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# Editorial Preface

This is the fourth issue of volume four of International Journal of Biometric and Bioinformatics (IJBB). The Journal is published bi-monthly, with papers being peer reviewed to high international standards. The International Journal of Biometric and Bioinformatics are not limited to a specific aspect of Biology but it is devoted to the publication of high quality papers on all division of Bio in general. IJBB intends to disseminate knowledge in the various disciplines of the Biometric field from theoretical, practical and analytical research to physical implications and theoretical or quantitative discussion intended for academic and industrial progress. In order to position IJBB as one of the good journal on Bio-sciences, a group of highly valuable scholars are serving on the editorial board. The International Editorial Board ensures that significant developments in Biometrics from around the world are reflected in the Journal. Some important topics covers by journal are Bio-grid, biomedical image processing (fusion), Computational structural biology, Molecular sequence analysis, Genetic algorithms etc.

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# Gene Expression Based Acute Leukemia Cancer Classification: a Neuro-Fuzzy Approach

**B. B. M. Krishna Kanth** bbkkanth@yahoo.com
*Research Scholar S.R.T.M.University*
*Nanded, Maharastra, India*

**U. V. Kulkarni** kulkarniuv@yahoo.com
*Dean of Academics and Head Department*
*of Computer Science S.R.T.M.University,*
*Nanded,Maharastra, India*

**B. G. V. Giridhar** murarihamlet@rediffmail.com
*Assistant Professor Department of Endocrinology*
*Andhra Medical College Visakhapatnam,*
*A.P, India*

## Abstract

In this paper, we proposed the Modified Fuzzy Hypersphere Neural Network (MFHSNN) for the discrimination of acute lymphoblastic leukemia (ALL) and acute myeloid leukemia (AML) in leukemia dataset. Dimensionality reduction methods, such as Spearman Correlation Coefficient and Wilcoxon Rank Sum Test are used for gene selection. The performance of the MFHSNN system is encouraging when benchmarked against those of Support vector machine (SVM) and the K-nearest neighbor (KNN) classifiers. A classification accuracy of 100% has been achieved using the MFHSNN classifier using only two genes. Furthermore, MFHSNN is found to be much faster with respect to training and testing time.

**Keywords:** gene expression data, cancer classification, AAL/AML, membership function, hypersphere

## 1. INTRODUCTION

Microarrays [1], also known as gene chips or DNA chips, provide a convenient way of obtaining gene expression levels for a large number of genes simultaneously. Each spot on a microarray chip contains the clone of a gene from a tissue sample. Some mRNA samples are labeled with two different kinds of dyes, for example, Cy5 (red) and Cy3 (blue). After mRNA interacts with the genes, i.e., hybridization, the color of each spot on the chip will change. The resulted image reflects the characteristics of the tissue at the molecular level. Microarrays can thus be used to help classify and predict different types of cancers. Traditional methods for diagnosis of cancers are mainly based on the morphological appearances of the cancers; however, sometimes it is extremely difficult to find clear distinctions between some types of cancers according to their appearances. Hence the microarray technology stands to provide a more quantitative means for cancer diagnosis. For example, gene expression data have been used to obtain good results in the classifications of Lymphoma, Leukemia [2], Breast cancer, and Liver cancer etc. It is challenging to use gene expression data for cancer classification because of the following two special aspects of gene expression data. First, gene expression data are usually very high dimensional. The dimensionality ranges from several thousands to over ten thousands. Second, gene expression data sets usually contain relatively small numbers of samples, e.g., a few tens. If we treat this pattern recognition problem with supervised machine learning approaches, we need to deal with the shortage of training samples and high dimensional input features.

Recent approaches to solve this problem include unsupervised methods, such as Clustering [3] and Self-Organizing Maps (SOM) [4] and supervised methods, such as Support Vector Machines (SVM)[5], Multi-Layer Perceptrons (MLP) [6], Decision Trees (DT) [7] and K-Nearest Neighbor(KNN) [8, 9]. Su et al [10] employs modular neural networks to classify two types of acute leukemia's and the best 75% correct classification was reached. Xu et al [11] adopted the ellipsoid ARTMAP to analyze the AAL/AML data set and the best result was 97.1%. But most of the current methods in microarray analysis can not completely bring out the hidden information in the data. Meanwhile, they are generally lacking robustness with respect to noisy and missing data. Some studies have shown that a small collection of genes [12] selected correctly can lead to good classification results [13]. Therefore gene selection is crucial in molecular classification of cancer. Although most of the algorithms mentioned above can reach high prediction rate, any misclassification of the disease is still intolerable in acute leukemia's treatment. Therefore the demand of a reliable classifier which gives 100% accuracy in predicting the type of cancer therewith becomes urgent.

In this paper, we apply a robust MFHSNN classifier which is an extension of Fuzzy Hypersphere Neural Network (FHSNN) proposed by Kulkarni et al [14] to the problem of cancer classification based on gene expression data. To reduce the dimensionality of genes correlation method such as Spearman Correlation Coefficient and statistical method such as Wilcoxon Rank Sum Test are used. The MFHSNN utilizes fuzzy sets as pattern classes in which each fuzzy set is a union of fuzzy set hyperspheres. The fuzzy set hypersphere is an n-dimensional hypersphere defined by a center point and radius with its membership function. We first experiment the classifier with 38 leukemia samples and test the classifier with another 34 samples to obtain the accuracy rate. Meanwhile, this study reveals that the classification result is greatly affected by the correlativity with the class distinction in the data set. The remainder of the paper is organized as follows. The gene selection methods for choosing effective predictive genes in our work are introduced in Section 2. Then Sections 3 gives a brief introduction for the architecture of the MFSHNN, followed by its learning algorithm in section 4. Section 5 examines the experimental results of the classifiers operated on leukemia data set. Conclusions are made in Section 6.

## 2. GENE SELECTION METHODS

Among the large number of genes, only a small part may benefit the correct classification of cancers. The rest of the genes have little impact on the classification. Even worse, some genes may act as noise and undermine the classification accuracy. Hence, to obtain good classification accuracy, we need to pick out the genes that benefit the classification most. In addition, gene selection is also a procedure of input dimension reduction, which leads to a much less computation load to the classifier. Maybe more importantly, reducing the number of genes used for classification can help researchers put more attention on these important genes and find the relationship between the genes and the development of the cancer.

### 2.1. Correlation Analysis for Gene Selection

In order to score the similarity of each gene, an ideal feature vector [15] is defined. It is a vector consisting of 0's in one class (ALL) and 1's in other class (AML). It is defined as follows:

$$ideal_i = (0,0,0,0,0,0,1,1,1,1,1,1) \qquad (1)$$

The ideal feature vector is highly correlated to a class. If the genes are similar with the ideal vector (the distance from the ideal vector and the gene is small), we consider that the genes are informative for classification. The similarity of $g_i$ and $g_{ideal}$ using similarity measure such as the Spearman coefficient is defined as follows

$$\text{SC}= 1-\frac{6\sum_{i=1}^{n}\left(\text{ideal}_i - g_i\right)^2}{n\times\left(n^2-1\right)} \tag{2}$$

Where *n* is the number of samples; $g_i$ is the $i_{th}$ real value of the gene vector and $\text{ideal}_i$ is the corresponding $i_{th}$ binary value of the ideal feature vector.

### 2.2. Wilcoxon Rank-Sum Test (WRST) for Gene Selection

The Wilcoxon rank-sum test [16, 17] is a big category of non-parametric tests. The general idea is that, instead of using the original observed data, we can list the data in the value ascending order, and assign each data item a rank, which is the place of the item in the sorted list. Then, the ranks are used in the analysis. Using the ranks instead of the original observed data makes the rank sum test much less sensitive to outliers and noises than the classical (parametric) tests [18]. The WRST organizes the observed data in value ascending order. Each data item is assigned a rank corresponding to its place in the sorted list. These ranks, rather than the original observed values are then used in the subsequent analysis. The major steps in applying the WRST are as follows:

(i) Merge all observations from the two classes and rank them in value ascending order.

(ii) Calculate the Wilcoxon statistics by adding all the ranks associated with the observations from the class with a smaller number of observations.

