ECG Biometrics Using a Dissimilarity Space Representation

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Abstract: Electrocardiogram (ECG) biometrics are a relatively recent trend in biometric recognition, with at least 13 years of development in peer-reviewed literature. Most of the proposed biometric techniques perform classification on features extracted from either heartbeats or from ECG based transformed signals. The best representation is yet to be decided. This paper studies an alternative representation, a dissimilarity space, based on the pairwise dissimilarity between templates and subjects' signals. Additionally, this representation can make use of ECG signals sourced from multiple leads. Configurations of three leads will be tested and contrasted with single-lead experiments. Using the same *k*-NN classifier the results proved superior to those obtained through a similar algorithm which does not employ a dissimilarity representation. The best Authentication EER went as low as 1.53% for a database employing 503 subjects. However, the employment of extra leads did not prove itself advantageous.

1 INTRODUCTION

1.1 ECG Basics

Humans possess an intrinsic ability to recognize patterns and observations as part of a certain class. Often the class-assigning process is immediate and deemed obvious. However, when asked to explain how that conclusion was achieved, the human observer is unable to detail the iterations that led him to it.

A biometric system attempts to replicate this behaviour and pursue an even more demanding goal – subject identification. For that purpose a specific procedure must be designed which will employ sensors to measure the data requested by it.

In what concerns the field of Electrocardiogram (ECG) Biometrics the sensors record the heart's electrical activity – the ECG itself – and build a procedure for feature extraction and classification. An ECG heartbeat is composed by three main components: P wave, QRS complex, and T wave, illustrated in Figure 1.

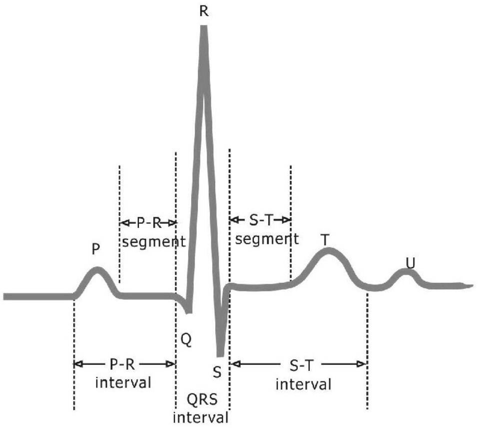

Figure 1: A labeled ECG waveform.

The measurement of an ECG is obtained via correct placement of a number of electrodes in specific parts of the body and by tracing voltages between them. Specific linear combinations between electrode potentials result in different leads. For instance, *lead I* corresponds to the voltage between the electrodes in the right and left arms, as stated by Einthoven's Triangle (Conover, 2003) shown in Figure 2.

An ECG biometric system works just like any other biometric system or any supervised learning algorithm. Its functioning can be divided into two modes of operation – enrolment and classification.

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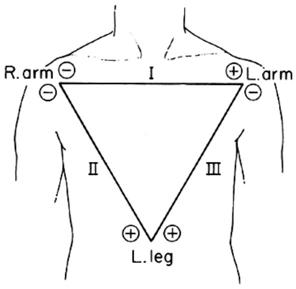


Figure 2: Figure representing Einthoven's Triangle and respective leads. The lead voltages are taken from the plus to the minus signs.

During *enrolment* the system is given a user's ID and extracts his/her information – the training data. From this data the classifier generates the templates which best represent the user and build the system's database. More enrolled subjects imply greater difficulty for identification as the number of possible choices increases (and the probability of having an individual with similar data also increases). This effect can be countered by storing more templates for a given subject.

The second mode, *classification* extracts a current user's data and compares it to the registered training data. It then outputs the best match, i.e. the correct user in the case of a biometric system. Classification can be divided into two procedures, *authentication* and *identification*.

Authentication
The system is provided an ID and will confirm or deny that a given user is who he/she claims to be. For that purpose the classifier performs only comparisons with respect to the given ID's stored templates.

Identification
In this case, the classifier is not given any ID by the user. As a result, it must search its entire database for the subject whose templates best match the input data.

1.2 ECG Biometrics

All the studies on ECG biometrics are based on one-lead, two-lead, three-lead, or 12-lead ECG signals, mirroring what is most commonly employed in clinical situations (Odinaka et al., 2012). The most widespread lead configuration used in ECG biometrics is by far the one-lead configuration as (Biel et al., 2001) demonstrated that a signal from one lead contains enough information to form the basis for a biometric system. Nonetheless, some studies have resorted to multiple-lead ECG signals in their biometric strategy. (Ye et al., 2010) utilized two leads (Fang and Chan, 2009) (Wübbeler et al., 2007) and (Labati et al., 2013) opted for three leads and (Biel et al., 2001) and (Agrafioti and Hatzinakos, 2008) used 12 leads. The technique proposed in this article will be tested in a single and triple-lead scenario, employing the limb-lead *I* or all the limb-leads *I*, *II* and *III* respectively.

With an ECG signal in hand, regardless of the lead, there are several existing techniques for carrying out the feature extraction procedure. These fall into three different categories in what concerns the type of features they employ (Odinaka et al., 2012).

