Personal Biometric Identification Based on ECG Features

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Key Words: *ECG signal; ECG wavelet; ECG segmentation; PCI feature extraction; ECG biometric personal identification.*

Abstract. *In this paper, a new approach for personal biometric identification is presented based on extraction of ECG features. We perform denoising and segmentation on the input signal, after which we realize dimensionality reduction and select the features for recognition. The final stage of the proposed approach is classification and recognition of the extracted features.*

1. Introduction

1.1. State of the Art

The importance of the personal biometric identification has been growing over the last 20 years. There are several biometrics that have proven to be robust and are used in major identification tasks – such as fingerprint, signature, voice, and face. In recent years efforts have been made to improve the existing technology and to introduce new biometrics for identification purposes – such as human DNA and electrocardiogram (ECG). Some of the major biometric modalities will be covered in short in this section.

There exist many fingerprint recognition systems. Data acquisition in such systems is rather noninvasive and high recognition rates can be achieved, even for large databases [9]. In personal identification systems where signatures are used for recognition, high accuracy rates have been achieved, although this modality is in strong influence from the person's physical and mental disposition at time of acquisition. The acquisition techniques are non-invasive, but relatively obtrusive [9].

In face recognition systems, high precision levels are achieved nowadays. There are several problems regarding acquisition and training of the classifiers, such as: illumination conditions, necessity of many samples per person for the correct classifier training. The main advantages are the non-invasive and possibly unobtrusive acquisition techniques.

The emerging fields of ECG and DNA recognition are characterized by high precision rates achieved, especially for DNA analysis which is used mainly during forensics. Personal identification through ECG features has been introduced recently [2,13,15,16,17]. There exist several techniques with high recognition rate which proves the relative time invariance of the unique ECG characteristic for different persons [2]. This modality is strongly influenced by the sensor noise, as well as the physical condition of the recognized individual [4]. The classical approach for ECG personal identification is to use a set from amplitude and temporal features (interval, amplitude, angle etc.) as input data for the classifier [13]. However the amplitude parameters could not be considered as reliable features (they depend on the used hardware, placement of the electrodes, etc.).

An alternative method for ECG personal identification is presented in [15]. It combines autocorrelation function with Discrete Cosine Transform (DCT). The advantage of the method is avoiding the ECG segmentation, which is a very complicated task. This method involves performing DCT over an autocorrelation function of the ECG signal and classification based on significant DCT coefficients.

In recent research, new techniques have been proposed for signal denoising and segmentation [4]. The research in the field of ECG analysis has produced several features that are considered to be suitable for identification, such as – low-dimensionality subspace projection, described in [3].

The rest of the paper is organized as follows: in section 2 we give a detailed overview of the proposed personal biometric identification system. In section 2.1 a short description of ECG signal acquisition is given. We describe the main methods for signal denoising and segmentation in point 2.2. In the next section 2.3 we present our approach for dimensionality reduction of the decomposed signal and feature selection. Section 2.4 provides details on the classifiers that we used for recognition. In section 3 we have shown experimental results. Finally, in section 4 we conclude and give a future roadmap of our research.

2. Description of the Proposed Approach

The sequence of procedures in the ECG personal identification algorithm is illustrated in *figure 1*. A detailed overview of each procedure is presented in the next sections.

2.1. ECG Signal Acquisition

The ECG sequences are acquired with one channel standard analogue electrocardiograph. The used lead is right arm – left arm from the Einthoven triangle [7]. The signals are resampled at sampling rate of 512 Hz and 12 bit resolution. The acquired signals are high-pass filtered with a zero-phase digital filter with cut-off frequency of 0.5 Hz in order to remove the possible baseline drift.