## 3. MODIFIED FUZZY HYPERSPHERE NEURAL NETWORK CLASSIFIER

The MFHSNN consists of four layers as shown in Figure 1(a). The first, second, third and fourth layer is denoted as $F_R$, $F_M$, $F_N$ and $F_O$ respectively. The $F_R$ layer accepts an input pattern and consists of n processing elements, one for each dimension of the pattern. The $F_M$ layer consists of q processing nodes that are constructed during training and each node represents hypersphere fuzzy set characterized by hypersphere membership function. The processing performed by each node of $F_M$ layer is shown in Figure 1(b). The weights between $F_R$ and $F_M$ layer represent centre points of the hyperspheres. As shown in Figure 1(b), $C_j = \left(c_{j1}, c_{j2}, c_{j3}.........c_{jn}\right)$ represents center point of the hypersphere $m_j$. In addition to this each hypersphere takes one more input denoted as threshold T, which is set to one and the weight assigned to this link is $\xi_j$. The $\xi_j$ represents radius of the hypersphere $m_j$, which is updated during training. The center points and radii of the hyperspheres are stored in matrix *C* and vector $\xi$ respectively. The maximum size of hypersphere is bounded by a user defined value $\lambda$, where $0 \le \lambda \le 1$. The $\lambda$ is called as growth parameter that is used for controlling maximum size of the hypersphere and it puts maximum limit on the radius of the hypersphere. Assuming the training set defined as $R \in \left\{R_h \middle| h = 1,2,.....P\right\}$, where $R_h = \left(r_{h1}, r_{h2}, r_{h3}.....r_{hn}\right) \in I^n$ is the $h_{th}$ pattern the, membership function of the hypersphere node $m_j$ is $m_j\left(R_h, C_j, \zeta_j\right) = 1 - f\left(l, \zeta_j, \gamma\right)$ (3)

where $f(\ )$ is three-parameter ramp threshold function defined as

$$f\left(l, \zeta_j, \gamma\right) = \begin{bmatrix} 0, \ if \ \ (0 \le l \le \zeta_j) \\ (l - \zeta_j)\gamma, \ if \ \ (\zeta_j \le l \le 1) \\ 1, \ if \ \ (l \ge 1) \end{bmatrix} \tag{4}$$

and the argument $l$ is defined as,

$$l = \left( \sum_{i=1}^{n} \left( c_{ji} - r_{hi} \right)^{2} \right)^{1/2} \tag{5}$$

The membership function returns $m_j$ =1, if the input pattern $R_h$ is contained by the hypersphere. The parameter $\gamma$, $0 \le \gamma \le 1$, is a sensitivity parameter, which governs how fast the membership value decreases $R_h$ outside the hypersphere when the distance between $R_h$ and $C_j$ increases.

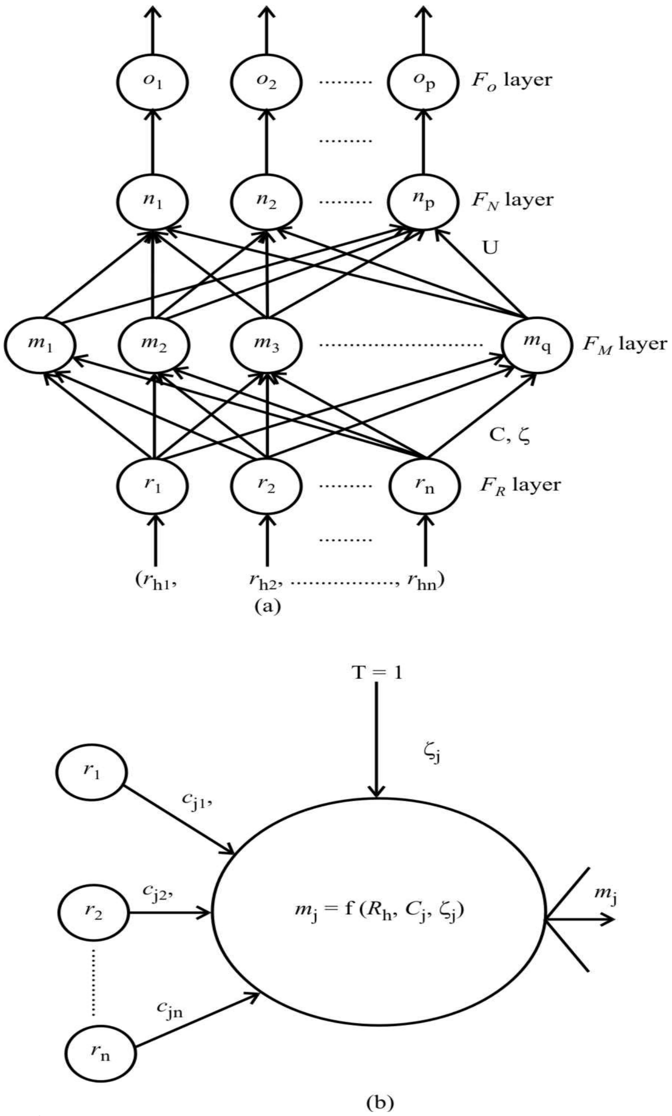

**FIGURE 1: (a)** Modified Fuzzy Hypersphere Neural Network **(b)** Implementation of Fuzzy Hypersphere

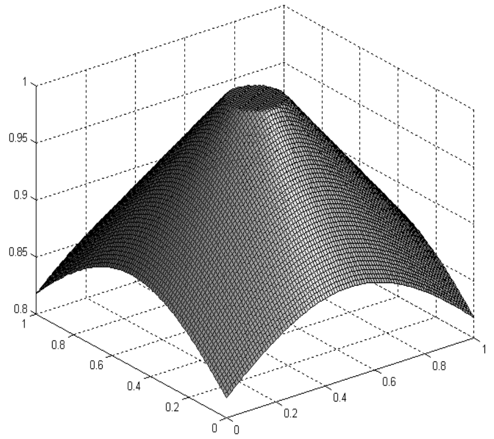

**FIGURE 2:** Plot of Modified Fuzzy Hypersphere Membership Function for $\gamma = 1$

The sample plot of membership function for MFHSNN with centre point [0.5 0.5] and radius equal to 0.3 is shown in Figure 2. It can be observed that the membership values decrease steadily with increasing distance from the hypersphere.

Each node of $F_N$ and $F_O$ layer represents a class. The $F_N$ layer gives fuzzy decision and output of $k_{th}$ $F_N$ node represents the degree to which the input pattern belongs to the class $n_k$ .The weights assigned to the connections between $F_M$ and $F_N$ layers are binary values that are stored in matrix $\mathrm{U}$ and updated during learning as

$$u_{jk} = \begin{cases} 1 \text{ if } m_j \text{ is a hypershere of class } n_k \\ 0 \text{ otherwise} \end{cases} \qquad (6)$$

For $k = 1, 2, 3, ..p$ and $j = 1, 2, 3, ...q$

where $m_j$ is the $j_{th}$ $F_M$ node and $n_k$ is the $k_{th}$ $F_N$ node. Each $F_N$ node performs the union of fuzzy values returned by the fuzzy set hyperspheres of same class, which is described by equation (7).

$$n_k = \max_{j=1}^{q} m_j u_{jk} \text{ for } k = 1, 2, .....p \qquad (7)$$

Each $F_O$ node delivers non-fuzzy output, which is described by equation (8).

$$o_k = \begin{cases} 0 \text{ if } \mathrm{n}_k \leq T \\ 1 \text{ if } \mathrm{n}_k = T \end{cases} \text{ for } k = 1, 2, 3, ....p \qquad (8)$$

Where $T = \max(n_k)$ for $k = 1, 2, 3, ....p$

## 4. MFHSNN Learning Algorithm

The supervised MFHSNN learning algorithm for creating fuzzy hyperspheres in hyperspace consists of three steps

1. Creation of hyperspheres
2. Overlap test, and
3. Removing overlap.

These three steps are described below in detail.

### 4.1 Creation of Hyperspheres

Given the $h_{th}$ training pair $(R_h, d_h)$ find all the hyperspheres belonging to the class $d_h$. These hyperspheres are arranged in ascending order according to the distances between the input pattern and the center point of the hyperspheres. After this following steps are carried sequentially for possible inclusion of input pattern $R_h$ .

Step 1: Determine whether the pattern $R_h$ is contained by any one of the hyperspheres. This can be verified by using modified fuzzy hypersphere membership function defined in equation (3). If $R_h$ is contained by any of the hypersphere then it is included, therefore in the training process all the remaining steps are skipped and training is continued with the next training pair.

Step 2: If the pattern $R_h$ falls outside the hypersphere, then the hypersphere is expanded to include the pattern if the expansion criterion is satisfied. For the hypersphere $m_j$ to include $R_h$ the following constraint must be met defined as:

$$\left( \sum_{i=1}^{n} \left( c_{ji} - r_{hi} \right)^2 \right)^{1/2} \le \lambda \tag{9}$$

If the expansion criterion is met then the pattern $R_h$ is included as

$$\zeta_j = \left( \sum_{i=1}^{n} \left( c_{ji} - r_{hi} \right)^2 \right)^{1/2} \tag{10}$$

Step 3: If the pattern $R_h$ is not included by any of the above steps then new hypersphere is created for that class, which is described as

$$C_{new} = R_h \text{ and } \zeta_{new} = 0 \tag{11}$$

### 4.2 Overlap Test

The learning algorithm allows overlap of hyperspheres from the same class and eliminates the overlap between hyperspheres from different classes. Therefore, it is necessary to eliminate overlap between the hyperspheres that represent different classes. Overlap test is performed as soon as the hypersphere is expanded by step 2 or created in step 3.

