training data (including both the input and the desired output) is provided. Learning basically refers to the process of adjusting the weights to optimize the network performance. ANNs belongs to machine-learning algorithms because the changing of a network's connection weights causes it to gain knowledge in order to solve the problem at hand. Neural networks have been widely used for both classification and prediction [5].

The Backpropagation algorithm, in particular, adaptively changes the internal network free parameters based on external stimulus. After trained, a neural network can make predictions about the membership of every test example. MLP is trained with the Backpropagation algorithm suffers from the high number of parameters that need to be tuned, like learning rate, number of neurons, momentum rate, etc. However, the motivations to select this algorithm arise after observing that they have been used to solve problems in different domains, moreover, the output can be directly used for ranking purposes [1]. The algorithm was popularized by [6] and the same has been summarized below. To train a

network, it is necessary to have a set of input patterns and corresponding desired outputs, plus an error function (cost function) that measures the "cost" of differences between network outputs and desired values. The basic steps includes:

1. Present a training pattern and propagate it through the network to obtain the outputs.
2. Compare the outputs with the desired values and calculate the error.
3. Calculate the derivatives $\partial E/\partial w_{ij}$ of the error with respect to the weights.
4. Adjust the weights to minimize the error.
5. Repeat until the error is acceptably small or time is exhausted.

The error function measures the cost of differences between the network outputs and the desired values.

4. Genetic Algorithm

Genetic Algorithm can be considered as a mathematical optimization algorithm whose workings are metaphorically inspired by neo-Darwinian evolution. GA are based on biological evolutionary theories to solve optimization problems. The GA adopts a population unit of analysis, and each member of the population corresponds to an encoding of a potential solution to the problem of interest. Traditionally, the encodings (or *genotypes*) were binary strings (0,1,0,1,...), but the GA also can operate on integer or real-valued encodings. The genotypes can be interpreted (or decoded) in a wide variety of ways depending on the nature of the problem. For example, a genotype could be interpreted to produce a problem solution (the *phenotype*) [23]. The steps of the GA algorithm are outlined in Figure 2 [10]. First, the solution-encoding scheme is designed and the problem specific fitness function is formulated. An initial (random) population of n chromosomes (solutions) is generated, and these solutions are evaluated based on the value of their scaled fitness. Depending upon the fitness function value some solutions from the old population are chosen for mating using a selection scheme like roulette wheel or tournament selection. The crossover operator is applied to the selected parents. Generally, a single point crossover is recommend if the chromosome size is small [10, 21]. Crossover is performed until m new offspring are generated, where m is equal to n of the old population. There is a possibility that the initial population was created in such a way that the GA cannot generate some solutions of interest. To avoid this and make the GA more robust, a mutation operator is used. Mutation operator alters the value at some genes using the mutation probability [10, 21].

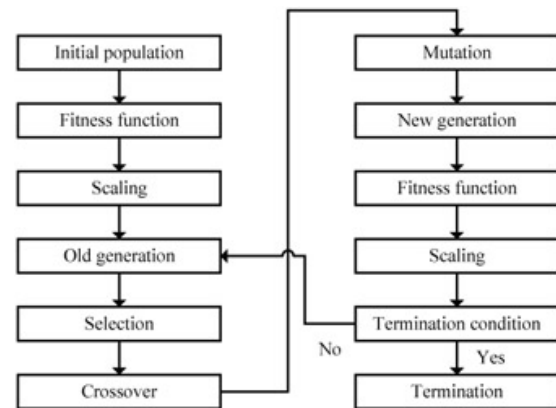


Figure 2: Genetic algorithm

This allows the exploration of the previously unattainable search space. After crossover and mutation are carried out, a new population is generated. The fitness of the new solutions is evaluated to measure their goodness. If the GA termination condition is not satisfied, then the new population becomes the old population and all the steps are repeated [9]. In this study, Genetic algorithms is applied which aim to obtain a general method of variable selection where only the fitness function will be dependent on the particular problem.