2.2. ECG Signal Denoising and Segmentation

The removal of the muscle artifacts' noise from real world ECG signals is most difficult to achieve. This noise is additive and often modeled with Gaussian white noise [4]. For this reason, a Wavelet denoising with soft threshold of the Wavelet coefficients is realized. We have used the SWT De-noising 1-D packet from Matlab®. The signals are 5 level decomposed with

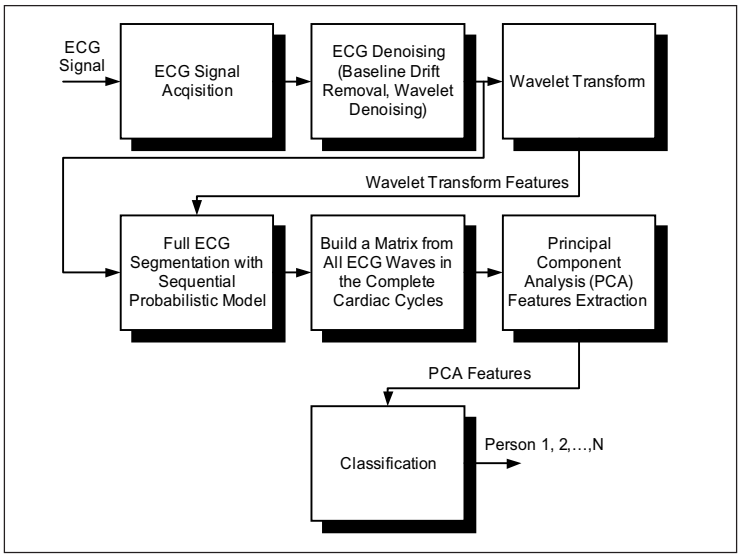


Figure 1. Sequence of procedures for ECG personal identification

Haar wavelet and the unscaled white noise is chosen for noise type.

In the normal ECG, there are defined several standard regions of interest named waves, complexes and segments (P wave, QRS complex, T wave). These components are related to distinct states of the cardiac muscle [7] (*figure 2*). The remaining part from ECG is called isoelectric line (baseline). The ECG segmentation (onset/offset determination of the ECG components) is a very important process in order to perform dimensionality reduction techniques such as PCA. In this project the ECG is segmented into complete cardiac cycles. It is desirable to incorporate full segmentation (boundary detection of all standard ECG waves and complexes) because some of the ECG intervals are considered to be discriminative enough and can be used as features for personal identification, too.

The ECG signal represents a random process. Despite this, the signal has strong cyclic recurrence (for healthy persons). Due to these reasons, in our approach we use a sequential probabilistic model such as Hidden Markov Model (HMM) [1,8,12]. The segmentation process is to assign each signal sample to a given class - wave, complex, etc. – so that classification and boundaries detection are performed within a single procedure.

The HMM is a probabilistic model which describes the statistical dependency between an observation sequence O and a sequence of hidden states S. A HMM λ is denoted with:

$$\lambda = (\mathbf{A}, \mathbf{B}, \mathbf{q}), \quad (1)$$

where $\mathbf{A}$ is the transition probability matrix, $\mathbf{B}$ is the observation probability distribution matrix and $\mathbf{q}$ is the initial distribution vector. In this work a first order Markov process (Markov chain) is used:

$$P(s_{t+1} \mid s_t, s_{t-1}, s_{t-2}, \ldots) = P(s_{t+1} \mid s_t), \quad (2)$$

where s_t is the state (ECG component) for time t.

The purpose of ECG segmentation is to find the optimal state sequence S' given the HMM parameters λ and observation sequence O:

$$\begin{aligned} S' &= \underset{S}{argmax}\{P(S \mid O, \lambda)\} = \\ &= \underset{S}{argmax}\left\{\frac{p(S, O \mid \lambda)}{p(O \mid \lambda)}\right\} = \\ &= \underset{S}{argmax}\{p(S, O \mid \lambda)\} \end{aligned} \quad (3)$$

The optimal state sequence S' in (3) is determined as the most probable state sequence given the observation. The final result is achieved by using the Bayesian rule. An effective way to calculate (3) is to use the Viterbi algorithm [6].

HMM learning (finding the HMM parameters λ) is a task, which can be realized using supervised or unsupervised techniques. The unsupervised learning is related to maximum likelihood:

$$\lambda' = \underset{\lambda}{argmax}\{p(\mathbf{O} \mid \lambda)\}, \quad (4)$$

where λ' represents HMM parameters that maximize the probability, and $\mathbf{O} = \{O_1, O_2, \ldots, O_N\}$ are the observation ECG-sequences.

The model architecture can be seen in *figure 2*. It is designed in accordance with the standard ECG components and it is valid for most common ECG morphology with positive deflected waves.

