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Feature selection algorithm for ECG signals using Range-Overlaps Method

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ABSTRACT

This study proposes a simple and reliable feature selection algorithm for ECG signals, termed the Range-Overlaps Method. The proposed method has the advantages of good detection results, no complex mathematic computations, fast and low memory space and low time complexity. Both cluster analysis and fuzzy logic methods are applied to evaluate the performance of the proposed method. Experimental results show that the total classification accuracy is above 93%. Thus, the proposed algorithm provides an efficient, simple and fast method for feature selection on ECG signals.

1. Introduction

According to the medical definition in Rangayyan (2001), the most important information in the ECG signal is concentrated in the P wave, QRS complex and T wave. These data include positions and/or magnitudes of the QRS interval, PR interval, QT interval, ST interval, PR segment, and ST segment (see Fig. 1). Based on the above data, doctors can correctly diagnose human heart diseases. Therefore, analyzing the ECG signals of cardiac arrhythmia is very important for doctors to make correct clinical diagnoses. In order to perform ECG signals classification of the cardiac arrhythmia, the first important task is to determine an appropriate set of features. The feature selection method which chooses the best features from original features to have the maximum recognition rate, simplify classified computation and comprehend the causal relation of classified question. In other words, the goal of feature selection is to find the optimal subset consisting of m features chosen from original features (total n features) and m is as small as possible. Such as, let $X = \{x_1, x_2, \ldots, x_n\}$ be a n-dimensional PQRST complex feature set, its subset $X' = \{x_1, x_2, \ldots, x_m\}$ is the optimal subset which consists of qualitative features if it can be able to represent the original PQRST complex features faithfully so that minimal useful information is lost (see Fig. 2), where $m \leqslant n$.

Feature selection (Dash & Liu, 1997) is an extensively adopted dimensionality reduction technique, and has been the focus of much research in pattern recognition, machine learning and data mining. Feature selection also improves understanding of data identifying the important features and their interrelationships. Principal Component Analysis (PCA) (Pattarin, Paterlini, & Minerva, 2004) and Fisher's Linear Discriminate Analysis (Fisher's LDA) (Ren & Chang, 2005) have been extensively adopted in pattern recognition and general feature selection problems. These methods find a mapping between the original feature space and a lower-dimensional feature space. Several investigations on feature selection for pattern classification have been performed in recent years. For instance, Lin and Meador (1992) proposed stepwise discriminant analysis for feature selection, producing results that can be adopted as inputs to a neural network that performs pattern recognition of circuitry faults. Lisboa and Mehri-Dehnavi (1996) presented a multilayer perception for feature selection. Genetic algorithms by Biswas, Goel, Mukerjee, and Shawky (2005) and Oh, Kim, and Min (2005) are adopted to find solutions of optimization problems, which in turn might adopt some estimation model for objective function evaluation. In statistics and machine learning, random multinomial logit (Prinzie & Van den Poel, 2008) is a technique for (multi-class) statistical classification using repeated multinomial logit (RML) analyses via Leo Breiman's random forests. This method is also known in statistics as ridge regression (Biswas et al., 2005; Chiang, Urbang, & Baldridge, 1996; Tarantola, 2004), and is related to the Levenberg–Marquardt algorithm for non-linear least-squares problems. All the above methods require some complicated mathematical calculations to achieve their aims, as is well known. However, fast, reliable and efficient algorithms become much important if the analysis of ECG signals for cardiac arrhythmia measurement systems is applied to areas involving limited energy consumption. Hence, this study proposes a simple, fast and reliable method called "Range-Overlaps Method" (ROM) for effective feature selection.

In this study, the proposed Range-Overlaps Method for ECG classification of the cardiac arrhythmia is a simple and reliable

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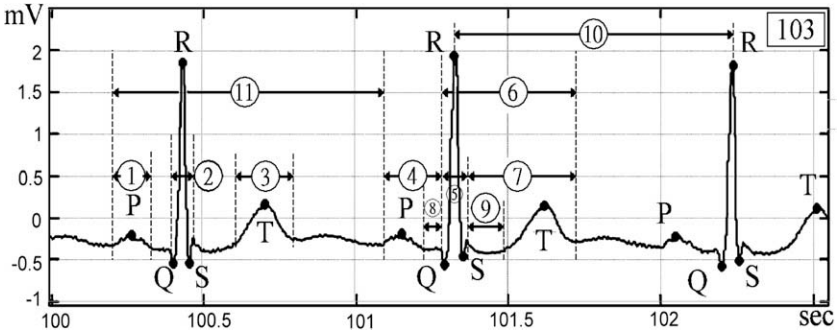

Fig. 1. ECG waveform: (1) P wave; (2) QRS complex; (3) T wave; (4) PR interval; (5) QRS interval; (6) QT interval; (7) ST interval; (8) PR segment; (9) ST segment; (10) R-R interval; (11) cardiac cycle.

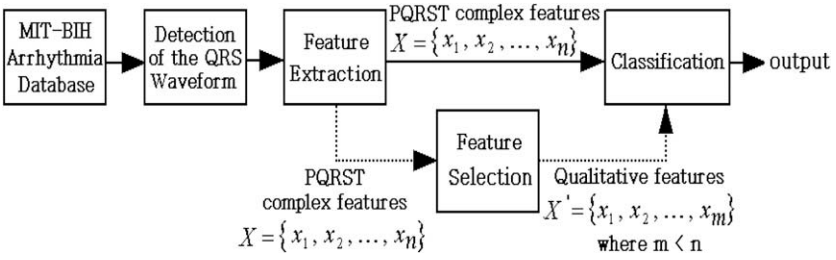

Fig. 2. Block diagram of feature selection.

feature selection method. This study consists of three major steps: (i) QRS extraction stage for detecting QRS waveform using the Difference Operation Method (DOM) proposed in Yeh and Wang (2008); (ii) qualitative features stage for qualitative feature selection for an ECG signal; and (iii) evaluation. The ECG records available in the MIT-BIH arrhythmia database (Massachusetts Institute of Technology, 1998) are experimented to illustrate the effectiveness of the proposed method.

The paper is organized as follows. Section 2 shows QRS extraction stage for detecting QRS waveform. In Section 3, the PQRST complex feature extraction of an ECG signal is introduced. Section 4 presents the qualitative feature selection which uses the Range-Overlaps Method, and the effectiveness of the proposed method is evaluated in Section 5. The paper is briefly concluded in Section 6.

2. QRS extraction stage: Difference Operation Method (DOM)

This section briefly reviews our previously proposed scheme called the "Difference Operation Method (DOM)" in Yeh and Wang (2008) for detecting QRS complex.

2.1. The difference equation operation

A difference equation is a formula for calculating an output sample at time n based on the past and present input samples and the past output samples in the time domain (Deeba & Korvin, 1995). A general difference equation (or digital filtering operation) is written as

$$y(n) = b(0)x(n) + b(1)x(n-1) + b(2)x(n-2) + \cdots + b(m)x(n-m) - a(1)y(n-1) - a(2)y(n-2) - \cdots - a(k)y(n-k) \quad (1)$$

where x, y, $b(i)$, and $a(j)$ are the input signal, the output signal, and the constant coefficients, respectively for $i = 0, 1, 2, \ldots, m$ and $j = 0, 1, 2, \ldots, k$. Notably, Eq. (1) concerns the past output samples (such as $y(n-1), y(n-2), \ldots, y(n-k)$) in the calculation of the present output $y(n)$. This form with past output samples is called "feedback". Any filter having one or more feedback paths is called a recursive digital filter or an infinite-impulse-response (IFIR) digital filter. Conversely, a filter without feedback is called a non-recursive or finite-impulse-response (FIR) digital filter. This study adopts an FIR digital filter has been adopted:

$$y(n) = b(0)x(n) + b(1)x(n-1) + b(2)x(n-2) + \cdots + b(m)x(n-m) = x(n) - x(n-1) \quad (2)$$

where we set the constants $b(0) = 1, b(1) = -1$, $b(2) = b(3) = \cdots = b(m) = 0$, and $a(j) = 0$; *for* $j = 0, 1, 2, \ldots, k$. Eq. (2) is called "difference operation" in this paper. For instance, Fig. 3 shows a difference operation with the original input signal $x(n)$ and the output signal $y(n)$.

The difference operation inhibits the low-frequency component of a signal, and enhances its high-frequency component. The violent variation of the signal is emphasized as an eminent impulse when the difference operation is applied to the relatively higher-frequency component of the ECG signals (such as QRS complex). Conversely, the relatively lower frequency part of the ECG signals (such as baseline drifting signal with slow variation) is often negligible when it is passed through the difference operation due to its nearly zero amplitude. The MIT-BIH arrhythmia database is adopted here to illustrate the effectiveness of difference operation. For instance, Tape 234 (see Fig. 4a) contains an ECG signal with baseline drifting, making a fixed reference line for obtaining point R difficult to achieve. If the difference operation is applied to the ECG signal, then the difference signal with eminent impulse without baseline drifting is obtained (shown in Fig. 4b). Therefore, point R is easy to obtain. Consider another example. Tape 228 (see Fig. 5a) has much larger variation on the amplitude size than Tape 234. The difference operation produces a series of positive impulse and negative impulse pairs (see Fig. 5b). Since the difference operation has the above capability (inhibits the low-frequency component of a signal, and enhances its high-frequency component), it is adopted herein to detect QRS in ECG signals, as discussed in detail in the following paragraph.

