Volume 1, No. 1, August 2010

Journal of Global Research in Computer Science

RESEARCH PAPER

Available Online at www.jgrcs.info

Neural Network Model in HIV / AIDS Application

M.Lilly Florence*[1] and Dr.P.Balasubramanie[2]

[1]Adhiyamaan College of Engineering, Hosur, Asst. Prof / MCA,
E- Mail : lilly_swamy@yahoo.co.in
[2]Kongu Engineering College, Perundurai, Erode, Prof. & Head, PG (CT)

***Abstract*:** HIV / AIDS is an incurable disease. More than millions of people have HIV positive. However, new medications not only can slow the progression of the infection, but also can suppress the virus, thereby restoring the body's immune function and permitting many HIV-infected individuals to lead a normal, disease-free life. Many research are going on to predict a better treatment for HIV patients, such as HIV drug prediction, drug resistance testing, predicting side effects for certain regimens etc. The prediction of regimen specification is a challenging research. Since all the patients are unique in their medical history, side effects and allergic in patricular drugs, the physician cannot treat all the patient in the same way. It is common that if a patient with set of certain sympotms consult the physician, the patient may get different opinions regarding the type of the underlying disease. A physician judegement is an important role in this regard. Recent research shows that computational intelligence has been widely used on medical diagonosis to solve complex problem by developing decision support system with the application of Neural Network algorithms. Neural Network is very good area to practice most of the medical problems. It has many algorithms for classification, prediction, image processing etc.A proper utilization of a Neural Network technique to implement a large – scale health services research dataset is one of the most difficult areas in the Neural Network field. It is further complicated due to ill-defined and ill-structured factors affecting a functional health status of HIV /AIDS patients. Many of the studies have applied Neural Network technique to classify and predict desired solution or to improve methodological aspects. In this proposed work, we have taken 300 HIV / AIDS patient's medical history and constructed a model to predict the appropriate regimen specification, which could help the patient to prolong their for maximum years. To construct this model we had been implemented Back Propagation Neural Network algorithm, ART1 Network and Radial Basis Function Network. Back Propagation Neural Network algorithm is used for classification and prediction purpose and also it would work with huge amount of data with large number of iterations. Due to its feed backward nature it could be act as better prediction algorithm. Similary the ART1 Neural Network algorithm has used to classify the patients into two groups active and inactive based on their regimen specification and the Radial Basis Neural Network has also used to prdict the regimen specification. All these three algorithms have used in this work to predict better regimen specification for HIV / AIDS patients.

Keywords; ANN, BPNN, ART1, RBNN AND HIV / AIDS

INTRODUCTION

Decisions about medical treatments are best made by a trained and experienced physician. These decision makers can benefit from historical data and artificial intelligence tools. Computer scientists have dreamed of creating an electronic brain. Intelligent computers are able to store and process vast stores of knowledge. The hope was that they would become perfect doctors in a box, assisting or surpassing clinicians in tasks like diagnosis, prescribing suitable drug specification etc. Today the importance of drug specification is a task requiring computer support in routine clinical situations which receives much less emphasis. The strict focus on the medical setting has now broadened across the healthcare spectrum and instead of AI medical system it is more typical to describe them as clinical Decision support system [1]. Our goal is to provide a means of constructing a model for prediction system for HIV/AIDS regimen specification using Neural Network algorithms. In particular we had been used Back Propagation Neural Network, Adaptive Resonance Theory1 and Radial Basis Function Network. In a large number of medical applications in which classification was desired to have the goal of discriminating a pattern with low frequency from a pattern with high frequency (e.g. No disease). Even though the patterns for certain conditions and diseases were well known to the medical community, others may not be well defined. For example, we still do not know why some patients with the HIV virus survive longer than others who had been infected for similar periods of time. In this work we have practiced some of the Neural Network algorithms for predicting HIV/AIDS regimen specification to improve the Patient's life time.

