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Electrocardiogram Based Identification using a New Effective Intelligent Selection of Fused Features

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ABSTRACT

Over the years, the feasibility of using Electrocardiogram (ECG) signal for human identification issue has been investigated, and some methods have been suggested. In this research, a new effective intelligent feature selection method from ECG signals has been proposed. This method is developed in such a way that it is able to select important features that are necessary for identification using analysis of the ECG signals. For this purpose, after ECG signal preprocessing, its characterizing features were extracted and then compressed using the cosine transform. The more effective features in the identification, among the characterizing features, are selected using a combination of the genetic algorithm and artificial neural networks. The proposed method was tested on three public ECG databases, namely, MIT-BIH Arrhythmias Database, MITBIH Normal Sinus Rhythm Database and The European ST-T Database, in order to evaluate the proposed subject identification method on normal ECG signals as well as ECG signals with arrhythmias. Identification rates of 99.89% and 99.84% and 99.99% are obtained for these databases respectively. The proposed algorithm exhibits remarkable identification accuracies not only with normal ECG signals, but also in the presence of various arrhythmias. Simulation results showed that the proposed method despite the low number of selected features has a high performance in identification task.

Key words: *Biometrics, identification, electrocardiogram, genetic algorithm, neural networks*

INTRODUCTION

Biometric systems are able to do identification with enhanced security based on biological and behavioral data, which are always available. Fingerprint, iris, face and electrocardiogram (ECG) are examples of biological data that are used in biometric systems. On the other hand, gait, speech, and signature are some of the behavioral characteristics used in these systems. Biometric systems designed based on each of these biometrics are different in terms of performance, permanence, collectability, circumvention, uniqueness, and acceptability.[1,2]

Studies have shown that ECG signal is one of the most accurate biometrics.[3,4] Identification based on ECG was first performed by Biel *et al*.[5] The authors of this study and other related studies showed that details of the electrical activity of the heart observed in the ECG signal can be used in identity recognition systems.[6,7] The ECG signal formation is a function of structural and functional anatomy of the heart and its surrounding tissues. Therefore, it is expected that the ECG biometric is unique. ECG signal confirm the viability and cannot be easily forged. Moreover, this signal provides a considerable amount of information about mental, physiological, and clinical status of subjects.[8]

Electrocardiogram based biometric systems can be categorized according to its characteristics such as the number of data channels, operating environment, feature extraction, and classification techniques. Among these characteristics, feature extraction method can have great influence on the system performance. In many studies, nonfiducial features extracted from the frequency content of the ECG signal (wavelet and Fourier coefficients) have been used.[9]

Frequency content based ECG features compared to its spatial features can be more easily extracted. Obtaining the ECG signal spatial features, its different fiducial points should be localized while the extraction of frequency-based features needs one or more ECG segments, so it is only necessary to locate the position of the R peaks.[9]

However, the numbers of nonfiducial features extracted from discrete wavelet transform (DWT) and discrete Fourier transform (DFT) coefficients are too much. It is expected

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that these features are not of equal Importance in various issues such as arrhythmia detection, identification, and authentication. Review of the studies done on each of these areas shows that the optimal set of features for a specific application (different from other uses) is not so far selected.

For example, 256 biorthogonal DWT coefficients of each RR segment of ECG have extracted by Wan and Yao.[10] Belgacem *et al*.[11] have used five levels of db3 DWT coefficients of the mean RR cycles. Chiu *et al*.[12] connected Samples around the R-peak of ECG signal (43 before and 48 after) for 4 beats and formed the input signal of 512 samples for each individual. Nine-level Haar DWT coefficients are then extracted as features. Nonzero coefficients in the discrete cosine transform (DCT) of auto-correlated (AC) ECG signal are used as a feature by Wang *et al*.[13] Fang and Chan[14] are also used a composition of the reflection and DCT coefficients. Plataniotis *et al*.[15] extracted features by applying DCT on AC sequences of ECG segments. AC and DCT or linear discriminant analysis were merged by Agrafioti and Hatzinakos.[16] Ye *et al*.[17] were applied DWT and independent component analysis (ICA) onto the two most routinely leads used for the continuous monitoring of cardiac signals to extract features. They extracted 118 coefficients of db8 wavelet components and 18 ICA components from each heartbeat segment. Gurkan *et al*.[18] were used a combination of 20 AC/DCT features and 13 *Mel-frequency cepstral coefficient* features. In addition, information of the QRS complex have been considered as the third feature set using 120 samples of ECG signal around the R-peak (60 samples each side of R-peak). Saechia *et al*.[19] were used significant components of the Fourier transform of the ECG signals as features.