	0	1	2	3	4	5	6	7	8	
x(n)	1	5	2	6	3	7	9	4	6	← x(n) is the original input signal

	1	2	3	4	5	6	7	8	
y(n)	4	-3	4	-3	4	2	-5	2	← y(n) is the original input signal after the difference operation

Fig. 3. An example for the difference operation.

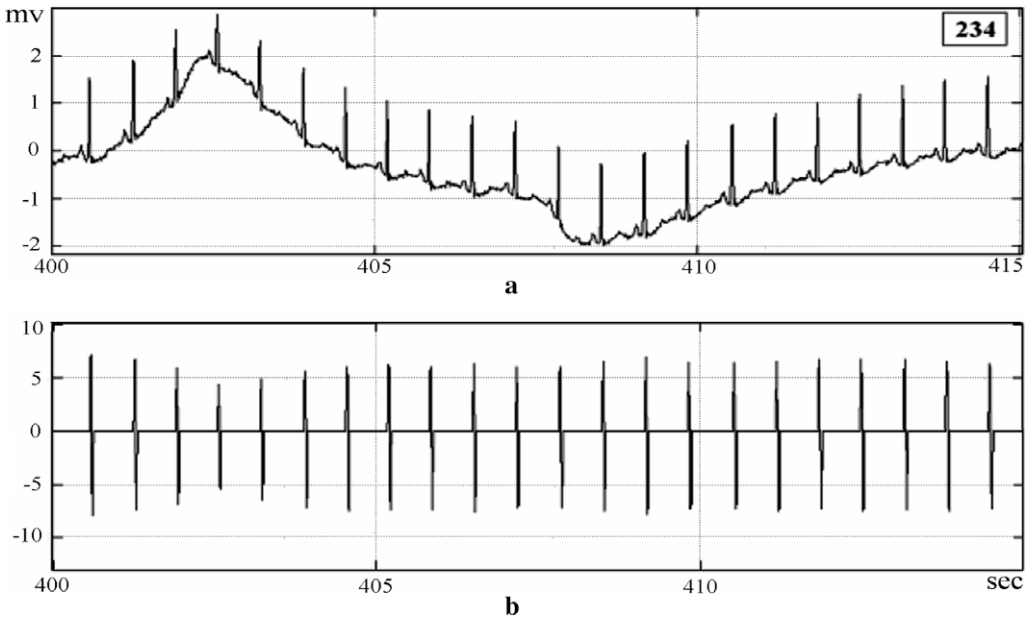

Fig. 4. (a) The original ECG signal in the database of MIT-BIH – Tape 234; (b) the difference signal without baseline drifting after applying the difference operation.

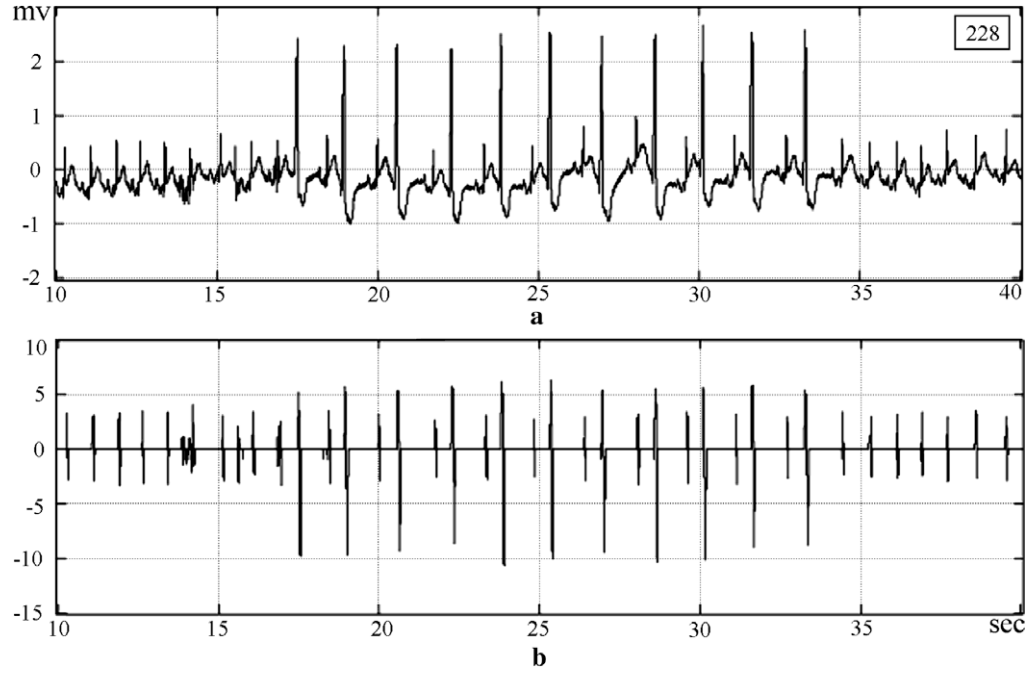

Fig. 5. (a) The original ECG signal in the database of MIT-BIH – Tape 228; (b) the difference signal without baseline drifting after applying the difference operation.

2.2. Difference Operation Method (DOM)

This section will review the DOM which uses the operation of difference equation (difference operation) to detect the QRS complex, P wave, and T wave in the original ECG signals. The DOM procedure is presented as follows:

Step 1-1: Download the original ECG signal x (see Fig. 6a).

Step 1-2: Use a digital filter to eliminate noise from the ECG signals.

The preprocessing filtration was based on methods in Zhao and Chen (2006), Friesen et al. (1990), Raphisak, Schuckers, and Curry (2004), and Hamilton and Curley (2000), and the following procedures are realized:

(i) 60 Hz power-line interference (see Fig. 7a). The 60 Hz notch filter is used for rejecting the power-line interference (Zhao & Chen, 2006).

(ii) Baseline drift (see Fig. 7b). The high-pass filter with a cut-off frequency 0.5 Hz is used to remove interference from baseline drift (Zhao & Chen, 2006).

(iii) Electromyogram (EMG) (see Fig. 7c). The morphological filter for a unit square-wave structuring (the best width is 0.07 s) is used to remove EMG interference (Friesen et al., 1990; Raphisak et al., 2004).

(iv) Motion artifacts (see Fig. 7d). The adaptive filter (duration time is about 100–500 ms) is employed to remove the interference of motion artifacts (Hamilton & Curley, 2000).

Step 1-3: Obtain the difference signal x_d by the following equation

$$X_d(n) = x(n) - x(n-1) \tag{3}$$

where $x(n)$ and $x_d(n)$ are the input signal and the difference output signal at time n (see Fig. 6b), respectively.

