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Reducing Process-Time for Fingerprint Identification System

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ABSTRACT

Fingerprints are the most widely used biometric feature for person identification and verification in the field of biometric identification. Fingerprints possess two main types of features that are used for automatic fingerprint identification and verification: (i) Ridge and furrow structure that forms a special pattern in the central region of the fingerprint and (ii) Minutiae details associated with the local ridge and furrow structure. In a traditional biometric recognition system, the biometric template is usually stored on a central server during enrollment. The candidate biometric template captured by the biometric device is sent to the server where the processing and matching steps are performed. This paper presents an approach to speed up the matching process by classifying the fingerprint pattern into different groups at the time of enrollment, and improves fingerprint matching while matching the input template with stored template. To solve the problem, we take several aspects into consideration like classification of fingerprint, singular points. The algorithm result indicates that this approach manages to speed up the matching effectively, and therefore prove to be suitable for large database like forensic divisions.

Keywords: Biometrics, identification, verification, minutiae points, singular points.

1. INTRODUCTION

Fingerprint is one of the most mature biometric traits and considered legitimate proof of evidence in courts of law all over worldwide. Fingerprints are, therefore, used in forensic divisions worldwide for criminal investigations. More recently, an increasing number of civilian and commercial applications are either using or actively considering using fingerprint-based identification because of a better

understanding of fingerprints as well as demonstrated matching performance than any other existing biometric technology. Modern fingerprint matching techniques were initiated in the late 16th century [1]. Henry Fauld, in 1880, first scientifically suggested the individuality and uniqueness of fingerprints. At the same time, Herschel asserted that he had practiced fingerprint identification for about 20 years [2]. This discovery established the foundation of modern fingerprint identification. In the late 19th century, Sir Francis Galton conducted an extensive study of fingerprints [2]. He introduced the minutiae features for single fingerprint classification in 1888. The discovery of uniqueness of fingerprints caused an immediate decline in the prevalent use of anthropometric methods of identification and led to the adoption of fingerprints as a more efficient method of identification.
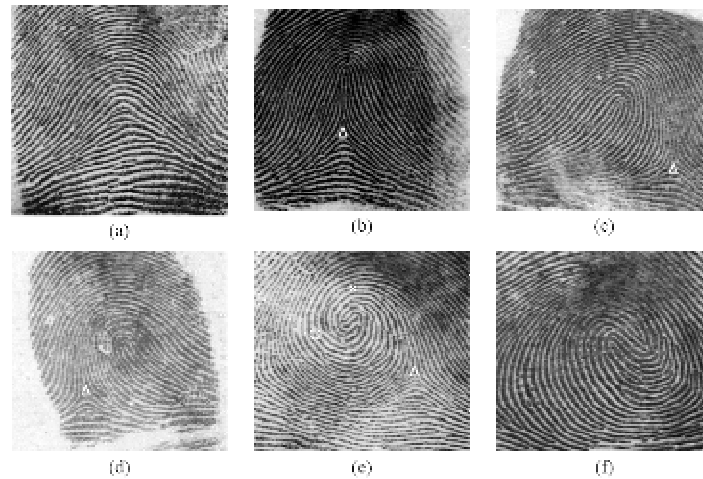
FIGURE 1: Fingerprints classification involving six categories: (a) arch, (b) tented arch, (c) right loop, (d) left loop, (e) whorl, and (f) twin loop. Critical points in a fingerprint, called core and delta, are marked as squares and triangles. Note that an arch does not have a delta or a core.

An important advance in fingerprint identification was made in 1899 by Edward Henry, who established the famous "Henry system" of fingerprint classification [1, 2]: an elaborate method of indexing fingerprints very much tuned to facilitating the human experts performing (manual) fingerprint identification. In the early 20th century, fingerprint identification was formally accepted as a valid personal identification method by law enforcement agencies and became a standard procedure in forensics [2]. Fingerprint identification agencies were setup worldwide and criminal fingerprint databases were established [2]. Loop, whorl, and twin loop.

1.1 Fingerprint Feature Extraction

The human fingerprint is comprised of various types of ridge patterns, traditionally classified according to the decades-old Henry system: left loop, right loop, arch, whorl, and tented arch.
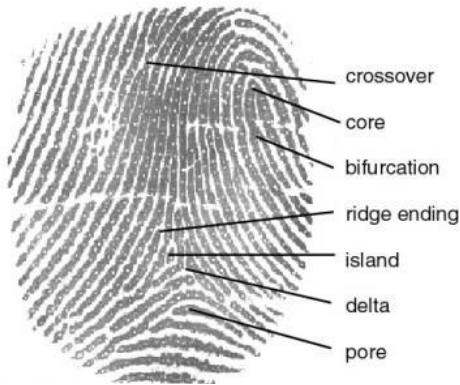
FIGURE 2: Minutiae- points on a fingerprint.

Loops make up nearly 2/3 of all fingerprints, whorls are nearly 1/3, and perhaps 5-10% are arches [3]. These classifications are relevant in many large-scale forensic applications, but are rarely used in biometric authentication. Many types of minutiae exist, including dots (very small ridges), islands (ridges slightly longer than dots, occupying a middle space between two temporarily divergent ridges), ponds or lakes (empty spaces between two temporarily divergent ridges), spurs (a notch protruding from a ridge), bridges (small ridges joining two longer adjacent ridges), and crossovers (two ridges which cross each other) [4].