Sometimes the JT segment is hard to distinguish, so the model allows direct transition from QRS complex to T wave. Since the model is trained with ECG signals from healthy persons, all remaining transitions are according to *figure 2*.

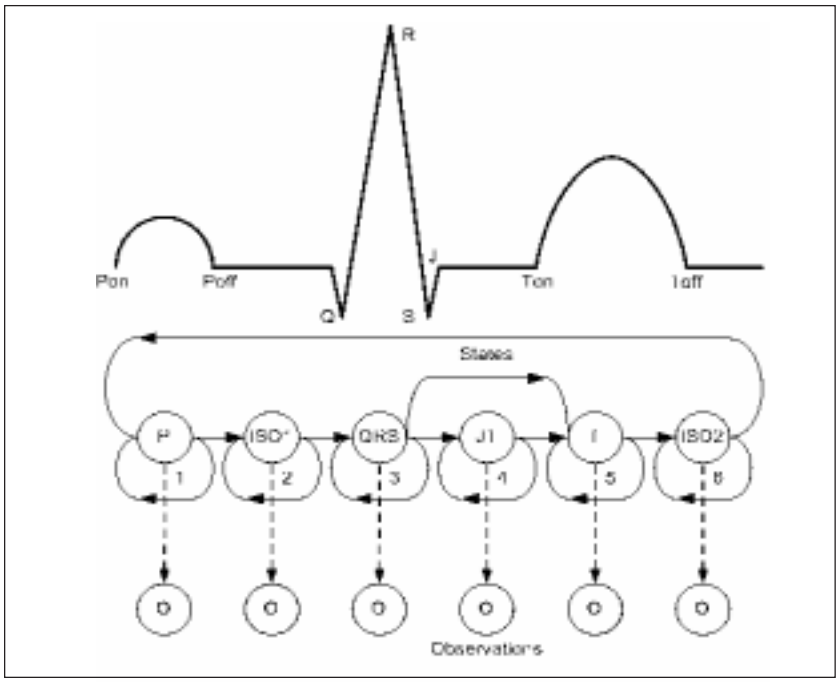


Figure 2. Architecture of the sequential probabilistic models for ECG segmentation

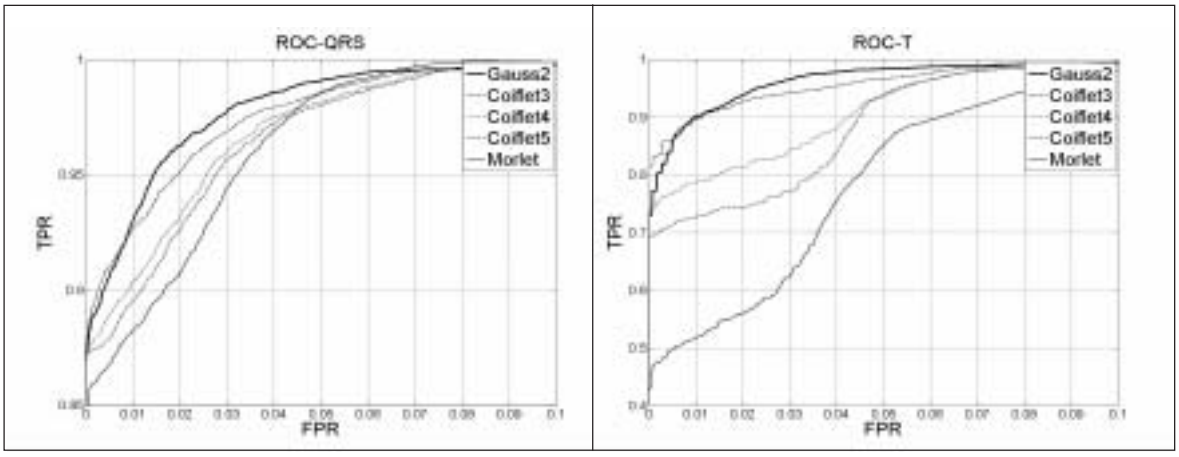
Although it is possible to use signal samples as observations, a better approach is to use observation vectors which are built from a mulitiscale linear transform such as the wavelet transform:

$$(5) \quad W_x(s,\tau) = \langle x, \psi_{s,\tau} \rangle = \frac{1}{\sqrt{s}} \int_{-\infty}^{\infty} x(t) \psi^* \left(\frac{t-\tau}{s} \right) dt,$$

where $x(t)$ is the ECG signal and ψ is the wavelet function [10]. The coefficients from the wavelet transform W serve as similarity measure between the signal and a wavelet function at different scales s and time shifts τ as parameters. The wavelet function ψ must satisfy several requirements: maximum similarity between ψ and ECG components; minimal effective width; it is also desirable for to be symmetric in order to avoid complicated phase corrections. The wavelet functions, which can fulfill these requirements, are: second derivative of the Gaussian function (Mexican hat), Morlet and the last three wavelets from Coiflet family. The optimal parameters for wavelet transform (wavelet function and scales) are chosen according to segmentation performance evaluation with different wavelet functions (*figure 3a* and *figure 3b*) and different scales.

The segmentation performance is evaluated by using the Receiver Operating Characteristics (ROC). The ROC analysis confirmed that the best suited wavelet function for the purpose is the second derivative of the Gaussian. The optimal scales are dyadic from 2 up to 64. The features (observation vectors) for the ECG segmentation are selected according to:

$$(6) \quad \mathbf{O}'_\tau = \left[W_x(2^k, \tau) \right]^T, k = 1,...,6, \tau = 0,...,N-1,$$



a b

Figure 3. The performance of HMM – SGM based ECG segmentation with different wavelet functions for QRS complex (a) and T wave (b)

where *N* is the number of samples in the ECG signal.

Because the features in a given class are not normally distributed, the used HMM has a Gaussian Mixture Model core (HMM-GMM). In this way, an arbitrary Probability Density Function (PDF) can be approximated as a weighted sum of Gaussians. Some experiments have been made by using HMM with a single Gaussian model (HMM-SGM) but with considerably lower performance. We have also experimented with another sequential probabilistic model (Conditional Random Field – CRF) for ECG segmentation purposes [14]. As can be seen from the evaluation of the experimental results, the achieved performance is not satisfying.

2.3. Feature Extraction from ECG Using Linear Subspace Projection

The principal component analysis (PCA) is a well-known technique for dimensionality reduction that concentrates the discriminative information into a low number of coefficients [4]. The main goal behind the reduction of a complex set of data to a lower dimension is to reveal the simpler structure that underlies it. The previous stage of our approach provides noise reduction and segmentation of the ECG signal. We consider each segmented and labeled cardiac cycle a row vector with a finite number of elements *N*. The matrix $\mathbf{X}$ is formed from the vectors for each cardiac cycle:

$$\mathbf{X} = \begin{pmatrix} x_{11} & x_{12} & \dots & x_{1N} \\ x_{21} & x_{22} & \dots & x_{2N} \\ \dots & \dots & \dots & \dots \\ x_{M1} & x_{M2} & \dots & x_{MN} \end{pmatrix}, \tag{7}$$

where M is the number of the cardiac cycles. The used segments for complete cardiac cycles are taken from P wave onset to T wave offset (PQRST segments), so most of the isoelectric line is discarded from the analysis. This assures much smaller length's variability for the vectors (observations) [3]. Such variability is much higher when using RR segments, for example. For the purposes of our experiment we have selected a fixed number M of training cycles per person that are strongly correlated. The input data $\mathbf{X}$ is sorted according to its correlation matrix and the first 10 vectors are used for PCA transformation, thus avoiding incorrectly segmented cardiac cycles. In order to prepare the transformation in PCA subspace, we subtract the mean vector from the data:

$$x_{ij} = x_{ij} - \frac{1}{N}\sum_{k=1}^{N} x_{ik}. \tag{8}$$

The covariance matrix of the input data $\mathbf{\Sigma_X}$ is calculated according to:

$$\mathbf{\Sigma_X} = E\{\mathbf{X}\mathbf{X}^T\} = \frac{1}{N-1}\mathbf{X}\mathbf{X}^T. \tag{9}$$