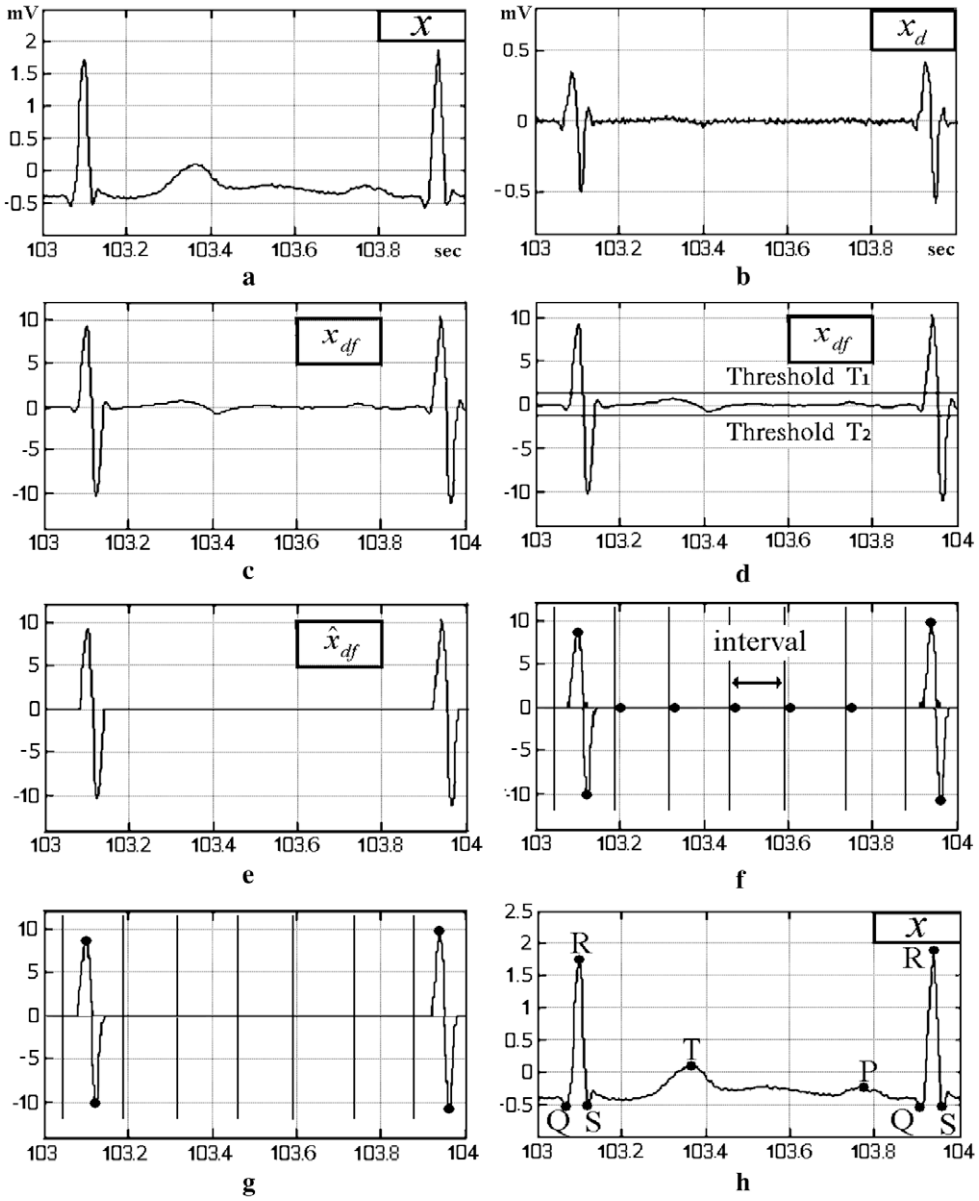

Fig. 6. (a) x, the original ECG signal; (b) x_d, the ECG signal after applying the difference operation; (c) x_{df}, the signal after applying a low pass filter; (d) the setting of the threshold values; (e) $\hat{x}_{df}$, the signal after going through thresholds; (f) pick up the extreme value points (where "•" represents extreme value points); (g) selecting the correct extreme value points; (h) the position of positive maximum value is the point R.

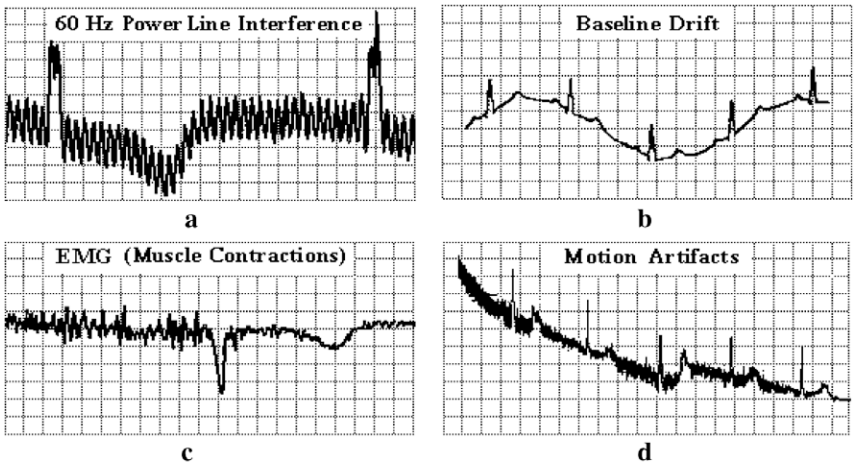

Fig. 7. Noise of ECG signal: (a) 60 Hz power-line interference; (b) baseline drift; (c) EMG; (d) motion artifacts.

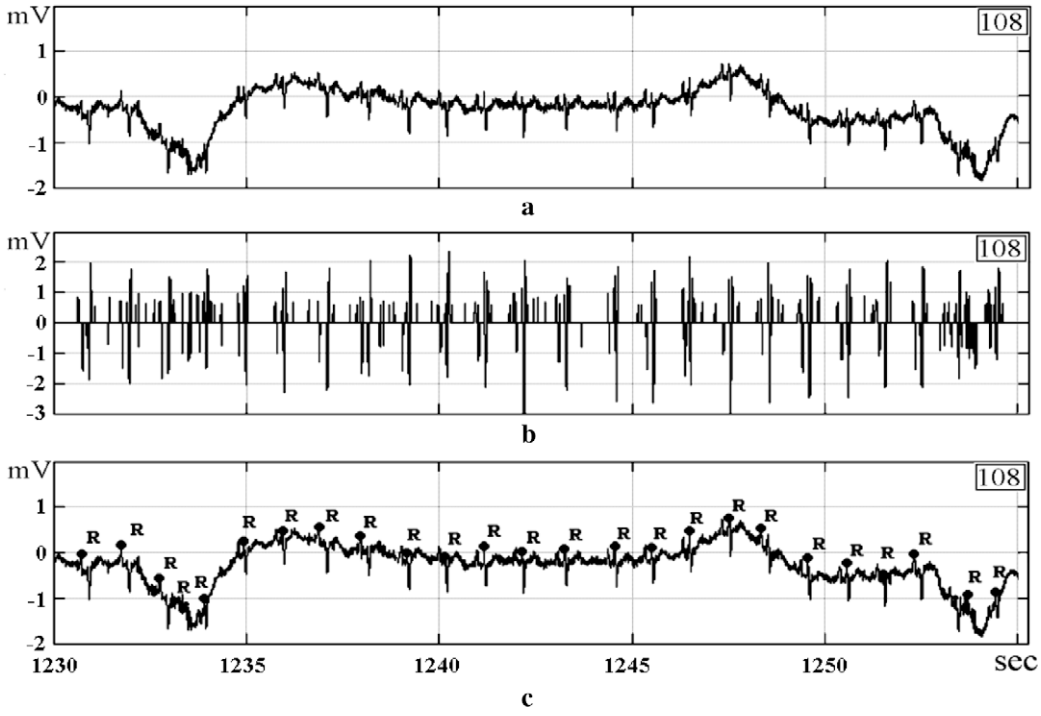

Fig. 8. Tape #108, (a) the original ECG signal; (b) the signal after difference operation; (c) the detected R waves.

Table 1
Description of the PQRST complex features.

Feature's serial #	Feature's symbol	Feature description	Units
1	H-QR	The amplitude between Q and R in a QRS complex	mV
2	H-RS	The amplitude between R and S in a QRS complex	mV
3	QRS-dur	The time duration between Q and S in a QRS complex	ms
4	QTP-int	The time duration between Q and T' in a QRS complex	ms
5	Ratio-RR	The ratio of RR_s and RR_a, RR_s is the length of a single RR-interval and RR_a is the average length of all RR-intervals	–
6	Slope-QR	The slope between Q and R in a QRS complex	mV/ms
7	Slope-RS	The slope between R and S in a QRS complex	mV/ms
8	Area-QRS	The area of QRS complex	mV × ms
9	Area-R′ST′	The area of R', S, and T' in a QRS complex. The point R' is the previous point which has the same amplitude as the point T'	mV × ms

Step 1-4: Apply any low pass filter with a cut off frequency about 100 Hz to x_d for eliminating the small amplitude but high frequency variation waveform (see Fig. 6c). The filtered signal is denoted by x_{df}.

Step 1-5: Get the final signal $\hat{x}_{df}$ (see Fig. 6e).

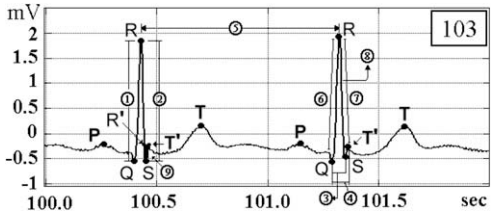

Fig. 9. The PQRST complex features: (1) F_1: H-QR; (2) F_2: H-RS; (3) F_3: QRS-dur; (4) F_4: QTP-int; (5) F_5: Ratio-RR; (6) F_6: Slope-QR; (7) F_7: Slope-RS; (8) F_8: Area-QRS; (9) F_9: Area-R′ST′.

Table 2
Heartbeat cases associated with the extracted beats for the full database from the MIT-BIH arrhythmia database.

	Heartbeat case						Total beats
	NORM	LBBB	RBBB	VPC	APC	Others	
Number of beats	75,054	8074	7259	7129	2544	9432	109,492
% of total beats	68.5	7.4	6.6	6.5	2.3	8.7	100.0

Table 3
Annotations of the MIT-BIH database ("–"represents no such heartbeat case in this Tape).

Tape no.	Total beats (30-min)	Heartbeat case				
		NORM	LBBB	RBBB	VPC	APC
103	2085	2083	–	–	–	2
111	2124	–	2123	–	1	–
113	1795	1789	–	–	–	6
118	2278	–	–	2166	16	96
123	1518	1515	–	–	3	–
200	2599	1743	–	–	826	30
212	2748	2073	–	675	–	–
214	2258	–	2002	–	256	–
221	2427	2031	–	–	396	–
222	2483	2274	–	–	–	209
231	1571	1007	–	562	2	–
232	1780	398	–	–	–	1382
233	3068	2230	–	–	831	7
234	2753	2700	–	–	3	50

$$\hat{x}_{df} = \begin{cases} 0, & \text{if } 0 < x_{df} < T_1, \text{ or } T_2 < x_{df} < 0 \\ x_{df}, & \text{if } x_{df} \geqslant T_1, \text{ or } x_{df} \leqslant T_2 \end{cases} \quad (4)$$

where $T_1 = 2 \times MV_p$ and $T_2 = 2 \times MV_n$ are thresholds (see Fig. 6d). MV_p and MV_n denote the mean values of all positive and negative waveform amplitudes in each MIT-BIH arrhythmia database record, respectively.

Step 1-6: Find the extreme value points for each interval, where each interval contains 50 sampling points with sampling frequency 360 Hz (see Fig. 6f).

