

# An efficient clustering-based non-fiducial approach for ECG biometric recognition

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**Abstract**—Recognition of individuals through different biometric traits is becoming increasingly important. Apart from traditional biomarkers (like fingerprints), many alternative traits have been proposed during the last two decades: ECG and EEG signals, iris or facial recognition, behavioral traits, etc. Several works have shown that ECG-based recognition is a feasible alternative for either stand-alone or multibiometric recognition systems. In this paper, we propose a novel, efficient and scalable clustering-based method for ECG biometric recognition. First of all, fixed length segments of the ECG are extracted without the need of computing any fiducial points. Unique traits for each subject are then obtained by computing the autocorrelation (AC) of each segment, followed by the discrete cosine transform (DCT) to compress the available information. Finally, hierarchical agglomerative clustering (HAC) is applied to generate the groups that will be used later on for classification. The combination of the DCT to reduce the feature dimensionality and the HAC to decrease the number of features required by the classifier results in an efficient method both from the memory storage and computational point of view. Furthermore, the proposed AC/DCT-HAC (ADH) approach is robust, since no fiducial points (which may be difficult to extract reliably) are required, scalable and attains a better performance than other approaches with higher storage/computational cost.

**Index Terms**—electrocardiogram (ECG), biometric recognition, non-fiducial methods, hierarchical agglomerative clustering

## I. INTRODUCTION

Correct identification of individuals through different biometric traits is becoming increasingly important. Traditional recognition systems, based on a combination of access cards and passwords, suffer from several well-known weaknesses: ease of identity impersonation, security breaches due to access card/password theft, denial of access to the intended user due to forgotten passwords or lost access cards, etc. As an alternative, biometric recognition systems rely on unique biological traits of the subjects which are difficult to falsify and cannot be lost or forgotten. Some traditional biomarkers (like fingerprints) have already been used for a long time, for example as part of national identification systems [1]. However, many alternative biometric measures have been proposed during the last two decades: ECG and EEG signals [2], [3], iris or facial recognition [4], [5], [6], behavioral traits [7], [8], etc.

In this paper, we focus on ECG-based biometric identification. Since the seminar works of Biel *et al.* [9], [10],

several authors have shown that ECG-based recognition is a feasible alternative either for stand-alone or multi-biometric recognition systems. On the one hand, several systems based on *fiducial methods*, which rely on using several fiducial points extracted from the detected QRS complexes (based on significant intervals and normalized amplitudes of the different waveforms), have been proposed [11], [12]. Unfortunately, extracting the fiducial points can be computationally demanding and cannot be reliably performed for all users. On the other hand, *non-fiducial methods*, which do not require the extraction of the QRS complexes from the signals and work directly with a transformed version of the raw data (e.g., DCT transform), have been considered [13], [14]. However, these studies have been performed on very reduced sets of subjects (14 and 27, respectively) and their scalability is still unclear. Odinaka *et al.* performed a comprehensive survey of existing methods in 2012, comparing several of them on a common dataset [2]. Unfortunately, the database used was not made publicly available. A more recent survey was undertaken by Fratini *et al.*, but no simulation study was performed [15]. Since then, several *deep learning* approaches, where the relevant features are automatically extracted by the network, have been proposed [16], [17], [18]. However, they have large memory storage and computational cost requirements that prevent their use in some applications, and their scalability is also unclear as it may require re-training the network whenever new data are available. Finally, several authors have also developed multi-modal biometric systems, where the ECG signal is combined with other biometric traits in order to enhance identifiability [19], [20], [21].