(a)Overlap test for step 2: Let the hypersphere $m_u$ is expanded to include the input pattern $R_h$ and expansion has created overlap with the hypersphere $m_v$, which belongs to other class. Suppose $C_u = (x_1, x_2 .......x_n)$ and $\zeta_u$ represents center point and radius of the expanded hypersphere and $C_v = \left[ x_1^{'}, x_2^{'} ........x_n^{'} \right]$ and $\zeta_v$ , are centre point and radius of the hypersphere of other class as depicted in Figure 3(a). Then if

$$\left( \sum_{i=1}^{n} \left( c_{ui} - c_{vi} \right)^2 \right)^{1/2} \le \zeta_u + \zeta_v \tag{12}$$

means those hyperspheres from separate classes are overlapping.

(b) Overlap test for step 3: If the created hypersphere falls inside the hypersphere of other class means there is an overlap. Suppose $m_p$ represents created hypersphere to include the input pattern $R_h$ and $m_q$ represents the hypersphere of other class as shown in Figure 4(a). The presence of overlap in this case can be verified using the membership function defined in the equation

(3). If $m_p\left(R_h, C_p, \zeta_p\right) = m_q\left(R_h, C_q, \zeta_q\right) = 1$ means two hyperspheres from different classes are overlapping.

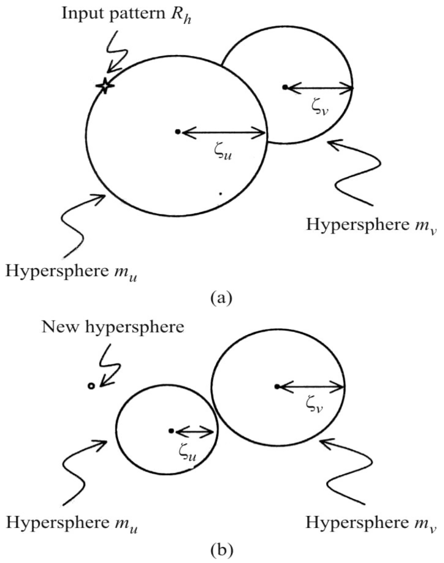

**FIGURE 3: (a)** Status of the hyperspheres before removing an overlap in step 2. **(b)** Status of the hyperspheres after removing an overlap in step 2

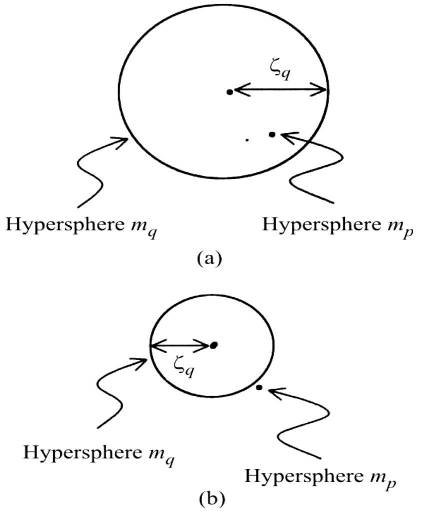

**FIGURE 4: (a)** Status of the hyperspheres before removing an overlap in step 3. **(b)** Status of the hyperspheres after removing an overlap in step 3

### 4.3 Removing Overlap

If step 2 has created overlap of hyperspheres from separate classes then overlap is removed by restoring the radius of just expanded hypersphere. Let, $m_u$ be the expanded hypersphere then it is contracted as $\zeta_u^{new} = \zeta_u^{old}$ (13)

and new hypersphere is created for the input pattern as described by equation (11). This situation is shown in Figure 3(b). If the step 3 creates overlap then it is removed by modifying the hypersphere of other class. Let $C_p = \left(x_1, x_2 .......x_n\right)$ and $\zeta_p$ represents centre point and radius of the created hypersphere, $C_q = \left[ x_1^{'}, x_2^{'} ........ x_n^{'} \right]$ and $\zeta_q$ are center point and radius of the hypersphere of other class. Then overlap is removed as

$$\zeta_q^{new} = \left( \sum_{i=1}^{n} \left( c_{pi} - c_{qi} \right)^2 \right)^{1/2} - \partial \qquad (14)$$

where $\partial$ is a small number selected just enough to remove the overlap. In our experiments the value of $\partial$ chosen is 0.0001. Hence, the hypersphere $m_q$ is contracted just enough to remove the overlap as shown in Figure 4(b).

## 5. EXPERIMENTAL RESULTS

Dataset that we have used is a collection of expression measurements reported by Golub et al [2]. Gene expression profiles have been constructed from 72 people who have either acute lymphoblastic leukemia (ALL) or acute myeloid leukemia (AML). Each person has submitted one sample of DNA microarray, so that the database consists of 72 samples. Each sample is composed of 7129 gene expressions, and finally the whole database is a 7129 X 72 matrix. The number of training samples in AAL/AML dataset is 38 which of them contain 27 samples of AAL class and 11 samples of AML class; here we randomly applied the training samples to the MFSHNN classifier. The number of testing samples is 34 where 20 samples belong to AAL and remaining 14 samples belongs to AML class respectively. This well-known dataset often serves as bench mark for microarray analysis methods. Before the classification, we need to find out informative genes (features) that are related to predict the cancer class out of 7129.

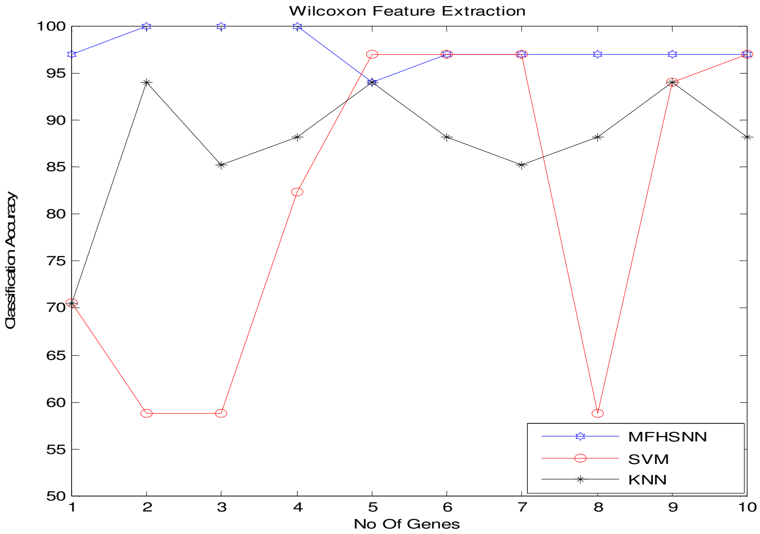

**FIGURE 5:** Comparison of classification accuracy among SVM, KNN(k= 5 neighbors) and MFHSNN classifiers with all the top 10 genes of Leukemia test data set selected by using Wilcoxon Rank Sum Test .

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Figures 5 and 6 shows the comparison of the classification performance with respect to the features and the classifiers. Spearman correlation coefficient and Wilcoxon rank sum test gene selection techniques achieved 100% prediction accuracy on the test data set using MFHSNN classifier. It should also be noted that this high classification accuracy has been obtained using only two genes with Gene id's 4847 and 1882 which are selected by using Spearman correlation and Wilcoxon rank sum test gene selection methods.

