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Person Identification in Irregular Cardiac Conditions using Electrocardiogram Signals

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Abstract— **This paper presents a person identification mechanism in irregular cardiac conditions using ECG signals. A total of 30 subjects were used in the study from three different public ECG databases containing various abnormal heart conditions from the Paroxysmal Atrial Fibrillation Predicition Challenge database (AFPDB), MIT-BIH Supraventricular Arrthymia database (SVDB) and T-Wave Alternans Challenge database (TWADB). Cross correlation (CC) was used as the biometric matching algorithm with defined threshold values to evaluate the performance. In order to measure the efficiency of this simple yet effective matching algorithm, two biometric performance metrics were used which are false acceptance rate (FAR) and false reject rate (FRR). Our experimentation results suggest that ECG based biometric identification with irregular cardiac condition gives a higher recognition rate of different ECG signals when tested for three different abnormal cardiac databases yielding false acceptance rate (FAR) of 2%, 3% and 2% and false reject rate (FRR) of 1%, 2% and 0% for AFPDB, SVDB and TWADB respectively. These results also indicate the existence of salient biometric characteristics in the ECG morphology within the QRS complex that tends to differentiate individuals.**

Index Terms— **Signal processing in physiological systems, ECG biometrics, irregular cardiac condition, cross correlation**

I. INTRODUCTION

In the recent decade, electrocardiogram (ECG) biometric has been a research interest for person identification since Biel et. al. in [1] proved that ECG can be used for identification purposes. This is supported by the fact that the physiological and geometrical differences of the heart in different individuals display certain uniqueness in their ECG signals [2]. The results in [3] also suggest the distinctiveness and stability of ECG as a biometric modality. Shen et. al. [4], Israel et. al. [5] and Wang et. al. [6] later used different methods and approaches to manifest ECG as a biometric mechanism. These findings open new techniques in establishing the identity of an individual based on the physical and behavioural attribute of a person for identity security.

Different biometric modalities have been reported in the past, examples of which includes physical characteristics such as voice, fingerprint, face, iris and behavioural attributes like keystroke and gait. However, these biometric modalities either are inadequate to provide reliable performance in terms of identification accuracy such as keystroke and gait or are not robust enough against false identity. For instance, fingerprint can be recreated by gummy fingers and latext, voice is easy to counterfeit and imitate, and iris can be dissembled by using contact lenses with copied iris features printed on. ECG signals not only being used for liveness detection but also to verify the identity of a certain individual.

Several methods [3], [4], [5], [6] have been suggested by researchers to prove the reliability and the robustness of ECG biometric against identity falsification. However, these studies were implemented with normal and healthy subjects without any severe cardiac diseases whereas in reality, not everyone has a normal sinus rhythm and healthy heart due to the influence of lifestyles and etc. The mechanism of using ECG as a medium of biometric for the same individual in different cardiac conditions is of great importance in real life situation. Cardiovascular diseases (CVD) can cause irrecoverable damage to the heart and effects the ECG signal morphology. The change in the signal morphology would influence an individual identification significantly. Different types of CVD would incur different forms of distorted morphologies which are inherited in the ECG signals. This would make the process of person identification much harder. Thus, in this paper, we present the idea of using a biometric matching algorithm implemented using three different public ECG databases. We investigated the possibility of using the existing biometric matching algorithm with defined threshold values for subject recognition in abnormal cardiac conditions. Our experimentation results suggest that ECG based biometric identification with irregular cardiac condition gives a higher recognition rate of different ECG signals when tested using three different abnormal cardiac databases with a false acceptance rate (FAR) of 2%, 3% and 2% and a false reject rate (FRR) of 1%, 2% and 0% for AFPDB, SVDB and TWADB respectively.