1.2 Fingerprint-Matching Process

Fingerprint matching techniques can be placed into two categories: minutiae-based and correlation based. But the commonly used technique with minimum FAR and FRR is Minutiae-based techniques. In this process we, first find minutiae points and then map their relative placement on the finger. However, there are some difficulties when using this approach. It is difficult to extract the minutiae points accurately when the fingerprint is of low quality. Also this method does not take into account the global pattern of ridges and furrows [5]. Fingerprint Verification System is a system that determines the correspondence of an input fingerprint with a template fingerprint stored in data base. A typical block diagram of biometric matching systems is shown in Figure 3.
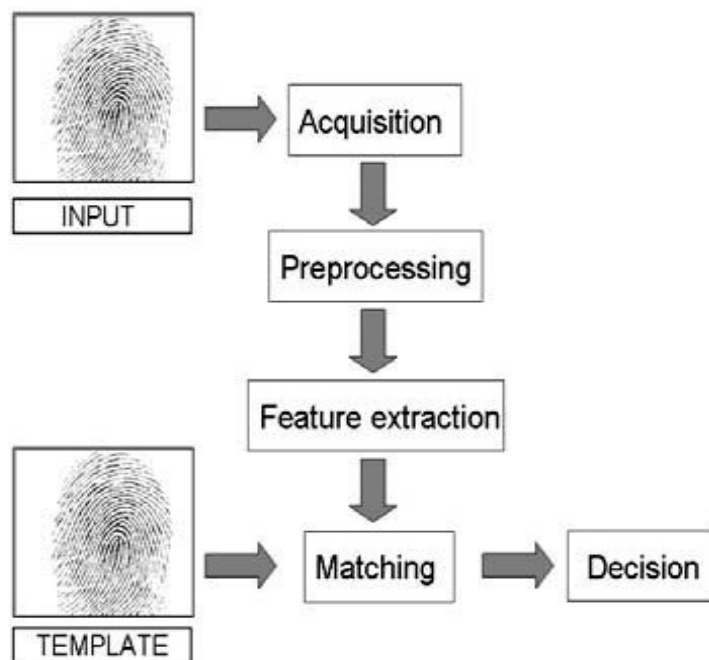
FIGURE 3: Block diagram of a typical Automatic Fingerprint Verification system.

In a verification fingerprint system, the template fingerprint image is obtained in the enrollment phase. After that verification process takes place by a inputting the sample of the user's fingerprint at sensor. Such input fingerprint must be processed, in the preprocessing step. The preprocessing includes image enhancement, gray level adjust, ridge thinning, etc. After the fingerprint image has been preprocessed, the feature extraction block extracts the relevant information that will be used for matching with the template fingerprint [6]. Finally a verification decision is made with the results or percentages of similarity obtained from the matching step. Section 2 describes the work in this field and the problems associated with this field. Section 3 describes the proposed work and the efficiency of proposed work based on experimental calculations.

2. Related Work

Figure3 above shows the process of matching for fingerprint. It is obvious that if fingerprint templates are stored in a particular manner then it will quite increase the efficiency of biometrics device. We have visited Madhuban Forensic Laboratory, Karnal to know which methods are used there as there are lots of templates in database. There we see the matching process of fingerprint identification among apx. 150000 database templates. The software being used there is FACTS (Finger Analysis Criminal Tracing System) developed by CMC and based on the theory of Dr. Henry Faulds. This approach involves the print of all the fingers of both hands and assign weights to each of fingers print pattern [7].

2.1 Explanation of the Henry Classification System

The Henry Classification System allows for logical categorization of ten-print fingerprint records into primary groupings based on fingerprint pattern types. This system reduces the effort necessary to search large numbers of fingerprint records by classifying fingerprint records according to gross physiological characteristics.
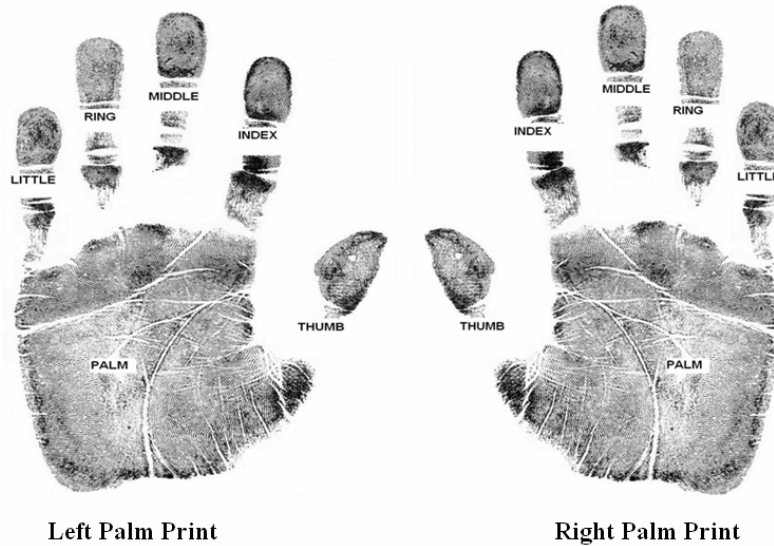
FIGURE 4: Both palm print of a single person.