ABOUT HIV / AIDS

HIV stands for Human Immunodeficiency Virus. It is the virus that causes AIDS. A member of a group of viruses called retroviruses, HIV infects human cells and uses the energy and

nutrients provided by those cells to grow and reproduce. AIDS stands for Acquired Immunodeficiency Syndrome. It is a disease in which the body's immune system breaks down and is unable to fight off infections, known as "opportunistic infections," and other illnesses that take advantage of a weakened immune system. When a person is infected with HIV, the virus enters the body and lives and multiplies primarily in the white blood cells. These white blood cells are immune cells that normally protect us from disease. The hallmark of HIV infection is the progressive loss of a specific type of immune cell called T-helper, or CD4 cells. As the virus grows, it damages or kills these and other cells, weakens the immune system and leaves the person vulnerable to various opportunistic infections and other illnesses ranging from pneumonia to cancer. A person can receive a clinical diagnosis of AIDS, if he or she has tested positive for HIV and meets one or both of these conditions [27]:

- The presence of one or more AIDS-related infections or illnesses;
- A CD4 count that has reached or fallen below 200 cells per cubic millimeter of blood. Also called the T-cell count, the CD4 count ranges from 800 to 1200 in healthy individuals.

In 2006 UNAIDS estimated that there were 5.6 million people living with HIV in India, which indicated that there were more people with HIV in India than in any other country in the world. In 2007, following the first survey of HIV among the general population, UNAIDS and NACO agreed on a new estimate – between 2 million and 3.1 million people living with HIV. In 2008 the figure was confirmed to be 2.31 million, which equates to a prevalence of 0.3%. While this may seem a low rate, because India's population is so large, it is third in the world in terms of greatest number of people living with HIV. With a population of around a billion, a mere 0.1% increase in HIV prevalence would increase the estimated number of people living with HIV by over half a million. The national HIV prevalence rose dramatically in the early years of the epidemic, but a study released at the beginning of 2006 suggests that the HIV infection rate has recently fallen in southern India, the region that has been hit hardest by AIDS. In addition, NACO released figures in 2009 suggesting that the number of people living with HIV has declined from 2.73 million in 2002 to 2.30 million in 2009. The presence of antibodies against HIV in human body is termed as HIV positive and the person is called HIV positive (seropositive). It takes 6-12 weeks after infection for antibodies to rise to detectable levels. Thus, there is a window period during which infected person may transmit his infection despite being seropositive [3]. Antibody test at this stage does not reveal the true status as it takes some time for formation of antibodies. Therefore, a person during this stage is not aware that he/she is infected and it is capable of transmitting the virus to others. Even after the test results positive, the person still continues to look and feel healthy and remains asymptomatic for a number of years. The infectivity of the virus is thus life long, though it may vary with time, being low in the initial stage of infection and high in the last stages when clinical manifestation appears. Most of the clinical manifestations occur during the stage of advanced immune depletion. Manifestations' pertaining to the different systems are followed by opportunistic infections [36].

OVERVIEW OF NEURAL NETWORKS

The human brain, the most complex known living structure in the universe, has the nerve cell or neuron as its fundamental unit. The number of neurons and connections between the neuron is enormous. This ensemble enables the brain to surpass the computational capacity of supercomputers in existence today. Artificial Neural Network (ANN) is models of the brain, which implement the mapping, f: X -> Y such that the task is completed in a certain sense. These networks are able to learn training samples as well as to generalize them, which makes them an interesting research area. Unfortunately, it is doubtful that current ANN models will ever have learning capacity that will match the performance of living systems. Furthermore, the number of iterations required for generalization is often excessive and this motivates us to look into network designs where learning is fast [1]. For comparison with biological systems, it should be noted that memory is not stored in a single area of the brain but distributed. Also, different parts of the brain are also required for processing different kinds of memories. Creating ANNs that can learn and generalize information seems to be the first step in the design of connectionist intelligent machines, and this is done by several ANN models. However, the learning and generalization time for the most popular models can be very large. The ability to store information quickly not only provides a capacity that is common in biological systems, but it also has obvious applications in computational systems [4]. Neural Networks, also known as connectionist systems or parallel distributed processing models, are computer-based, self-adaptive models that were first developed in the 1960s. But they reached great popularity only in the mid-1980s after the development of the Back Propagation algorithm by Rumelhart et al. in 1986. Initially derived from neuroscientists' models of human neurons, Neural Networks now encompass a wide variety of systems (many of which are in no way intended to mimic the functions of the human brain). Neural Network research has its origins in the work developed by McCullough and Pitts, who developed mathematical models based on observational studies of real neurons. Figure 1.1 compares the anatomies of real and artificial neural configurations.

