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ECG-Based Human Identification System by Temporal-Amplitude Combined Feature Vectors

EUNSANG BAK¹, GYU-HO CHOI¹, AND SUNG BUM PAN¹

IT Research Institute, Chosun University, Gwangju 61452, South Korea

Corresponding author: Sung Bum Pan (sbpan@chosun.ac.kr)

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ABSTRACT ECG data are biosignals with unique characteristics that can be obtained regardless of time and space constraints. Owing to these advantages, they have been widely used for not only diagnosing diseases but also recognizing people. Numerous studies have been conducted and various feature vectors from a large amount of data have been suggested to improve recognition performance. The key to extracting feature vectors is to extract differences in one-dimensional ECG signals without loss in order to recognize human identity. In this paper, we propose new feature vectors based on fiducial points. These feature vectors have simple and clear shapes that combine temporal and amplitude information. The discriminator operating in the proposed human identification system measures distance-based similarity. This method alleviates computational burden and enables the human identification system to run in real time. Based on the system, we conducted a number of recognition experiments. The experimental results proved that the proposed feature vectors are valid information that represents significant differences between individuals. In the experiments with 100 subjects, we obtained a recognition rate of over 94% when two or more than two heartbeat signals were used, and confirmed that as the number of input heartbeats increased the performance also improved proportionally.

INDEX TERMS Temporal-amplitude combined, feature vector, fiducial point, human identification.

I. INTRODUCTION

The biometric recognition technology, called biometrics, is a technology [1]–[20] that identifies people through statistical analyses by acquiring biometric information such as physiological and behavioral characteristics of human body. There are various types of biometric information available in body. ECG is one of them. Several conditions must be met for the information in body to have a meaning as biometric information. First of all, it should be something that everyone has, and it should have unique quality that does not change over time. Next, this information should be able to be measured externally and provided without any particular resistance. Lastly, it should be robust to falsification. Depending on the extent to which these conditions are met, the suitability of biometric information is determined [11].

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Consequently, it is difficult to find biometric information that everyone has, is hard to falsify, and is easy to obtain. Since 2001 researchers [2], [8], [9], [60] who have investigated on system access control have confirmed that ECG signals are a type of biometric information that satisfies the conditions mentioned above. At the beginning, ECG information aimed to diagnose diseases, but it has been widely used in biometric recognition over the last decade. This is because several features of ECG signals enable biometric recognition. The ECG-based biometric recognition technology started from the early studies mentioned in the work of Nasri *et al.* [14], Odinata *et al.* [15], Israel and Irvine [10] and, since then, has been continuously developed [21]–[25].

Let us examine how ECG signal generated by heart movement is used as information that can identify people. The heart is a muscle (myocardium) that carries blood to all over the body by contracting itself periodically. This contraction is initiated by an electrical stimulation generated at the sinoatrial (SA) node of the atrium (Fig. 1), which serves as a

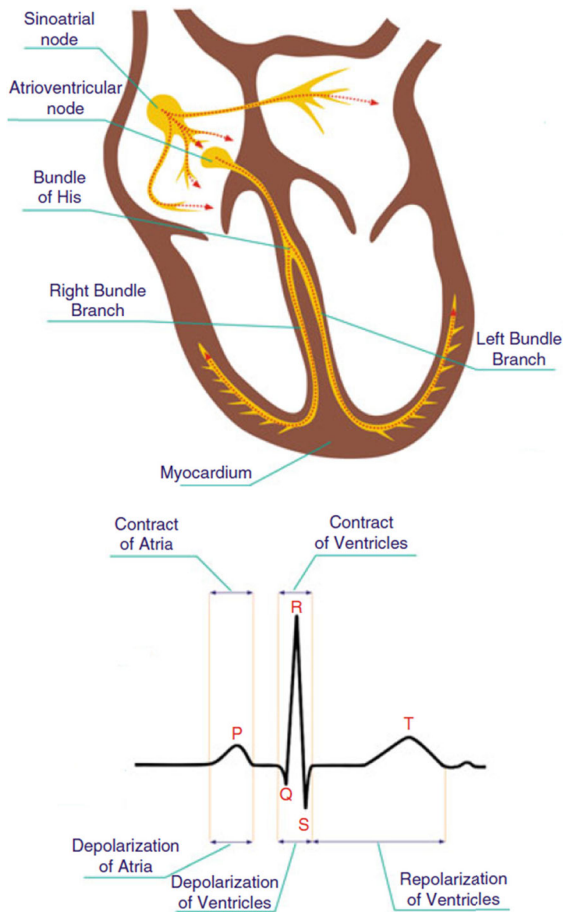


FIGURE 1. Structure of the heart and a heartbeat signal [28].

pacemaker of the body. This electrical stimulation propagation causes electric signals to flow on the surface of the body in a certain pattern. The record of such an electric signal flowing on the body is Electrocardiography (ECG) [26]–[29].

Generally a heartbeat of every person seems to have a similar shape, although there are clear differences [18] in its specific details. This is because each person has a different shape of the heart and its periphery. Such morphological differences are reflected in ECG signals, through which we are able to confirm the identity of a body.

In this paper, we propose new feature vectors that can successfully perform biometric recognition and also demonstrate a human identification system applying the proposed feature vectors. The proposed feature vectors can be extracted quickly from ECG data, and they are visually clear and discriminative. Thanks to these features, a human identification system based on the proposed feature vectors can reduce computational complexity, and yet achieving significant recognition performance in real time.

II. RELATED WORKS

Various types of feature vectors [30]–[42] have been proposed in relation to ECG signal. Feature vectors are generally classified into three types [7], [58], as follows: 1) temporal information, 2) amplitude information, and 3) morphological

information of ECG signals. The idea of using ECG information as a means of recognizing human identity was first proposed by Forsen *et al.* [43], although the first study of a human identification system was actually conducted by Biel *et al.* [2]. Researchers conducted experiments by combining features obtained from subjects using 12 leads. Oosterom *et al.* [41] found that the variations in ECG signals between individuals were related to the morphological difference of the heart. Based on these early research results, ECG-based biometrics (also known as heart biometrics) has been advanced.

In general, features extracted to distinguish the identity using ECG signals must meet the requirements of the discriminator and the real-time processing ability [19], [44]–[48] of the system. However, in the field of biometrics, there are no typical features [7] that can be extracted from ECG signals and no typical technology that can process them. The reason is that it is difficult to objectively compare the technologies because each researcher has developed a technology suitable for their own experimental conditions.

The conventional feature extraction methods [49]–[61] can be classified into fiducial-based approaches and nonfiducial-based approaches. Both approaches have pros and cons. The fiducial-based approach has clear fiducial points from which features can be extracted but the performance of the entire system can be affected depending on the accuracy in finding fiducial points. The nonfiducial-based approach eliminates the negative effects of the fiducial point detector, but it requires a more sophisticated algorithm because it utilizes various features contained in the entire data.

The fiducial-based approach finds specific fiducial points present in ECG signals, extracts numerous features based on these points, and uses the features as input into the human identification system. The peaks and valleys of a waveform of ECG signal are typical fiducial points. Apart from them, envelope and slope of the waveform can be also used as a fiducial point. The fiducial point detector [24], [62] can be implemented in several ways. The more fiducial points we set, the further the ability of the detector to extract them is degraded, which adversely affects the overall system performance. For this reason, most researchers use the limited number of fiducial points (P, Q, R, S, T).