5. The Neuro-Genetic Approach

ANNs and GAs have been combined by using GAs to optimize the parameters of an ANN. For instance, when the Gradient Descent Algorithm is used to modify the weights of an ANN, it needs to have a specific network topology, in particular, the number of hidden nodes and the number of connection weights. These values, if preset by hand are not usually optimal [12]. GAs have been used to search for the weights of the network, to search for appropriate learning parameters, or to reduce the size of the training set by selecting the most relevant features and to design the structure of the network. The structure largely determines the efficiency of the network and the problems that it can solve. It is well known that to solve non-linearly separable problems, the network must have at least one layer between the inputs and outputs; but determining the number and the size of the hidden layers is mostly a matter of trial and error. In [19], author compared a GA with 14 non-evolutionary attribute selection methods (some of them variants of each other) across 8 different data sets. GAs have been used to search for these parameters, as well as for the pattern of connections and for developmental instructions for the network.

The number of input variable determines size of the neural network. To avoid over-fitting problems and to give better performance the number of input variable should be less. In NN, there are several approaches like "forward", "backward" and "stepwise", are available. The Genetic Algorithm optimizes the inputs from a larger pool of variables, attempts to generate appropriate network architecture for a given data set. Data preprocessing is an essential step for knowledge discovery and eliminate some irrelevant and redundant features, many researchers in society of data mining have a broad interest in feature transformation and subset selection [17]. It is especially important to optimize network structure of ANNs. The standard individual representation for attribute selection consists simply of a string of N bits, where N is the number of original attributes and the i -th bit, $i=1, \dots, N$, can take the value 1 or 0, indicating whether or not, respectively, the i -th attribute is selected. For instance, in a 10-attribute data set, the individual "1 0 1 0 1 0 0 0 1" represents a candidate solution where only the 1st, 3rd, 5th and 10th attributes are selected. This individual representation is simple, and traditional crossover and mutation operators can be easily applied.

The new hybrid Neuro-Genetic approach is depicted in figure 3 and the same has been applied for the diagnosis of stroke disease. The results shows this hybrid approach has the potential to eventually improve the success rate better than traditional ANN monolithic design.