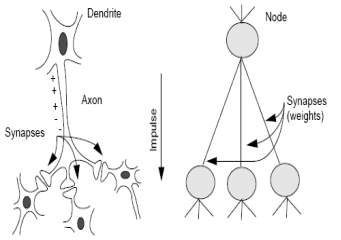

Figure 1.1 Real and artificial Neural Networks.

The neural body is represented in artificial Neural Networks as a circle, and it is called a node. The synapses are represented as lines connecting nodes, and are called weights. In artificial Neural Networks, the connections are called *weights* and are represented by real numbers. The Hebbian rule for learning simple neural models dictates that, if two connected neurons (or *nodes*, in the case of artificial Neural Networks) are simultaneously in an active state, the connection between them should be strengthened. Making a connection between two nodes stronger, means that, the real number is increased by a certain positive amount. Making a connection weaker requires that a negative number be added to the weight. Common learning rules used in artificial Neural Networks are derived from the Hebbian rule [12]. A Neural Network is a massively parallel distributed processor made up of simple processing units, which has a natural propensity for storing experiential knowledge and making it available for use. It resembles the brain in two respects: knowledge is acquired by the network from its environment through a learning process and inter neuron connection strengths, known as synaptic; weights are used to store the acquired knowledge. The procedure used to perform the learning process is called a learning algorithm, the function of which is used to modify the synaptic weights of the network [15].

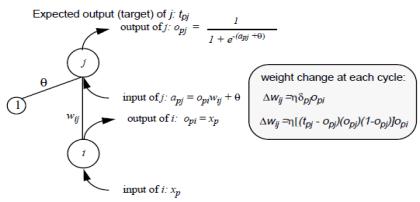

Figure1. 2 Learning in Neural Networks.

In Figure 1.2, the learning takes place when the logistic activation function is used. The change in weights is proportional to the derivative of the error function, and gradient descent is used. Note that the threshold, or bias q, can be modeled as a unit which always has activation 1, connecting to the output unit through weight q. This weight q is also learned using the delta rule. A neuron is an information processing unit that is fundamental to the operation of a Neural Network. The neuron consists of three basic elements, a set of synapses, and an adder for summing the input signals and an activation function. Every component of the model bears a direct analogy to the actual constituents of a biological neuron and hence it is termed as artificial neuron. The main characteristics of the Neural Network are;

- The NNs exhibit mapping capabilities that is they can map input patterns to their associated output patterns.
- The NNs learn by example
- The NNs possess the capability to generalize
- The NNs are robust system and fault tolerant.
- The NNs can process information in parallel at high speed and in a distributed manner.

Neural Networks have received a great deal of attention and produced astounding achievements in several medical applications. Back Propagation is a systematic method of training multilayer Artificial Neural Networks. It is built on high mathematical foundation and has very good application potential. Even though, it has its own limitations, it is applied to a wide range of practical problems and has successfully demonstrated it power. Back Propagation Neural Networks are by far the most commonly used Neural Network in the research community. The Back Propagation algorithm is a generalization of the Least Mean Square algorithm [20], that modifies network weights to minimize the Mean Square Error between the desired and the actual outputs of the network [18] [46] Back Propagation uses supervised learning in which the network is trained using data for known input as well as desired outputs. Once the network is trained, weights are frozen and can be used to compute output values for new input samples [5]. The learning rate is the key to influence the efficiency of the Back Propagation learning algorithm. In normal Back Propagation learning, the value of learning rate is constant. However, the optimum learning rate should be adjusted online; training process is done under the direction of summed squared error function and reaches the minimum through the weight adjustment [25].