Subsequent searches (manual or automated) utilizing granular characteristics such as minutiae are greatly simplified. Henry Classification System assigns each finger a number according to the order in which is it located in the hand, beginning with the right thumb as number 1 and ending with the left pinky/little as number 10. The system also assigns a numerical value to fingers that contain a whorl pattern; fingers 1 and 2 each have a value of 16, fingers 3 and 4 have a value of 8, and so on, with the final two fingers having a value of 1. Fingers with a non-whorl pattern, such as an arch or loop pattern, have a value of zero. Images of various fingerprint patterns are shown already in figure1. In accordance to the Henry Classification System, finger numbers and finger values are assigned as following: The fingerprint record's primary grouping is determined by calculating the ratio of one plus the sum of the values of the whorl-patterned, even-numbered fingers; divided by one plus the sum of the values of the whorl-patterned, odd-numbered fingers (Harling 1996). This formula is represented below [8]:

Henry Classification System Formula:

Primary Grouping Ratio (PGR) =

$$\frac{1+ \text{(Sum of whorled, EVEN finger value)}}{1+ \text{(Sum of whorled, ODD finger value)}}$$

	L Pinky	L Ring	L Middle	L Index	L Thumb	R Thumb	R Index	R Middle	R Ring	R Pinky
Finger Number	10	9	8	7	6	1	2	3	4	5
Value (if Whorl)	1	1	2	2	4	16	16	8	8	4

If, for example, an individual has a fingerprint record with a LWAALALWLA pattern series (the series begins with Finger 1, the right thumb and ending with Finger 10, the left pinky), the corresponding classification ratio would be 19:1. This example is calculated below [8] :

	L Pinky	L Ring	L Middle	L Index	L Thumb	R Thumb	R Index	R Middle	R Ring	R Pinky
Finger Number	10	9	8	7	6	1	2	3	4	5
Value (if Whorl)	1	1	2	2	4	16	16	8	8	4
Pattern Type	Arch	Loop	*Whorl*	Loop	Arch	Loop	*Whorl*	Arch	Arch	Loop
Finger Value	0	0	2	0	0	0	16	0	0	0

Example: $\dfrac{1+ \text{(Sum of Even finger value)}}{1+ \text{(Sum of Odd finger value)}} = \dfrac{1+ (16 + 2)}{1 + (0)} = \boxed{\dfrac{19}{1}}$

Therefore, this individual belongs to the 19:1 primary group. If, for example, an individual does not have any whorl-patterned fingerprints, his or her classification ratio, or primary group, would be 1:1. If an individual has all ten fingerprints containing a whorl pattern, his or her classification ratio would be 31:31. The Henry Classification System allows for up to 1,024 primary groupings.

2.2 Problems associated with Existing System

Above method work very efficiently when we have palm prints of all fingers of both hands. We assign weights to the person prints and calculate PGR. On the basis on PGR factor the search goes to particular domain and identified the proper match. But if we have only one finger print as input print, then there will be problem as in this case we can't find PGR factor. Further the problem can also arise if the criminal is made some trick while giving its input prints to the system. He can change the order of his fingerprint while giving input print, if this happen then his print can't be matched anywhere in the system.

3. PROPOSED WORK

Proposed work is based on the theory of fingerprint classification, we store only single finger print of person in the database. This single print can be thumb print or print of index finger. One obvious advantage of this approach is that it will considerably reduce the amount of memory required to store the fingerprint template as only one print is stored instead of 10 prints for an individual. Now let us see how the proposed system will work. First let us talk about the enrollment process; in conventional system the database contains the fingerprint templates in an ordinary manner. But here in our proposed system the database contains the different set of templates according to classification. During the enrollment process, sensor senses the fingerprint, then next step is feature extraction, here minutiae points are extracted. After this step we put a classifier to check the classification of input template that whether it is left-loop, right-loop, arch or whorl. The detail function of classifier is shown in figure 6. After classification the input template will be stored in particular domain. A domain in the database contains the templates of same classification. Normally the fingerprints are classified as Whorl, arch and loop. Loops make up nearly 65% of all fingerprints, whorls are nearly 30%, and perhaps 5% are arches [3]. These classifications are relevant in many large-scale forensic applications, but are rarely used in biometric authentication. Since the loops are 65%, we further divide this domain into two parts i.e. left loop 32% apx. and right loop 33% apx . So we have four different domains i) Left-Loop ii) Right-Loop iii) Arch and iv) Whorl as shown in figure5. Now let us come to the verification process, here the finger or finger print is placed at sensor and then its features are extracted and a final template is generated for matching. Now this template will not matched with every templates in the database rather it extracts its classified domain out of 4-domain and will perform match from this extracted domain. This process, no doubt will be fast and more efficient especially when the stored database is very large that is more than 1, 00000 templates. Let D and T be the representation of the Database Template and Stored Template respectively. Each minutia may be described by a number of attributes, including its location in the fingerprint image, orientation, type etc. Most common minutiae matching algorithms consider each minutiae as a triplet $m= \{x,y,\theta\}$ that indicates the minutiae location coordinates and the minutiae angle θ.

$D = \{m_1, m_2, \ldots\ldots m_n\}$　　　　　　$m_{i=}\{x_i, y_i, \theta_i\}$　i= 1…..m

$T = \{m'1, m'2, \ldots\ldots m'n\}$　$mj = \{x'j, y'j, \theta'j\}$　j= 1….n

Where m and n denotes the number of minutiae in D and T respectively.

Database Template and Stored Template and stored template will be matched, If we calculate Spatial Distance (SD) and direction difference (DD) that will not be below than specified value r0 and θ0 or we can write as [9].