Fiducial point-based features are represented by temporal, amplitude, and morphological information. The electrical conduction system of the heart involves a process where electrical stimulation occurs and is transmitted. The features existing on the temporal axis are the information between the key temporal points related to the stimulation propagation. As can be observed in Fig. 1, this stimulation begins at the SA node, passing through the atrioventricular (AV) node, the bundle of His (Fig. 1), and is transmitted to the Purkinje fibers of the ventricles. The key temporal points during this process are represented by the fiducial points (P, Q, R, S, T). They can be bases of discriminative features for biometrics. Fig. 2 shows several features [28] represented by temporal information. Of them, the most frequently used

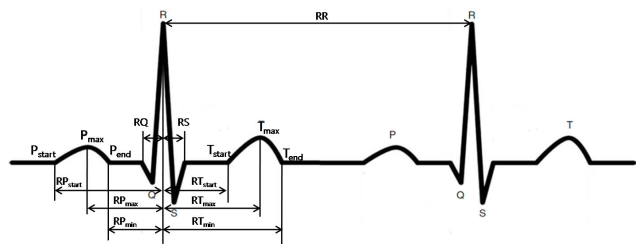


FIGURE 2. Temporal features of ECG.

features are the periods of the waves (P, QRS complex, T) and the temporal intervals [9], [12], [42] between them. The interval [16], [37] between the R point of the current signal and that of the next signal is also used as a feature.

The features present in signal strength (amplitude) use the differences in height [9] between the peaks of P, R, T and the valleys of Q, S. In general, given that R is the highest point, the amplitude can be expressed by its relative ratio to R, and the first and second derivatives [53] of the peaks are also used as features. Finally, morphological-based features use morphological information present in all or part of the ECG signals. For example, the average value [3], [48] of samples in a specific region can be used as a feature, and the slope of R toward S or the slope of S toward T [67] can also be used as a feature. Apart from them, many other features have been proposed.

There are various types of feature vectors and the number of feature vectors varies in each study. Furthermore, different types of discriminators have been used and the number of participants in the experiments ranged from as few as 20 to as many as several hundreds. A recognition rate of approximately over 92% was obtained in these various experimental environments [4], [19].

The nonfiducial-based approach has been reported since 2006 as a method that does not use a fiducial point detector. This method is based on the idea that ECG signals are repetitive. An earlier paper by Plataniotis [56] proposed a method for extracting normalized autocorrelation (AC)-based features. Various studies have been attempted using the wavelet distance [3], [48], template [31], spectrogram [38], MFCC [1], [61], autoregressive model [32], polynomial [52], [57], and others.

The last aspect to take into account when designing an ECG-based human identification system is the number of leads used to extract ECG signals. ECG signals developed for medical purposes basically obtain information using 12 leads [69]–[73]. However, when building a human identification system, we use only one lead [64]–[68] to obtain information by considering usability of the system. In other words, two electrodes, one for each hand, are used to extract information. The ECG data extracted through the above process go through preprocessing steps [30], [74]–[76] where unnecessary noise is removed, and they are converted into the signals from which the features for biometrics are to be extracted. In the next section, we examine the preprocessing technology applied to this study.

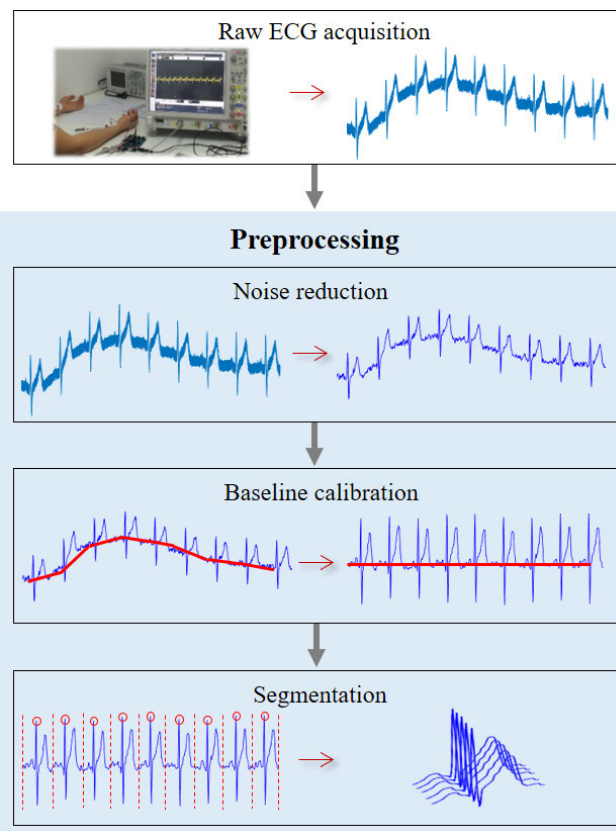


FIGURE 3. Preprocessing flowchart for ECG noise removal.

III. PREPROCESSING

With regard to the ECG data used in this study, we obtained ECG lead-I data repeatedly from a healthy person for a certain period of time using an in-house built device. The device used for measurement [77] was Psoc-5LP (ARM Cortex-M3 series). In the device, 128 samples were sampled in a second and the signal to noise ratio was 60 dB. Preprocessing goes through the three steps of noise removal, baseline calibration, and segmentation, as shown in Fig. 3.

The noises present in ECG signals are removed by frequency filtering, R point detection, and median filtering. Of them, the frequency filtering removes noises above 60Hz arising from a power line and noises below 0.5Hz arising from the connection surface of electrodes by using a bandpass filter. For signals passing through the bandpass filter, the QRS complex waveforms containing important information are separated by detecting the R point, and noises were removed by applying a median filter to the rest of the area except for the QRS complex part.

Even after the series of noise removal steps, the baseline fluctuation noises caused by subjects’ breathing could not be removed. Therefore, the variations in the baseline are estimated and are mapped on the horizontal line, and then the baseline fluctuation noises, in principle, are removed by zero-point calibration. However, due to the characteristics of the proposed features, the zero-point calibration is not necessary, which is an advantage for reducing computational

burden. The ECG baseline changed by subjects' breathing was estimated using a regression analysis, which only estimates a partial baseline. The estimation of the partial baseline is performed repeatedly to estimate the entire baseline. Finally, the entire baseline is completed as a stable baseline after the fluctuation noises are removed through projection and correction. Such a baseline calibration process does not affect the unique features of the individual present in ECG signals.

Such noise-removed ECG lead-I signals undergo a segmentation process in which the P wave, QRS complex, and T wave are grouped in a unit and then separated. The fiducial point-based segmentation method, which shows better performance, was selected as a segmentation method, thereby separating the lead-I signals into heartbeat signals composed of P wave, QRS complex, and T wave. For detailed information on the preprocessing steps, please refer to Choi *et al.* [74].

A. DB CONFIGURATION

The in-house database used in this study stored ECG data extracted from a total of 100 subjects, 89 of them males and 11 females. They were healthy when the ECG data was extracted, and individual medical history was not taken into account. Their age ranged from 23 to 34, and an amount of 2 min of ECG signals were extracted for each subject. We extracted signals for 10 sec, paused for 10 sec, and then measured again. We chose an amount of 10–50 sec of data and used them as a training dataset, and then used the next 10–30 sec of data as an evaluation dataset. To measure the recognition performance, the ECG signals were segmented into heartbeat signals, each of which was used as a data unit for training and evaluation. We used 50 data units (training data) for training and 10 data units (evaluation data) for evaluation per subject.