Fiducial Features
These methods use characteristic points of an ECG heartbeat and/or relationships between them as features – the fiducial features. Characteristic points include the peak of the R-wave, while a relationship between points can be the temporal duration of a QRS impulse. Several combinations of the four types of fiducial features have been used in the literature (Singla and Sharma, 2010) – temporal, amplitude, angle and dynamic (R-R intervals) (Odinaka et al., 2012).

Non-Fiducial Features
Techniques based on non-fiducial features do not use characteristic points as features. Despite that, most of them rely on some characteristic points for heartbeat segmentation (Chan et al., 2008) (Fatemian and Hatzinakos, 2009) while others simply create windows from the ECG recording (Wang et al., 2013) (Plataniotis et al., 2006) (Agrafioti and Hatzinakos, 2008) (Li and Narayanan, 2010). Afterwards these segments/windows are transformed into another domain so as to extract features from the resulting signals.

Hybrid Features
Algorithms in this group resort to both fiducial and non-fiducial features for their biometric system. Some use a combination of them as features (Wang et al., 2008) (Silva et al., 2007). Others design two classifiers where the first uses non-fiducial features to reduce the match set and the second outputs the classification while being fed with the fiducial features (Shen and Hu, 2011) (Shen et al., 2002).

Having assembled the feature space some algorithms additionally perform its dimensionality reduction. Afterwards, the reduced or raw feature space is then directly used for the training of classifiers. Regardless, it must be emphasised that the ideal feature representation is yet to be found – all the existing ones present pros and cons in relation to one another.

It is on these grounds that the current article introduces the concept of a feature space based on a Dissimilarity Representation for ECG biometrics by resorting to comparisons between signals as inspired by the study in (Duin and Pękalska, 2011). The current study explores this possibility by designing a multi-lead configuration and comparing it with the single-lead version. Dissimilarity Representations will be explained in Section 3.

Moreover Section 2 describes the notation used in this paper. Section 4 then outlines the pre-processing feature extraction and template generation carried out on the ECG signals, as well as the utilized classifier. Section 5 outlines the executed experiments and their results. This paper is concluded in Section 6 which draws the main findings and conclusions.

2 NOTATION

In order to better understand the methodology proposed in this paper as well as the process of building the dissimilarity representation, the notation that will be employed throughout the paper is here presented.

The basic element behind the proposed method's biometric system is the ECG heartbeat. Heartbeats will be employed as templates and dissimilarities will be calculated through comparisons between them. The current work utilized a Sampling Frequency of 500 Hz. With this in mind we shall consider:

- A population of $\boldsymbol{S}$ existing subjects;
- A percentage $\boldsymbol{p}$ which is considered sufficient to represent the whole population variation. From this percentage, a number of subjects $\boldsymbol{S_p}$ will be randomly chosen from S. For this work p is set to 15%.
- A set $\boldsymbol{C}$ of leads. For the scope of this work, $\boldsymbol{C}$'s elements will be either the single-lead $[I]$ or the 3 limb-leads $[I, II, III]$. The variable L is defined as $L = |C|$.
- $\boldsymbol{N_i}$ as the number of extracted heartbeats from subject i's ECG, $i = 1, \ldots, S$.
- $\boldsymbol{N} = \sum_{i=1}^{S} N_i$ as the number of all extracted heartbeats over all subjects.
- A heartbeat belonging to subject i is denoted by $h^l_{i_j}$ with $j = 1, \ldots, N_i$ and $l \in C$. The variable h_{i_j} implies a heartbeat originating from lead I. Beats are represented by a 600 ms window which is built having the R-peak as a reference at position 200 ms. Thus, for the employed Sampling Frequency, they are composed of 300 samples.
- A reference lead, $\boldsymbol{R}$, which for the scope of this work will be lead $\boldsymbol{I}$. Note that $h^R_{i_j}$ will correspond to signals taken from lead $\boldsymbol{R}$.
- A Feature Space $\boldsymbol{F}$, represented by an $\boldsymbol{N} \times \boldsymbol{M}$ matrix. $\boldsymbol{M}$ consists of the 300 samples present in a heartbeat.

Two metrics have been employed in various steps of the proposed methodology – the euclidean distance and the cosine similarity. For the sake of clarity they are respectively defined here in Equations 1 and 2.

$$D(h_{i_j}, h_{i_k}) = \sqrt{(h_{i_j} - h_{i_k})^T (h_{i_j} - h_{i_k})} \qquad (1)$$

$$D(h_{i_j}, h_{i_k}) = 1 - \frac{h_{i_j} \cdot h_{i_k}}{\|h_{i_j}\| \|h_{i_k}\|} \qquad (2)$$

where $\|.\|$ represents the euclidean norm.

3 DISSIMILARITY REPRESENTATION

A *Dissimilarity Representation* is built on the fact that similarity between objects plays a crucial role in class formation, i.e. a class is a set of similar objects (Duin and Pękalska, 2012). A universal object similarity, however, does not exist and always depends on the classification context, procedure and/or the domain of study. Moreover, the presence of other classes will influence the degree to which an object should or should not be assigned to a particular class.

This paper puts forward the notion of dissimilarity between ECG elements. Calculating a dissimilarity is simply comparing elements, pairwise, according to some pre-defined rules (Duin and Pękalska, 2012). Metrics, for instance, fit this criteria. The present study will explore two different ones – *euclidean* distance and *cosine* similarity.