SD (m'1, m1) = sqrt [(x'i - xi)2 + (y'i - yi)2] >= r0　　　---------------(1)

Similarly

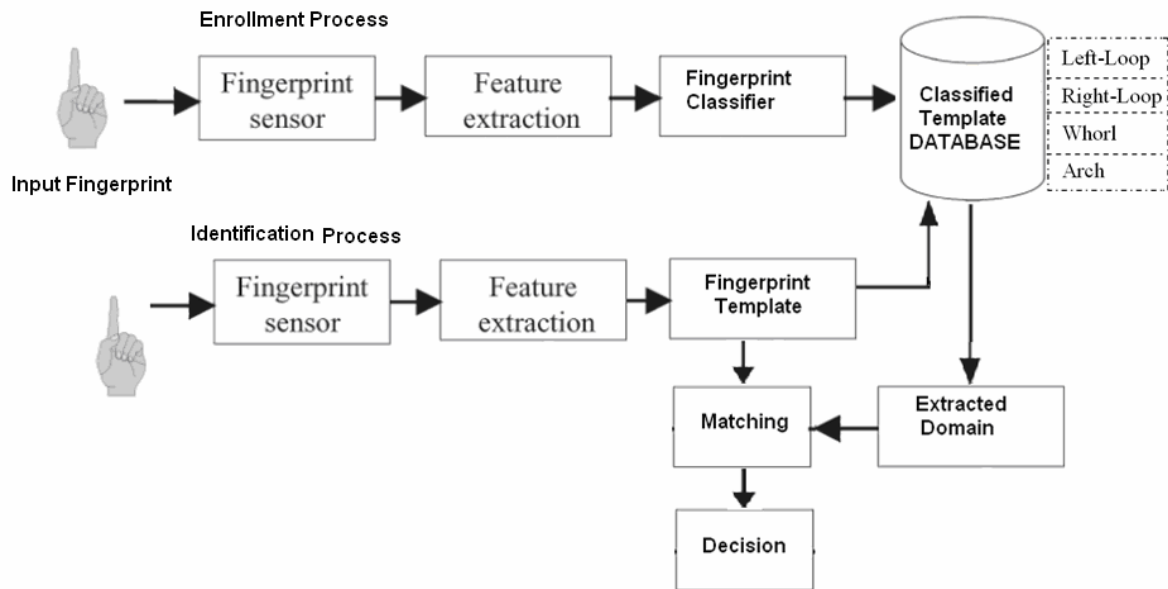DD (m'1, m1) >= θ0　　　　　　　　---------------(2)

FIGURE 5: Proposed scheme for Fingerprint Identification

3.1 Fingerprint Classifier

Fingerprint classifiers classify the input fingerprint into four major categories namely Left-Loop, Right-Loop, Whorl and Arch. The proposed classifiers works on the basis of singular point (Delta) extracted. If there are two deltas then it will be counted as whorl or twin loop. If there is no delta then it will be counted at arch. If only one delta is there then it will be either left loop or right loop.

| Whorl | Arch | Right-Loop | Left-Loop |
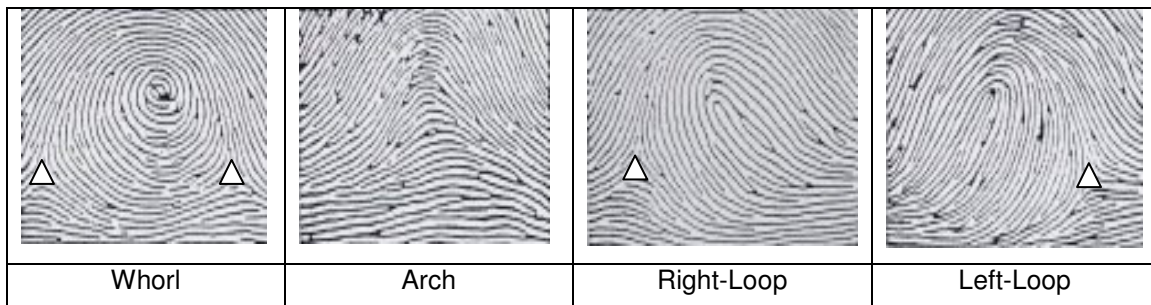
Figures 6. Position and numbers of deltas in different finger prints.

We further find the category of loop by measuring Relative position (R). If relative position, R of delta with respect to symmetry axis is R = 1 means the delta is on the right side of symmetry axis then it will be left loop otherwise it will be right loop [10]. On the basis of above idea, a flowchart (figure 6) for algorithm is designed to find the fingerprint classification.
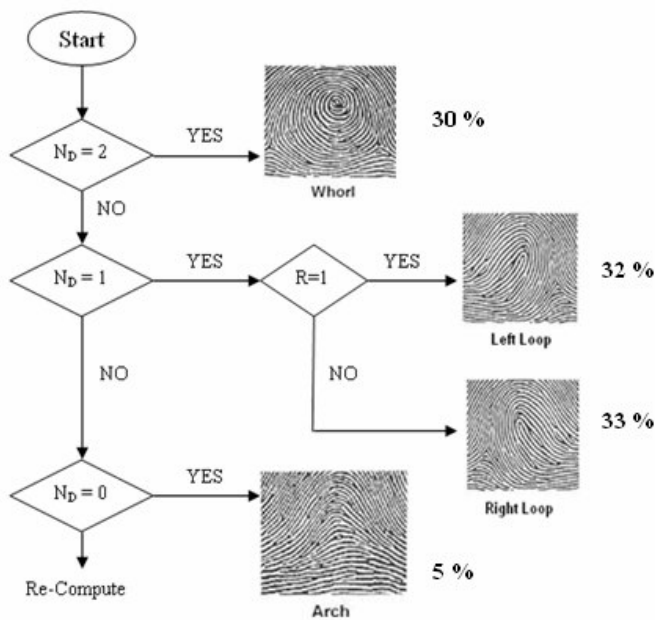
FIGURE 6: Proposed working of Fingerprint classifier.