There have been initial studies of ECG biometric authentication system in different cardiac conditions using various techniques in these recent years from [7], [8], [9]. In [7], Agrafioti et. al. obtained 96.2% recognition rate using Nearest Neighbour (NN) classifier when tested with 79 subjects from three different databases with Atrial Premature Contraction (APC) and Premature Ventricular Contraction (PVC). Autocorrelation/Linear Discriminant Analysis were used for feature extraction and dimensionality reduction. Later in [8], Shen et. al. monitored 23 subjects with peritoneal dialysis for a two year period and resulted in a decrease of subject recognition from 98.5% to 87.7%. Template matching and statistical t-test techniques were used as feature extraction

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mechanism. Longitudinal and cross section investigation were applied for subject recognition. And previously in [9], Ye et. al obtained 99.6% subject recognition using Support Vector Machine with Wavelet/Independent Component Analysis as the extracted features from three public databases. But one of the three public databases used in [9] was from MIT-BIH Normal Sinus Rhythm database (NSRDB) where the subjects had no significant arrhythmias.

These studies gives an interpretation that person identification technique is dependent on the type of cardiovascular condition. Thus, this has motivated us to proposed a simple yet effective method for subject recognition using databases with individuals having various cardiac conditions.

The remaining of the paper is organized as follows. The next section discusses the method of the study which includes the data acquisition process, feature extraction method and the biometric matching algorithm. Later, Section III discusses about the performance of the biometric matching algorithm applied to three ECG databases. Finally, in Section IV, we conclude the study based on the experimentation and results in the previous section.

II. SYSTEM AND METHODOLOGY

An ECG biometric system performs template matching by comparing two datasets which are called the enrolment and recognition ECG data. Recognition data can be categorised as either identification or verification data. Successful template matching recognizes an individual's identity and we represent it as $\mathbf{I_k}$, as shown in Fig. 1. Here, $k = 1, 2, 3, \cdots, M$ where M is the total number of individuals in the biometric database.

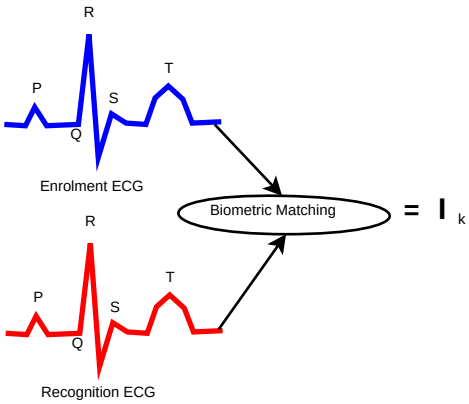

Fig. 1 – A typical ECG signal

The overall architecture of our proposed system starts with data acquisition of ECG signals, then identification of QRS complexes used as the feature extracted. Based on these QRS complexes, template matchings were then performed. After obtaining the CC values as a result of matching, the identity of an individual can be determined based on a defined threshold value. The proposed system is summarised as in Fig. 2.

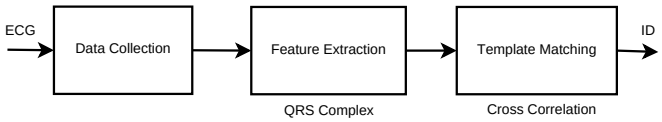

Fig. 2 – The proposed system

A. Data Acquisition

ECG data for 30 different individuals used in this research were taken from three different public databases containing various abnormal heart conditions. The databases involved are the Paroxysmal Atrial Fibrillation Predicition Challenge database (AFPDB), MIT-BIH Supraventricular Arrthymia database (SVDB) and T-Wave Alternans Challenge database (TWADB). A total of 10 subjects were from AFPDB, the other 10 subjects from SVDB and the remaining subjects were from TWADB with sampling rates of 128 Hz, 128 Hz and 360 Hz respectively. Each recording has 30 seconds of ECG signals. Ten ECG recordings were selected from AFPDB which contains subjects with paroxysmal atrial fibrillation (PAF). SVDB includes 10 ECG recordings of subjects which were identified to have had supraventricular arrythmia. While, 10 other ECG recordings were selected from TWADB which include subjects with myocardial infarctions, transient ischemia, ventricular tachyarrhythmias, and other risk factors for sudden cardiac death, as well as healthy controls and synthetic cases with calibrated amounts of T-wave alternans. These ECG entries are obtained from databases available online from PhysioBank [10] which has been extensively used for benchmarking algorithms pertaining to ECG diagnosis, compression and other related researches.