Step 1-7: Select the correct extreme value points (see Fig. 6g).

Step 1-8: Match the positions of those extreme points to the original ECG signal, the position of maximum positive value is point R in the interval (see Fig. 6h).

Step 1-9: Look for points Q and S based on point R to find the QRS complex (see Figs. 6h and 8).

Step 1-10: Find points P and T according to the method of Gritzali, Frangakis, and Papakonstantinou (1989) (see Fig. 6h).

Remark 1-10: Method in Gritzali et al. (1989) is based on a "length" transformation which exhibits interesting characteristics and can be utilized for one-channel or multichannel waveforms.

The paper (Yeh & Wang, 2008) showed that DOM is effective for finding QRS complexes correctly. In performing pattern classification, the first important task is to determine a suitable set of features. The classification accuracy and efficiency can be improved by selecting a proper subset of features. The qualitative features stage is described in the following two parts, namely the PQRST complex feature extraction and the other is the qualitative feature selection (Range-Overlaps Method).

3. PQRST complex feature extraction

The PQRST complex features are the location, duration, amplitudes, and shapes of the waves. These features can be recognized by the experienced cardio-doctors for diagnosing human heart diseases (Zigel, Cohen, & Katz, 2000). Based on many times of experiments, nine PQRST complex features listed in Table 1 are selected and their waveforms are shown in Fig. 9. Let F_i, $i = 1, 2, 3, 4, 5, 6, 7, 8, 9$, denotes PQRST complex features "H-QR", "H-RS", "QRS-dur", "QTP-int", "Ratio-RR", "Slope-QR", "Slope-RS", "Area-QRS", and "Area-R′ST′, respectively (see Fig. 9).

The MIT-BIH arrhythmia database contains forty-eight 30-min long records of ECG signals with a sampling rate of 360 Hz, there

Table 4
The ranges of the PQRST complex feature values for Tape #103.

Total beats: 2083	H-QR	H-RS	QRS-dur	QTP-int	Ratio-RR	Slope-QR	Slope-RS	Area-QRS	Area-R′ST′
Minimum	2.125	2.050	44.0	58.0	0.828	0.061	0.079	51.81	2.70
Maximum	2.665	2.625	64.0	75.0	1.145	0.095	0.156	79.20	6.01
Unit	mV	mV	ms	ms	–	mV/ms	mV/ms	mV × ms	mV × ms

Table 5
The ranges of the PQRST complex feature values for NORM case.

Total beats: 8087	H-QR	H-RS	QRS-dur	QTP-int	Ratio-RR	Slope-QR	Slope-RS	Area-QRS	Area-R′ST′
Minimum	0.695	0.800	33.0	43.0	0.800	0. 019	0.017	20.0	0.00
Maximum	2.690	3.645	79.0	90.0	1.200	0.134	0.214	82.0	24.50
Unit	mV	mV	ms	ms	–	mV/ms	mV/ms	mV × ms	mV × ms

Table 6
The ranges of the PQRST complex feature values for each case.

Features	Heartbeat case									
	NORM		LBBB		RBBB		VPC		APC	
	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean
H-QR	[0.695, 2.690]	2.178	[0.205, 2.060]	1.313	[0.695, 2.240]	1.629	[0.105, 3.095]	1.303	[0.275, 1.870]	0.882
H-RS	[0.800, 3.645]	2.630	[0.705, 2.815]	1.750	[0.955, 3.300]	2.309	[0.870, 3.575]	2.473	[0.490, 2.345]	1.263
QRS-dur	[33.0, 79.0]	55.0	[86.0, 153.0]	109.2	[46.0, 130.0]	74.6	[52.0, 210.0]	120.4	[34.0, 61.0]	54.3
QTP-int	[43.0, 90.0]	70.0	[135.0, 230.0]	172.8	[110.0, 210.0]	144.3	[120.0, 485.0]	291.8	[50.0, 112.0]	91.3
Ratio-RR	[0.80, 1.20]	0.995	[0.85, 1.30]	1.002	[0.775, 1.50]	1.028	[0.45, 0.76]	0.640	[0.41, 0.76]	0.706
Slope-QR	[0.019, 0.134]	0.067	[0.004, 0.050]	0.023	[0.012, 0.111]	0.049	[0.002, 0.061]	0.021	[0.006, 0.079]	0.022
Slope-RS	[0.017, 0.214]	0.138	[0.043, 0.055]	0.048	[0.023, 0.136]	0.063	[0.011, 0.108]	0.053	[0.013, 0.162]	0.064
Area-QRS	[20.0, 82.0]	24.9	[0.0, 146.15]	73.88	[25.01, 120.96]	60.17	[4.16, 289.92]	85.0	[10.59, 69.35]	27.43
Area-R′ST′	[0.0, 24.5]	9.3	[20.0, 32.0]	25.0	[34.0, 88.0]	55.8	[0.0, 265.0]	149.9	[0.0, 155.0]	8.00

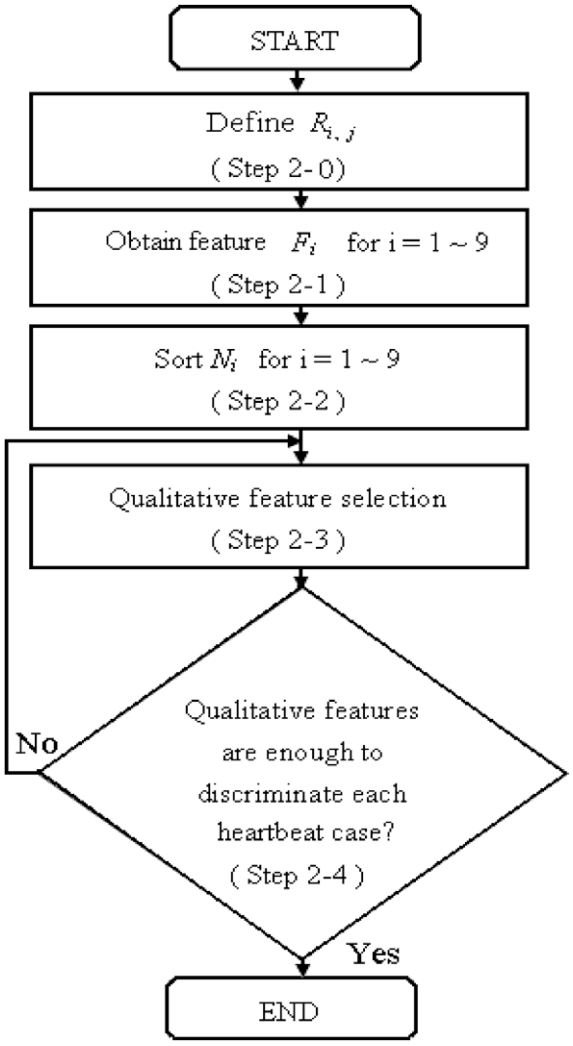

Fig. 10. Procedure QFS.

are about 109,492 labeled ventricular beats from 15 different heartbeat cases (see Table 2). The following five largest heartbeat cases in the MIT-BIH arrhythmia database were classified in this study, as listed in Table 2: (i) NORM – about 75,054 beats; (ii) LBBB – about 8074 beats; (iii) RBBB – about 7259 beats; (iv) VPC – about 7129 beats; (v) APC – about 2544 beats. Because NORM, LBBB, RBBB, VPC, and APC are symbols for labeling each heart "beat", and hence it can have different rhythms in different time sections. Table 3 lists annotations of the MIT-BIH database. For example, Tape #103 contains two cases of beats (NORM and APC), Tape #111 contains two cases of beats (LBBB and VPC). In this study, four records of NORM case (Tape #103:2083 beats, #113:1789 beats, #123:1515 beats, #234:2700 beats of MIT-BIH database, see Table 3) are used as examples to explain how to obtain the range of each complex feature value. For Tape #103, 30-min long ECG signals are selected. The ranges of the PQRST complex feature values are listed in Table 4. The same process is applied to the other three NORM cases, and then nine complex features of the files are united to obtain the results of the four records listed in Table 5. The same process is also applied to the abnormal heart ECG signals, and thus two records of the left bundle branch block (LBBB) database (Tape #111:2123 beats, #214:2002 beats), three records of the right bundle branch block (RBBB) database (Tape #118:2166 beats, #212:675 beats, #231:562 beats), three records of ventricular premature contractions (VPC) database (Tape #200:826 beats, #221:396 beats, #233:831 beats), and two records of atrial premature contractions (APC) database (Tape #222:209 beats, #232:1382 beats) are provided. Table 6 lists the ranges of the PQRST complex feature values for each case.

4. Qualitative feature selection: Range-Overlaps Method (ROM)

The qualitative features selection (QFS) is performed after obtaining the PQRST complex features.

The following procedure is run to perform QFS (see Fig. 10).

Step 2-0: Define $R_{i,j}$.