3.3 Performance Estimation of Proposed Scheme

Let us take the example of Madhuban forensic laboratory, Karnal where database of more than 1, 50000 templates are stored. We had performed an experiment at Madhubhan by inputting a single template at the sensor and started to identify it from their database. The process takes 25-30 minutes to identify and also gives 34 matched templates (equations 1, 2 satisfy for 34 templates) [7]. These 34 templates again have to match manually and consume around 5-6 hours i.e. it's a quite time consuming and complex task. First let us see why the system takes so much time.
Let's assume that time taken to perform a single match = 1 ms (1 milli seconds)

Performance of Existing System

For Best case i.e. the template is First match, Time required = 1 X 1 = 1 ms
For worst case i.e. the template is last match, Time required = 1 X 1, 50000 = 150 sec. = 25 min.
For an Average case, Time required= apx 10-20 min.

Performance of Proposed System

For Best case i.e. the template is First match, Time required = 1 X 1 = 1 ms
Now let us calculate for worst case
We have assumed 1, 50000 templates, According to classification there will be
45000 whorls (30%) + 48000 Left Loop (32%) + 49500 Right Loop (33%) + 7500 Arch (5%)
At First stage we get the template classification and accordingly particular domain will be extracted. Now we calculate the time taken for each classification
      For Whorl = 1ms X 45000 = 45 sec.
      For LL   = 1ms X 48000 = 48 sec.
      For RL   = 1ms X 49500= 49.5 sec
        For Arch = 1msX 7500= 7.5 sec.

Average time = 150/4= 37.4 sec.
For an Average case, Time required= apx 20-24 sec.

Performance Factor = Time take in worst case of existing system $\quad$ = $\quad$ 25 min $\quad$ = 40.1
$\qquad$ Time take in worst case of proposed system $\qquad$ 37.4 Sec

i.e. the new approach is apx 40 time better than the existing one.

4. CONCLUSION AND FUTURE SCOPE

An approach has been presented for fingerprint matching in an effective way to reduce time. The proposed scheme has been calculated as 40 times efficient as compared with an existing system. We have taken four major classifications of fingerprint, whorl, arch, left-loop and right-loop. But still there is some problem in existing system that is in our proposed system our pre-request is concern about our database. Our database should contain only one print of every individual not both palm prints. Proposed system will not work if we try to match fingerprint of middle finger or little finger. For that purpose we have to store all the fingerprints of a person but the turnaround time can be reduced by study further in this direction as 20-25 minutes are quite lengthy time to wait and moreover there is not single match in the result rather there are 35-50 templates matched.

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Designing an Artificial Neural Network Model for the Prediction of Thrombo-embolic Stroke

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ABSTRACT

In this study, a functional model of ANN is proposed to aid existing diagnosis methods. This work investigated the use of Artificial Neural Networks (ANN) in predicting the Thrombo-embolic stroke disease. The Backpropogation algorithm was used to train the ANN architecture and the same has been tested for the various categories of stroke disease. This research work demonstrates that the ANN based prediction of stroke disease improves the diagnosis accuracy with higher consistency. This ANN exhibits good performance in the prediction of stroke disease in general.

Keywords: Artificial Intelligence, BPN, Neural Network, Thrombo-embolic Stroke.

1. INTRODUCTION

Neural networks provide a very general way of approaching problems. When the output of the network is continuous, it is performing prediction and when the output has discrete values, then it is doing classification. A simple rearrangement of the neurons and the network becomes adept at detecting clusters. Computer Assisted Decision Support in medicine has at least the role of enhancing the consistency of care. Secondly, it has the potential to cover rare conditions, since no clinical expert can be expected to possess encyclopedic knowledge of all of the exceptional manifestations of diseases, even within a specialist domain. Thirdly, the expanding range of patient information that is made available in electronic form, makes it feasible to more accurately quantify important clinical indicators, such as the relative likelihood for competing diagnoses or the clinical outcome. In some cases, computer-assisted diagnoses have been claimed to be even more accurate than those by clinicians.

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 [1]. 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 Squeal, 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. In this paper, we propose an artificial neural network model for the prediction of Thrombo Embolic Stroke disease. The rest of the paper discusses about related studies, the proposed model, results and discussion along with conclusion.

2. RELATED STUDIES OF ANN IN MEDICINE

ANNs appear to be a valid candidate for the reliability analysis. Given a number of predictor variables, an opportunely structured and trained Multi Layer Perceptron (MLP) can identify the "causal path" leading to a certain value of the potential objective variables, with a certain degree of confidence. [3]. Several studies have applied neural networks in the diagnosis of cardiovascular disease, primarily in the detection and classification of at-risk people from their ECG waveforms [4]. In the works of [5], the application of neural networks to classify normal and abnormal (pathological) ECG waveforms and the abnormal ECG recordings had six different disease conditions. The classifier was able to recognize these waveforms with 70.9% accuracy.

The Study [6] suggested that the role of the ANN, which uses non-linear statistics for pattern recognition in predicting one-year liver disease-related mortality using information available during initial clinical evaluation. MLP with sigmoidal feed-forward and standard Back-Propagation (BP) learning algorithm was employed as a forecaster for bacteria-antibiotic interactions of infectious diseases. Comparing ANN ensembles with logistic regression models we found the former approach to be better in terms of ROC area and calibration assessments. Both ANN and logistic regression models showed intra-method variations, as a result of training the models with different parts of the study population. This variation was larger for the ANN ensemble models [7].