In previous researches, all wavelet and/or Fourier coefficients are used as the features. Obviously, only distinguishing unique features should be used in the identification. It is evident that all samples of the ECG signal in selected segments as well as all wavelet and/or Fourier transform coefficients do not have such a property. In this study, a new intelligent method for selecting the most distinguishing fused features that have unique values for each individual is proposed. The proposed feature selection method has been developed based on a combination structure of artificial neural networks (ANNs) and genetic algorithms (GAs).

The organization and structure of the study are such that the required primary concepts underlying the proposed method are firstly presented and then the proposed method is explained. Finally, simulation results, discussion, and conclusions are presented.

METHODS

The overall block diagram of the proposed method for selection of effective features in the identification using ECG signal is shown in Figure 1. Before describing the different stages of the proposed method, we first need to explain some basic concepts used. These concepts consist of discrete wavelet, Fourier and cosine transforms, reflection coefficients, GA and neural networks. Finally, the different steps of the procedure, including preprocessing, feature fusion, intelligent selection of fused features and classification will be described in detail.

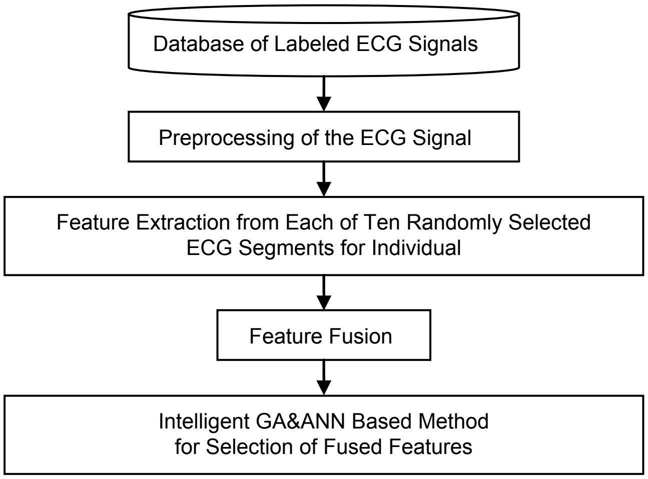

Figure 1: The overall procedure of the proposed algorithm

Discrete Cosine Transform

The DCT, and in particular the DCT-II, is often used in signal processing, especially for lossy data compression, because it has a strong "energy compaction" property.[20,21] Most of the signal information tends to be concentrated in a few low-frequency components of the DCT, approaching the Karhunen-Loève transform (which is optimal in the decorrelation sense) for signals based on certain limits of Markov processes. The DCT-II is probably the most commonly used form, and is often simply referred to as "the DCT".[20,21] The N real numbers $x_0, x_1, \cdots, x_{N-1}$ are transformed into the N real numbers $X_0, X_1, \cdots, X_{N-1}$ as it can be seen in Eq. 1.

$$X_k = \sum_{n=0}^{N-1} x_n \cos[\frac{\pi}{N}(n+\frac{1}{2})k] \qquad k = 0, \cdots, N-1 \qquad (1)$$

Discrete Fourier Transform

Analyzing the frequency content of the signal simply is possible using the DFT. The DFT coefficients (the absolute value of $X[k]$ in Eq 2) may be used in many practical applications such as feature selection.

$$X[k] = \sum_{n=0}^{N-1} x[n] e^{-jk\frac{2\pi}{N}n} \qquad k = 0, 1, \cdots, N-1 \qquad (2)$$

It should be noted that DFT does not provide any information about the local properties such as the location of frequency components appearance in the signal.

Discrete Wavelet Transform

The combined Time-Frequency analysis of non-stationary signals (such as the ECG) is an important issue. In addition to the features related to the frequency content of the ECG signal obtained using DFT, Time-Frequency features obtained from DWT is also used, so that will be described.

Reflection Coefficients

On the basis of auto-regressive (AR) or all-pole model, an ECG beat can be characterized as an output of a casual, stable, linear time invariant stationary system of Eq. 3 given by AR parameters.

$$x(n) = -\sum_{k=1}^{p} a_k x(n-k) + u(n) \tag{3}$$

AR parameters of this system $\{a_k\}$, commonly known as the linear prediction coefficients and $u(n)$ is assumed to be white Gaussian excitation with zero mean and variance σ_u^2. To calculate the AR parameters, often the Yule-Walker equations are used as in.[22] AR coefficients are very sensitive to noises. Therefore, instead of using them, reflection coefficients, $\{k_i\}$ are utilized.