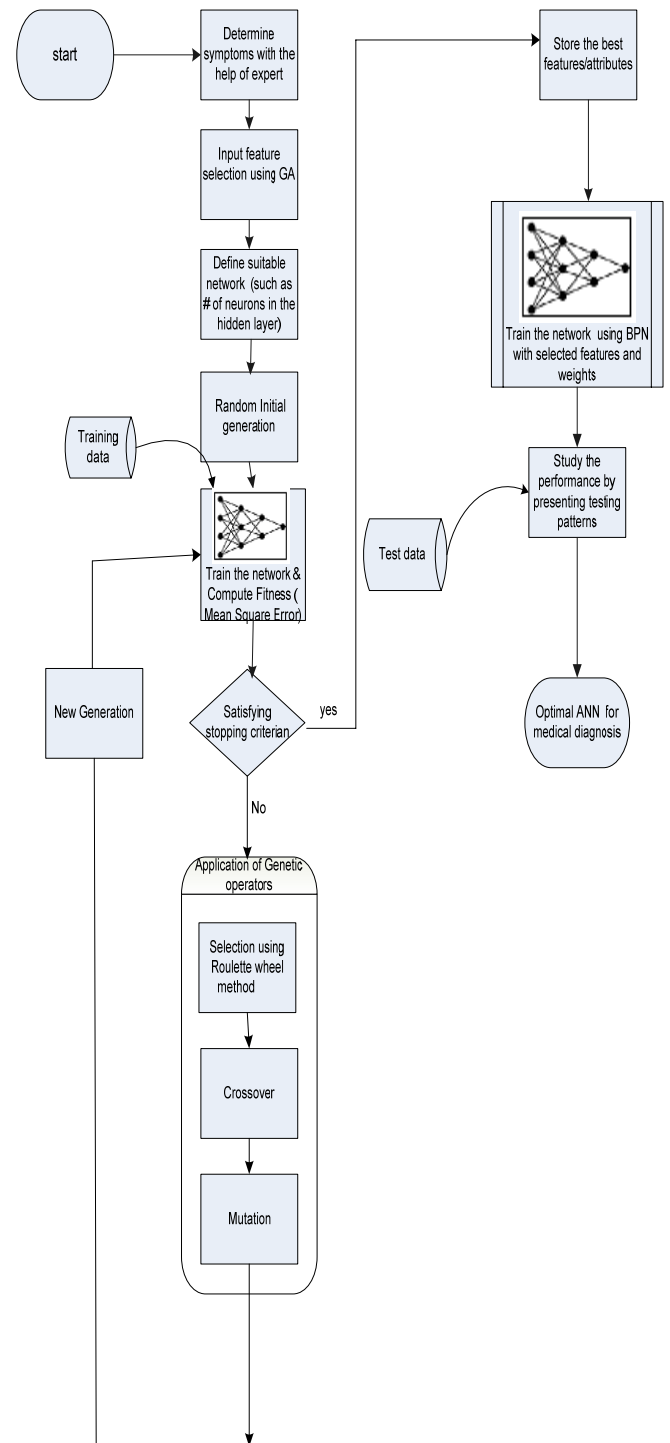


Figure 3: Hybrid Neuro- Genetic Approach

The process of GA-NN algorithm is presented below:

1. Determine the symptoms with help of Expert

2. Initialize count=0, fitness=0, number of cycles
3. Generation of Initial Population. The chromosome of an individual is formulated as a sequence of consecutive genes, each one coding an input.
4. Design suitable network (input layer, hidden layer, output layer)
5. Assign weights for each link
6. Train the network using BP algorithm
7. Find cumulative error and the fitness value. The genotypes are evaluated on the basis of the fitness function.
8. If (previous fitness < current fitness value) Then store the current features
9. count = count +1
10. Selection: Two parents are selected by using the roulette wheel mechanism
11. Genetic Operations: Crossover, Mutation and Reproduction to generate new features set (Apply new weights to each link)
12. If (number of cycles <= count) go to 4
13. Train the network with the selected features
14. study the performance with test data

6. Experimental Results and Discussion

The data for this work have been collected from 150 patients who have symptoms of stroke disease. The data have been standardized so as to be error free in nature. Table I below shows the various input parameters for the prediction of stroke disease.

Table 1: Input Parameters

Sl.No	Attributes
1.	Hypertensive
2.	Diabetes
3.	Myocardial
4.	Cardiac failure
5.	Atrial fibrillation
6.	Smoking
7.	Blood cholesterol
8.	Left arm and leg
9.	Right arm and leg
10.	Slurring
11.	Giddiness
12.	Headache
13.	Vomiting
14.	Memory deficits
15.	Swallowing
16.	Vision
17.	Double vision
18.	Vertigo

19.	Numbness
20.	Dizziness

7. Neural Network Based Feature Selection

Data are analyzed in the dataset to define column parameters and data anomalies. Data analysis information needed for correct data preprocessing. After data analysis, the values have been identified as missing, wrong type values or outliers and which columns were rejected as unconvertible for use with the neural network [3]. Feature selection methods are used to identify input columns that are not useful and do not contribute significantly to the performance of neural network. The removal of insignificant inputs will improve the generalization performance of a neural network. In this study, first Backward stepwise method is used for input feature selection. This method begins with all inputs and it works by removing one input at each step. At each step, the algorithm finds an input that least deteriorates the network performance and becomes the candidate for removal from the input set. The architecture of the neural network designed with 20 input nodes, 10 hidden nodes, and 10 output nodes. This ANN is trained using Back propagation algorithm and tested with the data and overall predictive accuracy was shown in table 10 against different datasets.

8. GA Based Feature Selection

In this neuro-genetic approach all the 20 symptoms are taken in to account. GA optimizes the 20 inputs in to 14. The genotype is represented by a sequence of symptoms. The number of individual in the initial population is 20. The fitness function is represented by means of root mean square error. The maximum number of generations are fixed at 20. The rest of the paper describes pre-processing, analysis, design, training and testing of ANN.

Table 2: Parameters used in GA

Search Method	Genetic Algorithm
Population size	20
Number of generations	20
Probability of crossover	0.6
Probability of mutation	0.033
Random number seed	1

At the first stage, two parents are selected from the population by the method of spinning the roulette wheel.