The studies of application of ARTMAP in medicine include classification of cardiac arrhythmias [8] and treatment selection for schizophrenic and unipolar depressed in-patients [9]. Another study revealed that fully connected feed forward MLP and BP learning rule, were able to predict patients with colorectal cancer more accurately than clinicopathological methods. They indicate that NN predict the patients' survival and death very well compared to the surgeons. The study [10] presents their study for the diagnosis of Acute Myocardial Infarction. The results show that NN performance is 0.84 and 0.85 under ROC.

A neural network can provide a considerable improvement in the diagnosis of early acute allograft rejection, though further development work is needed before this becomes a routine diagnostic tool. The selection of cases used to train the network is crucial to the quality of its performance. There is scope to improve the system further by incorporating clinical information[11]. Another methodology, which is based on ANNs, has been developed for the detection of ischaemic episodes in long-duration ECG recordings [12] . The raw ECG signal containing the ST segment

and the T wave of each beat is the input to the beat-classification system, and the output is the classification of the beat. The use of the ANN model as a data mining tool is very promising for new knowledge discovery in nephrology, to model complex behaviour of different molecular markers of dialysis treatment and for online treatment monitoring. [13]. The Study [14], presented a fully automated method using ANNs were compared with the clinical interpretation. The neural networks trained with both perfusion and ECG-gated images had a 4–7% higher specificity compared with the corresponding networks using perfusion data only, in four of five segments compared at the same level of sensitivity. The addition of functional information from ECG-gated MPS is of value for the diagnosis of myocardial infarction using an automated method of interpreting myocardial perfusion images.

3. THE PROPOSED MODEL

3.1 Patient Data

The data for this study have been collected from 50 patients who have symptoms of stroke disease. The data have been standardized so as to be error free in nature. All the fifty cases are analyzed after careful scrutiny with the help of the Physicians. Table-1 below shows the various input parameters for the prediction of stroke disease.

Sl.No.	Parameters
1	Age
2	Sex
3	Pre-stroke mobility
4	Hypertension
5	Diabetes Mellitus
6	Myocardial infarction
7	Cardiac failure
8	Atrial fibrillation
9	Smoking
10	High blood cholesterol
11	Alcohol abuse
12	Weakness of Left Arm and Left leg
13	Weakness of Right Arm and Right leg
14	Slurring of Speech
15	Giddiness
16	Headache
17	Vomiting
18	Memory Deficits
19	Swallowing Difficulties
20	Loss of Vision
21	Isolated vertigo
22	Transient Double Vision
23	Sudden difficulty in walking , dizziness or loss of balance
24	Hand / Leg numbness
25	Transient loss of consciousness

TABLE 1: Input Parameters for Prediction of Stroke

3.2 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[15]. Feature selection methods are used to identify input columns that are not useful and do not contribute significantly to the performance of neural network. In this study, Backward stepwise method is used for input feature selection. The removal of insignificant inputs will improve the generalization performance of a neural network. 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. Table 2 shows the finalized input parameters after applying feature selection method.

| Input column name	Code	Importance %
Hypertensive	X1	1.626103
Diabetes	X2	4.229285
Myocardial	X3	0.043249
Cardiac failure	X4	0.001659
Atrial fibrillation	X5	0.034991
Smoking	X6	2.061142
Blood cholesterol	X7	8.831646
left arm&leg	X8	19.209636
Right arm &leg	X9	2.832501
Slurring	X10	1.776497
Giddiness	X11	3.64891
Headache	X12	15.646755
Vomiting	X13	0.535259
memory deficits	X14	1.485701
Swallowing	X15	5.224413
Vision	X16	7.366008
Double vision	X17	1.13867
Vertigo	X18	15.471004
Numbness	X19	0.136173
Dizziness	X20	8.700397

TABLE 2: Percentage of Importance of Input Data

3.3 Neural Network   Architecture
The architecture of the neural network used in this study is the multilayered feed-forward network architecture with 20 input nodes, 10 hidden nodes, and 10 output nodes. The number of input nodes are determined by the finalized data; the number of hidden nodes are determined through trial and error; and the number of output nodes are represented as a range showing the disease classification. The most widely used neural-network learning method is the BP algorithm [16]. Learning in a neural network involves modifying the weights and biases of the network in order to minimize a cost function. The cost function always includes an error term a measure of how close the network's predictions are to the class labels for the examples in the training set. Additionally, it may include a complexity term that reacts a prior distribution over the values that the parameters can take.