B. Feature Extraction

The amplitude features of an ECG signal which depicts the morphological shape of the wave were used as part of the feature extraction method. This analytical based method captures the QRS complex in an ECG signal. Tawfik et. al in [11] proves the stability of the QRS complex to the heart rate variability and is convienient to be used alone as a biometric feature. Since in an ECG, the R wave denotes to the most obvious, highest and sharpest peak, it acts as the referral point when acquiring the ECG data. From the R wave, we select equal points from boths sides of the identified R wave. We repeat the process of selecting the points which actually covers the QRS complex. In order to automate the feature extraction process, First Derivative based Technique was implemented [12].

C. Biometric Algorithm

Cross correlation (CC) is a simple yet effective template matching algorithm to investigate the relationship between two unknown signals. In other words, CC is a technique used to match the similarity between two signals as represented in Eq. (1).

$$CC = \frac{1}{M}\sum_{i=1}^{M}\mathbf{x}(i) \times \hat{\mathbf{x}}(i) \quad (1)$$

where $\mathbf{x}(i)$, $\hat{\mathbf{x}}(i)$ are the ECG enrolmment and recognition data and M is the number of template matching instances.

Successful matching will be able to verify whether the two unknown signals come from the same or different sources. Furthermore, matching is dependent on the defined threshold values to differentiate between individuals. Thus, multiple instances have been taken from the same subject using few enrolment and recognition ECG datasets to obtain the minimum and maximum CC value which defines the threshold of a subject as shown in Table I, II and III. A random ECG recognition data from different instances will be matched with the ECG enrolment data as shown in Table IV, V and VI. When a person is considered within the minimum and maximum value, the person will be identified. The results of the experiment will be deduced in the next section.

III. EXPERIMENTATION AND RESULTS

A. Performance Analysis

For the self similarity of CC matching, the ECG for each subject consists of seven QRS complexes. In order to perform template matching for person identification, one QRS complex was used as an enrolment data, denoted as $E1$, and the remaining QRS complexes acts as the testing data which we represent as R_i where $i = 1, 2, \ldots, 6$. As a way to differentiate between subjects, we derive the threshold value for each subject by finding the minimum and maximum value as shown in Table I, II and III. These values will be used for CC matching against other subjects in the database as to verify the validity of the proposed system. A random ECG dataset from the same subject will then be matched against different subjects as shown in Table IV, V and VI. Furthermore, to verify that the QRS complexes of different individuals are not the same, Fig. 3 depicts example of three subjects from each database used in this study to show the self similarity in the QRS complex for each subject while at the same time differs from other subjects. Each subject has six QRS complexes overlapped with each other which also proves that the abnormal cardiac condition does not effect the QRS complex signal morphology of an individual where it remains consistent.

TABLE I – Self Similarity of CC Matching using AFPDB

AFPDB	(E1,R1)	(E1,R2)	(E1,R3)	(E1,R4)	(E1,R5)	(E1,R6)	min	max
afpdb04	0.031259	0.031230	0.031259	0.030355	0.031812	0.031382	0.030355	0.031812
afpdb06	0.117470	0.119350	0.119580	0.118710	0.124710	0.121000	0.117470	0.124710
afpdb07	0.151670	0.149030	0.155890	0.150940	0.153050	0.151380	0.149030	0.155890
afpdb09	0.017819	0.017507	0.017365	0.017306	0.016939	0.017508	0.016939	0.017819
afpdb11	0.097851	0.105870	0.098129	0.095020	0.097730	0.103570	0.095020	0.105870
afpdb12	0.079312	0.078307	0.077626	0.079353	0.078483	0.078179	0.077626	0.079353
afpdb13	0.215580	0.216860	0.215690	0.222680	0.217210	0.216390	0.215580	0.222680
afpdb16	0.061340	0.063902	0.058923	0.058684	0.063887	0.060902	0.058684	0.063902
afpdb25	1.262400	1.266800	1.305100	1.293900	1.259700	1.266200	1.259700	1.305100
afpdb26	1.527100	1.514000	1.491200	1.458600	1.455600	1.518300	1.455600	1.527100