In this paper, we propose a novel, efficient and scalable clustering-based method for ECG biometric identification. First of all, fixed length segments of the ECG are extracted without the need of computing any fiducial points. Unique traits for each subject are then extracted by computing the autocorrelation (AC) of each segment, followed by the discrete cosine transform (DCT) to compress the available information [13], [14]. Finally, hierarchical agglomerative clustering (HAC) is applied to generate the groups that will be used later on for classification. This is the main novelty of the paper, since a clustering-based classification approach had never been proposed for ECG biometric recognition as far as we know. The combination of the DCT to reduce the feature dimension-

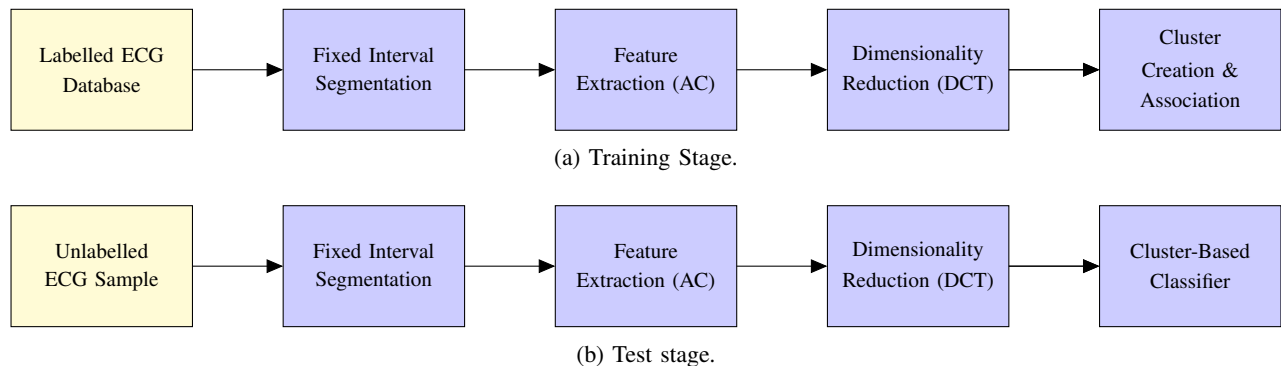


Fig. 1: Block diagram of the novel ECG-based biometric identification system proposed.

ality and the HAC to decrease the number of features required by the classifier results in an efficient method both from the memory storage and computational point of view. Furthermore, the proposed AC/DCT-HAC (ADH) approach is robust, since no fiducial points (which may be difficult to extract reliably) are required, scalable and attains a better performance than other approaches with higher storage/computational cost.

The paper is structured as follows. First of all, Section II provides an overview of the novel ECG-based biometric identification system developed. Then, the proposed clustering approach is described in Section III. Finally, the numerical results are shown in Section IV and the conclusions are provided in Section V.

## II. PROPOSED ECG-BASED IDENTIFICATION SYSTEM

The proposed system, both for the training and test stages, is described in Figure 1. During the *training stage*, we assume that a database with single-channel labelled ECG data is available. In this paper, we use the  $P = 548$  valid recordings from the PTB database [22], which is described in Section IV-A. These data are used as the input to the four blocks shown in Figure 1a:

- 1) A *segmentation* of the time-domain ECG signal in fixed blocks of  $T_b = 5$  seconds. This segmentation is performed without computing any fiducial points (i.e., without the need to detect the R peak or any other waveform inside the ECG) and without any overlap among the segments.
- 2) A *feature extraction* stage, which consists in computing the autocorrelation (AC) of the samples in the fixed length segment. This AC is unique for each subject, since the information about the length and height of the different relevant waveforms in the ECG (i.e., the so called P-QRS-T complexes) is embedded in the shape of the AC [13], [14].
- 3) A *dimensionality reduction* stage to reduce the large number of features extracted in the previous stage ( $N_f = T_b \cdot f_s + 1 = 5001$  for the PTB database considering only positive lags). This dimensionality reduction is based on the discrete cosine transform (DCT) [13], [14], which allows us to reduce the number of relevant features to

only  $N_c = 40$  (i.e., the first  $N_c = 40$  coefficients of the DCT) thanks to the DCT's energy compaction property.