The activation function considered for each node in the network is the binary sigmoidal function defined (with σ = 1) as output = $1/(1+e^{-x})$, where x is the sum of the weighted inputs to that particular node. This is a common function used in many BPN. This function limits the output of all nodes in the network to be between 0 and 1. Note all neural networks are basically trained until the error for each training iteration stopped decreasing. Figure 1 shows the architecture of the specialized network for the prediction of stroke disease. The complete set of final data (20 inputs) are presented to the generic network, in which the final diagnosis corresponds to output units.
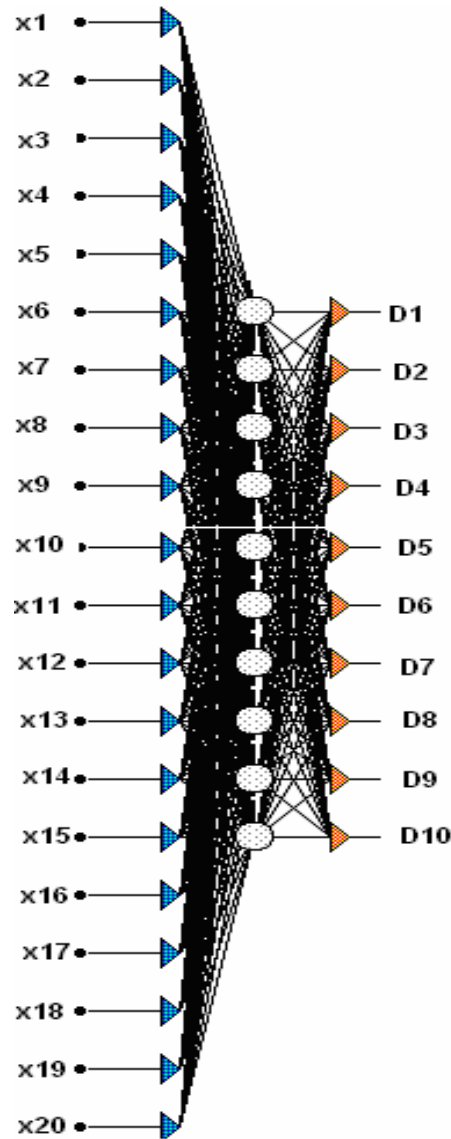
FIGURE 1: Artificial Neural Network Architecture for the prediction of stroke disease

The net inputs and outputs of the j hidden layer neurons can be calculated as follows

$$net_j^h = \sum_{t=1}^{N+1} W_{ji} x_i$$

$$y_j = f(net_j^h)$$

Calculate the net inputs and outputs of the k output layer neurons are

$$net_k^o = \sum_{j=1}^{J+1} V_{kj} y_j$$

$$Z_k = f(net_k^o)$$

Update the weights in the output layer (for all k, j pairs)

$$v_{kj} \leftarrow v_{kj} + c\lambda(d_k - Z_k)Z_k(1 - Z_k)y_j$$

Update the weights in the hidden layer (for all i, j pairs)

$$w_{ji} \leftarrow w_{ji} + c\lambda^2 y_j (1-y_j) x_i (\sum_{k=1}^{k} (d_k - z_k) z_k (1-Z_k) v_{kj})$$

Update the error term

$$E \leftarrow E + \sum_{k=1}^{k} (d_k - z_k)^2$$

and repeat from Step 1 until all input patterns have been presented (one epoch). If E is below some predefined tolerance level, then Stop. Otherwise, reset $E = 0$, and repeat from Step 1 for another epoch.

The inputs to the models were 20 variable training parameters and the output indicated the point at which training should stop. The following are the results generated from the input given to the neural network after going through the process of careful training, validation and testing using Neuro Intelligence tool. Table 3 shows the various categories of Stroke diseases and their classification.

Output	Code
TIA	D1
Left Hemiplegia	D2
Right Hemiplegia	D3
Dysphasia	D4
Monoplegia	D5
Left Hemianopia	D6
Aphasia	D7
Right Hemianesthesia	D8
Dysphagia	D9
Quadruplegia	D10

TABLE 3: Output Classification

4. RESULTS AND DISCUSSION

The Data have been analyzed using Neuro-intelligence tool [17].During analysis, the column type is identified. During data analysis, the last column is considered as the target one and other columns will be considered as input columns. The dataset is divided in to training set, validation set and test set.

Sl.No	Data Partition set	Records	Percentage
1.	Training set	34	68%
2.	Validation set	8	16%
3.	Test set	8	16%
4.	Ignored set	0	0%
	Total	50	100%

TABLE 4: Data Partition Set

Training a neural network is the process of setting the best weights on the inputs of each of the units. The goal is to use the training set to produce weights where the output of the network is as close to the desired output as possible for as many of the examples in the training set as possible. Also it has been proved that Genetic Algorithm and Back-Propagation neural network hybrids in selecting the input features for the neural network reveals the performance of ANN can be improved by selecting good combination of input variables [18]. The training set is a part of the input dataset used for neural network training, i.e. for adjustment of network weights**.** The validation set is a part of the data are used to tune network topology or network parameters other than weights. For example, it is used to define the number of units of to detect the moment when the neural network performance started hidden to deteriorate. To choose the best network (i.e. by changing the number of units in the hidden layer) the validation set is used. The test set is a part

of the input data set used to test how well the neural network will perform on new data. The test set is used after the network is ready (trained), to test what errors will occur during future network application. This set is not used during training and thus can be considered as consisting of new data entered by the user for the neural network application.