As a reflection coefficients estimation method, suppose that E is the amount of energy of the prediction error that is determined as follows.

$$E = \sum_{n=-\infty}^{\infty} e_n^2 = \sum_{n=-\infty}^{\infty} \left(x(k) + \sum_{k=1}^{p} a_k x(n-k) \right)^2 \tag{4}$$

The minimum prediction error of a P-pole model is given by

$$E_p = r_x(0) + \sum_{k=1}^{p} a_k r_x(k). \tag{5}$$

Where, $r_x(0)$ is energy of the signal $x[n]$. Based on the values of the correlation and the theory of minimum prediction error, by applying a recursive procedure of Levinson-Durbin, reflection coefficients are extracted directly. In this direct method, the following equations set are solved recursively for $i = 1, 2, \cdots, p$ to obtain reflection coefficients.

$$\begin{aligned}
k_i &= \frac{r_x(i) + \sum_{l=1}^{i-1} a_{i-1}(l) r_x(i-l)}{E_{i-1}} \\
a_i(i) &= k_i, \\
a_i(l) &= a_{i-1}(l) + k_i a_{i-1}(i-l), \quad l = 1, 2, \cdots, i-1 \\
E_i &= \left(1 - k_i^2\right) E_{i-1}
\end{aligned} \tag{6}$$

Where $E_0 = r_x(0)$.

Genetic Algorithm

Genetic algorithm is an optimization algorithm based on Darwin's theory of evolution that mimics the process of natural selection. The purpose of applying GA to the problems is to evaluate the ability of the algorithm to find optimal solutions in terms of convergence and its performance for different settings.[23] An overall framework of GA can be in the form of the following pseudo code.[24]

```
Step 0: Initialize parameters (e.g. population size, crossover rate, mutation rate and the maximum number of population generation)
Step 1: Create an initial population randomly $(P(0))$
Step 2: Evaluate current population (compute the fitness of all chromosomes)
Step 3: While (termination condition not satisfied) do (steps 4-8)
Step 4: Select $P(t)$ from $P(t+1)$ (perform selection)
Step 5: Recombine $P(t)$ (perform mutation and crossover)
Step 6: Evaluate current population (compute the fitness of all chromosomes)
Step7: $t = t+1$
Step8: Go to Step 3
```

Neural Networks

In this study, the selected features by GA are applied to a multi-layer perceptron neural network (MLP). MLP has a *feed-forward layer* structure with error-based learning algorithm. The MLP design is determined completely by an input layer where the number of neurons is equal to the number of selected features (m), one or more hidden layer (s) and an output layer where the number of neurons is equal to the number of the target classes (n). The input vector is applied to the input layer and on the track ahead passes through all layers. Each neuron in the hidden layer is related to all neurons in its previous and next layers. The process of classification begins by the input nodes allocation $x_i, i = 1, 2, \cdots, m$ to the corresponding input data vector components; then data will be released in a way ahead and through perceptron until reach the output nodes $o_j, j = 1, 2, \cdots, n$. MLP as a classifier estimates the necessary separator functions and assigns input vectors to the corresponding target class. A learning algorithm corrects the weights for minimizing the error between the desired output and the MLP output.

Data Preparation

Three well-known databases available on the Physionet website have been used for the implementation of this research.

The MIT-BIH Arrhythmia database includes 48 ECG records of 47 subjects consists of 25 men at the ages of 32–89 years, and 22 women at the ages 23–89 years. Each record lasts almost >30 min, and includes records of the top and bottom lids. Each record is digitized with a depth of 11-bit and sampled with a frequency 360 Hz and has been saved in the range of 10 mV.

The MIT-BIH Normal Sinus Rhythm database includes ECG records of 18 persons consists of 5 men at the ages of 36–45 years and 13 women at the ages of 20–50 years. Normal heart function of these people was a factor of choosing them. All records were sampled with a rate of 250 Hz.

The European ST-T database includes ECG records of 78 individuals contains 70 men at the ages of 30–84 years and 8 women at the ages of 55–71 years. Recording of each ECG signal lasts 2 h and sampled with a rate of 250 Hz and resolution of 12 bits and has been saved in the range of 20 mV.

Preprocessing of the Electrocardiogram Signal

In the preprocessing stage, after noise removal, individuals ECG records are segmented and then normalized. Noise components in the recorded ECG signals created by various noise sources include base line wander, the AC noise and high frequency noises. Removal of additive noise (Eq. 7) is performed using wavelet and Butterworth filtering.

$$ECG^n = ECG + u(t) \qquad (7)$$

Where ECG^n is the noisy signal; ECG is the cleared signal and $u(t)$ is additive white noise. The ECG signal can be shown by coefficients obtained by DWT. The Key for eliminating noise is to remove all wavelet coefficients that are produced by noise. So the coefficients exceed to a certain extent must be eliminated and removed by thresholding. Generally four types of the thresholding methods exist that are universal, minimax, Stain's unbiased risk, and hybrid. Furthermore, two types of standard threshold function in applications of noise removal called the hard and soft thresholding are given in Eqs. 8 and 9.[25]

$$THRH_H(Y,T) = \begin{cases} Y, & |Y| \geq T \\ 0, & |Y| < T \end{cases} \qquad (8)$$

$$THR_S(Y,T) = \begin{cases} sign(Y)(|Y| - T), & |Y| \geq T \\ 0 \qquad\qquad , & |Y| < T \end{cases} \qquad (9)$$