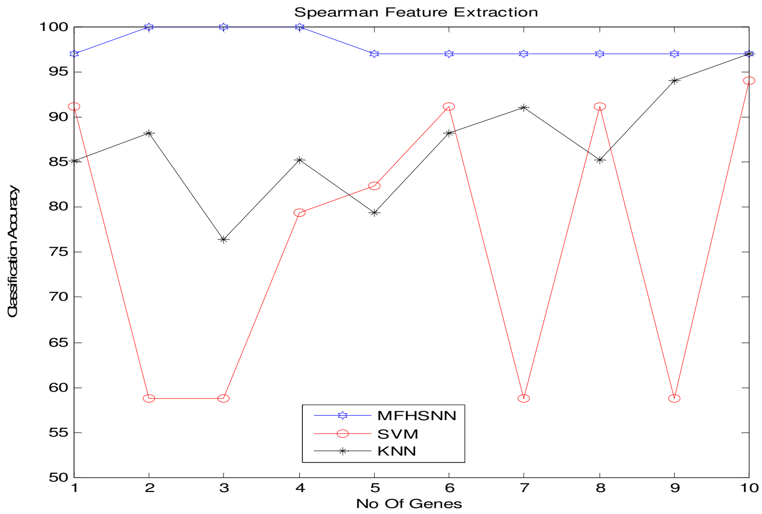

**FIGURE 6:** Comparison of classification accuracy among SVM, KNN (k= 5 neighbors) and MFHSNN classifiers of Leukemia test data set by using Spearman Correlation Coefficient**.**

But traditional classifiers such as Support vector machine and K-nearest neighbor produced the best accuracy of 97.1% using all the top 10 genes. As shown from Table 1 the average training time and testing time of MFHSNN classifier is in the range of 0.25 -0.39 seconds which is very fast compared to any other classifier published so far. Meanwhile the average training and testing time of SVM and KNN classifiers is around 2.60-3.5 seconds respectively which is very slow comparative to MFHSNN classifier.

| **Classifier** | **Average Training time (seconds)** | **Average Testing time (seconds)** |
|---|---|---|
| MFHSNN | 0.25 | 0.39 |
| KNN | 2.60 | 2.65 |
| SVM | 3.20 | 3.50 |

**TABLE 1:** Comparison of training and testing time for the classifiers

The average classification accuracy of the three classifiers with all the 10 genes is shown in Table 2. The highest average classification accuracy achieved by MFHSNN is 97.94% which clearly dominates the other classifiers.

| **Gene selection\Classifier** | **MFHSNN** | **KNN** | **SVM** |
|---|---|---|---|
| Wilcoxon Rank Sum Test | 97.647 | 87.633 | 81.176 |
| Spearman Coefficient | 97.941 | 87.045 | 76.471 |

**TABLE 2:** Average classification accuracy

| Gene Rank | Spearman Correlation Coefficient | Wilcoxon Rank Sum Test |
|---|---|---|
| 1 | 4847 | 4847 |
| 2 | 1882 | 1882 |
| 3 | 3320 | 3320 |
| 4 | 6218 | 6218 |
| 5 | 1834 | 760 |
| 6 | 760 | 1834 |
| 7 | 2020 | 1745 |
| 8 | 5039 | 2020 |
| 9 | 1745 | 4499 |
| 10 | 4499 | 5039 |

**TABLE 3:** List of top 10 ranked genes (values are the Gene ids in the columns)

Table 3 shows the list of top 10 ranked genes that are chosen as the features of the input patterns to the classifiers. It is found that these top 10 genes selected by the gene selection methods are very informative features for the accurate prediction of cancer.

## 6. CONCLUSIONS

In order to predict the class of cancer, we have demonstrated the effectiveness of the MFHSNN classifier on Leukemia data set using an informative genes extracted by methods based on their correlation with the class distinction, and statistical analysis. Experimental results show that the MFHSNN classifier is the most effective in classifying the type of leukemia cancer using only two of the most informative genes. MFHSNN yields 100% recognition accuracy and is well suited for the AAL/AML classification in cancer treatment. By comparing the performance with previous publications that used the same dataset, we confirmed that the proposed method provided the competitive, state-of-the-art results. Under the same context, it not only leads to better classification accuracies, but also has higher stability and speed. The training and testing time of MFSHNN is less than 0.4 seconds which will further drastically reduce if the proposed classifier is implemented in hardware. Our future work will focus on exploring unsupervised methods such as clustering combined with fuzzy classifier and the corresponding feature selection methods. Besides, we will further validate the performance of MFSHNN on more data sets.

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# Bimodal Biometric Person Authentication System Using Speech and Signature Features

**Prof. M.N. Eshwarappa** jenutc@rediffmail.com
*Assistant professor Department of Telecommunication*
*Engineering, Sri Siddhartha Institute of Technology,*
*Tumkur-572101, Karnataka, India*

**Prof. (Dr.) Mrityunjaya V. Latte** mvlatte@rediffmail.com
*Principal and Professor Department of Electronics*
*and Communication Engineering, JSS*
*Academy of Technical Education,*
*Bangalore-560060, Karnataka, India*

## Abstract

Biometrics offers greater security and convenience than traditional methods of person authentication. Multi biometrics has recently emerged as a means of more robust and efficient person authentication scheme. Exploiting information from multiple biometric features improves the performance and also robustness of person authentication. The objective of this paper is to develop a robust bimodal biometric person authentication system using speech and signature biometric features. Speaker based unimodal system is developed by extracting Mel Frequency Cepstral Coefficients (MFCC) and Wavelet Octave Coefficients of Residues (WOCOR) as feature vectors. The MFCCs and WOCORs from the training data are modeled using Vector Quantization (VQ) and Gaussian Mixture Modeling (GMM) techniques. Signature based unimodal system is developed by using Vertical Projection Profile (VPP), Horizontal Projection Profile (HPP) and Discrete Cosine Transform (DCT) as features. A bimodal biometric person authentication system is then built using these two unimodal systems. Experimental results show that the bimodal person authentication system provides higher performance compared with the unimodal systems. The bimodal system is finally evaluated for its robustness using the noisy data and also data collected from the real environments. The robustness of the bimodal system is more compared to the unimodal person authentication systems.

**Keywords:** Biometrics, Speaker recognition, Signature verification, Multimodal biometrics.

## 1. INTRODUCTION

Biometrics is the development of statistical and mathematical methods applicable to data analysis problems in the biological sciences. Introduction of this technology brings new security approaches to computer systems. Identification and verification are the two ways of using biometrics for person authentication. Biometrics refers to the use of physical or physiological, biological or behavioral characteristics to establish the identity of an individual. These characteristics are unique to each individual and remain partially unaltered during the individual's life time [1]. Biometric security system becomes a powerful tool compared to electronics based security [2]. Any physiological and/or behavioral characteristic of human can be used as biometric feature, provided it possesses the following properties: universality, distinctiveness, permanence, collectability, circumvention, acceptability and performance [3]. The physiological biometrics related to the shape of the body. The oldest traits, that have been used for more than 100 years are fingerprints. Other examples are Face, Hand Geometry, Iris, DNA, Palm-prints and so on. Behavioral biometrics related to the behavior of a person. The first characteristic to be used, still widely used today, is the signature. Others are keystroke, Gait (way of walking), Handwriting and so on. Speech is the unique biometric feature that comes under both the categories [9]. Based on the application, selecting the right biometric is the crucial part. Unimodal biometric system, which operates using any single biometric characteristic, is affected by problems like noisy sensor data, non-universality and lack of individuality of the chosen biometric trait, absence of an invariant representation for the biometric trait. For instance, speech is a biometric feature whose characteristics will vary significantly if the person is affected by cold or in different emotional status. Some of these problems can be relived by using multimodal biometric system that consolidates evidence from multiple biometric sources. Multimodal or Multi-biometric systems utilize more than one physiological or behavioral biometrics for enrolment and identification. This work presents, such a multimodal biometric person recognition system and results obtained are compared to the unimodal biometric systems.

There are several multimodal biometric person authentication systems developed in the literature [3-7]. In 2004, A. K. Jain *et. al.*, proposed the frame work for multimodal biometric person authentication [3]. Even though some of the traits offering good performance in terms of reliability and accuracy, none of the biometrics is 100% accurate. With increasing global need for security, the demand for robust automatic person recognition systems is evident. For applications involving the flow of confidential information, the authentication accuracy of the system is always the prior concern. From this basic reason the use of multimodal biometrics are encouraged. Multi-biometrics is an integrated prototype system embedding different types of biometrics [35]. Multimodal biometric fusion and identity authentication technique help to achieve an increase in performance of identity authentication system [8]. Multimodal biometrics can reduce the probability of denial of access without sacrificing the False Acceptance Rate (FAR) performance by increasing by discrimination between the genuine and impostor classes. There are several multimodal biometric person authentication systems developed in the literature [4-8]. Applications of multi-biometrics are widely spread throughout the world. A wide variety of systems require reliable personal recognition schemes to either confirm or determine the identity of an individual requesting their services. The purpose of such schemes is to ensure that the rendered services are accessed only by a legitimate user, and not anyone else. Examples of such applications include secure access to buildings, computer systems, laptops, cellular phones and ATMs. In the absence of robust personal recognition schemes, these systems are vulnerable to the wiles of an impostor. Authentication systems built upon only one modality may not fulfill all the requirements, due to the limitations of unimodal systems. This has motivated the current interest in multimodal biometrics, in which several biometric traits are simultaneously used in order to make an identification decision. The objective of the present work is to develop a bimodal biometric system using speech and signature features to mitigate the effect of some of the limitations of unimodal biometric systems.