The PCA is a linear transform:

$$\mathbf{Y} = \mathbf{P}^T\mathbf{X}, \tag{10}$$

where $\mathbf{Y}$ is the transformed data and $\mathbf{P}$ is the matrix for linear transformation. In terms of dimensionality reduction the goal is to diagonalize the covariance matrix of the output data:

$$\mathbf{\Sigma_Y} = diag\{\lambda_1, \lambda_2, ..., \lambda_M\}. \tag{11}$$

For $\mathbf{\Sigma_Y}$, the following is valid:

$$\mathbf{\Sigma_Y} = \frac{1}{N-1}\mathbf{Y}\mathbf{Y}^T = \frac{1}{N-1}(\mathbf{P}^T\mathbf{X})(\mathbf{P}^T\mathbf{X})^T = \frac{1}{N-1}(\mathbf{P}^T\mathbf{X}\mathbf{X}^T\mathbf{P}) = \\ = \frac{1}{N-1}(\mathbf{P}^T\mathbf{X}\mathbf{X}^T\mathbf{P}) = \mathbf{P}^T\mathbf{\Sigma_X}\mathbf{P}. \tag{12}$$

The columns of $\mathbf{P}$ consist of the eigenvectors of $\mathbf{\Sigma_X}$. Let $\mathbf{\Lambda}$ be a diagonal matrix whose diagonal is formed from the eigenvalues of $\mathbf{\Sigma_X}$. The eigenvalue and eigenvector decomposition are according to:

$$\mathbf{\Sigma_X}\mathbf{P} = \mathbf{P}\mathbf{\Lambda}. \tag{13}$$

$\mathbf{\Sigma_X}$ is symmetric, so $\mathbf{P}$ is an orthonormal matrix and the eigenvalues of $\mathbf{\Sigma_X}$ are real numbers. For the orthonormal matrix $\mathbf{P}$:

$$\mathbf{P}^T\mathbf{\Sigma_X}\mathbf{P} = \mathbf{P}^T\mathbf{P}\mathbf{\Lambda} \tag{14}$$

and

$$\mathbf{P}^T\mathbf{\Sigma_X}\mathbf{P} = \mathbf{\Lambda}. \tag{15}$$

Obviously $\mathbf{\Sigma_Y} = \mathbf{\Lambda}$. The calculation of eigenvectors and eigenvalues is realized in two steps. The first step is to evaluate the eigenvalues, which are the solution of a polynomial with degree M. The second step is to find the eigenvectors corresponding to the eigenvalues and sort them in descending-energy order.

The original basis is with dimension MxM. The new basis is with reduced size MxL ($L << M$). The criterion for is the following:

$$RMSE(L) = \frac{\sum_{i=1}^{L}\lambda_i}{\sum_{i=1}^{M}\lambda_i} > 0.95. \tag{16}$$

PCA is an optimal method which delivers the opportunity to perform back-projection to signal space – the Mean Square

Error (MSE) between the restored signal and the original one is minimized.

When using the transposed input matrix, the energy concentration of the PCA scores can be used as indicator for morphological regularity of the PQRST segments [3]. Thus if the identified person has irregular rhythm the identification procedure has to be stopped. If the identification system uses combination from different biometric modalities (face, fingerprint, etc.) it should rely on the other modalities, rather than ECG. In case of cardiac disease with permanent influence in the ECG waveform, a new profile should be created for the identified person.

2.4. Classification

The proposed ECG personal identification algorithm is intended to be a part of personal identification system, which will use a combination from different kind of biometric modalities. So it is desirable the classifier's output to contain confidence values [11]. The chosen classifier is Bayesian, i.e. the posterior probabilities are according to Bayes formula:

$$P(C_k \mid \mathbf{f}) = \frac{p(\mathbf{f} \mid C_k) P(C_k)}{p(\mathbf{f})}, \tag{17}$$

where C_k is the given class (person), $\mathbf{f} = [f_1, f_2, ..., f_D]^T$ is the feature vector obtained from PCA transform, $p(\mathbf{f} \mid C_k)$ is the PDF of class C_k in the feature space and $P(C_k)$ is the prior probability and $\sum_{k=1}^{K} P(C_k) = 1$. The scaling factor $p(\mathbf{f})$ is according to:

$$p(\mathbf{f}) = \sum_{i=1}^{K} p(\mathbf{f} \mid C_i) P(C_i). \tag{18}$$

The major problem in the Bayesian classifier is class-conditional PDF $p(\mathbf{f} \mid C_k)$ [11]. The distribution is estimated from the training set using Gaussian Mixture Model (GMM). In *D*-dimensional space the Gaussian PDF is defined as:

$$\square(\mathbf{f}; \boldsymbol{\mu}_\mathbf{f}, \boldsymbol{\Sigma}_\mathbf{f}) = \frac{1}{(2\pi)^{D/2} \sqrt{|\boldsymbol{\Sigma}_\mathbf{f}|}} \exp\left[-\frac{1}{2} (\mathbf{f} - \boldsymbol{\mu}_\mathbf{f})^T \boldsymbol{\Sigma}_\mathbf{f}^{-1} (\mathbf{f} - \boldsymbol{\mu}_\mathbf{f}) \right], \tag{19}$$

where $\boldsymbol{\mu}_\mathbf{f}$ is the mean vector and $\boldsymbol{\Sigma}_\mathbf{f}$ is the covariance matrix. GMM is a mixture (weighted sum) from several Gaussian distributions (6 in our case):

$$p(\mathbf{f}; \theta) = \sum_i \alpha_i \square\left(\mathbf{f}; \boldsymbol{\mu}_{\mathbf{f}_i}, \boldsymbol{\Sigma}_{\mathbf{f}_i}\right)$$
$$\theta = \left\{\alpha_1, \boldsymbol{\mu}_{\mathbf{f}_1}, \boldsymbol{\Sigma}_{\mathbf{f}_1}, \alpha_2, \boldsymbol{\mu}_{\mathbf{f}_2}, \boldsymbol{\Sigma}_{\mathbf{f}_2}, ...\right\} \tag{20}$$

where α_i is the weight of the *i*-th component. The model parameters are evaluated using the Maximum Likelihood Estimation (MLE). Let $\square = \{\mathbf{f}_1, \mathbf{f}_2, ..., \mathbf{f}_\mathbf{N}\}$ be a set from independent samples drawn from a single distribution described by a PDF $p(\mathbf{f}; \theta)$, where θ is the PDF parameter list. The likelihood function:

$$\square(\square; \theta) = \prod_i p(\mathbf{f}_i; \theta) \tag{21}$$

tells the likelihood of the features $\square$ given the distribution parameters θ. The goal is to find $\hat{\theta}$, which maximizes the likelihood:

$$\hat{\theta} = \arg\max_\theta \square(\square; \theta). \tag{22}$$

Usually this function is maximized indirectly using log-likelihood function $L(\square; \theta) = \ln \square(\square; \theta)$. Setting the derivatives of log-likelihood function to zero is according to Expectation Maximization (EM) algorithm.

3. Experimental Results

3.1. Example for Denoising

A SWT denoised real-word ECG signal is shown in *figure 4*. It is obtained by using Wavelet *De-noising* 1-D Toolbox form Matlab®. The levels of decomposition are 5 and the used