The threshold value of $T = \sigma\sqrt{2\ln(\mathrm{N})}$ in DWT was introduced by Donoho where N is the length of the noisy signal and σ is the standard deviation of noise.[25] In this study, "db6" was used as a mother wavelet. ECG signals were decomposed to five levels, and the universal soft thresholding is applied on each level.

In addition, there is the possibility of baseline shift of the ECG signal because of the presence of artifacts. This problem should be resolved after clearing the signal by wavelet transform and before signal segmentation stage. To remove base line shifts, a simple second-order Butterworth low-pass filter with a cutoff frequency of 40 Hz has been used.

For effective segmentation of the ECG records, Pan and Tampkin's algorithm have been used in order to detect R-wave.[26,27] Then the RR cycles are re-sampled to have similar lengths.

Afterward, each RR cycle of the filtered ECG signal is normalized by the following equation.

$$x_{norm} = \frac{x - \mu_X}{\sigma_X} \qquad (10)$$

In this formula $x_{norm}, x, \mu_X, \sigma_X$ respectively shows the normalized ECG signal with zero mean and unit variance, filtered ECG signal, the mean, and standard deviation. Figure 2 shows two RR segments of ECG signal before and after preprocessing stage.

Finally, to reduce the data acquisition time, which is an important issue in biometric systems, only ten RR cycles were selected randomly from each person's ECG record and will be sent to the feature extraction stage.

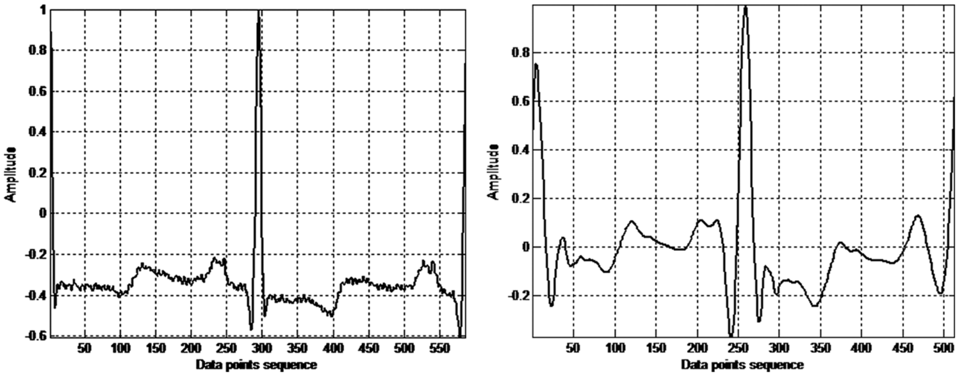

Figure 2: Two electrocardiogram segments before (left) and after (right) preprocessing

Feature Extraction and Fusion

In this research work, wavelet, Fourier, and reflection coefficients were extracted from individual's ECG segments. Then these features were combined and fused to form the basic features set.

To access to more effective frequency domain features, ECG segments are divided into five sub segments. DFT is then taken on these sub segments, and subsequently in order to compress the energy, only important coefficients of these five sub segments are selected using DCT.

Time-Frequency features suitable for identification are extracted using five level coefficients (A_5 and D_1 to D_5) of db6 wavelet. Obviously other wavelets used in previous researches on the ECG signal[28-33] were evaluated for this application and among them, db6 wavelet have been selected by trial and error.

Consuming DWT coefficients as the features increases the dimensions of the features set. So the DCT, were applied to the DWT coefficients at different levels. Then the main coefficients of DCT were considered as the features.

Reflection coefficients, which are obtained from AR modeling of the ECG signal, when used in conjunction with DCT coefficients, provide excellent results for human identification.[34] In this study, ten reflection coefficients extracted from each segment of individuals ECG record and added to the features set.

Intelligent Genetic Algorithm and Artificial Neural Network Based Selection of Fused Features

Most of the classifiers in the lower dimensions of the features provide acceptable results; however, in large dimensions of the features, they are confused and faced with the famous problem of the curse of dimensionality.[35] In general, it is not clear, which features subset makes the highest distinction for the desired pattern classes; on the other hand, the possibility of evaluating all existing subsets is not affordable. So to find the best and most appropriate features subset among a large collection of features is a problem, which in many cases we are faced with it.