Then, a new offspring is generated from these parents using arithmetic crossover and non-uniform mutation operators, which are governed by the probabilities of crossover and mutation, respectively. These operators decrease the training time in a great extent and help in locating an optimum solution relatively faster. In this work, the probability of crossover is 0.6 and the probability of mutation is 0.033. These probabilities are chosen by trial and error through experiments for good performance.

Table 3: Categories of the Initial Population

Merit	Scaled	Subset
0.45539	0.44916	1 2 4 5 6 9 18 20
0.51887	0.52459	4 5 6 7 8 12 15 18
0.48656	0.4862	1 2 5 9 14 18 20
0.52876	0.53635	3 8 14 18 20
0.58999	0.6091	2 4 5 7 8 9 11 13 14 15 16 17 19 20
0.58216	0.59979	1 3 5 7 8 11 13 14 15 18 20
0.50912	0.513	4 5 6 8 11 13 16 17 18 20
0.23355	0.18557	10 19
0.55665	0.56948	7 8 10 16 20
0.07737	0	4
0.51	0.51404	2 3 4 5 6 7 8 11 12 13 17 18 19
0.58009	0.59733	1 2 3 7 9 13 16 17 18 20
0.6072	0.62954	1 2 3 7 12 13 14 15 16 17 19 20
0.57602	0.5925	1 2 3 5 6 7 8 9 10 11 15 19 20
0.49339	0.49432	4 5 7 8 9 12 13 14 19
0.47447	0.47183	2 4 11 12 14 16 17 18
0.48826	0.48822	1 2 3 5 6 7 9 10 11 15 19
0.44613	0.43816	1 2 7 9 11 17 19
0.51073	0.51491	1 3 4 5 7 8 9 11 12 14 17 19
0.54487	0.55548	2 3 4 5 7 8 9 13 15 17 18 19

The subset categories after 20 generations using GA are given in Table 4 below:

Table 4: Subset category after 20 generations

Merit	Scaled	Subset
0.72162	0.94337	1 3 6 7 8 9 10 12 13 14 15 16 18 20
0.72162	0.94337	1 3 6 7 8 9 10 12 13 14 15 16 18 20
0.72376	0.96412	3 6 7 8 9 10 12 13 14 15 16 18 20
0.72073	0.93473	2 3 6 7 8 9 10 12 13 14 15 16 18 20
0.72051	0.93258	2 3 6 8 9 10 12 13 14 15 16 18 20
0.70528	0.78496	1 2 3 6 7 8 9 10 12 13 14 15 16 18 19 20
0.63263	0.08094	1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 20
0.62428	0	1 2 3 6 8 9 10 13 16 18 20
0.69269	0.66298	1 2 3 6 7 8 9 10 11 12 13 15 16 18 20
0.69313	0.66729	1 3 6 7 8 9 10 11 12 13 14 15 16 18 19 20
0.66708	0.41485	1 3 6 7 8 9 10 11 12 13 15 16 18
0.68071	0.54693	1 3 6 7 8 9 10 11 13 14 15 16 18 20
0.67375	0.47939	1 2 3 6 7 8 9 13 15 16 18 20
0.71529	0.88203	1 2 3 6 7 8 9 10 12 13 14 15 16 18 20
0.72073	0.93473	2 3 6 7 8 9 10 12 13 14 15 16 18 20
0.71796	0.90784	2 3 6 7 8 9 10 12 14 15 16 18 20
0.68307	0.5698	2 3 6 7 9 10 12 13 14 15 16 18 20
0.68396	0.57835	1 3 6 7 8 10 12 13 14 15 16 18 19 20
0.72162	0.94337	1 3 6 7 8 9 10 12 13 14 15 16 18 20
0.70172	0.75052	1 3 6 7 8 9 10 11 12 13 14 15 16 18 20

It is very important to identify which features are relevant to misuse classification. The irrelevant features add noise to the data which makes it more difficult to distinguish between one category of disease to another. In this work the neural network is employed to find the relationship between input and output for the diagnosis of the stroke disease. In this paper, GA is used to find the best combination of input features to provide the solution with less computational process and more accuracy. The selected attributes using GA are 1,3,6,7,8,9,10,12,13,14, 15,16,18,20.