IMPLEMENTATION OF BPNN

The construction of the neural network involves three different layers with feed backward architecture. The input layer of this network is a set of input units, which accept the elements of input feature vectors. The input units (neurons) are fully connected to the hidden layer with the hidden units. The hidden units (neurons) are also fully connected to the output layer. The output layer supplies the response of neural network to the activation pattern applied to the input layer. The information given to a neural net is propagated layer- by-layer from input layer to output layer through one or more hidden layers. The number of hidden layers and the number of hidden units are obtained by experiment. In the experiments, we found out that single hidden layer network structure cannot get the needed accuracy. When we adopted the two hidden layer network structure, we found out that the number of first hidden layer should be at least twice the number of input layer units. The number of second hidden layer should be at least being the larger one of the hidden input units and the output units. If we increase the number of the hidden layer units, accuracy can be improved, but it needs more learning time. The basic algorithm loop structure is given as;

Initialize the weights
Repeat
    For each training pattern
    Train on that pattern
End
Until the error is acceptably low.

Once the network has been structured for this application, that network is ready to be trained. To start this process, the initial weights are taken as existing regimen specification. The ANN

has been trained by exposing it to sets of existing data (based on the follow up history of HIV patients) where the outcome is known. The physician must consider many factors when selecting a regimen for a patient. The input vectors are the normalized data of each patient, it has taken as a 7 X 1 matrix (age, sex, weight, CD4 count, CD8 count, HB and TB)and the weight matrix of input layer to hidden later was taken as 1 X 3 matrix (Zidovudin or Stavudine, Lamivudine, Nevirapine or Efavirenz), then the network was presented with a training data set. Weight training in ANN's is usually formulated as minimization of an error function by iteratively adjusting connection weights. Weights are adjusted in such a way that each weight adjustment increases the likelihood that the network will compute. A small change is done at each cycle of the network training phase. The error value had been calculated using the output of the network, in the first iteration the error has calculated as 0.1247, the difference between these error and the expected output (1) was not closed to the threshold, so the weight was adjusted,(the regimen specification matrix got updated) and the process was repeated using the same input parameters. The weights of synapses connecting the output layer gave the proposed regimen specification for the given set of input. Once the process converges, the final weights should be the expected regimen specification of this work.

IMPLEMENTATION OF ART1

The ART1 algorithm begins with an initialization of the weight matrices $W^{1:2}$ and $W^{2:1}$. The intial $W^{2:1}$ matrix is set to all 1's. thus, the first time a new neuron in Layer 2 wins a competition, resonance will occur, since $a^1 = p \cap w_j^{2:1} = p$ and therefore $\| a^1 \|^2 / \| P \|^2 = 1 > \rho$. This means that any untrained column in $W^{2:1}$ is effectively a blank slate and will cause a match with any input pattern. After initialization, the ART1 algorithm proceeds as follows [15]:

1. First, we present an input pattern to the network. Since Layer 2 is not active on initialization,the output of Layer1 is $a^1 = P$.

2. Next, we compute the input to layer 2, $W^{1:2}\ a^1$, and activate the neuron in Layer 2 with the largest input

$$a_i^{\,2} = \begin{cases} 1, & \text{if } ((w_i^{1:2})^T a^1 = max [(w_k^{1:2})^T a^1]) \\ 0, & \text{otherwise} \end{cases}$$

In case of a tie, the neuron with the smallest index is declared the winner.

3. We then compute the L2 –L1 expectation
$W^{2:1}\ a^2 = W_j^{2:1}$

4. Now that Layer 2 is active, we adjust the Layer 1 output to include the L2-L1 expectation

$$a^1 = p \cap w_j^{2:1}$$

5. Next, the Orienting Subsystem determines the degree of match between the expectation and the input pattern

$$a^0 = \begin{cases} 1, & \text{if } \| a^1 \|^2 / \| P \|^2 = 1 < \rho \\ 0, & \text{otherwise} \end{cases}$$

6. If $a^0 = 1$, then we set $a_j^2 = 0$, inhibit it until an adequate match occurs, and return to step 1. If $a^0 = 0$, we continue with step 7.