It is expected that all of the features that can be extracted from the ECG signal, don't have equal importance in various applications such as arrhythmia detection or identification. A good selection of features increases the recognition rate and speed and has a positive effect on the storage, retrieval and processing of data. This method is developed in such a way that it is able to select important features that are necessary for identification using analysis of ECG signal.

The aim of different feature selection methods is to find the best subset among 2^N candidate subsets. As it was mentioned before, in all these methods, based on the application, a subset is selected as an answer that is able to optimize an evaluation function. It is evident that the final goal of a pattern recognition problem is to minimize the classification error in all classes. Despite the fact that each method will try to select the best features, but due to the extent of the possible responses and the set of answers that can be increased by N powers, it is difficult to find the optimal answer and in the medium and large Ns is very costly and sometimes impossible. Hence in the problems with the high number of candidate features, Metaheuristic optimization algorithms such as GA have been proposed to perform feature selection.[36,37]

In this study, ANN has been used as a classifier for evaluation of the features subset produced by GA. The number of input layer neurons depends on the number of desired features. Each subset has an estimated error that its inverse is considered as a criterion of eligibility of the features subset.

The overall proposed feature selection process by GA-ANN is shown in Figure 3. Moreover, parameters for GA and ANN are reported in Tables 1 and 2 respectively.

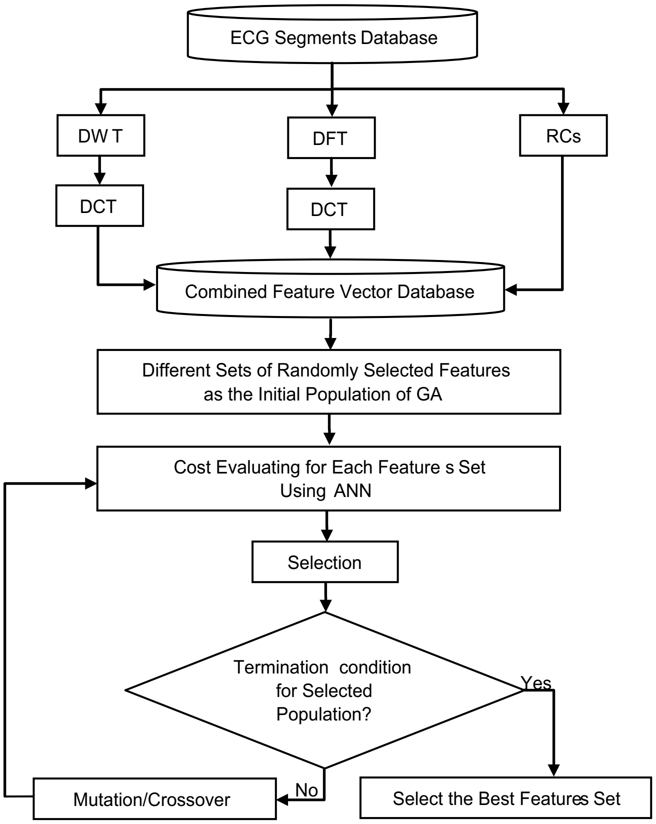

Figure 3: Feature selection process by genetic algorithm-artificial neural network

In this feature selection issue, cost function or estimation error should be minimized. In addition, additional and irrelevant features also should be removed from the features set. So, the cost function is normalized by a penalty term as follows.

$$J = MSE \times \left(\frac{D-d}{D-1}\right) \qquad (11)$$

In the above formula, D is the total number of the features, d is the number of selected features and MSE is mean squared error. So, NN orients the GA to find the most optimal solution by giving value to each chromosome string.

In the feature selection problem, the chromosomes (possible answers) are considered as binary strings, and their dimensions are proportional to the features vector. Each bit of the binary string represents a feature value. Ones and zeros for each bit string, indicating the participation or nonparticipation of its corresponding feature value respectively. For example, chromosome 00101000 means that the third and the fifth features are selected. Figure 4 illustrates a chromosome used in this method.

Table 1: Parameters of GA

Generations	Initial range	Population size
50	[0; 1]	10
Crossover function	Mutation function	Selection function
Scattered	Uniform	Stochastic uniform

GA – Genetic algorithm

Table 2: Parameters of ANN

Number of layers	Maximum number of epochs	Performance goal	Maximum time to train
3	100	0	Inf
Activation function	Learning rule	Maximum validation failures	Minimum performance gradient
Tan sig	Scaled conjugate gradient	5	1e-6

ANN – Artificial neural networks

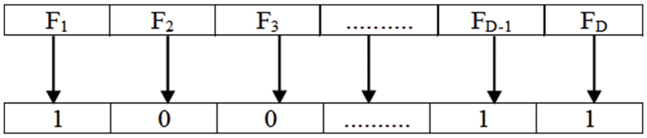

Figure 4: Displaying a chromosome and how to select features

Each chromosome represents a subset of features. Using ANN, cost (MSE) of features subset (after training) is obtained for the test set. Then the bests are selected as parents of the next generation.