The present work mainly deals with the implementation of bimodal biometric system employing speech and signature as the biometric modalities. This includes feature extraction techniques and modeling techniques used in biometric system. The organization of the paper is as follows: Section 2 deals with bimodal databases used in bimodal person authentication system. Section 3 deals with unimodal biometric speech based person authentication system and section 4 deals with unimodal biometric signature based person authentication system. Bimodal biometric system by combining speaker and signature recognition systems is explained with different fusion techniques in section 5. Section 6 concludes the paper by summarizing the present work and adding few points regarding the future work.

## 2. BIMODAL DATABASES FOR PERSON AUTHENTICATION

**IITG Speech database (standard)**
Number of speakers: 30(20 male, 10 female)
Sampling frequency: 8000Hz
Sentences considered for each speaker: 4
Number of utterances of each sentence for each speaker: 24
Training session: first 16 utterances
Testing session: remaining 8 utterances of each sentence of each speaker

**IITG Signature database (standard)**
Number of writers: 30 (20 male, 10 female)
Scanner: HP Scan jet 5300C
Resolution: 300dpi (digits per inch)
Data storage: 8-bit Gray scale image
Saved format: bmp (bits mapping)
Number of sample signatures of each writer: 24
Training session: First 16 signatures of all the writers
Testing session: remaining 8 signatures of all the writers

**SSIT Speech database**
Number of speakers: 30(20 male, 10 female)
Sampling frequency: 8000Hz
Sentences considered for each speaker: 4
Number of utterances of each sentence for each speaker: 24
Training session: first 16 utterances
Testing session: remaining 8 utterances of each sentence of each speaker

**SSIT Signature database**
Number of writers: 30 (20 male, 10 female)
Scanner: HP Scan jet 5300C
Resolution: 300dpi (digits per inch)
Data storage: 8-bit Gray scale image
Saved format: bmp (bits mapping)
Number of sample signatures of each writer: 24
Training session: First 16 signatures of all the writers
Testing session: remaining 8 signatures of all the writers

## 3. UNIMODAL SPEECH BASED PERSON AUTHENTICATION SYSTEM

As any other pattern recognition systems, a speech based person authentication system also consists of three components: (1) Feature extraction, which transforms the speech waveform into a set of parameters carrying salient speaker information; (2) Pattern generation, which generates from the feature parameters a pattern representing the individual speaker: and (3) Pattern matching and classification, which compares the similarity between the extracted features and a pre-stored pattern or a number of pre-stored patterns, giving the speaker identity accordingly. There are two stages in a speaker recognition system, training and testing. In the training stage, speaker models (or patterns) are generated from the speech samples with some feature extraction and modeling techniques. In testing stage, feature vectors are generated from the speech signal with the same extraction procedure as in training. Then a classification decision is made with some matching technique. Person authentication is a binary classification task [22]. The features from the testing signal are compared with the claimed speaker pattern and a decision is made to accept or reject the claim [10]. Depending on the mode of operation, speaker recognition can be classified as text dependent recognition and text independent recognition. The text dependent recognition requires the speaker to produce speech for the same text, both during training and testing: whereas the text independent recognition does not on a specific text being spoken [11]. The present work follows text dependent speaker recognition approach.This work uses feature extraction techniques based on (1) Mel Frequency Cepstral Coefficients (MFCC) derived from Cepstral analysis of the speech signal and (2) Wavelet Octave Coefficients of Residues (WOCOR) derived from the Linear Prediction (LP) residual. The time frequency analysis of the LP residual signal is performed to obtain WOCOR [14]. WOCOR are generated by applying a pitch-synchronous wavelet transform to the residual signal. Experimental results show that the WOCOR parameters provide complementary information to the conventional MFCC features for speaker recognition [14]. The Vector Quantization (VQ) and Gaussian Mixture Modeling (GMM) are used for modeling the person information from these MFCC and WOCOR features [13-15]. State of the art system uses MFCC derived from speech as feature vectors and GMM as the modeling technique [13].

## Feature Extraction from Speech Information

The speaker information is present both in the vocal tract and excitation parameters [12]. The vocal tract system can be corresponds to processing of speech in short (10-30ms) overlapped (5-15ms) windows. The vocal tract system is assumed to be stationary within the window and it can be modeled as all-pole-filter using LP analysis [21]. The most used form of speech signal for feature extraction is the Cepstrum. Different forms of Cepstral representation include Complex Cepstral Coefficients (CCC), Real Cepstral Coefficients (RCC), Mel Frequency Cepstral Coefficients (MFCC) and Linear Prediction Cepstral Coeeficeints (LPCC). Among these the mostly used one includes MFCC. In all the Cepstral analysis techniques the vocal tract information is obtained by taking *log* over spectrum of the speech signal. The LP residual signal, though not giving the true glottal pulse, is regarded as a good representative of the excitation source. The Haar transform and Wavelet transform are applied for the multi-resolution analysis of the residual signal and the derived the feature vectors termed as Wavelet Octave Coefficients of Residues (WOCOR). WOCOR are believed to be effectively capturing the speaker specific spectro-temporal characteristics of the LP residual signal.

## Extraction of MFCC Feature Vectors

The state of the system builds a unimodal system by analyzing speech in blocks of 10-30 ms with shift of half the block size. The MFCC are used as feature vectors extracted from each of the blocks. The MFCCs from the training or enrolment data are modeled using Vector Quantization (VQ) and Gaussian Mixture Modeling (GMM) technique [12]. The MFCCs from the testing or verification data are compared with respective model to validate the identity claim of the speaker. The MFCCs represent mainly the vocal tract aspect of speaker information and hence take care of only physiological aspect of speech biometric feature. Another important physiological aspect contributing significantly to speaker characteristics is the excitation source [13]. A speech signal is obtained by the convolution of vocal parameters v(n) and excitation parameters x(n) given by equation (3.1). We can not separate these parameters in time domain. Hence we go for Cepstral domain. The Cepstral analysis used for separating the vocal tract parameter v(n) and excitation parameters x(n), from speech signal s(n).

$$s(n) = v(n) * x(n) \tag{3.1}$$

The Cepstral analysis gives the fundamental property of convolution used for separating the vocal tract parameters and excitation parameters [27]. The Cepstral Coefficients (C) of length M can be obtained by using equation (3.2).

$$C = \text{real}\ (\text{IFFT}\ (\log |\text{FFT}\ (s(n))|\ )) \tag{3.2}$$

The nonlinear scale i.e., relation between the Mel frequency ($f_{Mel}$) and physical frequency ($f_{Hz}$) is used for extracting spectral information from the speech signal by using Cepstral analysis.

$$f_{Mel} = 2595 \log_{10} \left(1 + \frac{f_{Hz}}{700}\right) \tag{3.3}$$

Using equation (3.3) we construct a spectrum with critical bands which are overlapped triangular banks i.e., we map the linear spaced frequency spectrum ($f_{Hz}$) into nonlinearly spaced frequency spectrum ($f_{Mel}$). By this we can mimic the human auditory system and based on this concept MFCC feature vectors are derived. Windowing eliminates the Gibbs oscillations, which occur by truncating the speech signal. Using equation (3.4), Hamming window coefficients are generated, with which corresponding speech of frame is scaled.

$$w(n) = 0.54 - 0.46 \cos\left(\frac{2\pi n}{N-1}\right) \tag{3.4}$$

But, due to Hamming windowing, samples present at the verge of window are weighted with lower values. In order to compensate this, we will try to overlap the frame by 50%. After windowing, we compute the log magnitude spectrum of each frame for finding the energy coefficients using equation (3.5).

$$Y(i) = \sum_{k=0}^{\frac{N}{2}} \log |S(k,m)| Hi\left(k \frac{2\pi}{N-1}\right) \tag{3.5}$$

where $H_i\left(k \frac{2\pi}{N}\right)$ is the i$^{th}$ Mel critical bank spectra and N is the number of points used to compute the discrete Fourier transform (DFT). The M number of Mel frequency coefficients computed by using discrete Cosine transforms (DCT), by using equation (3.6), which is nothing but the real IDFT of critical band filters log energy outputs.

$$C(n,m) = \left(\frac{2}{N}\right) \sum_{k=1}^{\frac{N}{2}-1} Y(k) \cos\left(k \frac{2\pi}{N} n\right) \tag{3.6}$$

Where n=1, 2, 3………..M.

The present work also takes care of channel mismatch by using the Cepstral Mean Subtraction (CMS) and the effect of different roll off from the different channels on Cepstral coefficients by Liftering procedure [21].