7. Resonance has occurred. Therefore we update row j of $W^{1:2}$

$$_jW^{1:2} = \frac{\xi a^1}{\xi + \| a^1 \|^2 - 1}$$

8. We now update column j of $_jW^{1:2}$

$$_jW^{1:2} = a^1$$

9. We remove the input pattern, restore all inhibited neurons in Layer 2, and return to step 1 with a new input pattern.

The input vectors has taken as the same set of parameters (age, sex, weight, CD4 count, CD8 count, HB and TB) what we had been used in BPNN. The top down weights are the regimen specification which had been taken from the outcome of the BPNN. The output was propagated to the upper layer, since all unit activities were equal, we have taken the first unit as winner, then the output of layer2 was fed to layer 1 and the output was calculated. The activity value had calculated, based on the positive value the output has calculated and the bottom-up weight matrix has updated. The input patterns continue to be applied to the network until the weights stabilize. The result of this network was either 0 or 1, it was consider as two groups of patients. One group was an active group and other one was an inactive group. The patients under active groups are prescribed to take the weight of the network as their regimen specification, this regimen specification was closer to the regimen specification predicted using BPNN, and hence our proposed regimen specification would give better performance.

IMPLEMENTATION OF RBFN

Radial basis function networks consist of two layers: a hidden radial basis layer of S^1 neurons, and an output linear layer of S^2 neurons.

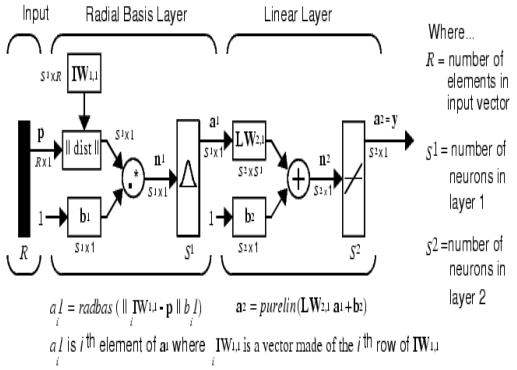

Figure 5.3 RBFN Architecture

The || dist || box in Figure 5.3 accepts the input vector **p** and the input weight matrix $\mathbf{IW}^{1,1}$, and produces a vector having S_1 elements. The elements are the distances between the input vector and vectors $_i\mathbf{IW}^{1,1}$ formed from the rows of the input weight matrix. The following steps are involved to construct RBFN model;

1. Calculate the center value using K – means clustering alghorithm [28]. The basic step of k-means clustering is simple. In the beginning we determined number of cluster K and we assumed that the centroid are center of these clusters. We could take any random objects as the initial centroids or the first K objects in sequence can also serve as the initial centroids. Then the K means algorithm will do the three steps below until convergence.

Iterate until *stable* (= no object move group):

- Determine the centroid coordinate
- Determine the distance of each object to the centroids
- Group the object based on minimum distance

2. When the RBF centres have been established, the width of each RBF unit can be calculated. The dimension of the centres is determined by the number of input variables or nodes of the input layer. The cluster centres become the centres of the RBF units. We have taken 10 RBF centres since it performed best at ten centres [43].

3. Computation of the weights between the hidden nodes and the output nodes

4. The output of the i^{th} unit, $a_i (X_t)$ in the hidden layer for the above input pattern is equal to ,

$$a_i (X_t) = exp \left(- \sum_{j=1}^{r} [x_{jt} - \hat{x}_{jt}]^2 / \sigma_i^2 \right)$$

where

$\hat{x}$ is center of i^{th} RBF unit for input variable j

σ_i is the width of the RBF unit

x_{jt} is j^{th} variable of input pattern t

5. Connection between the hidden units and the output units are weighted sum. The output value (y_{mt}) of the m^{th} output node is equal to the summation of the wieghted outputs of the hidden units are calculated as

$$Y_{mt} = \sum_{i=1}^{H} W_{im} \; a_i (X_t) + W_0$$

where

H = number of hidden layer nodes

Y_{mt} = output value of m^{th} node in output layer for t^{th} incoming Pattern

W_{im} = weight between i^{th} RBF unit and m^{th} output node.

W_0 = biasing term at m_{th} output node.