EXPERIMENTAL RESULTS

In this section, performance of the proposed algorithm is evaluated by testing it on ECG records available in three popular databases of Physionet website. Ten segments of the ECG records of each individual are considered. After features extraction and fusion of each individual sample, the best and most appropriate subset of features for identification is selected by the proposed method and applied to an MLP classifier. The average of ten implementation identification rate over 20% of each individual samples have been reported. To ensure the over training does not occur, 20% of the each individual samples were used for validation. The remaining 60% of each individual samples were used for the training process.

In this research, more comprehensive database is selected compared with similar studies. In order to demonstrate the generalization ability of the algorithm, implementation results have been reported on three common databases. In addition, the training and testing samples for each class (individual) have been considered more comparing similar studies. For each person, the algorithm runs ten times. In each run, ten randomly selected ECG segment are used. This means that for each individual, 100 ECG segment are selected.

The remaining wavelet, Fourier and reflection coefficients after feature selection stage, for four different samples of a person, as well as samples from four different people, which are selected randomly from the MITBIH database are shown in Figures 5-8.

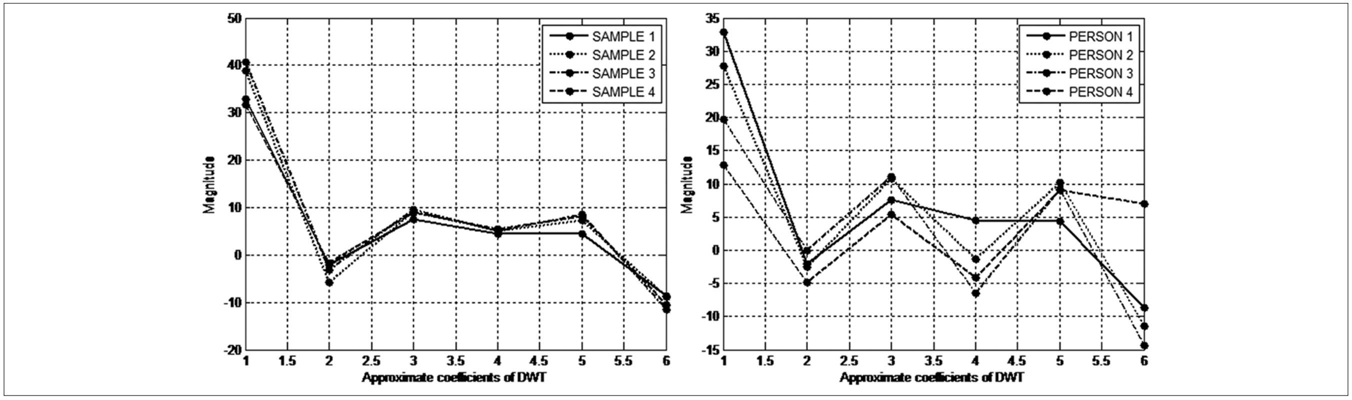

Figure 5: Wavelet approximation coefficients for different samples of an individual (left) and samples of different individuals (right)

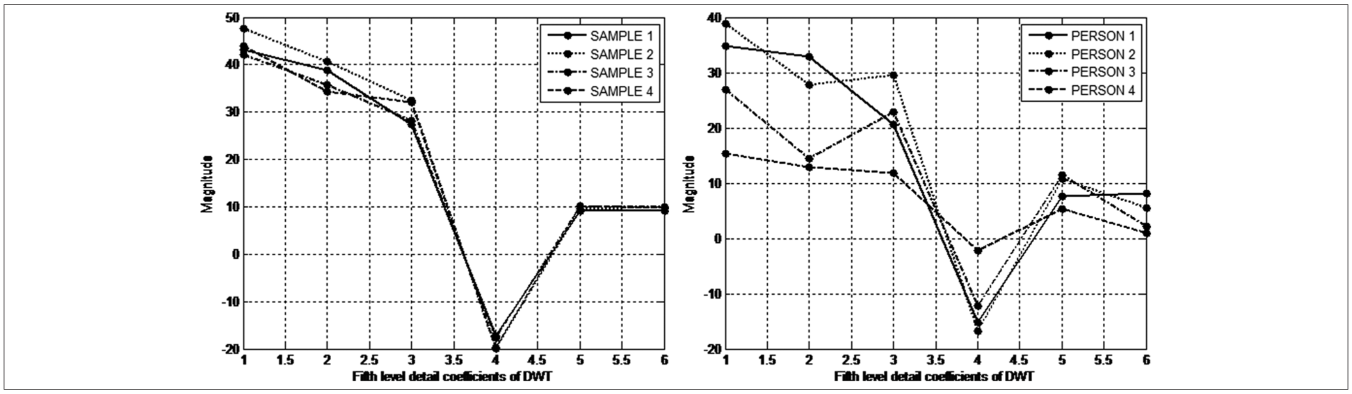

Figure 6: Wavelet fifth level detail coefficients for different samples of an individual (left) and samples of different individuals (right)