The input data are preprocessed and are encoded by the range $[-1..1]$ and most of the inputs are of two-state except desired output column. Initially 150 rows and 16 columns including output column were analyzed. The data is partitioned are done randomly and the following table shows the no of records in the training set, validation set and test set.

Table 5: Data Partition Set

Sl.No	Data Partition set	Records	Percentage
1.	Training set	104	69.33%
2.	Validation set	23	15.33%
3.	Test set	23	15.34%
4.	Ignored set	0	0%
	Total	150	100%

The Experimental results have been depicted in the following tables:

Table 6: Mean, Standard Deviation and Percentage of Input Importance of various attributes of Stroke disease.

Attributes	Min	Max	Mean	S.D	Input importance (%)
Hypertensive	0	1	0.693	0.463	0.087828
Myocardial	0	1	0.18	0.385	0.026777
Smoking	0	1	0.32	0.468	1.787629
Blood cholesterol	0	1	0.193	0.396	4.25239
Left arm&leg	0	1	0.253	0.456	32.37366
Right arm &leg	0	1	0.3	0.46	10.560274
Slurring	0	1	0.68	0.468	0.469455
Headache	0	1	0.327	0.471	11.30842
Vomiting	0	1	0.12	0.326	0.07021
Memory deficits	0	1	0.58	0.495	1.762396
Swallowing	0	1	0.267	0.444	13.868064
Vision	0	1	0.22	0.416	7.553708
Vertigo	0	1	0.207	0.406	3.385088
Dizziness	0	1	0.353	0.48	12.48966

In this work, Neural network contains one input, one hidden, and one output layer. Each ANN has 14 input neurons corresponding to the inputs, 7 hidden neurons and the output layer has 10 neurons. The first 14 input nodes represent the symptoms for the diagnosis of stroke disease. The output layer consists of 10 output nodes that represents the predicted type of the stroke disease. The sigmoidal function is used as input and output activation function. The network is trained using Back-propagation algorithm. The error rates on the training and test data are shown in table 7 below:

Table 7: Error rates on training and test data

Method	Training data	Test data
Correlation coefficient	0.9967	0.9996
Mean absolute error	0.0049	0.0019
Root mean squared error	0.0402	0.0133
Relative absolute error	1.0659 %	0.4107%
Root relative squared error	8.3576 %	2.8359 %

Table 8 shows the percentage of the total relevant records retrieved by the search (Recall) for dysphagia is 0 and for Right hemiplegia is 0.95 and for others is 1 and it has been reflected in the precision. The harmonic mean of precision and recall is specified as F-Measure for each class. It also shows the True positive rate and False positive rate of each class.

Table 8: Detailed accuracy by class

TP Rate	FP Rate	Precision	Recall	F-Measure	Class
1	0	1	1	1	Left Hemiplegia
1	0.008	0.962	1	0.98	TIA
0.95	0.008	0.95	0.95	0.95	Right Hemiplegia
1	0	1	1	1	Dysphasia
1	0	1	1	1	Monoplegia
1	0	1	1	1	Left Hemianopia
1	0	1	1	1	Aphasia
0	0	0	0	0	Dysphagia
1	0	1	1	1	Right Hemianesthesia
1	0	1	1	1	Quadruplegia

The confusion matrix for the various categories of stroke and the prediction classification by the neuro-genetic approach is depicted in table 9.

Table 9: Confusion Matrix for Stroke Disease Classification

A	B	C	D	E	F	G	H	I	J	Classified as
4 5	0	0	0	0	0	0	0	0	0	A = Left Hemiplegia

0	2 5	0	0	0	0	0	0	0	0	B=TIA
0	1	1 9	0	0	0	0	0	0	0	C= Right Hemiplegia
0	0	0	1 8	0	0	0	0	0	0	D=Dysphasia
0	0	0	0	1 4	0	0	0	0	0	E-Monoplegia
0	0	0	0	0	1 2	0	0	0	0	F= Left Hemianopia
0	0	0	0	0	0	5	0	0	0	G=Aphasia
0	0	1	0	0	0	0	0	0	0	H= Dysphagia
0	0	0	0	0	0	0	0	6	0	I= Right Hemianesthesia
0	0	0	0	0	0	0	0	0	4	J= Quadruplegia