Let $R_{i,j}$ be the feature value range of the ith PQRST complex feature for the jth heartbeat case. The sub-index i = 1, 2, 3, 4, 5, 6, 7, 8, 9 denotes "H-QR", "H-RS", "QRS-dur", "QTP-int", "Ratio-RR", "Slope-QR", "Slope-RS", "Area -QRS", and "Area-R′ST′, respectively. The sub-index j = 1, 2, 3, 4, 5 denotes the heartbeat cases of "NORM", "LBBB", "RBBB", "VPC", and "APC", respectively. According to Table 6, $R_{i,j}$ are shown in Fig. 11. In Fig. 11, the X-axis of each figure is the feature value ranges and the Y-axis denotes the "heartbeat case". For example, $R_{1,1}$ = [0.695, 2.69] mV, $R_{1,2}$ = [0.205, 2.06] mV, $R_{1,3}$ = [0.695, 2.24] mV, $R_{1,4}$ = [0.105, 3.095] mV, and $R_{1,5}$ = [0.275, 1.870] mV in Fig. 11a. Similarly, $R_{3,1}$ = [33, 79] ms, $R_{3,2}$ = [86, 153] ms, $R_{3,3}$ = [46, 130] ms, $R_{3,4}$ = [52, 210] ms, $R_{3,5}$ = [34, 61] ms in Fig. 11c.

Step 2-1: Obtain feature F_i using the following algorithm:

If $\widetilde{R} = 1$, then feature F_i (see Fig. 9) is obtained for $1 \leqslant i \leqslant 9$, $1 \leqslant k \leqslant 5$, $1 \leqslant j \leqslant 5$, $k \neq j$, where $\widetilde{R} = R_{i,k} \cap R_{i,j}$, and the index i, j (or k) is defined as the same as that of $R_{i,j}$ (see Fig. 11), Fig. 12 shows the flowchart of Step 2-1.

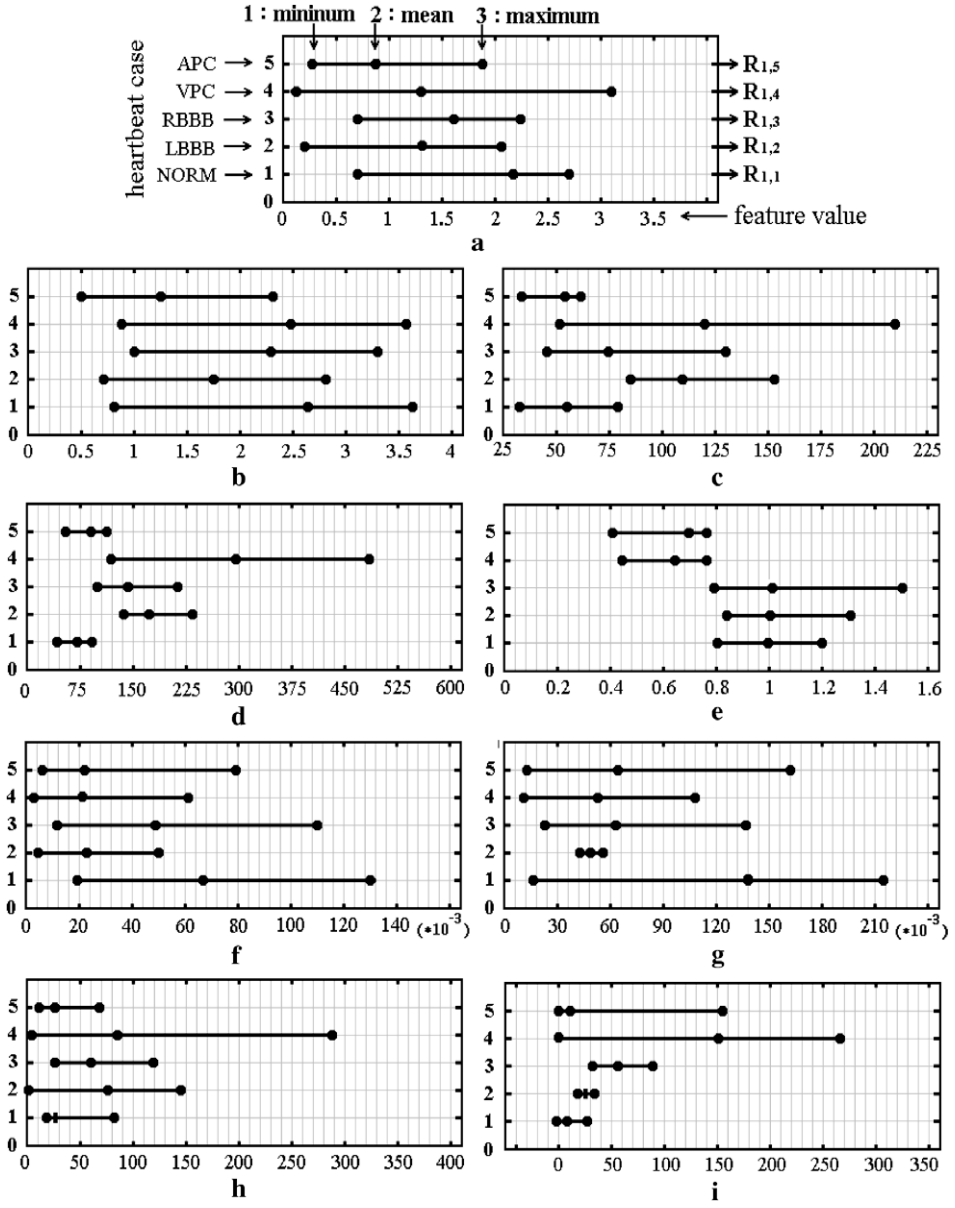

Fig. 11. The feature value range of each PQRST complex feature for each heartbeat case of the corresponding feature range: (a) R_1: H-QR; (b) R_2: H-RS; (c) R_3: QRS-dur; (d) R_4: QTP-int; (e) R_5: Ratio-RR; (f) R_6: Slope-QR; (g) R_7: Slope-RS; (h) R_8: Area-QRS; (i) R_9: Area-R′ST′. (Note – 1: minimum value, 2: mean value, 3: maximum value.)

Remark 2-1: Let $\widetilde{R} = R_{i,k} \cap R_{i,j} = 1$ if the two feature value ranges $R_{i,k}$ and $R_{i,j}$ do not overlap. Thus, feature F_i is obtained to discriminate heartbeats case-k and case-j, and NF_i is increased by 1, where NF_i denotes the total number of cases in which feature F_i can discriminate two disjoint heartbeats case-k and case-j. For instance, if $R_{3,1}$ = [33, 79] ms, $R_{3,2}$ = [86, 153] ms (see Fig. 11c), then $\widetilde{R} = R_{3,1} \cap R_{3,2} = 1$, meaning that feature F_3 (“QRS-dur”) can discriminate heartbeats case-1 (NORM case) and case-2 (LBBB case), the experiment results of $\widetilde{R} = R_{3,k} \cap R_{3,j}$ for feature F_3 see Table 7. Similarly, let $\widetilde{R} = R_{i,k} \cap R_{i,j} = 0$ if $R_{i,k}$ and $R_{i,j}$ overlap, that is, feature F_i is not obtained and heartbeats case-k and case-j cannot be discriminated. In this case, the value of NF_i remains unchanged. For instance, if $R_{1,1}$ = [0.695, 2.69] mV, $R_{1,2}$ = [0.205, 2.06] mV (see Fig. 11a), then $\widetilde{R} = R_{1,1} \cap R_{1,2} = 0$, meaning that feature F_1 (“H-QR”) cannot discriminate heartbeats case-1 (NORM case) and case-2 (LBBB case), the experiment results of $\widetilde{R} = R_{1,k} \cap R_{1,j}$ for feature F_1 see Table 8. Table 9 shows the experimental results of Step 2-1. In Table 9, for instance, the feature F_3 (“QRS-dur”) or F_4 (“QTP-int“) can discriminate heartbeats case-1 (NORM case) and case-2 (LBBB case). Let us see another example, the feature F_4 (“QTP-int“) or F_9 (“Area-R′ST′”) can discriminate heartbeats case-1 (NORM case) and case-3 (RBBB case) (see Table 9).

Step 2-2: Sort NF_i, $i = 1, 2, \ldots, 9$, with the order of decreasing values, and then select the index with the highest value, that is,

$$i = \arg(Max\{NF_i\}, \quad i = 1, 2, \ldots, 9) \tag{5}$$

For instance, suppose that NF_1 = 4, NF_2 = 2, NF_3 = 3, the sorted sequence becomes NF_1, NF_3 and NF_2.Thus, the index with the biggest value is NF_1 and the sequence of sub-indexes NF_i with the order of decreasing values of NF_i is 1, 3, and 2.