The mean square difference between the target outputs and predicted output is the error associated with the testing subset. This procedure is repeated with different training and testing set to obtain the optimum network structure with the minimum MSE. The training data has to select first. We had been collected the training data in an ART centre. Then we have to select the structure of the network that is how many hidden layers and hidden nodes . once the model constructed, we have to identify the training and testing data. Then the clustering is take place using any clustering algorithm, in our work we have used k- Means clustering algorithm [28]. The network parameters were identified, the network output is calculated and compare with the calculated error value. The validation is true, the average error value is calculated and check for convergence. If the network is converged, the network parameters are set to produce optimum network. Otherwise it repeat the above said setps. The model developed to predict a regimen specification for HIV/AIDS patients is a three layer Radial Basis Function Network. It was implemented using MATLAB neural network tool (nntool). An input layer is used to represent set of input variables (seven input variables). An output layer is used to represent an output variable. A hidden layer has three hidden nodes. Input pattern has the seven variables: age, ses, weight, CD4 count, CD8 count, HB rate and TB. Each of these variables is entered into the corresponding input layer of the network. These values are multiplied by computer generated random numbers, resulting in the input values of the hidden layer. Each value is placed in a logistic function that computes the net activation of the hidde layer, becoming input values of the output la $\hat{}$ This value is entered into the same logistic function that computes the activation of the output layer. The network architecture is designed to be the three layer RBF networks. The RBF has a linear approximation function for the input layer and a logistic function for the output layer. After configuring the network, we assign a learning rate (0.6),

initial weight (regimen specification obtained from BPNN), momentum learning epoch to the system to initiate the training. Once the system is designed a certain percent over total pattern is used to extract the training set and the test set. The training data has clustered using the k-means algorithm, it was implement using MATLAB. The patient's age, sex, weight, CD4 count, CD8 count, HB and TB are taken as network paramenter. The network was trained very similar to BPNN. The error value will be calculated using OLS and it was compared with tolerance. If it is less than the tolerance, the calculated wieghted layer would be considered as a proposed regimen specification.

RESULTS AND DISCUSSION

The proposed ANN model is able to predict the regimen specification for HIV / AIDS patients, so that, the patients can survive more than 10 years. To construct this model we have taken age, weight, sex, HB rate, CD4 count, CD8 count and TB rate as input parameters. Three types of regimens had been considered as the weight of the synapses. Using three different types of neural network algorithms the model has been constructed and trained with 300 patients' medical history. First the Back Propagation algorithm has been experimented using C++ language. In this, the initial weight of synapses connecting the input neuron and hidden neurons are taken as the default regimen specification. Then compute the input for the hidden layer by multiplying the corresponding weights of synapses, then the output layer evaluate the output using sigmoidal function and calculate the error. Compare the error with the threshold. The threshold value used in this work was 0.001. If the error value is less than the threshold, then the calculated weight would be the proposed regimen specification of the patient. Otherwise the weight will be adjusted and repeat the above process unit. The convergence in the error rate is less than the tolerance value. The result of this model was tested using 100 patients medical information and observed that, if the physician treats the patients with this proposed regimen specification could prolong the life time of the patients for more than 10 years. This work indicates that Back Propagation could be effectively applied for regimen specification. This prediction could help physician to plan for a better medication and reduce number of death caused by HIV / AIDS disease.

Patient_ID	Sex	Age	Weight	HB	CD4	CD8	TB
A	M	50	35	10	36	430	619
B	M	23	43	10	187	721	1769
C	F	40	45	10	98	1498	860
D	F	40	35	8	38	812	1169
E	F	35	35	8	148	940	1023
F	M	39	58	12.5	113	408	114
G	M	44	31	9	21	293	413
H	M	45	35	9.2	172	722	1032
I	M	35	41	8	69	555	772
J	F	49	40	10	184	265	1421