A dissimilarity-based representation can be constructed from any type of elements which can be any kind of feature array possible. Also, they can be built from as many comparisons between elements as one wishes. Consequently, note that this process is easily extensible to using more than one-lead by simply comparing one lead's elements with another lead's elements.

A dissimilarity space intends to take the original feature space F and output another one, F_D, by taking pairwise distances between ECG elements i, where $i = 1, \ldots, N$. This paper proposes two different approaches for defining the dissimilarity space. Subsection 4.4 details their development.

4 PROPOSED METHODOLOGY

The whole methodology for the proposed technique is summarized in Figure 3.

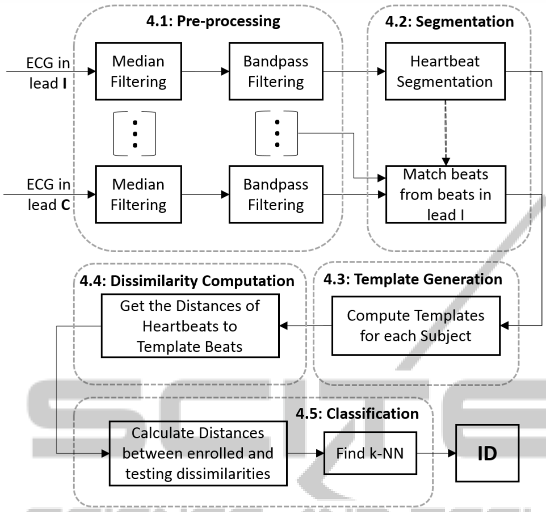


Figure 3: Block diagram of the proposed ECG biometric system. Note that lead **C** simply refers to an arbitrary lead. Also, the suspension points underline the possibility of using additional leads.

4.1 Pre-processing

Due to the presence of several noise sources during measurement – power line interference, electrode contact loss, baseline drift due to respiration and motion artefacts, for example (Friesen et al., 1990)– it is imperative to filter the signal to facilitate the procedure of feature extraction.

In order to remove baseline drift from raw ECG signals we apply the method by (de Chazal et al., 2004). It applies two median filters (of 200 ms and 600 ms respectively) to the raw ECG signal and then proceeds to subtract the resulting waveform to the raw ECG.

Afterwards, an additional filtering stage eliminates the effect of other noise sources through bandpass filtering. The filter consists of a 5 → 20 Hz bandpass FIR filter with order 150. This frequency band removes a substantial part of the information present in heartbeats but compensates by successfully cleaning the signal of any motion artefacts and power line interference as well as reducing electromyographic noise effects.

4.2 Segmentation

In order to segment the ECG signal into heartbeats, R-peak detection is first carried out as in (Hamilton, 2002). Beat detection is performed over a transformed signal which is obtained according to the diagram in Figure 4. Its basic detection rules are as follows:

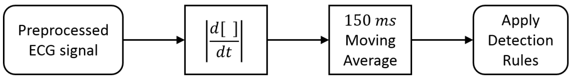


Figure 4: Transformation process applied to the ECG signal so as to perform beat detection.

1. Ignore all peaks that precede or follow larger peaks by less than 200 ms.
2. If the peak occurred within 360 ms of a previous detection and had a maximum slope less than 0.7×the maximum slope of the previous detection assume it is a T-wave.
3. If the peak is larger than the *detection threshold – DT* – call it a QRS complex; otherwise call it noise.
4. If an interval equal to 1.5 times the average R-to-R interval has elapsed since the most recent detection, check for a peak larger than $\frac{DT}{2}$ within that interval. If the peak followed the *preceding* detection by at least 360 ms then classify that peak as a QRS complex.

The *detection threshold – DT* mentioned in rules 3 and 4 – resorts to the following data structures:

QRS-peak buffer
Stores the 8 most recent R-peak values. Its entries are used in the *detection threshold – DT* – calculation. It is initialized with the highest-valued peaks in one second intervals for 8 seconds;

Noise-peak buffer
Behaves like the previous structure but stores the 8 most recent *noise*-peak values instead. It is, however, initialized at 0;

RR-interval buffer
Stores the 8 most recent interval between R-peaks. These are initialized at a value corresponding to a 1 s interval.

The *DT* threshold is computed as:

$$\begin{aligned} DT = {} & Noise\_Peak\_Buff_{med} \\ & + TH(QRS\_Peak\_Buff_{med} \\ & - Noise\_Peak\_Buff_{med}) \end{aligned} \tag{3}$$

where $Noise\_Peak\_Buff_{med}$ and $QRS\_Peak\_Buff_{med}$ are the median of the *Noise-peak buffer* and *QRS-peak buffer* arrays respectively. $TH = 0.45$ was empirically found most suitable for the database used in testing.

However, the peaks detected on the transformed signal do not map directly to the R-peaks in the ECG signal. A post-processing phase is necessary so as to perform adequate R-peak detection. The points found are then mapped to the exact R-peak location by searching within ±150 ms and choosing the highest sloped peak of the two largest ones found in that interval. This process is executed only for lead I – the beats are then matched on the other utilized leads by once again looking for the highest sloped peak of the two largest ones, but this time in a smaller interval consisting of ±60 ms.