B. FIDUCIAL POINTS DETECTION

Various algorithms [62], [63] have been proposed for the methods to detect fiducial points. However, although their own performance could affect the final recognition performance, there were no significant differences in performance between the techniques. Besides, standard databases used for ECG research are provided in such a way that they are already divided into heartbeat signals and contain fiducial point information. Therefore, researchers have conducted their studies based on the given fiducial point information without developing additional detectors.

In this study, we built our own database by extracting ECG data using the in-house built device. Since the database did not have additional information unlike the standard databases, we obtained fiducial point information by employing a fiducial point detector that we designed. The following Algorithm 1 is the design steps of the fiducial point detector of our own.

Algorithm 1

1. A smoothing filter is applied to a heartbeat signal.
 2. Find candidates of fiducial points by applying a derivative filter to the smoothed signal (Fig. 4(a)).
 - 2.1 If a point with zero slope occurs consecutively, let the median point be a valley or a peak.
 - 2.2 If there are valleys and peaks within a certain distance from the candidates, they are regarded as noise and removed.
 3. Regard the two highest peaks as the R and T points. If the first peak is selected, regard it as the P point, and find the next two highest peaks for R and T points (Fig. 4(b)).
 - 3.1. If the T point is not located at the end part of the signal, find the T point again.
 4. Let both adjacent valleys to the R point be the Q and S points (Fig. 4(b)).
 - 4.1 Revise the location of the Q and S points if they are not the last two lowest valleys.
 5. Determine the final locations in the original signal corresponding to the P, Q, R, S, and T points of the smoothed signal (Fig. 4(c)).
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C. NORMALIZATION

The ECG signals are normalized properly after noise reduction. The purpose of normalization [21], [30] is to minimize the effects of the noise reduction process and to maximize the discrimination between feature vectors. When a heartbeat signal of our database is displayed in an X-Y coordinates as in Fig. 4, the variation of the amplitude components (y axis) ranges from approximately 0.5 mV to 3.1 mV and the temporal components (x-axis) consists of 95 samples which corresponds to an amount of 0.7 seconds. Therefore, if the numerical value in seconds is used as the digital value on the horizontal axis, it becomes a graph with the vertical length (0.5 ~ 3.1) of the ECG signal longer than the horizontal length (0.0 ~ 0.7).

The feature vectors proposed in this paper (described in detail in the next section) are composed of length and slope, and the horizontal axis represents temporal information. This temporal information indicates individual differences when the electrical stimulation of the heart propagates, thus the feature vectors can have better discrimination when the horizontal direction has sufficient length compared to the vertical direction. We found the ratio maximizing the discrimination between feature vectors through experiments. As a result, we normalized the variation on the x-axis ranges between 0 and 7 while the variation on the y-axis ranges between 0.5 and 3.1.

IV. METHODOLOGY

A. FEATURE EXTRACTION AND SELECTION

Heartbeat signals making up ECG signals have a specific shape. A heartbeat signal, which is a one-dimensional signal,

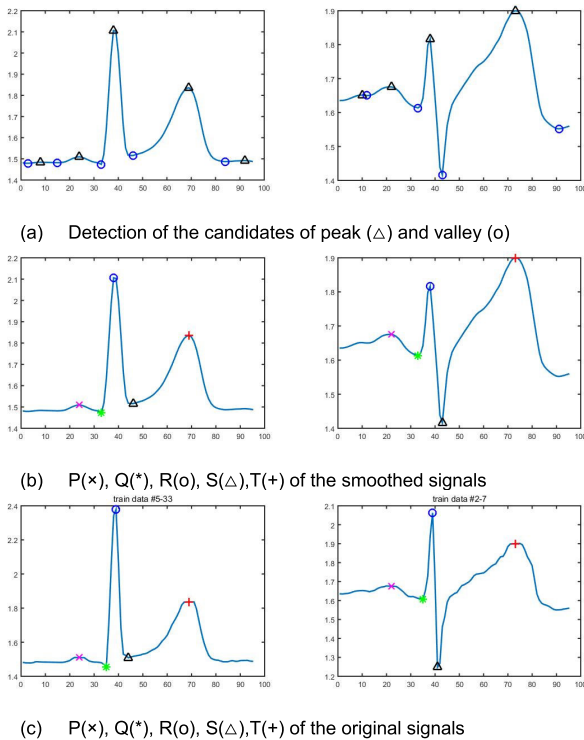


FIGURE 4. The results of the fiducial point detector in each step.

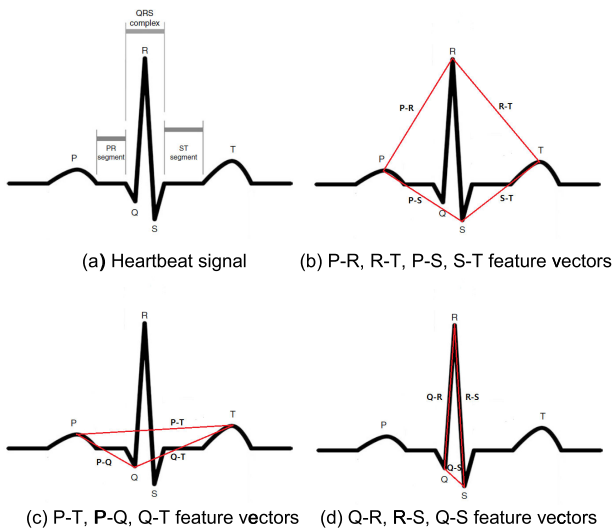


FIGURE 5. The proposed feature vectors in a heartbeat signal.

has peaks and valleys at certain locations, which are denoted as the fiducial points P, Q, R, S, and T, as shown in Fig. 5 (a). As described previously, one of the methods to extract feature vectors is based on the fiducial points. In particular, features are extracted from several fiducial points, which are the strength or period of the P wave, T wave, and QRS complex, in an ECG waveform. We tried to find the identity of ECG data by operating a discriminator based on the differences between these feature vectors. If discrimination can be maximized by transforming this morphological difference into a

feature vector with minimum loss, it will be the most effective feature extraction method. It will also be very efficient if a feature vector is visible enough to be confirmed by naked eyes.

In this paper, we propose a new feature vector extraction method that has such advantages and demonstrate an ECG-based human identification system applying the new feature vectors. This method is based on the P, Q, R, S, and T points that can be detected in the ECG signal of a healthy person. The purpose of the proposed system is not for medical diagnosis but for biometrics, and thus, it does not require high precision when detecting fiducial points. Therefore, computational burden is small and the effect of fiducial point detection performance on the entire system is not significant.

Now, let us examine the proposed feature vectors. A line segment can be created by selecting two different points from the peaks (P, R, T) and valleys (Q, S) present in a heartbeat signal. This line is proposed as a new feature vector (Fig. 5). There are 10 line segments (hereinafter referred to as 10 types of feature vectors) that can be created in this way, which are, P-R, R-T, S-T, P-S, P-T, P-Q, Q-R, Q-S, Q-T, and R-S. These feature vectors change in length and slope depending on both the location of the P, Q, R, S, and T points on the temporal axis and the variation in amplitude. In other words, we propose 10 types of feature vectors that combine the temporal and amplitude information of ECG signals. These feature vectors reflect unique characteristics of individuals as will be seen in the followings.