The results of the CC matching between subjects from three public databases represented by ECG enrolment and recognition data from each subject are shown in Table IV, V and VI. For example in Table IV, afpdb04 in row 1 with afpdb04 in column 1 means that a random ECG enrolment and recognition data from the same subject was matched to check whether it is in the range of the defined threshold value. While, afpdb04 in row 1 against afpdb06 in column 2 denotes matching of two different subjects in comparison with the defined threshold value of afpdb04. This process is also repeated for subjects from SVDB and TWADB as shown in Table V and VI.

TABLE II – Self Similarity of CC Matching using SVDB

SVDB	(E1,R1)	(E1,R2)	(E1,R3)	(E1,R4)	(E1,R5)	(E1,R6)	min	max
svdb803	0.108210	0.115420	0.108750	0.107610	0.113090	0.107070	0.107070	0.115420
svdb806	0.059809	0.058578	0.058639	0.059719	0.059612	0.059281	0.058578	0.059809
svdb809	0.440160	0.426670	0.428330	0.451080	0.420850	0.408380	0.408380	0.451080
svdb810	0.364930	0.362030	0.369260	0.345740	0.345740	0.370970	0.345740	0.370970
svdb824	0.176000	0.171710	0.171430	0.145100	0.176710	0.150000	0.145100	0.176710
svdb840	0.081276	0.086495	0.086807	0.080631	0.082676	0.085242	0.080631	0.086807
svdb863	0.515870	0.517900	0.469680	0.499920	0.510950	0.488670	0.469680	0.517900
svdb870	1.023700	1.051500	1.008600	1.094900	1.075600	0.957280	0.957280	1.094900
svdb888	0.174270	0.200070	0.191930	0.201690	0.188770	0.222600	0.174270	0.222600
svdb892	0.130870	0.137030	0.130710	0.130220	0.128150	0.137450	0.128150	0.137450

TABLE III – Self Similarity of CC Matching using TWADB

TWADB	(E1,R1)	(E1,R2)	(E1,R3)	(E1,R4)	(E1,R5)	(E1,R6)	min	max
twadb01	0.283690	0.279850	0.282550	0.277730	0.285440	0.277020	0.277020	0.285440
twadb09	0.177710	0.167250	0.171530	0.176770	0.170470	0.165090	0.165090	0.177710
twadb12	2.741800	2.670900	2.774900	2.763100	2.804500	2.752100	2.670900	2.804500
twadb18	0.406420	0.409750	0.410320	0.416140	0.417090	0.413420	0.406420	0.417090
twadb24	0.353750	0.360560	0.355320	0.354440	0.356400	0.349440	0.349440	0.360560
twadb25	0.375230	0.367620	0.377210	0.370120	0.367700	0.377690	0.367620	0.377690
twadb33	0.066054	0.067587	0.067103	0.067599	0.068074	0.067496	0.066054	0.068074
twadb42	0.222870	0.213870	0.217870	0.215980	0.222080	0.217270	0.213870	0.222870
twadb47	0.133030	0.136100	0.130770	0.126770	0.135690	0.131540	0.126770	0.136100
twadb50	0.097282	0.099084	0.101750	0.097214	0.096814	0.097585	0.096814	0.101750

In order to measure the performance of the algorithm, we used two important biometric performance metrics that were defined in [13] which are False Acceptance Rate (FAR) and False Reject Rate (FRR).