Having the location of the R-peaks for all leads, the segments are constructed simply by taking the ECG window from 0 ms to 600 ms, where 200 ms correspond to the R-peak. As mentioned in Section 2, all segments have a fixed length of 600 ms.

4.2.1 Outlier Detection

Outlier removal is performed as in (Lourenço et al., 2013). It will only be executed for lead *I* – the beats here discarded will be discarded for the other employed leads as well.

This algorithm receives as input the N_i heartbeats for subject i and begins by calculating the average beat via:

$$h_i^{av} = \frac{1}{N_i}\sum_{j=1}^{N_i} h_{i_j}, \tag{4}$$

Heartbeats which stray away from the average beat are discarded according to the following procedure:

1. For each h_{i_j}, compute its distance $D(h_{i_j}, h_i^{av})$ to the mean waveform h_i^{av}.
2. Compute the 1^{st} and 2^{nd} order statistical moments of the distances $D(\cdot, h_i^{av})$; $\mu_{D(\cdot,h_i^{av})}$ corresponds to the mean value and $\sigma_{D(\cdot,h_i^{av})}$ to the standard deviation.
3. Compute the median of the *minimum* and *maximum* values over all templates h_{i_j}, denoted as $h_{i_{min}}^{med}$ and $h_{i_{max}}^{med}$ respectively.
4. Verify the conditions below for every h_{i_j}. If any is confirmed, then h_{i_j} is discarded as an outlier:
   (a) $h_{i_{j_{min}}} < 1.5 \times h_{i_{min}}^{med}$, $h_{i_{j_{min}}}$ is the minimum value for beat h_{i_j};
   (b) $h_{i_{j_{max}}} > 1.5 \times h_{i_{max}}^{med}$, $h_{i_{j_{max}}}$ is the maximum value for beat h_{i_j};
   (c) $D(h_{i_j}, h_i^{av}) > \mu_{D(h_{i_j},h_i^{av})} + 0.5 \times \sigma_{D(h_{i_j},h_i^{av})}$;

Note that $D(h_{i_j}, h_i^{av})$ can refer to any distance metric. The present work utilizes the cosine distance in 2.

4.3 Template Generation

The problem of template selection may be posed as follows: given a set of N heartbeats, select K templates that "best" represent the variability as well as the typically observed patterns according to a given similarity criterion (Lourenço et al., 2014).

Clustering methods are especially adequate for this task, and have already been used for template selection in other modalities (Uludag et al., 2004; Connell and Jain, 1999; Liu and Wang, 2008; Lumini and Nanni, 2006). In this paper the K-means algorithm was used, with K empirically set to 5, the cluster's centroids being used as templates (Lourenço et al., 2014).

4.4 Dissimilarity Computation

Dissimilarities can be calculated by measuring a distance between beats according to a metric. Two such metrics have been explored in this study – euclidean distance and cosine similarity referred respectively in Equations 1 and 2. In Section 5 their effects can be contrasted.

Two different dissimilarity extraction techniques are hereby proposed.

Subject based

This first and simplest approach computes the distance $D(h_{i_j}^R, h_{i_t}^l)$ between each segment $h_{i_j}^R$ and the set of $h_{i_t}^l$ template beats for each lead in set C. The process is repeated for all subjects S. It is presented in pseudo-code below.

```
for each subject $i$ in $S$ do
    for each beat $j$ in $N_i$ do
        $ds_{i_j} = [\,]$
        for each lead $l$ in $C$ do
            for each template $t$ do
                $ds_{i_j}$.append($D(h_{i_j}^R, h_{i_t}^l)$)
```

Considering T templates per subject, the resulting dissimilarity representation is then an $\boldsymbol{N \times T{*}L}$ matrix composed by N dissimilarity arrays with $T * L$ components.

Inter-subject based

A second strategy computes the distance $D(h_{i_j}^R, h_{i_t}^l)$ between each segment $h_{i_j}^R$ and the set of $h_{i_t}^l$ template beats of the randomly chosen S_p subjects for each lead in set C. The following pseudo-code outlines these steps.

```
for all $S$ subjects do
    for each beat $j$ in $N$ do
        $ds_j = [\,]$
        for each lead $l$ in $C$ do
```

```
for each subject $s$ in $S_p$ do
    for each template $t$ do
        $\mathrm{ds}_j.\mathrm{append}(D(h_j^R, h_{s_t}^l))$
```

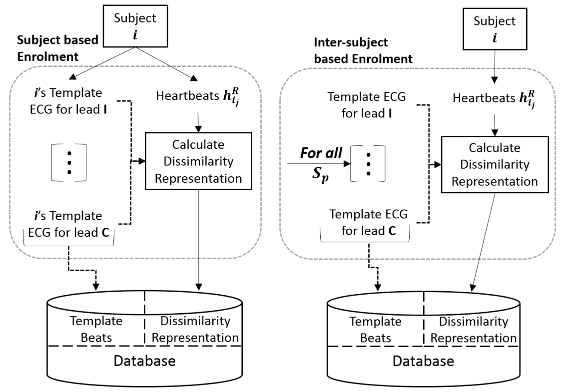
Once again, considering T templates per subject, the obtained dissimilarity representation is an $N \times T*S_p*L$ matrix consisting of N dissimilarity arrays composed by $T*S_p*L$ elements.