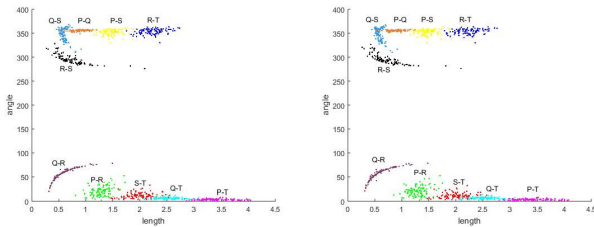
First of all, let us focus on the 4 types of feature vectors (which is interchangeably used with the 4 feature vectors) of the 10 types of feature vectors. The S-T and R-T feature vectors contain information from the depolarization to the repolarization of the ventricles. As observed in Fig. 5(b), these two feature vectors contain information about the periods of QRS complex, ST segment, and P wave. The length information of the R-T vector indicates the time difference between the maximum depolarization and the repolarization of the ventricles, and that of the S-T vector contains information on the ventricular contraction and relaxation immediately after the maximum depolarization. The variations in these feature vectors occur due to the different size and structure of the heart and its periphery. The S-T and R-T vectors could be complementary to each other because they are feature vectors representing similar phases in the electrical conduction system of the heart. In fact, the experimental results in Table 1 for verifying the discrimination by a single feature vector showed that they achieved the first and third highest recognition performance.

The P-R feature vector is related to atrial depolarization. Atrial depolarization begins at the sinoatrial node (SA), contracts the right and left atrium, and propagates to the AV node (Fig. 1) during the PR segment. Therefore, the length information of the P-R feature vector represents the time from atrial depolarization to the highest point of ventricular depolarization, and the relative ratio of signal amplitude is

TABLE 1. Performance by the accumulated feature vectors (%).

Single feature vector	P*	2 accumulated feature vectors	P*
S-T	65	(S-T) + (P-R)	96
P-R	50	(S-T) + (R-T)	89
R-T	49	(S-T) + (P-S)	86
P-S	47	3 or more accumulated feature vectors	P*
P-T	46	(S-T) + (P-R) + (R-T)	97
Q-T	45	(S-T) + (P-R) + (R-T) + (P-S)	99
R-S	41	(S-T) + (P-R) + (R-T) + (P-S) + (P-T)	99
Q-S	31	...	
Q-R	25	...	
P-Q	20	Using 10 feature vectors	99

P*: Performance



(a) Distribution of feature vectors in training data (b) Distribution of feature vectors in test data

FIGURE 6. Distribution of the proposed feature vectors.

represented by the slope of the P-R feature vector. The P-S vector is similar to the P-R vector and contains information about the periods of P wave, PR segment, and QRS complex. These two feature vectors are also complementary to each other because they are the feature vectors representing similar phases in the electrical conduction system of the heart. In fact, in the experiment in Table 1 for confirming the discrimination by a single feature vector, they showed the second and fourth highest recognition performance.

The four feature vectors mentioned above can be seen as the line segments (Fig. 5(b)) representing the outermost shape of a heartbeat signal. In other words, they are regarded as the feature vectors representing the most significant characteristics of a heartbeat signal. We conducted experiments to verify this, and the results using the 4 feature vectors are presented in Table 1. The performance using the 4 feature vectors are not significantly different from those using all of the 10 feature vectors. Therefore, if we need to design a small-size human identification system restricted to computational capacity, we can build a system using only the 4 feature vectors out of the 10 feature vectors. In other words, we can build a system with 60% reduction in computation but with no significant difference in performance.

Fig. 6 shows the distribution of the 10 types of feature vectors extracted from the training and test data of 100 subjects. The distribution of the 10 types of feature vectors in the 2D space shows that there are not much overlapping

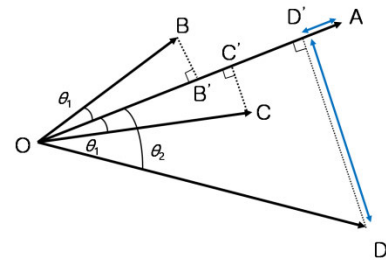


FIGURE 7. Distance-based similarity.

areas. Therefore, if the average value (average length, average angle) is calculated for each type of the feature vector per person and is used as a representative vector, a simple discriminator can be built.

B. SIMILARITY FUNCTION

A discriminator plays a critical role in a human identification system. A discriminator determines the identity of input biometric information by measuring similarity between the representative feature vectors obtained from the training process and unknown input feature vectors. The feature vectors used in this study are the vectors connecting two points between P, Q, R, S, and T, and these vectors are represented by length and slope. Therefore, the role of the discriminator is to determine how similar such feature vectors are. The similarity measurement used in the study is distance-based as shown in Fig. 7.

In order to find which vector is more similar to the vector OA, the vector OB and OC are projected on the vector OA respectively. And then the length difference between the projected vectors and the vector OA are measured. The vector that makes the length difference smaller between the projected vector and the vector OA is more similar to the vector OA. In this case, AC' is smaller than AB' so that the vector OC is more similar to the vector OA. This method is available because the angle between the vector OA and the vector OC is the same as the one between the vector OA and the vector OB.

In the case that the angle is not the same, the similarity using only a projected vector is not sufficient. Considering the vectors OB and OD in Fig. 7, these two vectors make different angles against the vector OA. Thus the similarity should consider not only the projected vectors OB', OD' but also the height vectors BB', DD' as in Eq. (1) and (2).

Similar to vector subtraction, the similarity of two vectors can be determined in such a way that the two vectors with the smallest sum of length difference (AB', AD') and height (BB', DD') are the most similar to each other as in Eq. (3) and (4).

$$\overline{OB'} = \overline{OB} \cdot \cos \theta_1, \quad \overline{AB'} = \overline{OA} - \overline{OB'}, \quad \overline{BB'} = \overline{OB} \cdot \sin \theta_1 \tag{1}$$

$$\overline{OC'} = \overline{OC} \cdot \cos \theta_1, \quad \overline{AC'} = \overline{OA} - \overline{OC'}, \quad \overline{CC'} = \overline{OC} \cdot \sin \theta_1$$

$$\overline{OD'} = \overline{OD} \cdot \cos \theta_2, \quad \overline{AD'} = \overline{OA} - \overline{OD'}, \quad \overline{DD'} = \overline{OD} \cdot \sin \theta_2 \tag{2}$$

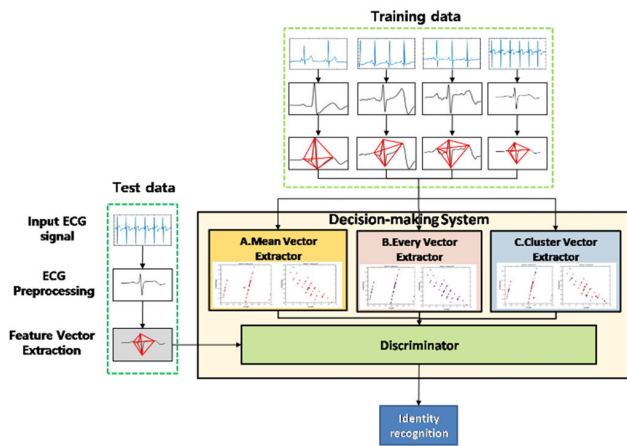


FIGURE 8. Structure of the proposed human identification system.

$$\begin{aligned}
 \text{Similarity}(A, B) &= (\overline{OA} - \overline{OB}') + \overline{BB'} \\
 &= (\overline{OA} - \overline{OB} \cdot \cos \theta_1) + \overline{OB} \cdot \sin \theta_1 \\
 &= AB' + BB'
 \end{aligned} \tag{3}$$

$$\begin{aligned}
 \text{Similarity}(A, D) &= (\overline{OA} - \overline{OD}') + \overline{DD'} \\
 &= (\overline{OA} - \overline{OD} \cdot \cos \theta_2) + \overline{OD} \cdot \sin \theta_2 \\
 &= AD' + DD'
 \end{aligned} \tag{4}$$

C. DECISION-MAKING SYSTEM

When a feature vector is inputted through the discriminator, the human identification system proposed in this study (Fig. 8) determines from whose heartbeat the feature vector was extracted. For this purpose, the decision-making system must store (or register) the representative vectors extracted through the training process. Therefore, it is essential to go through the training process before operating the system.