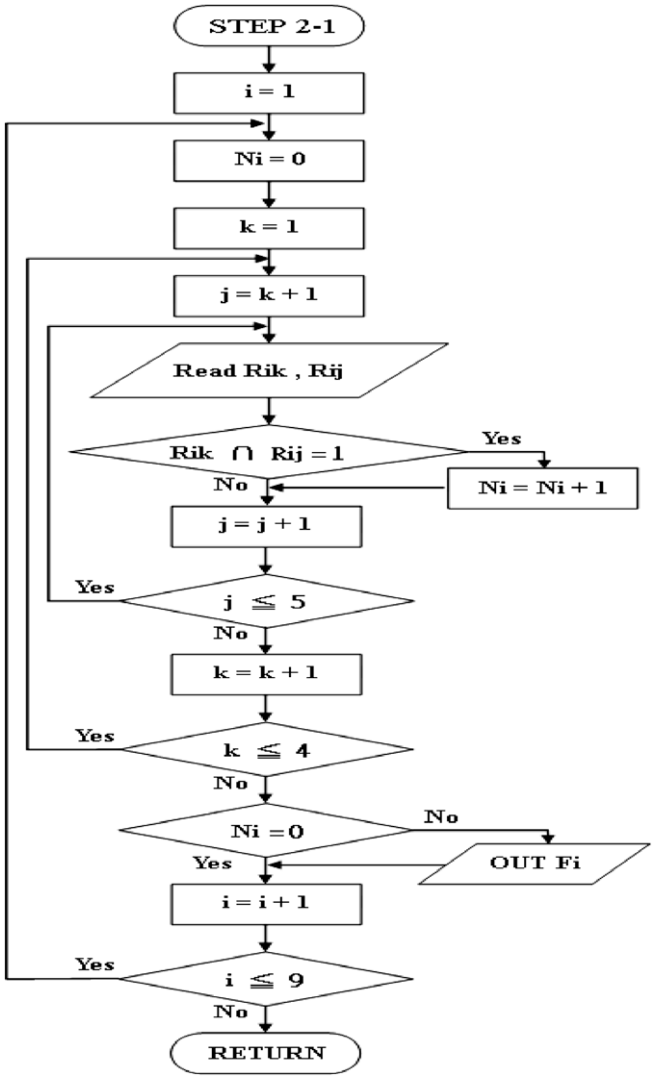

Fig. 12. A flowchart of Step 2-1.

Step 2-3: Obtain qualitative feature F_i.

A feature F_i is selected as a qualitative feature if it satisfies both the following conditions:

Table 9
Summary of the experiment results of Step 2-1.

Heartbeats case	NORM	LBBB	RBBB	VPC	APC
NORM	–	F_3, F_4	F_4, F_9	F_4, F_5	F_5
LBBB	F_3, F_4	–	F_9	F_5	F_3, F_4, F_5
RBBB	F_4, F_9	F_9	–	F_5	F_4, F_5
VPC	F_4, F_5	F_5	F_5	–	F_4
APC	F_5	F_3, F_4, F_5	F_4, F_5	F_4	–

Condition 1: Feature F_i can discriminate heartbeats case-k and case-j, where sub-indexes i are obtained from Step 2-2.

Condition 2: The qualitative feature for discriminate between heartbeats case-k and case-j is not found yet, where $k, j = 1, 2, 3, 4, 5$, and $k \neq j$.

If the feature F_i is selected as qualitative feature, then both heartbeat cases k and j are recorded in data items for the feature F_i and OUT F_i (that is, F_i is a qualitative feature). If the feature F_i cannot be selected as qualitative feature, then go to Step 2-4. Fig. 13 shows the flowchart of Step 2-3.

Remark 2-3: Index k and $j = 1, 2, 3, 4, 5$ denote the heartbeat cases of "NORM", "LBBB", "RBBB", "VPC" and "APC", respectively.

Step 2-4: Obtain the next qualitative feature.

If the qualitative features obtained from Step 2-3 are enough to discriminate each heartbeat case, then go to Step 2-5, otherwise go to Step 2-3.

Step 2-5: End.

After performing the Procedure QFS, four qualitative features QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′ are selected. Fig. 14 shows that each heartbeat case has its own range of values for each qualitative feature. Thus, these specific value ranges can be used to determine whether the patient has the case of cardiac arrhythmia by the existing methods.

5. Evaluation

The heartbeat classification abilities are compared by the five statistical indices: sensitivity (Se), specificity (Sp), positive predictive value (PPV), negative predictive value (NPV), and total classification accuracy (TCA), which are defined in Eqs. (6)–(10), respectively (Christov et al., 2006; Dokur & Olmez, 2001).

Table 7
The experiment results of $\widetilde{R} = R_{3,k} \cap R_{3,j}$ for feature F_3, where $1 \leqslant k \leqslant 5$, $1 \leqslant j \leqslant 5$, and $k \neq j$.

Heartbeats case	NORM($j = 1$)	LBBB($j = 2$)	RBBB($j = 3$)	VPC($j = 4$)	APC($j = 5$)
NORM($k = 1$)	–	$R_{3,1} \cap R_{3,2} = 1$	$R_{3,1} \cap R_{3,3} = 0$	$R_{3,1} \cap R_{3,4} = 0$	$R_{3,1} \cap R_{3,5} = 0$
LBBB($k = 2$)	$R_{3,2} \cap R_{3,1} = 1$	–	$R_{3,2} \cap R_{3,3} = 0$	$R_{3,2} \cap R_{3,4} = 0$	$R_{3,2} \cap R_{3,5} = 1$
RBBB($k = 3$)	$R_{3,3} \cap R_{3,1} = 0$	$R_{3,3} \cap R_{3,2} = 0$	–	$R_{3,3} \cap R_{3,4} = 0$	$R_{3,3} \cap R_{3,5} = 0$
VPC($k = 4$)	$R_{3,4} \cap R_{3,1} = 0$	$R_{3,4} \cap R_{3,2} = 0$	$R_{3,4} \cap R_{3,3} = 0$	–	$R_{3,4} \cap R_{3,5} = 0$
APC($k = 5$)	$R_{3,5} \cap R_{3,1} = 0$	$R_{3,5} \cap R_{3,2} = 1$	$R_{3,5} \cap R_{3,3} = 0$	$R_{3,5} \cap R_{3,4} = 0$	–

Table 8
The experiment results of $\widetilde{R} = R_{1,k} \cap R_{1,j}$ for feature F_1, where $1 \leqslant k \leqslant 5$, $1 \leqslant j \leqslant 5$, and $k \neq j$.

Heartbeats case	NORM($j = 1$)	LBBB($j = 2$)	RBBB($j = 3$)	VPC($j = 4$)	APC($j = 5$)
NORM($k = 1$)	–	$R_{1,1} \cap R_{1,2} = 0$	$R_{1,1} \cap R_{1,3} = 0$	$R_{1,1} \cap R_{1,4} = 0$	$R_{1,1} \cap R_{1,5} = 0$
LBBB($k = 2$)	$R_{1,2} \cap R_{1,1} = 0$	–	$R_{1,2} \cap R_{1,3} = 0$	$R_{1,2} \cap R_{1,4} = 0$	$R_{1,2} \cap R_{1,5} = 0$
RBBB($k = 3$)	$R_{1,3} \cap R_{1,1} = 0$	$R_{1,3} \cap R_{1,2} = 0$	–	$R_{1,3} \cap R_{1,4} = 0$	$R_{1,3} \cap R_{1,5} = 0$
VPC($k = 4$)	$R_{1,4} \cap R_{1,1} = 0$	$R_{1,4} \cap R_{1,2} = 0$	$R_{1,4} \cap R_{1,3} = 0$	–	$R_{1,4} \cap R_{1,5} = 0$
APC($k = 5$)	$R_{1,5} \cap R_{1,1} = 0$	$R_{1,5} \cap R_{1,2} = 0$	$R_{1,5} \cap R_{1,3} = 0$	$R_{1,5} \cap R_{1,4} = 0$	–

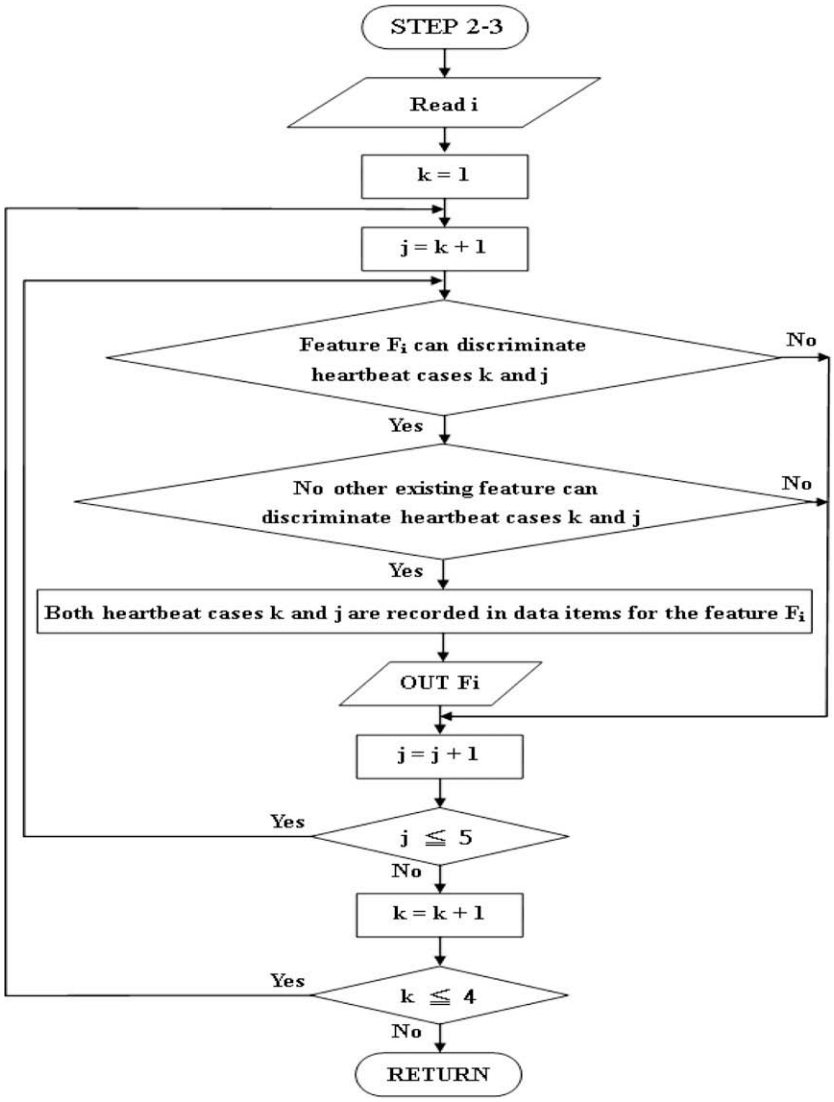

Fig. 13. A flowchart of Step 2-3.