4.5 Classification

In classification, both authentication and identification follow the same principles for matching. A feature space comprising dissimilarities supports a large variety of classifiers (Duin et al., 2010). The current work employs a k-Nearest Neighbours (k-NN) model applied to dissimilarity arrays, with k set to 3.

The steps taken during the classification process depend on the dissimilarity representation approach taken in Sub-section 4.4. During enrolment, for a *Subject based* approach, the classifier will store all the S users' template heartbeats $h_{i_t}^l$ for all C leads.

As for the *Inter-subject* method the algorithm saves only the template beats belonging to the S_p subjects (which have been recorded prior to enrolment) over the C used leads.



(a) Enrolment for a Subject based Dissimilarity Representation. (b) Enrolment for an Inter-subject based Dissimilarity Representation.

Figure 5: Enrolment for both approaches.

Both methods store their N respective *template* dissimilarity arrays calculated for all the extracted heartbeats h_{ij}^R over S. Consider v_t as one such template. See Figure 5 for an illustration of this mode. As for authentication and identification, for each dissimilarity representation approach:

Subject based
Authentication or identification determine the set of retrieved $h_{i_t}^l$ templates – in the former they only originate from the requested subject while in the latter they are obtained from the S subjects.

Inter-subject based
In this case, the classifier calculates one single dissimilarity representation with respect to the templates originating from the S_p determined subjects – regardless of the procedure taken.

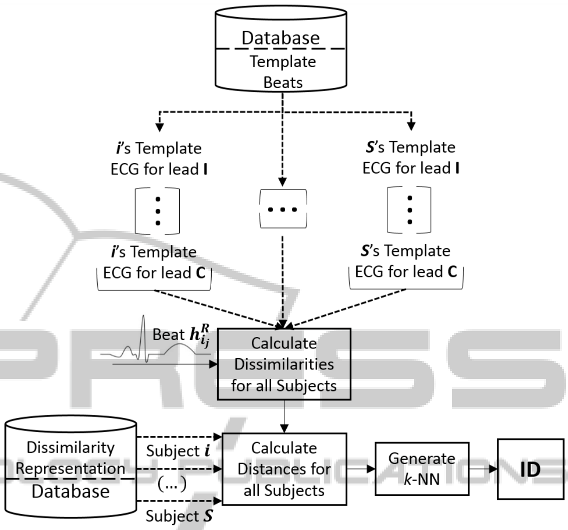


Figure 6: Block diagram illustrating the identification procedure for the Subject based dissimilarity approach.

The obtained dissimilarity arrays are called v_{id}. Then, the template dissimilarity arrays v_t chosen for the determination of the 3-NN are either sourced from the input subject – for authentication – or obtained from all subjects – for identification.

Distances between dissimilarity vectors $D(v_{id}, v_t)$ are once again measured according to both euclidean distance and cosine similarity referred in Equations 1 and 2. In Section 5 their effect in classification is compared as well. See Figures 6 and 7 for the classification procedure for the Subject based and Inter-subject based dissimilarity approaches respectively.

After calculating all the $D(v_{id}, v_t)$, the 3 smallest distances are taken as the 3-Nearest Neighbours. They will then be compared with a threshold, th_{auth} for authentication or th_{id} for identification. This threshold will validate the distances' votes according to:

$$d_k <= th \tag{5}$$

where d_k is one of the 3 resulting distances and th is either th_{auth} or th_{id} according to the chosen mode. Distances d_k not respecting Equation 5 are not considered in the final classification. If at least 2 d_k distances have been validated, then for authentication the input user is confirmed as valid. In identification the most voted user corresponding to those d_k is provided as

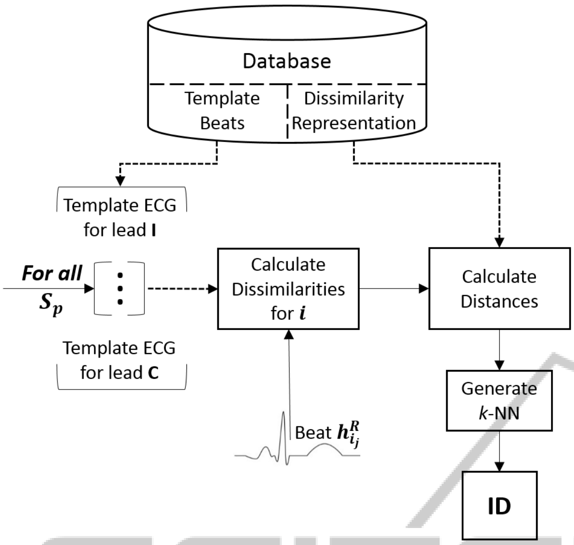


Figure 7: Block diagram illustrating the identification procedure for the Inter-subject based dissimilarity approach.

output. However, for this mode, if no majority exists for the valid d_k, then identification fails.