FAR exists when the numerical values produced during the matching process exceeds the threshold values and overlaps with different individuals while FRR is imposed when the numerical values obtained as a results of matching are within the threshold but not accepted by the system. FAR is more related to impostors attempts where they have numerical

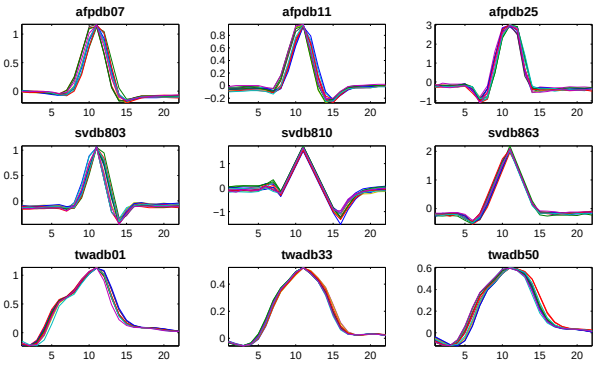

Fig. 3 – QRS complexes of Different Individuals From Different Databases

TABLE IV – CC Matching for AFPDB subjects

AFPDB	afpdb04	afpdb06	afpdb07	afpdb09	afpdb11	afpdb12	afpdb13	afpdb16	afpdb25	afpdb26
afpdb04	0.0305	0.0467	0.0718	0.0194	0.0552	0.0434	0.0564	0.0368	0.1800	0.1834
afpdb06	0.0452	0.1202	0.1133	0.0330	0.0957	0.0957	0.0496	0.0686	0.3312	0.3289
afpdb07	0.0654	0.1062	0.1528	0.0429	0.1211	0.1069	0.1279	0.0842	0.4187	0.4576
afpdb09	0.0213	0.0303	0.0425	0.0180	0.0329	0.0326	0.0327	0.0286	0.1254	0.1421
afpdb11	0.0493	0.0950	0.1202	0.0323	0.0987	0.0902	0.0845	0.0665	0.3355	0.3583
afpdb12	0.0437	0.0926	0.1148	0.0287	0.0940	0.0812	0.0704	0.0642	0.3119	0.3143
afpdb13	0.0596	0.0480	0.1325	0.0322	0.0928	0.0693	0.2189	0.0684	0.3367	0.4045
afpdb16	0.0392	0.0688	0.0899	0.0311	0.0700	0.0652	0.0707	0.0613	0.2626	0.2814
afpdb25	0.1796	0.3239	0.4288	0.1273	0.3448	0.3158	0.3212	0.2585	1.2673	1.3384
afpdb26	0.1956	0.2919	0.4244	0.1411	0.3438	0.3452	0.4080	0.2702	1.2987	1.4686

TABLE V – CC Matching for SVDB subjects

SVDB	svdb803	svdb806	svdb809	svdb810	svdb824	svdb840	svdb863	svdb870	svdb888	svdb892
svdb803	0.1088	0.0818	0.1868	0.1711	0.1266	0.0856	0.1943	0.2632	0.1247	0.0918
svdb806	0.0801	0.0613	0.1378	0.1335	0.0975	0.0687	0.1340	0.1777	0.0971	0.0742
svdb809	0.2050	0.1478	0.4353	0.4160	0.2262	0.1378	0.4129	0.6061	0.2441	0.2518
svdb810	0.1773	0.1303	0.3846	0.3759	0.1856	0.1244	0.3400	0.4928	0.2139	0.2073
svdb824	0.1272	0.0943	0.1934	0.2056	0.1976	0.1328	0.1785	0.1970	0.1920	0.1110
svdb840	0.0762	0.0612	0.1033	0.1108	0.1156	0.0882	0.0925	0.0941	0.1142	0.0457
svdb863	0.2200	0.1505	0.4462	0.3808	0.2006	0.1147	0.4891	0.7401	0.2001	0.2632
svdb870	0.2721	0.1831	0.5948	0.4929	0.1995	0.1039	0.6587	1.0566	0.2039	0.3629
svdb888	0.1201	0.0919	0.2156	0.2134	0.1493	0.1095	0.1926	0.2521	0.1850	0.0921
svdb892	0.1223	0.0894	0.2201	0.2000	0.1332	0.0902	0.2245	0.3280	0.1411	0.1337