The training process requires a certain quantity of ECG data for people whose identities are already confirmed. Using this data, we extract feature vectors and make representative vectors by manipulating feature vectors according to the purpose. Depending on how many representative vectors are extracted from ECG data in the training step, the size of the system storage is determined, and at the same time, the processing speed is affected accordingly. Let us have a closer look at the training process. In total, 50 heartbeat signals are used as the training data for each one of the 100 subjects. These heartbeat signals have already been preprocessed to remove unnecessary noise. The location of the P, Q, R, S, T points has already been detected by the fiducial point detector. Representative vectors are determined from the feature vectors of such heartbeat signals. In this study, we conducted experiments in the following three ways for determining representative vectors.

1) REGISTER THE AVERAGE VALUE OF FEATURE VECTORS AS A REPRESENTATIVE VECTOR

From a single heartbeat signal, the 10 types of feature vectors can be extracted. As 50 heartbeat signals per person are used as training data, 50 training feature vectors (or training vectors) are used for each type of feature vector. Each training vector is expressed by length and slope. Therefore, a representative vector can be obtained by calculating a 2-dimensional mean vector from 50 training vectors in length and slope. As there are the 10 types of feature vectors, each person obtains 10 mean vectors as representative vectors. Thus, 1000 representative vectors of the 100 subjects are registered in the human identification system.

The similarity of the stored representative vectors is calculated along with the feature vectors of input ECG data, and the identity of input ECG data is considered to be the same person as the one from which the representative vector with the highest similarity is calculated.

2) REGISTER EVERY FEATURE VECTOR AS A REPRESENTATIVE VECTOR

This method registers every feature vector extracted from training data as a representative vector instead of mean vectors. That is, as there are 50 training data per person, there are 50 representative vectors for each type of the feature vector. Therefore, 500 representative vectors are given to each person. Given that there are 100 subjects, the number of representative vectors registered in the system is 50,000. Compared to the system using a mean vector as a representative vector, 50 times more storage space is required, and thus, the processing time is increased proportionally.

We conducted experiments in two ways to compare the similarity in the discriminator. The first one determines the similarity by the highest value between an input feature vector and the representative vectors. The other one determines the similarity by a sum of K highest values (K-nearest neighbors) between an input feature vector and the representative vectors. A sum of K values can alleviate the problem of being excessively biased toward particular data during the similarity measurement process.

3) REGISTER THE CENTER POINT OF A CLUSTER AS A REPRESENTATIVE VECTOR

Clustering is a method of partitioning data by assigning individual data to the nearest cluster according to the data distribution. One of the typical clustering methods is the K-means clustering method, which is used in the experiment. It creates N clusters by applying the K-means clustering algorithm to each of the 10 types of feature vectors consisting of 50 training data units and uses the center points of the N clusters as representative vectors (X in blue in Fig. 9). This method compromises between using a mean vector as a representative vector and using every vector as a representative vector. It keeps balance between recognition performance and processing speed.

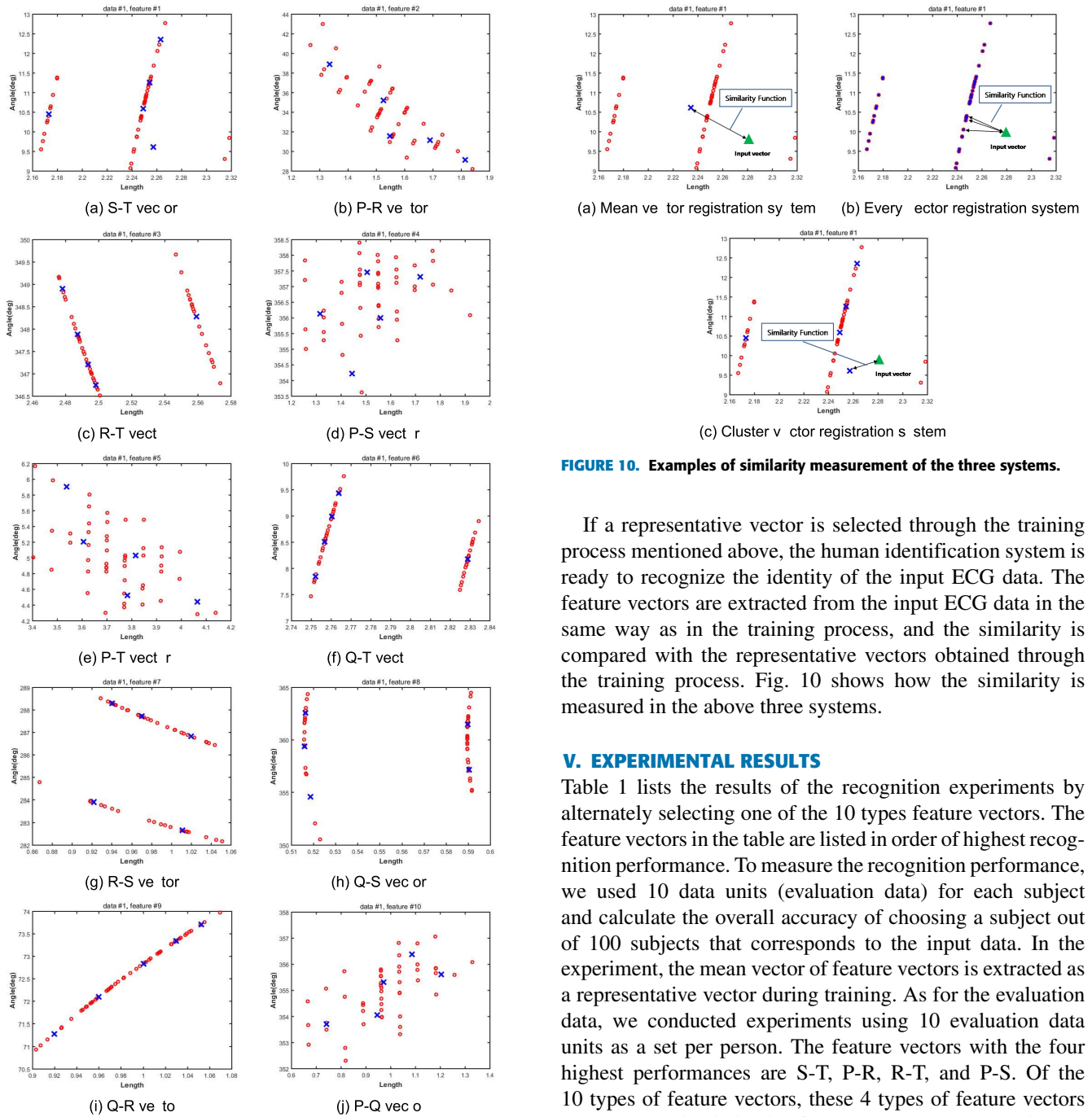


FIGURE 9. The representative vectors of the 10 types of feature vectors using 5 fixed clusters.