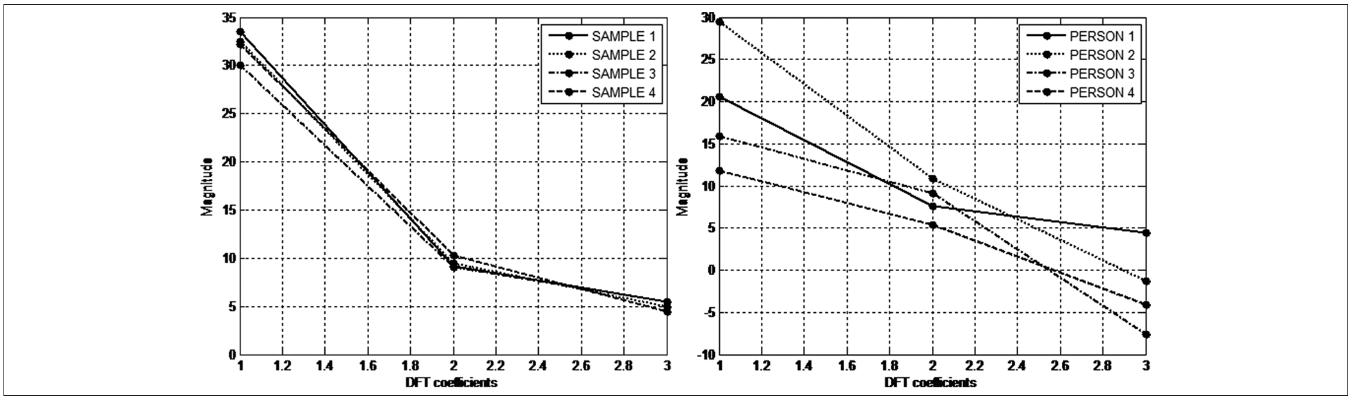

Figure 7: Discrete Fourier transform coefficients for different samples of an individual (left) and samples of different individuals (right)

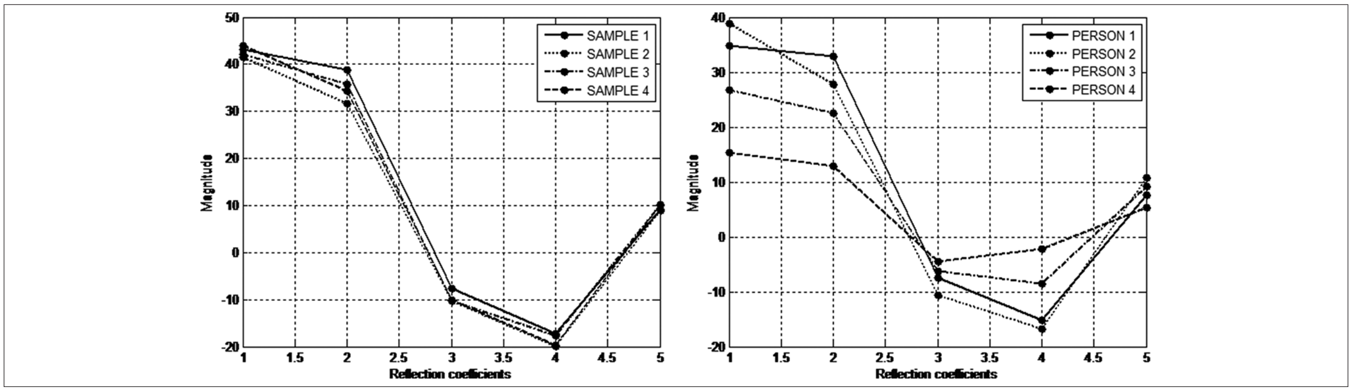

Figure 8: Reflection coefficients for different samples of an individual (left) and samples of different individuals (right)

Some studies in the field of ECG biometrics and their results are reported in Table 3. The rates of decrease in the dimensions of the features set, before and after compression and intelligent selection process, as well as the correct identification rates, have been reported in Table 4. Correct identification rate is defined as the rate at which the system rightly states a match between the person's biometrics and those biometric records previously collected.[38]