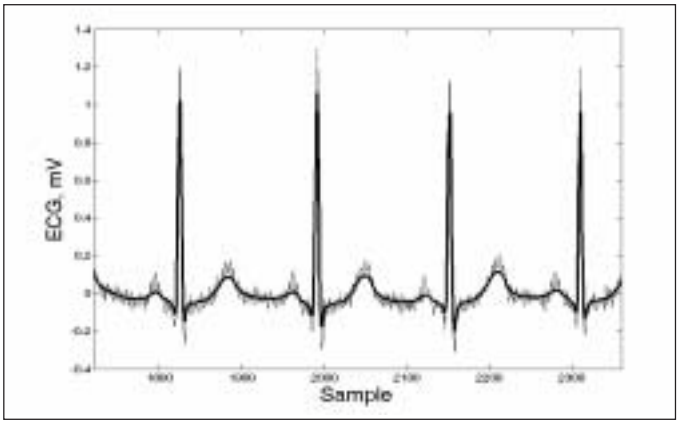


Figure 4. ECG SWT denoising example

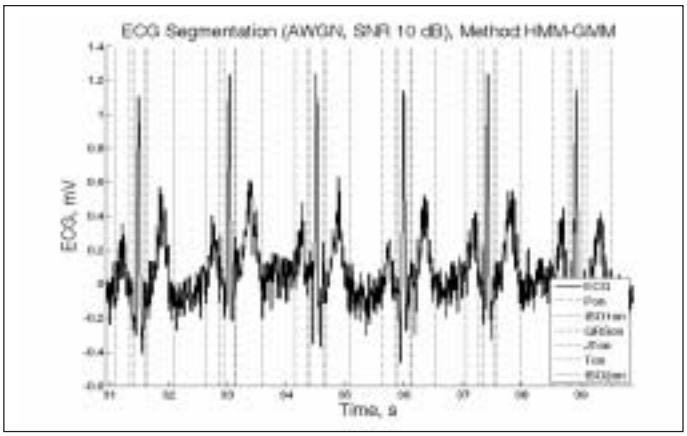


Figure 5. ECG segmentation result with HMM-GMM and AWGN influence (SNR=10 dB)

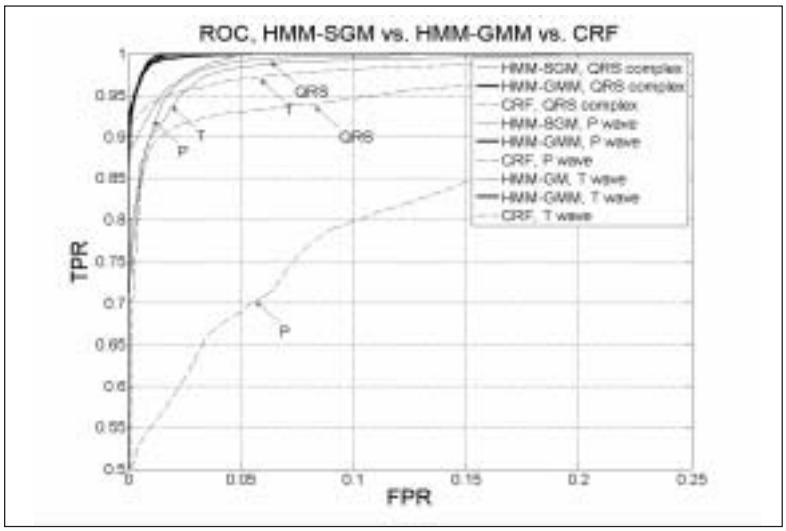


Figure 6. Segmentation performance comparison between HMM-GMM (8 components), HMM-SGM and CRF

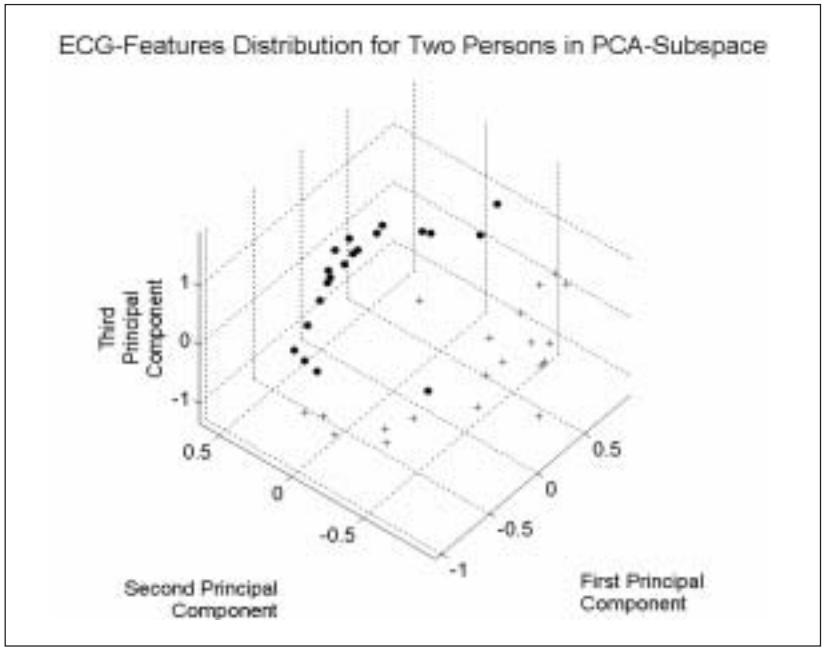


Figure 7. ECG-Features Distribution for two persons (o and +) according to the first 3 principal components in PCA subspace