When applying the clustering method, we need to determine the number of clusters to which we assign the data. Depending on the characteristics of the data, the number of clusters may be determined in advance, and then clustering can be executed (fixed clustering), or the number of clusters can be changed during a clustering process (variable clustering). In this study, we evaluated the performance by applying both methods. Fig. 9 shows representative vectors (X in blue) obtained through the fixed clustering (5 clusters in total) method for each of the 10 feature vectors.

FIGURE 10. Examples of similarity measurement of the three systems.

If a representative vector is selected through the training process mentioned above, the human identification system is ready to recognize the identity of the input ECG data. The feature vectors are extracted from the input ECG data in the same way as in the training process, and the similarity is compared with the representative vectors obtained through the training process. Fig. 10 shows how the similarity is measured in the above three systems.

V. EXPERIMENTAL RESULTS

Table 1 lists the results of the recognition experiments by alternately selecting one of the 10 types feature vectors. The feature vectors in the table are listed in order of highest recognition performance. To measure the recognition performance, we used 10 data units (evaluation data) for each subject and calculate the overall accuracy of choosing a subject out of 100 subjects that corresponds to the input data. In the experiment, the mean vector of feature vectors is extracted as a representative vector during training. As for the evaluation data, we conducted experiments using 10 evaluation data units as a set per person. The feature vectors with the four highest performances are S-T, P-R, R-T, and P-S. Of the 10 types of feature vectors, these 4 types of feature vectors are the most discriminative feature vectors that determine the outer shape of a heartbeat signal. The next discriminative feature vector is the P-T vector, which represents the entire process of the heartbeat period.

We observed how the performance changed when accumulating the feature vectors by adding one feature vector at a time. In the case where we accumulated two feature vectors, we were able to achieve the performance with the recognition rate of 96% when using (S-T + P-R), followed by (S-T + R-T) and (S-T + P-S) with 89% and 86%, respectively. This result shows that an increase in the number of feature vectors by adding feature vectors in descending order of performance leads to the highest performance. In this way,

we conducted experiments by continuously increasing the number of feature vectors, such as three vectors (S-T + P-R + R-T), four vectors (S-T + P-R + R-T + P-S) up to ten vectors (S-T + P-R + R-T + P-S ... + P-Q). The experimental results are listed in Table 1. When we accumulated feature vectors up to 4, the performance is continuously improved, whereas the performance remained when using more than 4 vectors.

The evaluation data sets used in the following experiments were composed as follows. As each person can use 10 data units for evaluation, we prepared the 10 data sets by randomly selecting a data unit N ($N = 1, 2, \dots, 9$) times from 10 evaluation data units. That is, we prepared 10 evaluation sets each of which consists of 1 evaluation data unit, and prepared another 10 evaluation sets each of which consists of 2 evaluation data units and repeated until the number of evaluation data units becomes 9. Since we conducted experiments using the 10 different sets, the average value of the 10 sets is used as the overall recognition performance. This method shows the recognition performance that gradually changes according to the change in the number of input evaluation data units. Now, let's take a look at the performance of the three systems that are configured differently depending on how the representative vectors are selected.

First, let us consider the performance of the system (denoted as System 1) using a mean vector as a representative vector. Table 2 shows in detail the performance measured for each set when the number of input data units changes from 1 to 9. System 1 has the fastest processing speed. However, as a representative vector per a type of feature vector is just a mean vector, there is a limit for effectively representing various characteristics of the training data.

When two or more heartbeat signals are inputted, System 1 shows over 92.7% of recognition performance, which indicates that the proposed feature vectors are suitable for biometric information. Since the discriminator has a simple structure in this system, it has possibility to improve the performance. In terms of real time processing, System 1 can achieve a performance of 94.8% after approximately two seconds in which three heartbeat signals are received.

If a human identification system uses a fiducial point detector, the performance of the entire system can be adversely affected when the exact location of the fiducial points cannot be found. For example, the P point appears to be normal when the stimulus of the heart begins at the SA node. However, in the case of the junctional rhythm [26] or the SA block that occurs at the atrioventricular (AV) node rather than at the SA node, the P point may not appear in ECG signals. In addition, the P point might disappear [49] when the heart rate increases. Therefore, Kim *et al.* [36] attempted to extract feature vectors without the P point.

Let us see how the proposed method changes the performance in the same situation, where the four feature vectors (P-Q, P-R, P-S, P-T) associated with the P point are unavailable. Consequently, the system performance can only be measured using the rest of the six feature vectors. Table 3 com-

TABLE 2. System 1 performance (%).

Test set	Number of evaluation data units								
	1	2	3	4	5	6	7	8	9
1 st set	7	91	95	91	96	97	98	98	98
2 nd set	81	92	98	97	98	95	98	98	99
3 rd set	79	90	96	94	98	97	99	98	99
4 th set	84	97	97	97	98	98	97	98	99
5 th set	82	94	95	95	95	96	99	98	99
6 th set	80	89	90	94	96	99	99	97	99
7 th set	82	95	99	98	97	99	97	98	98
8 th set	81	94	94	97	98	99	98	99	99
9 th set	77	93	89	99	99	97	99	99	99
10 th set	84	92	95	99	95	97	97	99	99
average	81.0	92.7	94.8	96.1	97.0	97.4	98.1	98.2	98.8

TABLE 3. In cases where P, Q or S is excluded (%).

Exclusion of the point	Number of evaluation data units								
	1	2	3	4	5	6	7	8	9
P	79.7	91.1	91.7	94.3	95.9	96.3	96.9	96.8	97.6
Q	77.2	90.9	92.7	95.4	96.2	95.6	97.2	97.5	98.2
S	65.0	81.4	86.9	90.0	90.8	92.1	94.9	94.8	95.2

pare only the average values from the 10 evaluation sets according to the change in the number of evaluation data units, as in Table 2.

The results show that the performance without the P point is approximately 98% of the performance obtained with the P point, regardless of the number of input data units. This proves that the overall system performance is not significantly affected even though we could not find the P point by a fiducial point detector. Likewise, we observed the effect on the overall performance in cases where the Q or S points do not appear just like the P point. As presented in Table 3, when there are no feature vectors associated with the Q point, the performance is almost similar to or even better than that of P point case. In the absence of the S point, the performance is relatively large decreased. However, when three or more evaluation data units are inputted, the performance is close up to 90 ~ 95% compared to the performance when the S point is present. In conclusion, the detection of fiducial points does not significantly affect the proposed system, given that at least the R and T points must be accurately detected by a fiducial point detector, which could be a drawback of the proposed method in a sense.

Second, let us consider the performance of the system (denoted as System 2) registering every feature vector

TABLE 4. System 2 performance according to the change in K (average, %).

K	Number of evaluation data units								
	1	2	3	4	5	6	7	8	9
1	83.8	91.3	95.4	96.8	98.4	98.5	99.5	99.7	99.9
5	85.5	94.0	95.5	97.5	98.8	98.8	99.2	99.5	99.8
10	86.2	94.6	96.2	97.4	98.3	98.7	98.9	99.3	99.3
20	85.1	94.3	95.4	97.1	97.6	97.9	98.6	98.9	99.0
50	79.5	88.3	89.7	91.0	92.0	92.8	92.5	93.0	93.2

extracted from the training data as a representative vector. Given that 50 heartbeat signals are used as the training data, 50 times more representative vectors are used compared to the System 1. Considering the total number of subjects who participated in the experiment is 100, a total of 50,000 representative vectors were generated through the training process. The discriminator compares the similarity between the representative vectors generated in this way and input feature vectors; then, the subject with the highest similarity is found and is considered to be the same person that the input ECG data was extracted from.