- 4) A *clustering* approach to group the extracted features into separate clusters associated to each user. Hierarchical, agglomerative clustering (with different distance metrics and linkages) is used here, but other clustering approaches will be explored in future works. Note that the important problem of cluster association has to be addressed. A detailed description of this stage is provided in Section III.

During the *test stage* a new unlabelled sample is provided to the system in order to identify the unknown user. As shown in Figure 1b, the first three blocks are the same as in the training stage: segmentation, feature extraction and dimensionality reduction. The only difference occurs in the last block, where the clustering approach is substituted by a classifier to determine the identity of the user. Here, we use a simple  $K$  nearest neighbours ( $k$ -NN) classifier with  $K = 1$ , since we focus on efficiency and scalability, and it still provides an excellent performance, as shown in Section IV. However, more sophisticated classifiers can also be used.

Note that the  $k$ -NN classifier could be applied directly using the samples from the training set after the feature extraction and dimensionality reduction. However, by adding the clustering stage the number of samples for the  $k$ -NN classifier is substantially reduced (see Section IV). As a result, biometric recognition during the test stage becomes much more efficient and the proposed scheme is better prepared to incorporate new users (i.e., it becomes more scalable) in the future.

## III. CLUSTERING METHOD

In this section, we describe in detail the central stage of the proposed ECG-based system: the clustering method. We briefly describe first the method used for the creation of the clusters, hierarchical agglomerative clustering, followed by the description of the cluster association approach followed, which is based on majority voting.

### A. Hierarchical Agglomerative Clustering

We propose to use a hierarchical agglomerative clustering approach for the creation of the clusters, since it is a simple

and well-known clustering approach that we have recently used to construct multi-scale dictionaries for ECG modeling [23]. However, note that the goal of the clustering stage is completely different now. On the one hand, in [23] we were looking for a few representative waveforms that allowed us to build compact and representative dictionaries to perform sparse modelling of a wide range of ECG signals. On the other hand, here we want to obtain a set of  $Q \geq P$  clusters that allow us to discriminate among all the  $P$  subjects in our database. Finally, note that we also need to solve the important cluster association problem (i.e., assigning one or more clusters to every user in the database), which was unnecessary in [23].

The hierarchical agglomerative clustering technique starts with  $R = LP$  singleton clusters, corresponding to all available samples from all subjects, and constructs the clusters iteratively following the hierarchical approach described in Algorithm 1.

Start with  $R$  singleton clusters;  
 Calculate the proximity matrix for the  $R$  clusters;  
**repeat**  
     Search for the pair of clusters  $C_i$  and  $C_j$  with the  
     minimal distance  $d_{i,j} = \min_{\substack{1 \leq m, l \leq R \\ m \neq l}} d(C_m, C_l)$ ;  
     Join clusters  $C_i$  and  $C_j$  to form a new cluster;  
**until** the desired number of clusters remains;

**Algorithm 1:** Hierarchical agglomerative clustering.

The key point in Algorithm 1 is the construction of the *proximity matrix* that quantifies the similarity or dissimilarity of each pair of identified clusters, and thus determines the cluster aggregations at each iteration of the algorithm. A proximity matrix can be defined as a square  $R \times R$  matrix,  $\mathbf{D}$ , whose  $(i, j)$ -th element contains the distance (dissimilarity)  $d_{i,j} = d(C_i, C_j)$  among each pair of clusters  $C_i$  and  $C_j$  for  $1 \leq i, j \leq R$ :

$$D = \begin{pmatrix} 0 & d_{1,2} & \cdots & d_{1,R} \\ d_{2,1} & 0 & \cdots & d_{2,R} \\ \vdots & \vdots & \ddots & \vdots \\ d_{R,1} & d_{R,2} & \cdots & 0 \end{pmatrix}. \quad (1)$$