5 RESULTS

In order to provide a thorough evaluation of the proposed method, we applied it to a database provided by a local cardiac hospital, Hospital de Santa Marta, that has been previously validated in terms of biometric performance in (Carreiras et al., 2014).

The used ECG records were acquired during normal hospital operation, encompassing scheduled appointments, emergency cases, and bedridden patients. This study focuses on signals originating from healthy individuals. All signals were acquired using Philips PageWriter Trim III devices, following the standard 12-lead placement, with a sampling rate of 500 Hz and 16 bit resolution. Each record has a duration of 10 s. 832 records were then employed belonging to 618 subjects.

The various results are compared through Receiver Operating Characteristic (ROC) and corresponding Equal Error Rates (EER) for the authentication mode of operation while the identification mode is characterized by its Identification Error (EID) as in:

$$E_{ID} = \frac{F_{ID}}{T_{ID} + F_{ID}} \tag{6}$$

where F_{ID} and T_{ID} correspond to the number of incorrect and correct identifications respectively.

All of the designed experiments were executed according to a simple random approach. The existing valid heartbeats were randomly partitioned into two sets, a training set containing 75% of those beats and a test set composed by the remaining 25%, whose beats are individually evaluated. This procedure was repeated 10 times and the average EER and EID were calculated from all these 10 runs. The minimum number of training heartbeats is 5, an amount demanded by the template generation block. Some subjects did not satisfy this requirement and were thus not considered for testing. The employed number of subjects thus becomes 503.

The following experimental set-ups were tested. The effect of the metric choice over both dissimilarity computation in Section 4.4 and classification in Section 4.5 was tested. The chosen metrics for both steps were the cosine similarity and euclidean distance. To test all the possible metric combination, 4 different scenarios are possible. Given the existence of two methods for dissimilarity computation, the number of experiments rises to 8 for each lead configuration C. Experiments over all metrics were only carried out with $C = [I, II, III]$. Due to time constraints, the set of metrics corresponding to the best results for each dissimilarity method were employed for $C = [I]$. The total number of experiments is then 10. Tags are given to these experiments so as to facilitate the observation of results.

Subject based (B)

This approach is given the tag B. The employed metric scenario for a given experiment will be described by two letters C or E whether the employed metric is a cosine similarity or euclidean distance respectively. The first letter will correspond to the metric utilized in the dissimilarity computation process while the second refers to the metric used in the classification procedure. The utilized set C is shown subscript to the letter B. As a result, a tag of $B_{I,II,III} - CE$ pinpoints the use of cosine similarity for dissimilarity calculation and the use of euclidean distance to get the distances between dissimilarity arrays, for a set $C = [I, II, III]$. As a result, for approach B there are:

- $B_{I,II,III} - CC$
- $B_{I,II,III} - CE$
- $B_{I,II,III} - EC$
- $B_{I,II,III} - EE$
- $B_I - CE$

Inter-subject based (I)

The tag I was attributed to experiments following this approach. The notation associated to them follows the same as in the previous method. As such:

- $I_{I,II,III} - CC$
- $I_{I,II,III} - CE$
- $I_{I,II,III} - EC$
- $I_{I,II,III} - EE$
- $I_I - CC$

Additionally, results obtained from the technique in (Carreiras et al., 2014) are contrasted with the ones hereby obtained. This technique is similar to the one presented in this paper but ditches the dissimilarity computation phase. Instead, it uses heartbeats as feature arrays and then applies k-NN directly to them. Also this method is exclusively single-lead. It shall be tagged with the expression O_I. Table 1 summarizes results obtained for all experiments in the form of averaged EERs and EIDs and respective standard deviations.

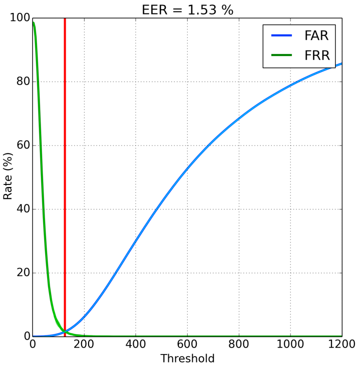
Table 1: Results all experiments' EER & EID rates.

		EER [%]	EID [%]
O_I		8.51 ± 0.30	12.04 ± 0.68
$B_{I,II,III}$	CC	21.55 ± 0.36	87.97 ± 2.21
	CE	4.45 ± 0.13	8.89 ± 1.11
	EC	30.25 ± 0.34	92.59 ± 1.78
	EE	1.53 ± 0.09	23.46 ± 1.96
B_I	CE	4.45 ± 0.09	9.92 ± 0.76
$I_{I,II,III}$	CC	2.46 ± 0.09	5.48 ± 0.33
	CE	4.76 ± 0.24	6.90 ± 0.38
	EC	10.75 ± 0.06	13.02 ± 0.68
	EE	3.83 ± 0.11	19.74 ± 0.50
I_I	CC	2.46 ± 0.09	5.37 ± 0.48