$$\text{(i)}\quad Se_i = \frac{TP_i}{TP_i + FN_i} \tag{6}$$

$$\text{(ii)}\quad Sp_i = \frac{TN_i}{TN_i + FP_i} \tag{7}$$

$$\text{(iii)}\quad PPV_i = \frac{TP_i}{TP_i + FP_i} \tag{8}$$

$$\text{(iv)}\quad NPV_i = \frac{TN_i}{TN_i + FN_i} \tag{9}$$

$$\text{(v)}\quad TCA = \frac{\textit{the number of correct diagnosis beats}}{\textit{the number of total beats}} = \sum_{i=1}^{5} \frac{TP_i}{T_r} \tag{10}$$

where TP_i (true positives) is the number of heartbeats of the ith class, which are correctly classified (that is, NORM classified as NORM); FN_i (false negatives) is the number of heartbeats of class i, classified in a different class (that is, NORM not classified as NORM); TN_i (true negatives) is the number of heartbeats not belonging to the ith class and not classified in the ith class (that is, LBBB, RBBB, VPC, and APC not classified as NORM); FP_i (false positives) is the number of the heartbeats classified erroneously in the ith class (that is, LBBB, RBBB, VPC, and APC classified as NORM); and T_r is the number of total heartbeats in Table 3. In this study, identification of TP, FN, TN, and FP are listed in Table 10.

This study uses two experiments for performance evaluation of the proposed method including Se, Sp, PPV, NPV, TCA, and Receiver Operating Characteristic (ROC) curves (Fawcett, 2006). In these experiments, the proposed method is implemented via MATLAB software on a personal computer. We explain these experiments in the following subsections.

5.1. The first experiment: fuzzy logic method (FLM)

Fuzzy logic theory (Zadeh, 1978) is widely adopted in various fields, such as pole-balancing robot control, electric washing machine control, speech recognition, image retrieval and pattern recognition. A fuzzy system is characterized by a set of linguistic statements according to experience and knowledge, usually of the form of If–Then rules, which can be easily implemented by fuzzy conditional statements via fuzzy logic. Fuzzy If–Then rules are expressions of the form IF A THEN B, where A and B denote labels of fuzzy sets characterized by appropriate membership functions.

This section introduces a fuzzy logic system for the diagnosis of the cardiac arrhythmia is. The fuzzy logic consists of four parts: fuzzy sets definition, fuzzy rule base establishment, fuzzy inference engine design and defuzzification (see Fig. 15) (Zadeh, 1978). The input variables of the fuzzy rule base are four qualita-

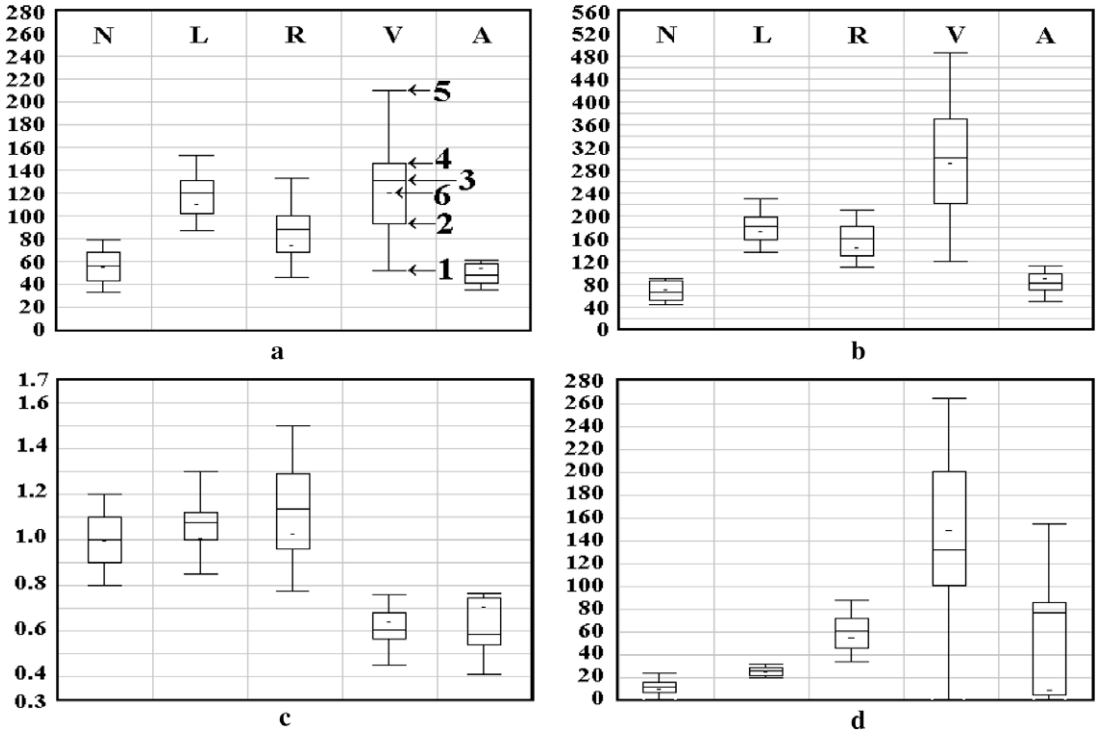

Fig. 14. Box-and-Whisker plots of the four qualitative feature values for each heartbeat case: (a) QRS-dur; (b) QTP-int; (c) Ratio-RR; (d) Area-R′ST′. (Note – 1: smallest value; 2: first quartile; 3: median; 4: third quartile; 5: largest value; 6: mean value; N: NORM; L: LBBB; R: RBBB; V: VPC; A: APC.)

Table 10
Identification of TP, FN, TN, and FP in this study for (i) NORM case; (ii) LBBB case; (iii) RBBB case; (iv) VPC case; and (v) APC case.

		Algorithm label				
		NORM	LBBB	RBBB	VPC	APC
Reference label	NORM	NN	NL	NR	NV	NA
	LBBB	LN	LL	LR	LV	LA
	RBBB	RN	RL	RR	RV	RA
	VPC	VN	VL	VR	VV	VA
	APC	AN	AL	AR	AV	AA

(i) NORM case: TP = NN; FN = NL + NR + NV + NA; FP = LN + RN + VN + AN; TN = LL + LR + LV + LA + RL + RR + RV + RA + VL + VR + VV + VA + AL + AR + AV + AA.
(ii) LBBB case: TP = LL; FN = LN + LR + LV + LA; FP = NL + RL + VL + AL; TN = NN + NR + NV + NA + RN + RR + RV + RA + VN + VR + VV + VA + AN + AR + AV + AA.
(iii) RBBB case: TP = RR; FN = RN + RL + RV + RA; FP = NR + LR + VR + AR; TN = NN + NL + NV + NA + LN + LL + LV + LA + VN + VL + VV + VA + AN + AL + AV + AA.
(iv) VPC case: TP = VV; FN = VN + VL + VR + VA; FP = NV + LV + RV + AV; TN = NN + NL + NR + NA + LN + LL + LR + LA + RN + RL + RR + RA + AN + AL + AR + AA.
(v) APC case: TP = AA; FN = AN + AL + AR + AV; FP = NA + LA + RA + VA; TN = NN + NL + NR + NV + LN + LL + LR + LV + RN + RL + RR + RV + VN + VL + VR + VV.

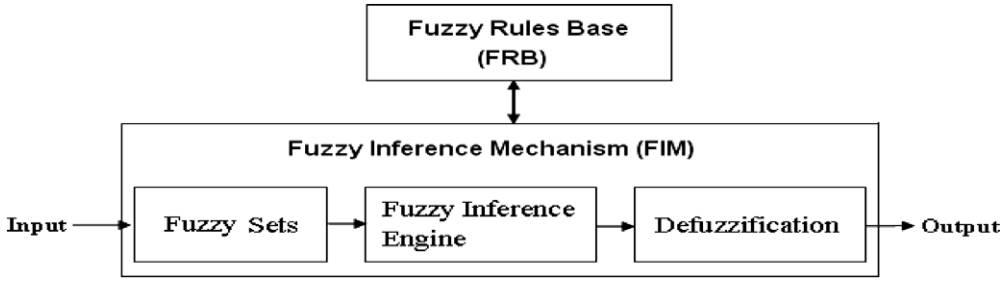

Fig. 15. Block diagram of fuzzy logic.

tive features, namely "QRS-dur", "QTP-int", "Ratio-RR" and "Area-R′ST′ "(see Fig. 14). The output variable is "Heartbeat case", which has five cases of NORM, LBBB, RBBB, VPC, and APC. The first experiment was performed on a portion of the MIT-BIH arrhythmia database records with four records from the NORM database (Tape #103 (2083 NORM beats), #113 (1789 NORM beats), #123 (1515 NORM beats) and #234 (2700 NORM beats), see Table 2), two records from the LBBB database (Tape #111 (2123 LBBB beats) and #214 (2002 LBBB beats)), three records from the RBBB database (Tape #118 (2166 RBBB beats), #212 (675 RBBB beats) and #231

Table 11
The first experiment results for four qualitative features (according to Table 3).