The similarity was measured in two ways. The first one finds the highest similarity for each type of the feature vectors and then adds them up to an accumulated value, which is the similarity between the corresponding training data and the input evaluation data. The other one calculates the similarity using the sum of the K highest similarities instead of using only the highest value when calculating the similarity of each feature vector.

Table 4 presents the change in performance when all the training data are used as representative vectors with $K = 1, 5, 10, 20,$ and 50 . The table only shows the average value according to the change in the number of evaluation data units. The experimental results show that there is no significant difference in performance except for $K = 50$. However, if we look at them in more detail, $K = 10$ shows better performance than $K = 5$ when the number of input data units is less than 3, and $K = 5$ shows better performance than $K = 10$ when the number of input data units is 4 or more. This indicates that the number of input data units and the number of representative vectors are complementary to each other. In other words, if the feature vectors that can represent unique characteristics of the ECG are not sufficient due to insufficient input data, this can be compensated by increasing the number of representative vectors in the training data. On the contrary, if the number of input data units is large, the performance can be maintained by an appropriate number of representative vectors. The performance improvement according to the increase in K is saturated and when K is more than 20, the performance of the discriminator becomes degraded.

The third system (denoted as System 3) uses a clustering method when extracting representative vectors in the training process. System 1 and System 2 have difficulty in balanc-

TABLE 5. System 3 performance according to the number of the fixed clusters (average, %).

# of clusters	Number of evaluation data units								
	4	5	6	7	4	5	6	7	4
5	85.6	94.7	96.4	98.1	99.0	99.2	99.7	99.7	99.9
10	86.4	94.5	95.6	97.6	98.7	99.3	99.6	99.6	99.8
15	84.3	94.0	95.4	97.0	98.4	99.1	99.8	99.7	99.9
20	86.2	93.9	95.3	96.7	97.4	98.0	99.5	99.8	99.9

ing an amount of computation and recognition performance. Therefore, we generated clusters by grouping adjacent data and designed the system using the center value of each of the generated clusters as a representative vector. The number of representative vectors affects not only the time of training process but also the speed of the human identification system that is expected to run in real time. Therefore, reducing the number of representative vectors is a way to design an effective system while maintaining proper performance.

We used the K-means algorithm for clustering. The algorithm is widely used because it is intuitive and can group adjacent data at high speed in a vector space. When we group feature vectors with this method, we proceed in two ways. The first one begins with a fixed number of clusters, which is, before starting to group feature vectors, the number of clusters is fixed. The other one is a variable number of clusters that determines the number of clusters at the point where a clustering error gets minimal while increasing the number of clusters. In the experiment, we applied both methods and observed the relationship between the number of clusters and the performance. Because of the characteristics of the K-means algorithm, we should determine the initial center values of the clusters at the beginning and how to terminate the iterations. In the experiment, we performed random sampling to set the initial center values and the iterations were terminated when there was no significant improvement in 5 consecutive iterations.

Let us examine the experimental results by the fixed cluster method. Table 5 presents the results of comparing the average performance of the 10 sets according to the change in the number of evaluation data, when the number of clusters changes to $N = 5, 10, 15,$ and 20 . Table 5 reveals that the overall improvement in performance is not significant when the number of clusters increases. Given that System 2 maintained effective performance until $K = 20$, we conducted an experiment increasing the number of clusters to 20 to compare them in the same condition. System 3, which uses the fixed cluster method, showed the most effective performance when the number of clusters was 5 or 10.

The variable cluster method does not set the number of clusters in advance. We obtained representative vectors by applying the variable clustering method to the 10 types of feature vectors. As the number of clusters is variable, different

TABLE 6. System 3 performance according to the number of the variable clusters (average value, %).

avg. # of clusters	Number of evaluation data units								
	1	2	3	4	5	6	7	8	9
4.8 (max 5)	86.2	94.4	96.3	98.3	98.9	99.4	99.6	99.6	99.8
7.2 (max 10)	85.1	94.5	95.6	97.6	98.4	98.8	99.0	99.2	99.8
7.4 (max 20)	85.8	93.6	95.2	97.0	98.2	99.1	99.6	100.0	100.0

TABLE 7. Comparison of system 1, 2, 3 performance comparison (%).

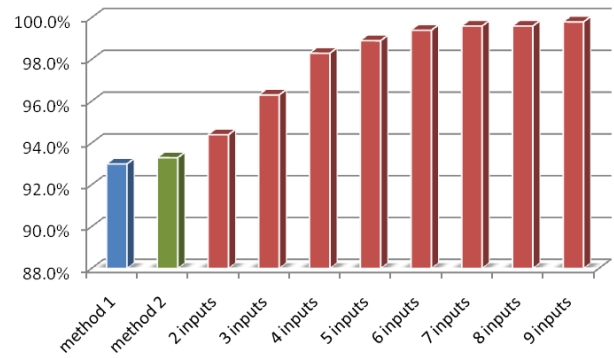
	Number of evaluation data units								
	1	2	3	4	5	6	7	8	9
System 1	81.0	92.7	94.8	96.1	97.0	97.4	98.1	98.2	98.8
System 2	85.5	94.0	95.5	97.5	98.8	98.8	99.2	99.5	99.8
System 3 (fix, 5)	85.6	94.7	96.4	98.1	99.0	99.2	99.7	99.7	99.9
System 3 (var., 4.8)	86.2	94.4	96.3	98.3	98.9	99.4	99.6	99.6	99.8

numbers of representative vectors are generated for each of the 10 types of feature vectors. Therefore, the overall number of representative vectors is obtained by calculating their average value.

Table 6 lists the average number of clusters and the average recognition performance when the variable clustering is performed with the maximum number of clusters set to 5, 10, and 20. The increasing input data leads to performance improvement in a moderate rate. In addition, even when the average number of clusters is as few as 4.8, the recognition rate is similar to that of the other cases. This indicates that an increase in the number of clusters does not necessarily improve the system performance as in the case of the experiment on the fixed cluster method. Consequently, this proves that the quality of representative vectors affects the performance more than their quantity.

Until now, we have examined the performance results of the three different human identification systems (System 1, System 2, System 3) with different structures of the discriminator. Table 7 presents the comparison of the highest performance of each system. The conclusion that can be drawn from this table is that an effective extraction of representative vectors can achieve effective performance with a small number of representative vectors. If we select System 3 (variable) as the final system, we can achieve a recognition performance with a rate of 94.4% or more when there are two or more evaluation data units. In other words, assuming that the period of an input heartbeat signal is approximately 0.7 sec, the identity of ECG data can be confirmed after 1.5 sec in which two heartbeat signals are received.