Figure 2 shows the various data set errors with respect to training set, validation set and the best network. After training through repeated iterations it reaches the level of best network.
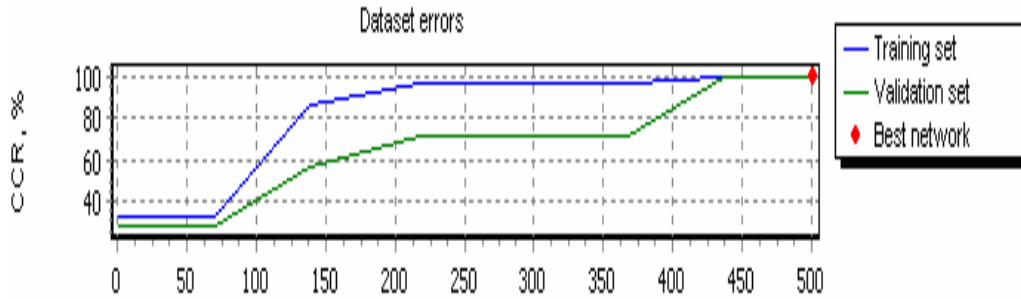

FIGURE 2: Data Set Errors

In the diagnosis of stroke , it is not always possible to make a clear-cut determination of disease, because of variability in the diagnostic criteria, age at onset, and differential presentation of disease. Mapping such diseases is greatly simplified if the data present a homogeneous genetic trait and if disease status can be reliably determined. Here, we present an approach to determination of disease status, using methods of artificial neural-network analysis. The Network errors have been shown graphically in figure 3. After 150 iterations, the network error has been decreased and from 300 iterations it is almost 0.
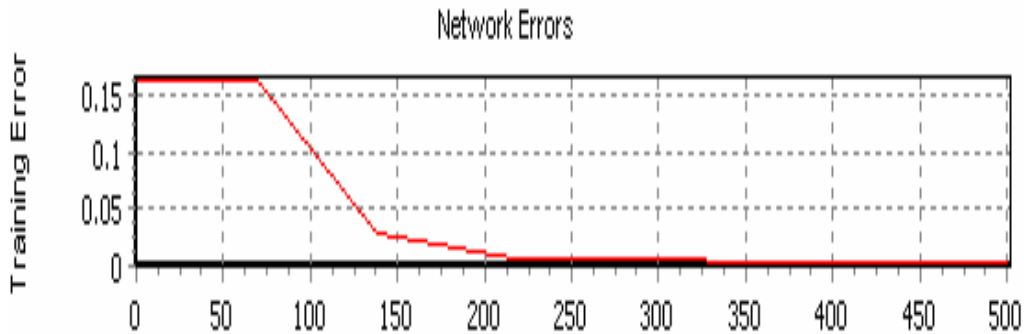
FIGURE 3: Network Errors vs. Training Error

The trained network has been tested with a test set, in which the outcomes are known but not provided to the network, to see how well the training has worked.. We used diagnostic criteria and disease status to train a neural network to classify individuals as "affected" by several categories of stroke as given below .

The analysis shows clearly that 32% of the respondents have the symptoms of Left Hemiplegia; 14% each have the symptoms of TIA and Right Hemiplegia respectively; 10% of the patients have the symptoms of Dysphasia and 6% are suffering from Monoplegia. 8% each have the symptoms of Left Hemianopia and Aphasia. In the meantime, 4% have the symptoms of Right Hemianesthesia. 2% each have the symptoms of Dysphagia and Quadruplegia respectively and is diagrammatically depicted in figure 4.
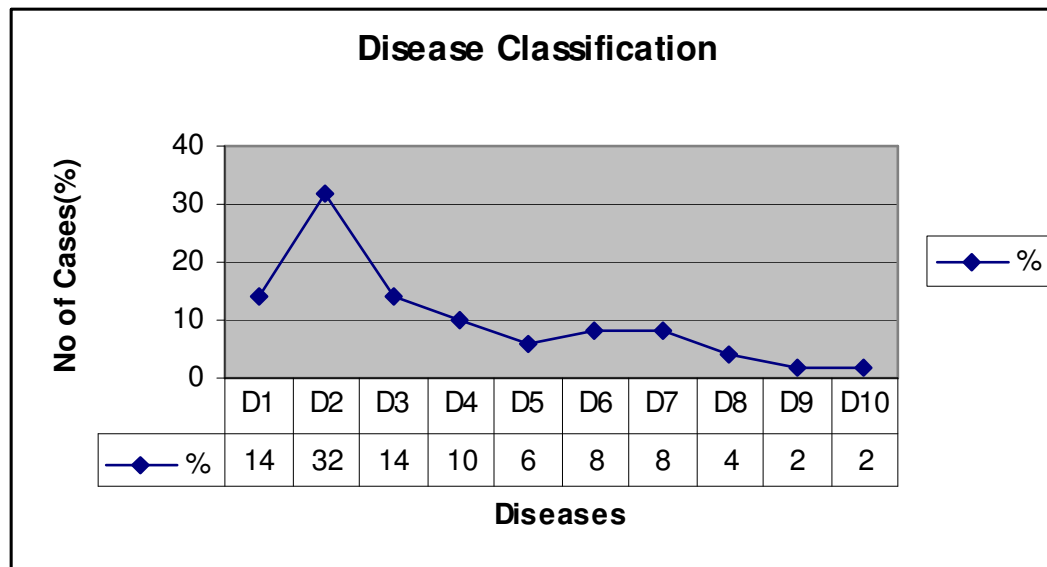
FIGURE 4: Various Stroke Diseases vs. Number of Cases

5. CONCLUSION

Neural networks have been proposed as useful tools in decision making in a variety of medical applications. Neural networks will never replace human experts but they can help in screening and can be used by experts to double-check their diagnosis. In general, results of disease classification or prediction task are true only with a certain probability. This work described here shows that the prediction of risk from stroke gives best results on the dataset used. The results generated by this system have been verified with the physicians and are found correct. This ANN model helps the doctors to plan for a better medication and provide the patient with early diagnosis as it performs reasonably well even without retraining.   In conclusion, when the ANN was trained and tested after optimizing the input parameters, the overall predictive accuracy obtained was 89%.

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