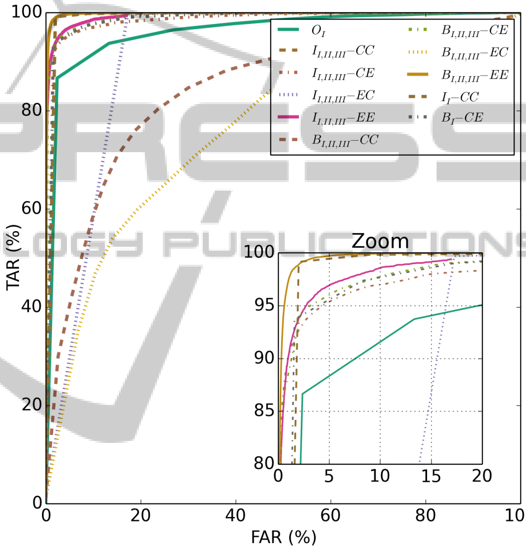
The ROC curve for the experiment $B_{I,II,III} - EE$ is shown in Figure 8(a). A ROC curve comparing all the experiments in authentication mode is shown in Figure 8(b).

The results in Table 1 suggest the following observations.

- Classifiers whose training computes dissimilarities based on a cosine metric proved much superior to their euclidean distance equivalents. This was expected due to the large initial feature size of $M = 300$. The exception concerns authentication results for CE vs EE, in which the latter is better.
- For a Subject-based approach, experiments employing a cosine similarity metric during classification present very high EER and EID indices. This was expectable due to the very small dissimilarity array size ($T * L = 15$) rendering the cosine similarity metric unable to extract viable information. Precisely the opposite can be said for an Inter-subject approach which presents a dissimilarity array size of ($T * S_p * L = 1125$).
- Both single-lead experiments present better results than those obtained from O_I. From here it is possible to conclude that a dissimilarity based representation can originate a more effective biometric system.
- Authentication EERs did not vary significantly by changing the lead-set C. However, EIDs for a triple-lead set improved in a subject based approach and deteriorated for an inter-subject based one. The following are the possible explanations for what happened.
  - For a subject based approach B, the single-lead dissimilarity array size is very small ($T * L = 5$). The three extra leads raise this dimension to 15 which is a significant increase in information.



(a) ROC curve and obtained EER for the experiment $B_S - EE$.



(b) ROC curve for all the executed experiments.

Figure 8: ROC curves outlining obtained results for authentication.

  - For an inter-subject based approach I, the single-lead dissimilarity array size is already relatively large ($T * S_p * L = 375$). Increasing it further does not contribute to the rise in information. Thus the EID degrades slightly.

- Lastly, the lowest EER for authentication originated from $B_{I,II,III} - EE$. However it also presents a high EID. The lowest EID is shown by $I_{I,II,III} - CC$ which also gave a good and second lowest EER value.

6 CONCLUSIONS AND FUTURE WORK

The number of possible ECG representations is endless and so far none has managed to stand out at the expense of all the others. In this paper a new ECG representation space is developed and integrated into an already existing biometric system. This feature space is built through dissimilarity computation, where the new features are a direct and pairwise comparison between those present in two signals, which here were taken via metrics.

Moreover, the computation of this novel representation can be extended to various types of ECG configurations or signals, underlining its versatility. The current study extended its usage to multi-lead ECG signals, where an EER rate of 1.53% has been achieved, for authentication over a database of 503 subjects as well as an EID rate of 5.65%. It should be emphasized that for authentication/identification a single heartbeat was used. The usage of a larger number of beats for classification will likely lead to better results. When contrasting with the original technique, which does not compute a dissimilarity representation, this feature space returns better results, proving the usefulness of such a representation. However, as in previous work, the usage of more than one lead did not significantly improve results.

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REFERENCES

Agrafioti, F. and Hatzinakos, D. (2008). Fusion of ECG sources for human identification. In *Communications, Control and Signal Processing, 2008. ISCCSP 2008. 3rd International Symposium on*, pages 1542–1547.

Biel, L., Pettersson, O., Philipson, L., and Wide, P. (2001). ECG analysis: a new approach in human identification. *Instrumentation and Measurement, IEEE Transactions on*, 50(3):808–812.

Carreiras, C., Lourenço, A., Fred, A., and Ferreira, R. (2014). ECG signals for biometric applications - are we there yet? In *11th Int. Conf. on Informatics in Control, Automation and Robotics*, pages 765–772. Scitepress.

Chan, A. D. C., Hamdy, M., Badre, A., and Badee, V. (2008). Wavelet distance measure for person identification using electrocardiograms. *Instrumentation and Measurement, IEEE Transactions on*, 57(2):248–253.

Connell, S. D. and Jain, A. K. (1999). Template-based online character recognition. *Pattern Recognition*, 34:1–14.

Conover, M. (2003). *Understanding Electrocardiography*. Mosby.

de Chazal, P., O'Dwyer, M., and Reilly, R. (2004). Automatic classification of heartbeats using ECG morphology and heartbeat interval features. *Biomedical Engineering, IEEE Transactions on*, 51(7):1196–1206.

Duin, R., Loog, M., Pękalska, E., and Tax, D. (2010). Feature-based dissimilarity space classification. In Ünay, D., Çtaltepe, Z., and Aksoy, S., editors, *Recognizing Patterns in Signals, Speech, Images and Videos*, volume 6388 of *Lecture Notes in Computer Science*, pages 46–55. Springer Berlin Heidelberg.