Furthermore, the proposed identification system performance was evaluated based on four other conventional statistical criteria called TPR (Recall) and TNR (Specificity) and FPR (Fall Out) and FNR (Miss Rate). The TPR and TNR statistical criteria are presented in Eqs. 12 and 13. The FPR and FNR statistical criteria are easily calculated from the TPR and TNR respectively (FPR = 1 − TNR and FNR = 1 − TPR).

$$TPR = \frac{TP}{TP + FN} \tag{12}$$

$$TNR = \frac{TN}{FP + TN} \tag{13}$$

TP, TN, FP and FN parameters used in the Eqs. 12 and 13 are presented in Table 5. TP is the number of samples of

Table 3: Results of some related researches

Study	Sample size	Feature extraction technique	Classification technique	Identification rate (%)	Database
Chiu *et al.*[12]	45	DWT	NC/ED	95.71	Qt
Wang *et al.*[13]	31	AC/DCT	NNC	97.80	PTB/MITBIH
Agrafioti and Hatzinakos[16]	27	AC/DCT	KNN/ED	96.30	PTB/MITBIH
Ye *et al.*[17]	18, 47	DWT/ICA	SVM	99.09	MITBIH/longterm-ST
Gurkan *et al.*[18]	30	AC/DCT/MFCC	LDA/NNC	97.30	PTB
Saechia *et al.*[19]	35	FT	MLP-BP	97.15	MITBIH
Irvine *et al.*[39]	43	PCA/eigen analysis	MD	91	Private database

AC – Auto correlation; DCT – Discrete cosine transform; DWT – Discrete wavelet transform; ED – Euclidian distance; FT – Fourier transform; ICA – Independent component analysis; KNN – K nearest neighbor; LDA – Linear discriminant analysis; MD – Minimum distance; MFCC – Mel frequency cepstral coefficient; MLP-BP – Multi-layer perceptron back propagation neural networks; NC – Nearest center; NNC – Nearest neighbor classifier; PCA – Principal component analysis; SVM – Support vector machine

Table 4: Results of applying the proposed algorithm on different databases

Database	MITDB	NSRDB	EDB
Number of people	48	18	78
Number of samples per individual	10	10	10
Dimensions of initial features set	1086	362	1086
Dimensions of selected features subset	51	31	54
Identification rate (%)	99.89	99.84	99.99

MITDB – MIT-BIH Arrhythmia Database; NSRDB – MIT BIH Normal Sinus Rhythm Database; EDB – European ST T Database

Table 5: TP, FN, TN and FP definition according to the classification accuracy of the cardiac cycle

Cardiac cycle	Correctly classified?	
	Yes	No
Cardiac cycle related to the individual	TP	FN
Cardiac cycle related to other people	TN	FP

TP – True positive; FN – False negative; TN – True negative; FP – False positive

Table 6: Classification performance of the proposed approach

Database	MITDB	NSRDB	EDB
TP rate	0.9545	0.9743	0.9882
TN rate	0.9990	0.9984	0.9998

TP – True positive; TN – True negative; MITDB – MIT-BIH Arrhythmia Database; NSRDB – MIT BIH Normal Sinus Rhythm Database; EDB – European ST T Database

the target class, which is assigned correctly to the target class. TN is the number of samples of other classes that are correctly assigned to other classes. FP is the number of samples of other classes, which mistakenly assigned to the target class. FN is the number of samples of the target class, the mistakenly assigned to other classes. The performance of the proposed algorithm using these parameters is reported in Table 6.

DISCUSSIONS AND CONCLUSIONS

In this study, a new intelligent method for selecting the most distinguishing fused features, which have unique values for each individual, is proposed. It is obvious that all samples of the ECG signal in selected segments as well as all wavelet and/or Fourier transform coefficients do not have such a property to distinguish each individual uniquely. Whereas, only distinguishing unique features should be used in the identification. For this purpose, features extracted from the DFT and DWT analysis of the ECG signal segments, were firstly compressed by the cosine transform to reduce redundancy of features. Some reflection coefficients also extracted from ECG signal segments and added to the fused features set and then an intelligent GA-ANN based method is utilized for selecting more effective subset of features for identification task.

Reflection coefficients when used in conjunction with DCT components provide excellent results for human identification. It is clearly observed from Figures 5-8 that selected features offers a great intraclass compactness and interclass separability.

Comparison of classification accuracies of Tables 3 and 4, and also the results reported in Table 6 shows that our new proposed method, which is validated by the greater number of one channel long/short term ECG records obtained from healthy and patient individuals available in three popular databases of physionet website despite the lower number of selected features gives better identification results than the other researches. Moreover, the proposed method requires less time to train and test the classifier and has a lower computational complexity. The results of the experiments shows, our new proposed algorithm has demonstrated remarkable performance compared to other ECG based identification techniques.

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