Table 6.1 Input data set

Table 6.1 shows patients' information which we have taken as input to construct this network model (only 100 patients' data had been given here). The physicians mainly consider this factors to prescribe the regimen specifications. The three types of regimen we have taken for this research was Zidovudine or Stavudine, Lamivudine and Nevirapine or Efavirenz. The patient infected with HIV as well as Tuberculosis has prescribed different set of regimens. The maximum age of the patient was considered as 50. The CD4 count and CD8 count is inversely propotional to each other. The data given in the table had normalized to maximum value and then given as a input to construct the model. This model was trained with 300 patients' information. The default regimen specification prescribed by the physician in the ART centre where we had collected our samples are given in Table 6. 2. If the patient is infected with Tuberculosis, he/she was prescribed to take Efavirenz. Similarly the HB rate of the patient is less than 8, he/she is prescribed to take Nevirapine otherwise he/she is prescribed to take Zidovudine. The physicians are prescribing constant regimen specification for the patient of their age is more than 30. Because of this, the physicians are not able to get better performance from the patient's CD4 count. In this research, there was no constant regimen specification; the regimen specification is only based on the patients' age, weight, CD4, CD8, HB, and TB rate. Table 6.3 shows the proposed regimen specification for the patients.

S.No.	Regimens	Specification (mg)	Tuberculosis	HB Rate
1	Zidovudine	40	-	> 8
2	Stavudine	150	-	-
3	Lamivudine	150	-	-
4	Nevirapine	250	-	< 8
5	Efavirenz	600	Y	-

Table 6.2. Existing Regimen Specification

S.No.	Regimens	Specification (X Weight mg)	Tuberculosis	HB Rate
1	Zidovudine	10	-	> 8
2	Stavudine	1	-	-
3	Lamivudine	5	-	-
4	Nevirapine	2	-	< 8
5	Efavirenz	20	Y	-

Table 6. 3. Proposed Regimen Specification

Second, the ART1 network model was implemented with the training data given in the Table 6.1, and the weight of layer has taken as the output of BPNN. Using ART1 network model, two clusters are obtained namely active and inactive. The active cluster has taken the regimen specification from the previous model outcomes. The inactive cluster had the default regimen specification which has been prescribed by the physicians. So here the group of patients under active cluster could prolong their life for maximum period. Table 6.4 shows the result obtained from ART1 model. It has been experimented in MatLab.

S.No.	Patient	Active (or) Inactive
1	A	Inactive
2	B	Active
3	C	Active
4	D	Active
5	E	Active
6	F	Inactive
7	G	Inactive
8	H	Active
9	I	Active
10	J	Active

Table 6.4

Finaly, RBFN had been implemented using the outcome of ART1 network model and using the regimen specification given in Table 6.2. RBFN was practiced using Matlab tool. The training data has clustered using the k-means algorithm, it was implemented using MATLAB. The patient's age, sex, weight, CD4 count, CD8 count, HB and TB are taken as network paramenter. The network was trained very similar to BPNN. The error value will be calculated using OLS and it was compared with tolerance. If it is less than the tolerance, the calculated wieghted layer would be considered as a proposed regimen specification.We obtained similar results what we got in BPNN which has shown in Table 6.3. Hence our proposed regimen specification decision support tool would help the physician to treat the HIV patients postiviely. In future, we could reduce number of death caused by the HIV/AIDS disease. This proposed regimen specification would be permitted for the age group from 12 to 50. The data which we had been used in this work was homogeneous and it had been collected in a ART centre, Tamil Nadu, India.

CONCLUSION AND FUTURE ENHANCEMENT

This research work had been implemented using Back Propagation Neural Network algorithm, ART1 network model and Radial Basis Function network. The result obtained from BPNN has taken as the weight matrix for ART1 network model, in this model the patients was grouped into two active and inactive based on its output. The active patients' information has taken as the training data to implement RBFN and the regimen specification has taken as the weight of the hidden layer. The network was trained and the weight of the hidden layer got adjusted. The final adjusted weight was the result of this model. The outcome of this research shows that the prediction model devised provides medical practitioners a convenient decision support tool that can be used to predict a suitable regimen specification for the patient. These findings of research indicate that this prediction method is a promising method for treating HIV / AIDS patients. It is concluded that this system have the potential to improve the quality of clinical decision making and improve the outcomes of health services and strengthen the life of AIDS patients. The following are the enhancements that can be incorporated in the continuation of this research.

- The data set can be used as heterogeneous from different area of an ART centre.
- Large data set can be used.
- Different sets of regimens can be considered. This will help to give a more precise solution to the problem.

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