**Extraction of WOCOR Feature Vectors**

The Linear Predictive (LP) residual signal is adopted as a good representative of the vocal source excitation, in which the speaker specific information resides on both time and frequency domains. The resulting vocal source feature, WOCOR feature, can effectively extract the speaker-specific spectro-temporal characteristics of the LP residual signal. Particularly, with pitch-synchronous wavelet transform, the WOCOR feature set is capable of capturing the pitch-related low frequency properties. Only voiced speech is kept for subsequent processing. In the source-filter model, the excitation signal for unvoiced speech is approximated as a random noise [22, 26]. Voicing decision and pitch extraction are done by the robust algorithm for pitch tracking [32]. We believe that such a noise-like signal carries little speaker-specific information in the time-frequency domain [28]. For each voiced speech portion, a sequence of LP residual signals of 30ms long is obtained by inverse filtering the speech signal, i.e.,

$$e(n) = s(n) - \sum_{k=1}^{12} a_k s(n-k) \tag{3.7}$$

where the filter coefficients $a_k$ are computed on Hamming windowed speech frames using the autocorrelation method [22]. The e(n)'s of neighboring frames are concatenated to get the residual signal, and their amplitude is normalized within [-1,1] to reduce intra-speaker variation. Once the pitch periods estimated, pitch pulses in the residual signal are located. For each pitch pulse, pitch-synchronous wavelet analysis is applied with a Hamming window of two pitch periods long. The windowed residual signal is denoted as $e_h(n)$. The wavelet transform of $e_h(n)$ is computed as

$$w(a,b) = \frac{1}{\sqrt{a}} \sum_n eh_{(n)} \psi^* \left(\frac{n-b}{a}\right) \tag{3.8}$$

Where a = {$2^k$|k=1, 2 ……….K} and b = 1, 2 …………N, and N is the window length. $\Psi^*(n)$ is the conjugate of the fourth order Daubechies wavelet basis function $\Psi(n)$, a and b are the scaling parameter and the translation parameters, respectively [33].

The four octave groups of wavelet coefficients, i.e.,

$$W_k = \{w(2^k, b) | b = 1, 2 \ldots\ldots N\}, \text{ where } k=1, 2, 3, 4. \tag{3.9}$$

Each octave group of coefficients is divided evenly into M subgroups, i.e.,

$$W_k^M(m) = \left\{ w(2^k, b) \mid b \in \left( \frac{(m-1)N}{M}, \frac{mN}{M} \right) \right\} \quad m = 1, 2........M \tag{3.10}$$

The two-norm of each sub-group of coefficients is computed to be a feature parameter. As a result, the complete feature vector is composed as

$$WOCOR_M = \{\|W_k^M(m)\| \text{ For m = 1, 2....M and k = 1, 2, 3, 4.}\} \tag{3.11}$$

where ‖.‖ denotes the two norm operation.

For a given speech utterance, a sequence of $WOCOR_M$ feature vectors is obtained by pitch-synchronous analysis of the LP residual signal. Each feature vector consists of 4M components, which are expected to capture useful spectro-temporal characteristics of the residual signal.

### Modeling Techniques

For speaker recognition, pattern generation is the process of generating speaker specific models with collected data in the training stage.The mostly used modeling techniques for modeling includes Vector Quantization (VQ) and Gaussian Mixture Modeling (GMM) [13-15]. The VQ modeling involves clustering the feature vectors into several clusters and representing each cluster by its centroid vector for all the feature comparisons. The GMM modeling involves clustering the feature vectors into several clusters and representing all these clusters using a weighted mixture of several Gaussians. The parameters that include mean, variance and weight associated with each Gaussian are stored as models for all future comparisons. For speaker recognition, the Gaussian Mixture Model (GMM) has been the most popular clustering technique. A GMM is similar to a VQ in that the mean of each Gaussian density can be regarded as a centroid among the codebook. However, unlike the VQ approach, which makes “hard” decision (only a single class is selected for feature vector) in pattern matching, the GMM makes a “soft” decision on mixture probability density function. This kind of soft decision is extremely useful for speech to cover the time variation.

### Vector Quantization (VQ)

Once the MFCC feature vectors are computed for the entire frame of the speech signal for the individual speaker, we have to find the sequence of feature vectors of training speech signal which is the text dependent template model. The dynamic time warping finds the match between the template matching and, it is time consuming as the number of feature vectors increases. For this reason, it is common to reduce the number of training feature vectors by some modeling technique like clustering. The cluster centers are known as code vectors, and the set of code vectors is known as codebook. In this work, the Vector Quantization (VQ) method is used for pattern matching [14]. Vector quantization process is nothing but the idea of rounding towards the nearest integer i.e. Minimum Mean Square Error (MMSE). The two popular codebook generation algorithms namely k-means algorithm [15-16] and Linde-Buzo and Gray (LBG) algorithm [17] are used for generating speaker based vector quantization (VQ) codebooks for speaker verification.

### Gaussian Mixture Modeling (GMM)

Generally, speaker models can be classified into two categories: the generative model and the discriminative model. Generative models attempt to capture all the underlying distribution, i.e., the class centroids and the variation around the centroids, of the training data. The most popular generative model in speaker recognition is the stochastic model, e.g., Gaussian Mixture Models (GMM), hidden Markov Model (HMM), etc. Discriminative models, on the other hand, not necessary model the whole distribution, but the most discriminative regions of the distribution. The template models, e.g., Vector quantization (VQ) codebooks, can also be regarded as a generative model, although it does not model the variations. Unlike the template models, the stochastic models aim at the distribution, i.e., the centroid (mean) and the scattering around the centroid (variance) as well, of feature vectors in a multi-dimensional space. The pattern matching can be formulated as measuring the probability density (or the likelihood) of an observation given the Gaussian. As for speaker recognition, the Gaussian Mixture Model (GMM) has been the most popular clustering technique. The likelihood of an input feature vectors given by a specific GMM is the weighted sum over the likelihoods of the M unimodal Gaussian densities [29], which is given by equation (3.12).

$$P(x_i \mid \lambda) = \sum_{j=1}^{M} w_j b\left(x_i \mid \lambda_j\right) \tag{3.12}$$

where b($x_i$|$\lambda_j$) is the likelihood of $x_i$ given the $j^{th}$ Gaussian mixture

$$b(x_i \mid \lambda_j) = \frac{1}{(2\pi)^{D/2} \mid \sum_j \mid} \exp\{-\frac{1}{2}\left(x_i - \mu_j\right)^T \sum_j^{-1}\left(x_i - \mu_j\right)\} \tag{3.13}$$

Where D is the vector dimension, $\mu_j$ and $\sum_j$ are the mean vectors and covariance matrices of the training vectors. The mixture weights $w_j$ are constrained to be positive and sum to one. The parameters of a GMM**,** $\mu_j$, $\sum_j$ and $w_j$ can be estimated from the training feature vectors using the maximum likelihood criterion, via the iterative Expectation-Maximization (EM) algorithm [31]. A GMM can be regarded as providing an implicit segmentation of the sound units without labeling the sound classes. The sound ensemble is classified into acoustic classes, each of which represents some speaker-dependent vocal system configurations, and modeled by a couple of Gaussian mixtures.

## Performance of Speaker Recognition System

In the recognition stage, feature vectors are generated from the input speech sample with same extraction procedure as in training. Pattern matching is the task of calculating the matching scores between the input feature vectors and the given models in recognition. The input features are compared with the claimed speaker pattern and a decision is made to accept or reject the claiming. The performance of a system operating in verification mode is specified in terms of two error rates. They are false acceptance rate (FAR) and false rejection rate (FRR). The FAR may be defined as the probability of an impostor being accepted as a genuine individual and FRR may be defined as the probability of a genuine individual being rejected as an imposter. In pattern matching, the training speech of each speaker is processed in blocks of 20ms and 10ms block shift to extract MFCC and WOCOR features. These features are modeled using VQ and GMM modeling techniques. In this way, speaker models are developed. We will have in total four models per speaker. These include VQ-MFCC, GMM-MFCC, VQ-WOCOR and GMM-WOCOR combinations. The testing speech is also processed in a similar way and matched with the speaker models using Euclidean distance in case of VQ and Likelihood ratio in case of GMM. Testing stage in the person authentication system includes matching and decision logic. During testing the test feature vectors are compared with the reference models. Hence matching gives a score which represents how well the feature vectors are close to the claimed model. Decision will be taken on the basis of matching score, which depends on the threshold value. The alternative is to employ verification through identification scheme. In this scheme the claimed identity model should give the best match. The test speech compared with the claimed identity model, if it gives best match, then it is accepted as genuine speaker, otherwise, rejected as imposter.

In order to check the performance of different algorithms, we use IITG standard speech database. The speaker verification system is implemented with different combination of feature extraction techniques and modeling techniques. As a result, the four unimodal biometric systems were developed individually and conducted experiments with 30 user's database. The performance of different unimodal systems, with and without noise (noise with SNR=15dB), and also there combination systems using some simple rules of combination like score level fusion are tabulated in Table1.