Duin, R. P. and Pękalska, E. (2011). The dissimilarity representation for structural pattern recognition. In San Martin, C. and Kim, S.-W., editors, *Progress in Pattern Recognition, Image Analysis, Computer Vision, and Applications*, volume 7042 of *Lecture Notes in Computer Science*, pages 1–24. Springer Berlin Heidelberg.

Duin, R. P. and Pękalska, E. (2012). The dissimilarity space: Bridging structural and statistical pattern recognition. *Pattern Recognition Letters*, 33(7):826 – 832.

Fang, S.-C. and Chan, H.-L. (2009). Human identification by quantifying similarity and dissimilarity in electrocardiogram phase space. *Pattern Recognition*, 42(9):1824 – 1831.

Fatemian, S. and Hatzinakos, D. (2009). A new ECG feature extractor for biometric recognition. In *Digital Signal Processing, 2009 16th International Conference on*, pages 1–6.

Friesen, G., Jannett, T., Jadallah, M., Yates, S., Quint, S., and Nagle, H. (1990). A comparison of the noise sensitivity of nine qrs detection algorithms. *Biomedical Engineering, IEEE Transactions on*, 37(1):85–98.

Hamilton, P. (2002). Open source ECG analysis. In *Computers in Cardiology, 2002*, pages 101–104.

Labati, R. D., Sassi, R., and Scotti, F. (2013). ECG biometric recognition: permanence analysis of qrs signals for 24 hours continuous authentication. In *IEEE International Workshop on Information Forensics and Security (WIFS)*, pages 31–36. Institute of electrical and electronics engineers.

Li, M. and Narayanan, S. (2010). Robust ECG biometrics by fusing temporal and cepstral information. In *Pattern Recognition (ICPR), 2010 20th International Conference on*, pages 1326–1329.

Liu, N. and Wang, Y. (2008). Template selection for on-line signature verification. In *Proc. of the 19th Int. Conf. on Pattern Recognition (ICPR)*, pages 1–4.

Lourenço, A., Carreiras, C., Silva, H., and Fred, A. (2014). ECG biometrics: A template selection approach. In *Medical Measurements and Applications (MeMeA), 2014 IEEE International Symposium on*, pages 1–6.

Lourenço, A., Silva, H., Carreiras, C., et al. (2013). Outlier detection in non-intrusive ECG biometric system. In *Image Analysis and Recognition*, pages 43–52. Springer Berlin Heidelberg.

Lumini, A. and Nanni, L. (2006). A clustering method for automatic biometric template selection. *Pattern Recognition*, 39(3):495–497.

Odinaka, I., Lai, P.-H., Kaplan, A., O'Sullivan, J., Sirevaag, E., and Rohrbaugh, J. (2012). ECG biometric recognition: A comparative analysis. *Information Forensics and Security, IEEE Transactions on*, 7(6):1812–1824.

Plataniotis, K., Hatzinakos, D., and Lee, J. (2006). ECG biometric recognition without fiducial detection. In *Biometric Consortium Conference, 2006 Biometrics Symposium: Special Session on Research at the*, pages 1–6.

Shen, T. W., Tompkins, W., and Hu, Y. H. (2002). One-lead ECG for identity verification. In *Engineering in Medicine and Biology, 2002. 24th Annual Conference and the Annual Fall Meeting of the Biomedical Engineering Society EMBS/BMES Conference, 2002. Proceedings of the Second Joint*, volume 1, pages 62–63 vol.1.

Shen, Tsu-Wang, T. W. J. and Hu, Y. H. (2011). Implementation of a one-lead ECG human identification system on a normal population. *Journal of Engineering and Computer Innovations*, 2(1):12–21.

Silva, H., Gamboa, H., and Fred, A. (2007). One lead ECG based personal identification with feature subspace ensembles. In Perner, P., editor, *Machine Learning and Data Mining in Pattern Recognition*, volume 4571 of *Lecture Notes in Computer Science*, pages 770–783. Springer Berlin Heidelberg.

Singla, S. and Sharma, A. (2010). ECG as biometric in the automated world. *International Journal of Computer Science & Communication*, 1:281–283.

Uludag, U., Ross, A., and Jain, A. (2004). Biometric template selection and update: a case study in fingerprints. *Pattern Recognition*, 37(7):1533–1542.

Wang, J., She, M., Nahavandi, S., and Kouzani, A. (2013). Human identification from ECG signals via sparse representation of local segments. *Signal Processing Letters, IEEE*, 20(10):937–940.

Wang, Y., Agrafioti, F., Hatzinakos, D., and Plataniotis, K. (2008). Analysis of human electrocardiogram for biometric recognition. *EURASIP Journal on Advances in Signal Processing*, 2008(1):148658.

Wübbeler, G., Stavridis, M., Kreiseler, D., Bousseljot, R.-D., and Elster, C. (2007). Verification of humans using the electrocardiogram. *Pattern Recognition Letters*, 28(10):1172 – 1175.

Ye, C., Coimbra, M., and Kumar, B. (2010). Investigation of human identification using two-lead electrocardiogram (ECG) signals. In *Biometrics: Theory Applications and Systems (BTAS), 2010 Fourth IEEE International Conference on*, pages 1–8.