TABLE VI – CC Matching for TWADB subjects

TWADB	twadb01	twadb09	twadb12	twadb18	twadb24	twadb25	twadb33	twadb42	twadb47	twadb50
twadb01	0.2804	0.2182	0.7400	0.3262	0.2719	0.3281	0.1334	0.2326	0.1820	0.1514
twadb09	0.2297	0.1738	0.5972	0.2609	0.2229	0.2579	0.1065	0.1870	0.1471	0.1213
twadb12	0.7399	0.5466	2.6913	1.0611	0.8979	0.8427	0.3597	0.7581	0.5699	0.4032
twadb18	0.3147	0.2342	1.0198	0.4078	0.3442	0.3566	0.1514	0.2957	0.2239	0.1705
twadb24	0.2682	0.2082	0.8603	0.3333	0.3553	0.2912	0.1304	0.2615	0.2116	0.1530
twadb25	0.3303	0.2480	0.8560	0.3790	0.3099	0.3780	0.1506	0.2662	0.2079	0.1693
twadb33	0.1328	0.1000	0.3585	0.1509	0.1271	0.1436	0.0664	0.1118	0.0854	0.0779
twadb42	0.2346	0.1758	0.7594	0.3090	0.2745	0.2656	0.1117	0.2249	0.1740	0.1262
twadb47	0.1847	0.1394	0.5838	0.2371	0.2139	0.2074	0.0886	0.1737	0.1353	0.1009
twadb50	0.1639	0.1243	0.4309	0.1831	0.1569	0.1777	0.0808	0.1355	0.1047	0.0977

values which are quite similar with other individuals whereas FRR is linked to the failure of the matching algorithm to detect a genuine acceptance where the system rejects the claimed identity.

Mathematically, FAR is defined as the ratio of the number of false instances to the total number of instances as described in Eq. 2.

$$FAR = \frac{1}{N}\sum_{i=1}^{N}\mathbf{FAR}(i) \tag{2}$$

where $num1$ = number of fraud attempts against a person i and $denum1$ = total number of fraud attempts against a person i. Thus, $\mathbf{FAR}(i) = \frac{num1}{denum1}$.

While, FRR is calculated by the ratio of the number of instances of false rejection to the total number of instances as denoted in Eq. 3.

$$FRR = \frac{1}{N}\sum_{i=1}^{N}\mathbf{FRR}(i) \tag{3}$$

where $num2$ = number of rejected attempts for qualified person i and $denum2$ = total number of rejected attempts for qualified person i. Therefore, $\mathbf{FRR}(i) = \frac{num2}{denum2}$.

The results of FAR and FRR for the AFPDB, SVDB and TWADB databases are shown as in Table VII.

TABLE VII – Performance Parameters using Cross Correlation

Database	FAR (%)	FRR (%)
AFPDB	2	1
SVDB	3	2
TWADB	2	0

Based on the results, we can point out three main deductions; (1) the random ECG dataset tested for self similarity were mostly in the defined threshold value (2) the threshold value defined from one individual in the database does not overlap other defined threshold values and (3) the QRS complexes from subjects with atrial fibrillation, supravenricular and T-wave alternans have very stable and uniform wave signals regardless of the abnormal heart condition as shown in Fig. 3.

IV. CONCLUSIONS

In this paper, we demonstrate the idea of person identification by using CC as the biometric matching algorithm implemented for three different public ECG databases consisting of subjects with abnormal heart conditions as a proof of concept. Our experimentation results suggest that ECG based biometric identification is possible with irregular cardiac condition acheiving high recognition rate of different ECG signals yielding FAR of 2%, 3% and 2% for AFPDB, SVDB and TWADB respectively. While the FRR value for the three databases are 1%, 2% and 0% respectively. These results also indicates the existence of salient biometric characteristics in the ECG morphology within the QRS complex that tends to differentiate individuals.

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