**Table1: Speaker system verification performance(IITG database)**

| Unimodal System | FAR (%) | FRR (%) | Average error (%) |
|---|---|---|---|
| MFCC-VQ (clean data) | 0.001 | 0.003 | 0.002 |
| MFCC-VQ (noise data) | 0.3862 | 12.1667 | 6.2765 |
| MFCC-GMM (clean data) | 0 | 0 | 0.000 |
| MFCC-GMM (noise data) | 2.4623 | 20.133 | 11.2976 |
| WOCOR-VQ (clean data) | 0.11 | 1.232 | 0.671 |
| WOCOR-VQ (noise data) | 1.242 | 28.1267 | 14.6844 |
| WOCOR-GMM (clean data) | 0 | 0 | 0.000 |
| WOCOR-GMM (noise data) | 0.0123 | 3.222 | 1.6725 |

The experiments are also conducted for SSIT database, which is our own database created under practical environments for 30 users. The experimental setup was same as that of IITG database. The experimental results are shown in Table 2. The Table 2 resembles the Table 1, which shows that the proposed techniques yield good performance irrespective of any database. The result comparative evaluation process is done with available literatures and the values listed out within bracket in Table 2, the average error obtained for clean data. The experimental result shows the present system performance is better.

**Table 2: Speaker system verification performance(SSIT database)**

| Unimodal System | FAR (%) | FRR (%) | Average error (%) |
|---|---|---|---|
| MFCC-VQ (clean data) | 0 | 0 | 0.00 (0.1) |
| MFCC-VQ (noise data) | 0.4885 | 14.1667 | 7.3276 |
| MFCC-GMM (clean data) | 0 | 0 | 0.0 (0.01) |
| MFCC-GMM (noise data) | 3.4483 | 25.133 | 14.29065 |
| WOCOR-VQ (clean data) | 0.22 | 1.624 | 0.922 (1.06) |
| WOCOR-VQ (noise data) | 2.0402 | 29.1667 | 15.60345 |
| WOCOR-GMM (clean data) | 0 | 0 | 0.0 (0.0) |
| WOCOR-GMM (noise data) | 0.0144 | 3.333 | 1.7241 |

## 4. UNIMODAL SIGNATURE BASED PERSON AUTHENTICATION SYSTEM

Unimodal signature based person authentication system is more commonly termed as signature verification system. Signature verification is the task of verifying signatories by using their signatures [18]. Signature verification systems require contact with the writing instrument and an effort on the part of the user. The signature verification system finds use in government, legal and commercial applications. Signature is a behavioral biometric which is characterized by a behavioral trait. Signature, which is similar to handwriting, is learnt and acquired over a period of time rather than a physiological characteristic. Signature verification methods are divided into two types, offline signature verification and online signature verification. Online signature verification uses additional information collected dynamically at the time of signature acquisition along with the signature information and is also called as dynamic signature verification [19]. Offline signature verification uses only the scanned signature image for verification which is static and is also called static signature verification. The offline signature signal is two-dimensional nature and offline signature recognition becomes a pattern recognition problem. The techniques used in the literature for offline signature recognition are Support Vector Machines (SVM), Hidden Markov Models (HMM), Neural Networks, Graph Matching, GSC features (gradient, structure and concavity) and Dynamic Time Warping [19]. The present work employs offline signature verification system for person authentication.

### Feature Extraction from Signature Information

Feature extraction plays a very important role in offline signature verification. In offline signature recognition there are two groups of features, static and pseudo dynamic features fall under one group, global and local features constitute the other group. In our work we implemented an offline signature identification system using Vertical Projection Profile (VPP), Horizontal Projection Profile (HPP) and Discrete Cosine Transform (DCT) features [23]. The VPP and HPP are static features of a signature and DCT is a global feature of a signature image. The size of VPP is equal to the number of columns in the signature image. VPP also a kind of histogram indicates the intensities around which the image pixels are concentrated. VPP gives the horizontal starting and ending points of the image. So, this can be used as a unique feature of a signatory. Since, the size of signature regions are not constant even for a single user, in this work we are taking average value of vertical projection profile as a feature. Horizontal Projection Profile (HPP) is an array contains sum of pixels of each row in a signature image. The size of HPP is equal to the number of rows in the signature image. HPP is also a kind of histogram. Just like histogram indicates the intensities around which the image pixels are concentrated. HPP gives vertical starting and ending points of the image. So, this can be used as a unique feature of a signatory.

Since, the size of signature regions are not constant even for a single user, in this work we are taking the average value of horizontal projection profile as a feature. The equations (4.1) and (4.2) give just average values of VPP and HPP of signature image.

$$vpp_{avg} = \frac{1}{N}\sum_{q=1}^{N}\sum_{p=1}^{M} A_{(p,q)} \tag{4.1}$$

$$hpp_{avg} = \frac{1}{M}\sum_{p=1}^{M}\sum_{q=1}^{N} A_{(p,q)} \tag{4.2}$$

where M is number of rows in an image, N is number of columns in an image, p and q are the row and column indices respectively, and A(p,q) is the intensity of the signature image at $p^{th}$ row and $q^{th}$ column. There are various transforms available to extract the feature of images. Among them, Karhunen-Loeve (KL), Discrete Fourier Transform (DFT) and Discrete Cosine Transform (DCT) are the transforms. Since DCT is real arithmetic and having less computational complexity to other transforms, in our work we are using analysis to extract the features of our signatures. Equation (4.3) shows the two dimensional discrete cosine transform of the input image A. Where $B_{pq}$ is the output DCT coefficient corresponding to $p^{th}$ row and $q^{th}$ column. M and N are total number of rows and columns of input image respectively.

$$B_{pq} = \alpha_p \alpha_q \sum_{m=0}^{M-1}\sum_{n=0}^{N-1} A_{mn} \cos\left(\frac{\pi(2m+1)p}{2M}\right)\cos\left(\frac{\pi(2n+1)q}{2N}\right) \tag{4.3}$$

Where $\alpha_p = \left\langle \frac{1}{\sqrt{M}} \right.$ for p=0 and $\alpha_p = \left\langle \sqrt{\frac{2}{M}} \right.$ for 1 ≤ p ≤ (M-1)

$\alpha_q = \left\langle \frac{1}{\sqrt{N}} \right.$ for q=0 and $\alpha_q = \left\langle \sqrt{\frac{2}{N}} \right.$ for $1 \le q \le (N-1)$

The performance of the signature recognition system depends on the way in which the DCT coefficients are considered. As DCT is a transform which has high energy compaction property, most of the energy in the signature image is concentrated in very few coefficients. In threshold coding, the DCT coefficients in the transformed image have been sorted and a particular number of DCT coefficients have been taken as a feature vector representing the signature image. Instead of threshold coding, the zonal coding DCT coefficients are used for the better performance, which gives energy concentration at low spatial frequencies. In this work we are considering zonal coding of DCT coefficients of signature image.

### Modeling Techniques

During training, calculate two-dimensional DCT of all the training images, and consider a specified number of coefficients according to zonal coding. Calculate the average value of all the average VPP values, average HPP values and all DCT coefficient vectors of all the signatures of a user. These become three kinds of feature models for signature recognition system. The simple time averaged VPP and HPP values cannot convey the person information present along its length. A modified system uses VPP and HPP vectors with Dynamic Time Warping (DTW) for the optimal cost. DTW is a pattern matching technique which aims at finding the minimum cost path between the two sequences having different lengths [23]. A very general approach to find distance between two time series of different sizes is to resample one of the sequence and comparing the sample by sample. The drawback of this method is that, there is a chance of comparing the samples that might not correspond well. This means that comparison of two signals correspond well when there is a matching between troughs and crests. DTW solves this method by considering the samples with optimum alignment. The DTW computation starts with the warping of the time indices of two sequences. The two sequences are compared with some distance measures like Euclidean distance at each and every point so as to obtain the Distance Matrix. These distances in the matrix are termed as local distances. Let the matrix be *d* and the sequences are A, B with lengths M, N respectively. Then *d* is calculated as:

$$d\,(i,j) = distance\ (A(i),B(j)) \tag{4.4}$$

where i vary from 1 to M and j varies from 1 to N.

The distance here considered is Euclidean distance. After computing this matrix, the minimum path is obtained from the matrix by considering some constraints. Apart from the direct Gray scale values in terms of VPP and HPP, some frequency information is obtained from DCT of the image. So, in order to use this information, zonal coding of DCT coefficients of signature image is considered. The modified feature vectors obtained from the signature image A(i,j) of size MXN are given in equations (4.5) and (4.6). Apart from the VPP and HPP vectors, DCT features with zonal masking are used as it is.

$$vpp(j)=\sum_{i=1}^{M}A(i,j) \quad \text{Where j= 1, 2, 3……………..……N} \tag{4.5}$$

$$hpp(i)=\sum_{j=1}^{N}A(i,j) \quad \text{Where i=1, 2, 3………………..M} \tag{4.6}$$

The VPP, HPP and DCT features gives three models namely, VPP-HPP model, DCT model and VPP-HPP-DCT model for training the signatures. The third model should give better performance compared to the other two, since all three different information about signature is used while modeling. In this work, we propose the new method using VPP-HPP features with DTW method, for signature verification, instead of simple averaged values of VPP, HPP features.