	P_{on}	$ISO1_{on}$	QRS_{on}	T_{on}
	μ_e, ms σ_e, ms	μ_e, ms σ_e, ms	μ_e, ms σ_e, ms	μ_e, ms σ_e, ms
Noise free ECG	*-3.8* *6.1*	*5.8* *4.2*	*-11.1* *5.1*	*-6.9* *7.2*
ECG with AWGN (SNR = 10 dB)	*7.5* *48.1*	*-4.8* *91.6*	*-16.2* *7.1*	*4.4* *12.3*

wavelet function is Haar. The noise is assumed as additive white Gaussian (AWGN).

This type of noise is used to evaluate the robustness of the probabilistic models for ECG segmentation. Also, a synthetic ECG has been corrupt with AWGN (SNR = 5 dB) and Wavelet-denoised according to the mentioned conditions. The MSE between original and denoised ECG is 0.6 %.

3.2. Example for Segmentation

The segmentation performance is evaluated by using a synthetic ECG signal composed from Gaussians with random parameters. This approach ensures that the ECG signal is noise free and eliminates the subjective criterion in terms to define onset and offset in ECG waves. Finally, the model performance is evaluated by segmenting the same synthetic signal corrupted with additive white Gaussian Noise (AWGN) (*figure 5*).

As can be seen from *figure 6* the comparative analysis for ECG segmentation performance confirms that HMM-GMM (8 components) outperforms HMM-SGM and CRF methods.

The ECG segmentation performance for HMM-GMM is additionally evaluated by using mean value μ_e and the standard deviation σ_e of the absolute error between expert annotated and detected ECG characteristic point (onset or offset of a given ECG wave or complex). The segmentation performance results for noise free synthetic ECG and synthetic ECG with AWGN can be seen in the *table*.

The probabilistic models for ECG segmentation are based on Conditional Random Field (CRF) Toolbox for Matlab [5].

3.3. Example for Feature Space Projection

In our experiments we have used real-world ECG data from 10 persons, which is acquired with industry-standard ECG hardware, equipped with PC-interface. The ECG-cycles projections for two different persons form clusters in PCA subspace are shown in *figure 7*.

3.4. Example for Classification

In the classification experiments we have used ECG PCA training set from 10 persons with 10 complete cardiac cycles for each. The classifier has been tested with other ECG records acquired from the same persons. In *figure 8* can be seen the ROC curve for the recognition performance of the first person.

4. Conclusion

In this work we have presented a new approach for personal biometric identification based on ECG features classification. We denoise the input signal and segment it into sequences. After that we perform dimensionality reduction of the input sequence and extract the PCA features. Then we apply GMM classifiers for recognition.

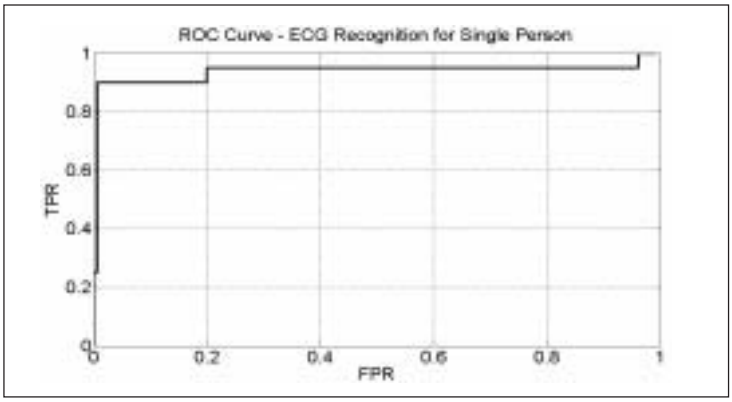


Figure 8. ECG classification performance for single person

The future development of the method will involve a combination with another biometric modality, such as face or fingerprint. Other methods for classification will also be researched. The plans are to use a combination from the output data, which will assure independence and flexibility of the subsystems.

It is planned to achieve more discriminative features for ECG personal recognition when implementing the Linear Discriminant Analysis (LDA) method.

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