The average prediction accuracy by the traditional Neural Network approach and the new hybrid Neuro-Genetic approach are depicted in table 10 below:

Table 10: Average Prediction Accuracy

Approach	Training	Validation	Testing
Neural Networks	78.52%	82.43%	90.61%
GA-NN	79.17%	83.88%	98.67%

The result shows clearly that our new hybrid neuro-genetic method provides better accuracy and faster convergence due to the complexity of the network. The prediction accuracy is 98.67% with the reduced features. Sometimes reduction of features yields the drop in accuracy. So the input parameters should be chosen with out compromising the accuracy.

9. Conclusion

In this paper, a new hybrid neuro-genetic approach has been proposed and the same has been used for the selection of input features for the neural network. Experimental results showed the performance of ANN can be improved by selecting good combination of input variables. It is shown that reduction of input variable reduces number of input neurons, size of the neural network and complexity of the ANN. From the results, GA-NN approach gives better average prediction accuracy than the traditional ANN.

10. References

- [1] Abdi, H. (1994). A neural network primer. Journal of Biological Systems, 2 (3), 247-283.

- [2] American Heart Association. Heart Disease and Stroke Statistics — 2004 Update. Dallas, Tex.: American Heart Association, 2003.
- [3] Baxt WG. Application of artificial neural networks to clinical medicine. *Lancet*. 1995; 346 (8983): 1135- 8.
- [4] D. Decker and J. Hintz, A (1993). Genetic Algorithm and Neural Network Hybrid Classification Scheme," *Proceedings of AIAA Computers in Aerospace Conference*, 1993.
- [5] Wang (ed), John.(2006) "Artificial Neural Networks for Prediction ". *Encyclopedia of Data Warehousing and Mining*, Volume I, A-H. IGI Publishing. © 2006.
- [6] D.E., Rumelhart, G.E. Hinton, and R.J. Williams. Learning internal representations by back-propagating errors. *Nature* 323:533—536, 1986 (reprinted in J.A. Anderson, and E. Rosenfeld, editors, *Neurocomputing*. MIT Press, Cambridge, 1988).
- [7] Dybowski R., Weller P., Chang R., Gant V (1996). "Prediction of outcome in the critically ill using an artificial neural network synthesised by a genetic algorithm," *Lancet*, 347: 1146–1150.
- [8] E. J. Chang and R. P. Lippmann (1991). Using Genetic Algorithms to Improve Pattern Classification Performance," *Advances in Neural Information Processing* 3, pp. 797-803.
- [9] Felici, Giovanni, and Carlo Vercellis (eds) (2008). *Mathematical Methods for Knowledge Discovery and Data Mining*. IGI Publishing.
- [10] Goldberg, D. E. (1989). *Genetic algorithms*. New York: Addison Wesley Longman, Inc.,
- [11] Gonzalez, J.S., Rodriguez, K., Garcia Nocetti, D.F. (1999). Model-based Spectral Estimation of Doppler Signals Using Parallel Genetic Algorithms. *Artificial Intelligence in Medicine* 19(1): 75–89.
- [12] Husbands, P., & Mill, F. (1991). Simulated co-evolution as the mechanism for emergent planning and scheduling. In *Proceedings of the Fourth Int. Conf. on Genetic Algorithms*, pp. 210–264.
- [13] Janson, D. J., & Frenzel, J. F. (1993). Training product unit neural networks with genetic algorithms. *IEEE Expert*, 8(5), 26–33.
- [14] K.J. Cherkauer and J.W. Shavlik (1996). Growing simpler decision trees to facilitate knowledge discovery. *Proc. 2nd Int. Conf. on Knowledge Discovery and Data Mining (KDD-96)*, 315–318. AAAI Press.
- [15] Larranaga, P., Sierra, B., Gallego, M.J., Michelena, M.J., Picaza, J.M.,(1997). Learning Bayesian networks by genetic algorithms: a case study in the prediction of survival in malignant skin melanoma. In *Proc. Artificial Intelligence in Medicine Europe* (E. Keravnou, C. Garbay, R.Baud, J. Wyatt, eds.), pp. 261–272.
- [16] Leung, F. H. F., Lam, H. K., Ling, S. H., & Tam, P. K. S. (2003). Tuning of the structure and parameters of a neural network using an improved genetic algorithm. *IEEE Transactions On Neural networks*, 14(1), 793–799.
- [17] Liu, H. and Motoda, H. (1998). "Feature transformation and subset selection", *IEEE Intelligent Systems and Their Applications*, Vol. 13, No. 2, pp. 26-28.
- [18] L. Jourdan, C. Dhaenens-Flipo and E.-G. Talbi (2003). Discovery of genetic and environmental interactions in disease data using evolutionary computation. In: G.B. Fogel and D.W. Come (Eds.) *Evolutionary Computation in Bioinformatics*, 297–316. Morgan Kaufmann.
- [19] M. Kudo and J. Sklansky (2000). Comparison of algorithms that select features for pattern classifiers. *Pattern Recognition* 33(2000), 25–41.
- [20] Mohr, J.P., (2001). *Stroke Analysis*, 4th Edition, Oxford Press, New York.
- [21] Pham, D., & Karaboga, D. (2000). *Intelligent optimization techniques*. London: Springer-Verlag.
- [22] Sugumaran (ed), Vijayan (2008). "Several Approaches to Variable Selection by Means of Genetic Algorithms". *Intelligent Information Technologies: Concepts, Methodologies, Tools, and Applications*. IGI Publishing.
- [23] Rabuñal, Juan R., and Julián Dorado (2006). *Artificial Neural Networks in Real-Life Applications*. Idea Group Publishing.
- [24] Vinterbo, S. and Ohno-Machado, L., (1999). A Genetic algorithm approach to multi-disorder diagnosis. *A1 in Medicine*, 18(2): 117–32.
- [25] Y Kim, W.N. Street and F. Menczer. (2000). Feature selection in unsupervised learning via evolutionary search. *Proc. 6th ACM SIGKDD Int. Conf on Knowledge Discovery and Data Mining (KDD-2000)*, 365–369. ACM.