**Performance of Signature Recognition System**

Signature verification is a pattern recognition problem [33]. After extraction of the features from a given image, distances are obtained from a testing image to all the users. Signature verification using VPP-HPP and DCT features involves the following steps:

a) Calculate the DTW distance values separately for VPP vectors and HPP vectors from all the users for all the training images to the testing image and obtain distances from each user using average distance method.

b) Obtain the two dimensional DCT and zonal coding of the coefficients for the testing image. Calculate the Euclidean distance of the signature feature vectors from the corresponding trained image DCT models. We get one distance for each model and for each user in the database.

c) Normalize each of the distance of a particular feature using one of the normalization methods and use sum rule for fusion of match scores obtained using each model.

d) Assign the test signature to the user who produces least distance in fused sum vector.

In order to check the performance of different algorithms, we use IITG standard signature database. Then, implemented signature verification system with different combination of feature extraction techniques and modeling techniques. The two unimodal biometric systems were developed individually and conducted experiments with 30 user's database. The results are tabulated for averaged values of VPP-HPP-DCT feature models and modified VPP-HPP-DCT feature models with DTW. Table 3 shows the performance of two different signature verification systems for with and without noise (salt and pepper noise=3%).

**Table3: Signature system verification performance(IITG database)**

| Unimodal System | FAR (%) | FRR (%) | Average error (%) |
|---|---|---|---|
| VPP-HPP-DCT (clean data) | 1.2232 | 36.23 | 18.7256 |
| VPP-HPP-DCT (noise data) | 2..342 | 70.161 | 36.251 |
| Modified VPP-HPP-DCT (clean data) | 0.061 | 3.212 | 1.6302 |
| Modified VPP-HPP-DCT (noise data) | 2.1332 | 66.426 | 34.2796 |

The experiments are also conducted for SSIT signature database. The experimental setup was same as that of IITG database. The results are shown in Table 4. The performance in Table 4 resembles the performance in Table 3. This means that the proposed technique gives good performance irrespective of any database. The result comparative evaluation process is done with available literatures and the values are listed out within the bracket in Table 4. The present system performed better with clean data.

**Table4: Signature system verification performance(SSIT database)**

| Unimodal System | FAR (%) | FRR (%) | Average error (%) |
|---|---|---|---|
| VPP-HPP-DCT (clean data) | 1.2931 | 37.5 | 19.396 (20.013) |
| VPP-HPP-DCT (noise data) | 2..4549 | 71.25 | 36.8534 |
| Modified VPP-HPP-DCT (clean data) | 0.1149 | 3.333 | 1.7241 (1.66) |
| Modified VPP-HPP-DCT (noise data) | 2.3994 | 69.583 | 35.994 |

## 5. BIMODAL PERSON AUTHENTICATION SYSTEM

The main module in the bimodal person authentication system is the biometrics. One commonly used approach to the development of biometrics block is combining person information from different biometric features. There are different ways of combining biometric features like decision level fusion, score level fusion, feature level fusion etc. The present work employs score level fusion for the development of bimodal biometric person authentication system. Once we have the biometric block obtained by the fusion process, the person authentication performance will increase and also its robustness.

In the score level fusion, scores obtained at the output of the classifier are fused using some rules. The simple rules of fusion are Sum rule, Product rule, Min rule, Max rule and Median rule. The Sum rule and Product rule assume the statistical independence of scores from the different representations [24-25]. In the present case, the entire work is carried out using Sum rule. The outputs of the individual matchers need not be on the same numerical scale. Due to these reasons, score normalization is essential to transform the scores of the individual matchers into a common domain prior to combining them. Score normalization is a critical part in the design of a combination scheme for matching score level fusion. Min-Max and Z-score normalization are the most popular techniques used for normalization [25]. Unimodal biometric person authentication systems are initially developed by using speech and signature biometrics features. The scores from the unimodal systems are normalized and combined. The combined score are treated as the output of bimodal biometric person authentication system. Therefore the combined score is evaluated to obtain the performance of bimodal person authentication system.

### Performance of Signature Recognition System

Table 5 shows the performance of the bimodal biometric person authentication systems using speech and signature information. These include (i) MFCC features with VQ model and GMM model for speech with VPP-HPP and DCT features for signatures (ii) WOCOR features with VQ model and GMM model for speech with VPP-HPP and DCT features for signature (iii) MFCC features with VQ model and GMM model for speech with modified VPP-HPP and DCT features for signature (iv) WOCOR features with VQ model and GMM model for speech and modified VPP-HPP and DCT features for signature, are tabulated separately. We have conducted experiments on bimodal biometric system with and without noise. The random noise (SNR=15dB) added to the speech files under testing in the speaker recognition case. Similarly in the signature recognition case, we added salt and pepper noise (3%) to the signature files under testing. The IITG standard database and SSIT database are used for checking the performance of bimodal system. As it can be observed, the performance of bimodal system is better in all the cases. This demonstrates the usefulness of using bimodal and hence multimodal biometric features for person authentication.

**Table5: Bimodal system verification performance(IITG database)**

| Bimodal System | FAR (%) | FRR (%) | Average error (%) |
|---|---|---|---|
| MFCC-VQ for speech and VPP-HPP-DCT for signature (clean data) | 0 | 0 | 0.00 |
| MFCC-VQ for speech and VPP-HPP-DCT for signature (noise data) | 1 | 70 | 35.5 |
| MFCC-GMM for speech and VPP-HPP-DCT for signature (clean data) | 0 | 0 | 0.00 |
| MFCC-GMM for speech and VPP-HPP-DCT for signature (noise data) | 2 | 70 | 36 |
| WOCOR-VQ for speech and VPP-HPP-DCT with DTW for signature (clean data) | 0 | 0 | 0.00 |
| WOCOR-VQ for speech and VPP-HPP-DCT with DTW for signature (noise data) | 1.86 | 57.75 | 30.72 |
| WOCOR-GMM for speech and VPP-HPP-DCT with DTW for signature(clean data) | 0 | 0 | 0.00 |
| WOCOR-GMM for speech and VPP-HPP-DCT with DTW for signature(noise data) | 0.86 | 54.75 | 27.8 |

**Table 6: Bimodal system verification performance(SSIT database)**

| Bimodal System | FAR (%) | FRR (%) | Average error (%) |
|---|---|---|---|
| MFCC-VQ for speech and VPP-HPP-DCT for signature (clean data) | 0 | 0 | 0.00 |
| MFCC-VQ for speech and VPP-HPP-DCT for signature (noise data) | 2.42 | 70 | 36.2 |
| MFCC-GMM for speech and VPP-HPP-DCT for signature (clean data) | 0 | 0 | 0.00 |
| MFCC-GMM for speech and VPP-HPP-DCT for signature (noise data) | 2.4 | 69.58 | 36 |
| WOCOR-VQ for speech and VPP-HPP-DCT with DTW for signature (clean data) | 0 | 0 | 0.00 |
| WOCOR-VQ for speech and VPP-HPP-DCT with DTW for signature (noise data) | 2.86 | 58.75 | 30.72 |
| WOCOR-GMM for speech and VPP-HPP-DCT with DTW for signature(clean data) | 0 | 0 | 0.00 |
| WOCOR-GMM for speech and VPP-HPP-DCT with DTW for signature(noise data) | 1.86 | 53.75 | 27.8 |

## 6. CONSLUSION & FUTURE WORK

In this work, we have implemented a bimodal biometric person authentication using Speech and Signature biometric traits. The better performance can be achieved with different features and with different modeling techniques. The MFCC features with VQ model or GMM model and the WOCOR features with GMM model are best system for speaker verification. For the signature verification, the VPP-HPP with DTW method based system gives better performance. Thus, the experimental results proved that, the bimodal biometric person authentication system with respect to more number of users, and more number of biometrics. The future work needs to be done with respect to more number of users, and more number of biometrics. The future work may also be including with different sessions for speech data collection and signature data collection in practical environments. The new speaker recognition methods may be developed to extract feature vectors by combining two features like WOCOR and MFCC, different windowing techniques like triangular or rectangular or hamming used for framing in a linear frequency scale. The new signature verification system may be developed with the modifications were made to the basic DTW algorithm to account for stability of various components of a signature. Finally, the modified bimodal system performed significantly better than the basic system.

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