The values of the elements in the proximity matrix depend on two parameters: the distance metric and the linkage function. On the one hand, we have to define a *distance metric* to determine the dissimilarity among any two samples  $\mathbf{x}_i$  and  $\mathbf{x}_j$ . A huge number of distances exist [24], but here we only consider four of the most common ones:

- **Euclidean:**  $d(\mathbf{x}_i, \mathbf{x}_j) = \|\mathbf{x}_i - \mathbf{x}_j\|_2$  with  $\|\cdot\|_2$  denoting the  $\ell_2$  norm.
- **City Block (a.k.a. Manhattan):**  $d(\mathbf{x}_i, \mathbf{x}_j) = \|\mathbf{x}_i - \mathbf{x}_j\|_1$  with  $\|\cdot\|_1$  denoting the  $\ell_1$  norm.
- **Cosine:** Defined as one minus the cosine of the included angle between the two vectors  $\mathbf{x}_i$  and  $\mathbf{x}_j$ . It can be easily computed as  $d(\mathbf{x}_i, \mathbf{x}_j) = 1 - \frac{\mathbf{x}_i^\top \mathbf{x}_j}{\|\mathbf{x}_i\|_2 \|\mathbf{x}_j\|_2}$ , where  $\mathbf{x}^\top$  denotes the transposed vector.

- **Correlation:** One minus the sample correlation between points (treated as sequences of values).

On the other hand, we also need to define the *linkage* function, which determines the distance among clusters and is based on the distance metric previously defined. Let us consider two clusters,  $C_i$  and  $C_j$ , whose elements are, respectively,  $\mathbf{x}_{ik}$  and  $\mathbf{x}_{j\ell}$  for  $k \in \{1, \dots, |C_i|\}$ ,  $\ell \in \{1, \dots, |C_j|\}$ , and  $|C|$  denoting the cluster's cardinality. We have considered the following linkages:

- **Single:** The distance between clusters  $C_i$  and  $C_j$  is determined by the distance among their nearest elements:  $d_{i,j} = \min d(\mathbf{x}_{ik}, \mathbf{x}_{j\ell})$  for  $k \in \{1, \dots, |C_i|\}$  and  $\ell \in \{1, \dots, |C_j|\}$ .
- **Complete:** The distance between clusters  $C_i$  and  $C_j$  is determined by the distance among their furthest elements:  $d_{i,j} = \max d(\mathbf{x}_{ik}, \mathbf{x}_{j\ell})$  for  $k \in \{1, \dots, |C_i|\}$  and  $\ell \in \{1, \dots, |C_j|\}$ .
- **Average:** The distance between clusters  $C_i$  and  $C_j$  is determined by the average distance among their elements:  $d_{i,j} = \frac{1}{|C_i||C_j|} \sum_{k=1}^{|C_i|} \sum_{\ell=1}^{|C_j|} d(\mathbf{x}_{ik}, \mathbf{x}_{j\ell})$ .
- **Ward:** Based on the incremental sum of squares, i.e., the increase in the total within-cluster sum of squares as a result of joining two clusters. It can be computed using the following formula:  $d_{i,j} = \sqrt{\frac{2|C_i||C_j|}{|C_i|+|C_j|}} \|\bar{\mathbf{x}}_i - \bar{\mathbf{x}}_j\|_2$ , where  $\bar{\mathbf{x}}_i$  denotes the centroid of the  $i$ -th cluster.

All possible combinations of distance metrics and linkages have been tested and the results are shown in Section IV.

## B. Cluster Association

Let there be a set of observations  $\mathbf{X}$  with  $P$  desired partitions  $S_i$  ( $i \in [1, P]$ ) corresponding to the identity of  $P$  subjects. Every single sample can be identified as  $\mathbf{x}_{ik} \in S_i$ , where  $k \in [1, L_i]$  and  $L_i = |S_i|$ . After the clustering stage described in the previous section, we obtain  $Q$  clusters,  $C_m$  for  $m \in [1, Q]$  and  $Q \geq P$ , where each cluster is composed of one or more observations  $\mathbf{x}_{ik}$ . The cluster association step consists in labeling each cluster  $C_m$  by assigning a single subjects' identity to it. Majority voting, based on the known labels from the training set, is used in this step.