Let us compare the performance obtained in this study with the conventional methods [77] obtained in the same

**FIGURE 11. Performance graph of the conventional methods and the proposed method. (conventional methods: method 1, method 2; proposed method: 2–9 inputs).****TABLE 8. Comparison of performance of conventional and proposed methods (%).**

Conventional		Proposed method							
Method 1	Method 2	Number of inputs							
		2	3	4	5	6	7	8	9
93.0	93.3	94.4	96.3	98.3	98.9	99.4	99.6	99.6	99.8

experimental environment. Table 8 presents the performance comparison. When we conducted an experiment for 100 subjects, the method using frequency properties [20] achieved a recognition rate of 93% (Table 8, Method 1), and the 2D-resize method, which extracts features using the spectrogram, achieved a recognition rate of 93.3% (Table 8, Method 2). The method 2 increases the discrimination of feature vectors by increasing the amount of data to extract effective features present in ECG signals.

In the proposed method, on the contrary, we selected a method of minimizing the amount of computation when extracting feature vectors and proposed the 10 types of feature vectors. As a result, the human identification system using the proposed feature vectors can process them in real time, and the result shows better performance than the conventional methods when two or more input data sets are inputted (Fig. 11). It could be a drawback of the proposed method that the recognition performance using a single heartbeat is not as good as expected. However it is a rare situation in which only a single heartbeat is available for human identification. In addition, given that the proposed method uses the accumulated similarity obtained from the entire input data, the recognition performance, unlike the conventional methods, increases in proportion to the increase in the number of input data units. Such a structure enables the human identification system to achieve an appropriate performance by adjusting the number of input data units according to the given conditions.

Table 9 is a modified confusion matrix of the proposed method with 2 inputs for the 100 subjects. Due to space restrictions, the original confusion matrix form has been reconfigured in a more compact fashion. In the table, the upper four rows show all the subjects which have been

TABLE 9. Confusion matrix for the proposed method with 2 inputs.

		Predicted				
		label (# of predictions)				
	label					
		#1	#1(10)			
	...					
	#N	#N(10)				
	...					
True	#13	#13(9)	#56(1)			With errors
	#15	#15(8)	#61(2)			
	#34	#34(8)	#64(2)			
	#35	#35(7)	#60(3)			
	#36	#36(3)	#76(2)	#85(5)		
	#38	#38(6)	#40(1)	#53(2)	#64(1)	
	#42	#42(7)	#44(2)	#82(1)		
	#47	#47(8)	#71(2)			
	#48	#48(8)	#54(1)	#67(1)		
	#50	#50(2)	#41(2)			
	#53	#53(7)	#38(3)			
	#54	#54(9)	#71(1)			
	#55	#55(8)	#16(2)			
	#56	#56(7)	#12(2)	#76(1)		
	#59	#59(9)	#20(1)			
	#61	#61(7)	#46(2)	#75(1)		
	#64	#64(8)	#15(1)	#37(1)		
	#65	#65(8)	#70(1)	#78(1)		
	#68	#68(7)	#48(3)			
	#72	#72(7)	#60(3)			
	#80	#80(8)	#43(2)			
	#87	#87(9)	#60(1)			
	#95	#95(9)	#60(1)			
	#100	#100(9)	#89(1)			

classified without errors. For instance, the 10 test inputs from the subject #1 were identified as ECG signals of the subject #1. All the test inputs from 76 subjects, which are 760 test inputs in total, were identified without decision errors.

On the other hand, the rest of the rows show the subjects that have been identified with errors. For instance, 8 of 10 test inputs from the subject #48 have been identified correctly and 2 test inputs were falsely identified into the subject #54, #67 respectively. Each of the 24 subjects contains at least one test input that was identified incorrectly.

Therefore the red-highlighted cells (diagonal cells in an original confusion matrix) show the TP (True Positive) or TN (True Negative), which are 944 in total, and the other cells (off-diagonal cells in an original confusion matrix) show prediction errors considered as FP (False Positive) or FN (False Negative), which are 56 in total.

Since it is not a binary classification, the micro-averaged recall (often called as micro-recall) and overall accuracy are

adopted for multi-class metrics.

$$\text{micro-recall} = \frac{TP}{TP + FN} = \frac{944}{944 + 56} = 94.4\%$$

$$\text{overall accuracy} = \frac{TP + TN}{TP + FN + TN + FP} = \frac{944 + 944}{944 + 56 + 944 + 56} = 94.4\%$$

Since precision is the same as recall in the micro-averaging case, the following always holds true:

$$\text{micro-recall} = \text{micro-precision} = \text{overall accuracy} = 94.4\%$$

Likewise FNR, FPR can be calculated in the form of micro-averaged metric as follows:

$$\text{micro-FNR} = \frac{FN}{TP + FN} = \frac{56}{944 + 56} = 5.6\%$$

$$\text{micro-FPR} = \frac{FP}{TN + FP} = \frac{56}{944 + 56} = 5.6\%$$

Consequently, Statistical characteristics of the multi-class classification in the proposed system can be summarized that its overall accuracy is 94.4% and error rate is 5.6%.

VI. CONCLUSION AND FUTURE WORK

The ECG-based human identification system recognizes the identity of a person using the uniqueness of ECG signals caused by morphological differences of the heart. In this study, we proposed new feature vectors based on fiducial points which are clear and visible. The human identification system applying the new feature vectors was designed considering the computational complexity. Accordingly, we designed the structure of the discriminator in a simple manner. Unlike the complex and overlapping information represented by feature vectors in the previous research, we proposed the 10 types of feature vectors that can be represented by the combination of temporal and amplitude information and verified the validity of these feature vectors. Consequently, we were able to confirm that the proposed feature vectors effectively represent the discriminative information present in ECG signals.

The direction of future research aims to build the structure of the proposed feature vectors hierarchically. As previously mentioned, the proposed feature vectors containing the most discriminative information were the four types of feature vectors representing the outer shape of heartbeat signals. Based on this concept, if we get the 10 types of the proposed feature vectors into a hierarchical structure, which has outer, middle, and inner layers, and then study the characteristics of each layer and design a suitable discriminator for each layer, we would be able to design an advanced ECG-based human identification system with better performance.

It should be noted that in many studies, the unit for extracting features is limited to a heartbeat signal itself, not taking into account the unique characteristics between heartbeat signals. Therefore, it is necessary to study a method that can

express not only the features within a heartbeat signal but those features between them. If we extend the concept in this way, there is a possibility of extending feature vectors based on fiducial points into feature vectors independent of fiducial points. In other words, the adjacent areas around the proposed feature vectors could contain highly discriminative information, and it could be possible to extract new feature vectors from them. Efforts to find these new methods should proceed in the direction of real-time processing. Consequently, the key to the development of new technology will be to extract feature vectors from the areas containing the most discriminative information of ECG signals, including fiducial points.

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EUNSANG BAK received the B.S. and M.S. degrees from Sogang University, Seoul, South Korea, and the Ph.D. degree from the University of North Carolina, Charlotte, in 2004. From 2004 to 2015, he worked as a Senior Research Engineer in Samsung Electronics Company, Ltd., Suwon, South Korea. He is currently a Research Member with Chosun University, Gwangju, South Korea. His research interests include statistical pattern recognition, machine learning, bioinformatics, and image processing.



GYU-HO CHOI received the B.S. degree in electronics engineering from Chosun University, Gwangju, South Korea, in 2015. He is currently pursuing the Ph.D. degree. His research interests include biometrics, pattern recognition, and wearable device.



SUNG BUM PAN received the B.S., M.S., and Ph.D. degrees in electronics engineering from Sogang University, South Korea, in 1991, 1995, and 1999, respectively. He was a Team Leader with the Biometric Technology Research Team, ETRI, from 1999 to 2005. He is currently a Professor with Chosun University. His current research interests are biometrics, security, and VLSI architectures for real time image processing.

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