D. Shanthi received her B.E. Computer Science and Engineering in 1992 from Madurai Kamarajar University, Tamil Nadu and M.E. Computer Science and Engineering in 2004 from Manonmaniam Sundaranar University, Tamil Nadu. She is currently working with

Department of Computer Science & Engineering, Birla Institute of Technology, Bahrain and pursuing her PhD in Soft Computing. She is member of various professional societies like CSTA, IAENG and IACSIT. Her other research interests include Genetic Algorithms, Neural Networks, Intelligent Systems, Image Processing, Embedded Systems and M-Learning. She has published more than 10 papers in International Conferences and Journals and also published 5 books in computing and applications.



Dr. G. Sahoo received his P.G. degree from Utkal University in the year 1980 and Ph.D degree in the area of Computational Mathematics from Indian Institute of Technology, Kharagpur in the year 1987. He is associated with Birla Institute of

Technology, Mesra, Ranchi, India since 1988. He is currently working as a professor and heading the Department of Computer Science and Engineering. His research interest includes theoretical computer science, parallel and distributed computing, image processing and pattern recognition.



Dr. N. Saravanan received his P.G. Degree in 1989 from Madurai Kamarajar University, Tamil Nadu and his Ph.D. in Computer Science and Engineering – Mathematics (Inter-disciplinary) in 2008 from Manonmaniam Sundaranar University, Tamil Nadu. He is currently working

with Department of Computer Science & Engineering, Birla Institute of Technology, Bahrain. His other research interests include Neuro-Fuzzy Systems, Intelligent Systems, Image Processing, Educational Technology and Web2.0. He has published more than 11 papers in International Conferences and Journals and also published

6 books in computing and applications. He has attended more than 20 workshops, symposia, seminars and short-term training programmes. He is a senior member of various international professional bodies like CSTA, IAENG and IACSIT and also a Life member of Ramanujan Mathematical Society, India.