However, if we set  $Q = P$  in the hierarchical agglomerative clustering algorithm, we may end up with some subjects not being assigned to any cluster after the majority voting. The simplest strategy for solving this issue (and determining the final value of  $Q$ ) consists in trying different increasing values of  $Q$  starting from  $P$  until all the subjects' identities have been associated to one or more clusters. The implementation of the aforementioned strategy, based on testing increasing values of  $Q$ , is summarized in Algorithm 2.

## IV. RESULTS

### A. PTB Database

In order to test the proposed approach, we use the Physikalisch-Technische Bundesanstalt (PTB) database, compiled by the National Metrology Institute of Germany for research, algorithmic benchmarking and teaching purposes

**Data:** $P$ : number of partitions of  $\mathbf{S}$  $linkage$ : Hierarchical clustering linkage of  $\mathbf{S}$  $Q_{MAX}$ : Value of  $Q$  in the most adverse clustering case**Result:** $C$ : partition of  $Q$  clusters $Q$ : number of clusters of  $C$  $Q \leftarrow P - 1$ ;**repeat** $Q \leftarrow Q + 1$ ; $C \leftarrow$  partition of  $Q$  clusters;**foreach** cluster  $Q_m$  of  $C$  **do**    Calculate the centroid  $centroid_m$  of  $Q_m$ ;    Obtain the subjects' identity label  $l_m$  associated to  $centroid_m$  by majority voting considering all  $s_{ij} \in Q_m$ ;**end****until**  $|\{l_m | m = 1, 2, \dots, Q\}| = P$ ;**Algorithm 2:** Algorithm for obtaining  $Q$ .

[22]. The ECGs were collected from healthy volunteers and patients with different heart diseases by Prof. Michael Oeff, at the Dep. of Cardiology of Univ. Clinic Benjamin Franklin in Berlin (Germany), and can be freely downloaded from Physionet [25].<sup>1</sup> The database contains 549 records from 290 subjects (aged 17 to 87 years) composed of 15 simultaneously measured signals: the 12 standard leads plus the 3 Frank lead ECGs [26], [27]. Each signal is digitized using a sampling frequency  $f_s = 1000$  Hz with a 16 bit resolution. Out of the 549 records, we used the  $P = 548$  records for which a valid V1 lead recording existed. Subject 285 in the PTB database has a single record that does not show any heartbeats on the V1 lead, so we removed it.

**B. Numerical Results**

Table I shows the performance (obtained using 40 Monte Carlo simulations in each case) for all the tested combinations of linkage and distance metrics with the training percentage that leads to the best performance. The table shows both the average accuracy ( $\overline{ACC}$ ) and the average percentage of  $Q$  normalized by the training set size ( $\overline{Q}/N_{training}(\%)$ ). On the one hand, when considering the  $\overline{ACC}$  as the performance metric we can see that the 10 different combinations of linkage-distance metrics and training percentages attain an average accuracy above 99.98%, which is an excellent result. On the other hand, the  $\overline{Q}/N_{training}(\%)$  allows us to estimate the reduction in the number of features attained by the proposed clustering stage. The most efficient combination corresponds to an average linkage with the cosine distance and 85% of the available samples assigned to the training set, since an  $\overline{ACC} = 0.999897$  is attained using only a 23.41% of the

TABLE I: Average accuracy ( $\overline{ACC}$ ) and average value of  $Q$  normalized by the training set size ( $\overline{Q}/N_{training}$ ) for different linkage-distance metrics and training percentages.

Linkage	Metric	Train (%)	$\overline{ACC}$	$\overline{Q} / N_{training} (\%)$
Complete	City Block	90	<b>0.999921</b>	32.6
Ward	City Block	90	<b>0.999917</b>	36.99
Single	City Block	75	<b>0.999916</b>	42.14
Ward	Correlation	90	<b>0.999909</b>	24.55
Ward	Cosine	90	<b>0.999902</b>	25.85
Average	Euclidean	90	<b>0.999901</b>	33.55
Ward	Euclidean	90	<b>0.999898</b>	34.51
Complete	Cosine	90	<b>0.999898</b>	27.5
Average	Cosine	85	<b>0.999897</b>	23.41
Single	Euclidean	75	<b>0.999894</b>	37.76

available samples in the training set (i.e., a compression by a factor larger than 4 has been attained).

In [28] we compared the performance of several fiducial methods using different dimensionality reduction and classification techniques on the same dataset as the one used here, although only the healthy subjects were used then. Comparing the average accuracy attained here to the accuracy of the fiducial ECG-based biometric identification approaches tested in [28] (99.65 – 99.85% for the best cases), we see that the proposed ADH method allows us to obtain even better performance while decreasing the storage and computational cost. Furthermore, extracting all the fiducial points requires a considerable amount of time and cannot always be performed reliably: from the 52 healthy patients of the PTB database, we were only able to compute all the required fiducial points for 48 subjects in [28]. In contrast, the non-fiducial, clustering-based approach proposed here does not require computing any fiducial points and thus can be reliably applied in all cases with little computational cost.

**C. Results for MIT-BIH Database**

Preliminary results have also been obtained from the MIT-BIH arrhythmia database. This database contains 48 records from 47 subjects, with a half-hour duration for each one [29], and can also be freely downloaded from PhysioNet [25].<sup>2</sup> Each record contains two simultaneously measured channels with a half-hour duration, taken at  $f_s = 360$  Hz with an 11 bit resolution. We used the second channel, which corresponds to a modified V1 lead in most subjects, with the exceptions of 4 subjects where a V2 lead was used, 5 with a V5 lead and one with a V4 lead. Although some signals from the MIT-BIH database are reasonably clean (e.g., the record from subject 103), in general MIT-BIH records generally present a higher amount of noise than those in PTB, and we want to investigate how this affects the recognition performance.

In terms of accuracy, the best result ( $\overline{ACC} = 0.9952$ ) is obtained using a simple linkage with Euclidean distance and 90% of the samples in the training set. However, for this approach we obtain a high value of  $\overline{Q}/N_{training}(\%) = 52.09$  (i.e., the feature size is only reduced by a factor of 1.92). In order to increase the compression, we need to slightly

<sup>1</sup>PTB database: <https://www.physionet.org/physiobank/database/ptbdb/>

<sup>2</sup>MIT-BIH database: <https://physionet.org/content/mitdb/1.0.0/>

decrease the accuracy. Using Ward linkage with city block distance and 75% of the samples in the training set we obtain  $\overline{Q}/N_{training}(\%) = 14.31$  (compression factor equal to 6.99, 3.62 times higher than before) with  $\overline{ACC} = 0.9934$  (i.e., only a 0.18% decrease in accuracy). Therefore, we see that the lower quality of the database has a small impact on the attained performance (0.64% decrease in average accuracy), but no impact at all in the achievable compression rate, which is even higher than before.

## V. CONCLUSIONS

In this paper, we have proposed a novel ECG-based biometric recognition scheme which is based on a clustering method (hierarchical agglomerative clustering). The developed approach is efficient (both from the computational cost and storage points of view), robust, scalable, and attains excellent results on all the subjects from the PTB database: average accuracy above 99.98% with a reduction in feature size by a factor of 4.27. Preliminary results on the MIT-BIH arrhythmia database also show very good results (99.34% accuracy in the best case with a reduction in feature size by a factor of 6.99) in spite of the lower quality and reduced sampling rate of this database. Future works will include testing the system on a larger number of subjects (e.g., on the recently released PTB-XL database) and considering other clustering techniques.

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