Tape #	Respective heartbeats	Classified results (%)				
		Se	Sp	PPV	NPV	TCA
103	NORM (2083 NORM beats)					
113	NORM (1789 NORM beats)					
123	NORM (1515 NORM beats)					
234	NORM (2700 NORM beats)	97.41	98.36	97.77	98.09	
111	LBBB (2123 LBBB beats)					
214	LBBB (2002 LBBB beats)	88.94	97.57	91.73	96.68	
118	RBBB (2166 RBBB beats)					
212	RBBB (675 RBBB beats)					
231	RBBB (562 RBBB beats)	87.36	96.91	86.93	97.03	
200	VPC (826 VPC beats)					
221	VPC (396 VPC beats)					
233	VPC (831 VPC beats)	96.17	98.95	87.65	99.70	
222	APC (209 APC beats)					
232	APC (1382 APC beats)	97.89	99.73	96.99	99.81	93.17

Table 12
The first experiment results for any three qualitative features (for example, QRS-dur, QTP-int, and Area-R′ST are selected).

	Se (%)	Sp (%)	PPV (%)	NPV (%)
NORM	65.84	92.43	86.55	78.54
LBBB	51.93	95.05	76.07	86.71
RBBB	52.20	94.89	70.58	89.42
VPC	43.89	82.52	16.28	94.99
APC	54.02	84.77	23.66	95.48

(562 RBBB beats)), three records from the VPC database (Tape #200 (826 VPC beats), #221 (396 VPC beats) and #233 (831 VPC beats)) and two records from the APC database (Tape #222 (209 APC beats) and #232 (1382 APC beats)).

Results of the first experiment indicate that the four qualitative features are the best choice for discriminating each heartbeat case using fuzzy logic. The verification procedure is described as follows. First, four qualitative features (QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′, see Fig. 14) are selected. In the experiments, the sensitivities were 97.41%, 88.94%, 87.36%, 96.17% and 97.89% for NORM, LBBB, RBBB, VPC and APC, respectively (see Table 11). The

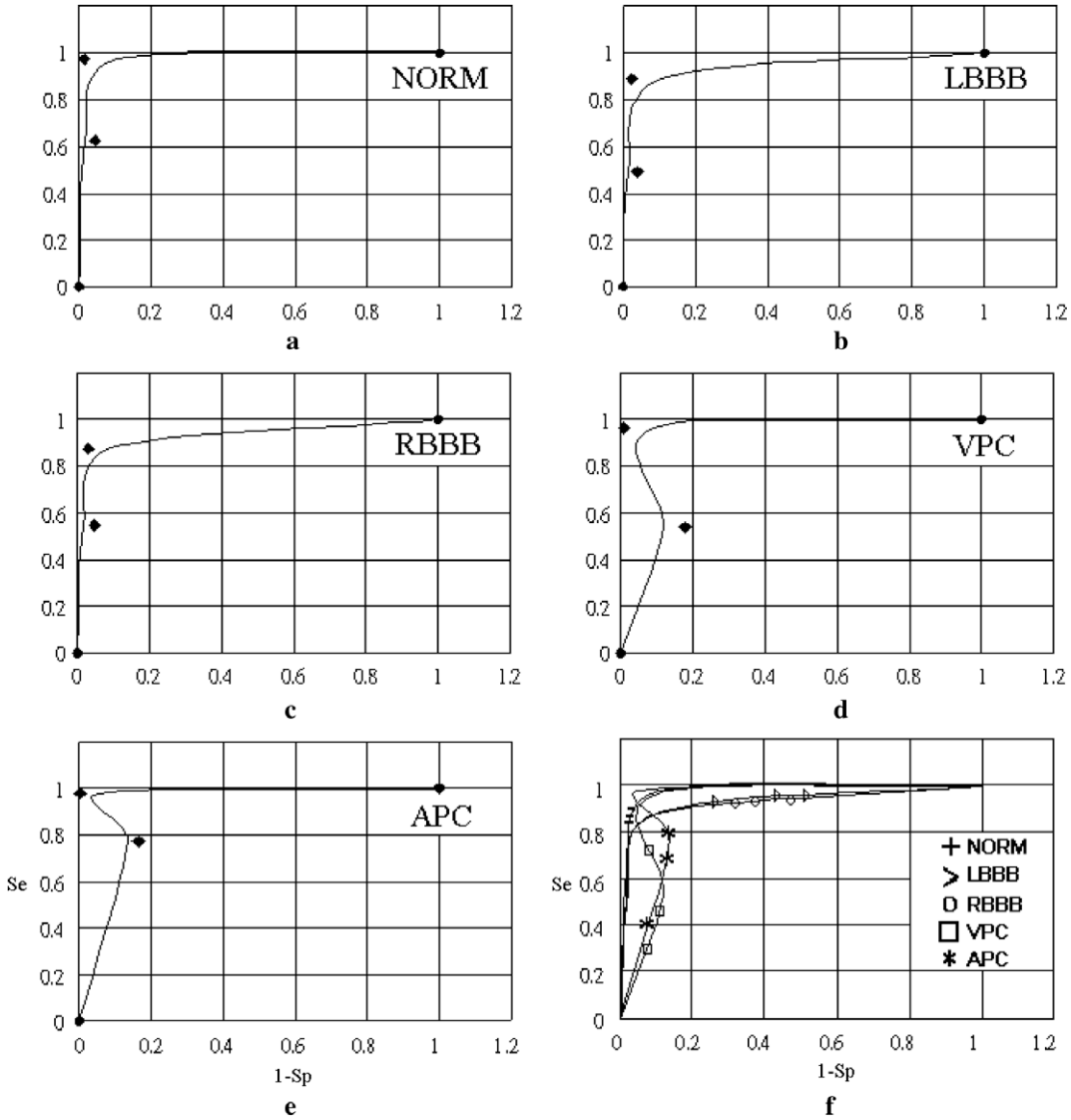

Fig. 16. ROC curves of fuzzy logic method.

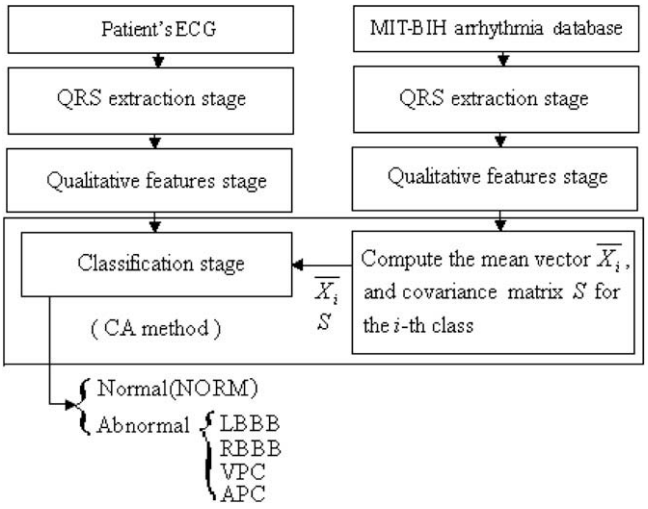

Fig. 17. A flowchart of the cluster analysis (CA) method.

Table 13
The second experiment results for four qualitative features.

Tape #	Respective heartbeats	Classified results (%)				
		Se	Sp	PPV	NPV	TCA
103	NORM (2083 NORM beats)					
113	NORM (1789 NORM beats)					
123	NORM (1515 NORM beats)					
234	NORM (2700 NORM beats)	98.28	98.04	97.38	98.72	
111	LBBB (2123 LBBB beats)					
214	LBBB (2002 LBBB beats)	90.35	97.28	90.97	97.08	
118	RBBB (2166 RBBB beats)					
212	RBBB (675 RBBB beats)					
231	RBBB (562 RBBB beats)	86.97	96.96	87.07	96.94	
200	VPC (826 VPC beats)					
221	VPC (396 VPC beats)					
233	VPC (831 VPC beats)	92.19	98.91	86.82	99.39	
222	APC (209 APC beats)					
232	APC (1382 APC beats)	94.86	99.41	93.87	99.51	93.57

total classification accuracy (TCA) was about 93.17%. Second, five disjoint features are selected from four qualitative features (QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′, see Fig. 14) and one feature from Table 6. The experimental results are similar to Table 11. Third, any three qualitative features, for example, QRS-dur, QTP-int, and Area-R′ST were selected. Experimental results indicate that the sensitivities were 65.84%, 51.93%, 52.20%, 43.89% and 54.02% for NORM, LBBB, RBBB, VPC and APC, respectively (see Table 12). Fig. 16 shows the ROC curves for the experiment results using three, four and five qualitative features, and indicates that the best choice is to use four qualitative features (QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′) to discriminate each heartbeat case.

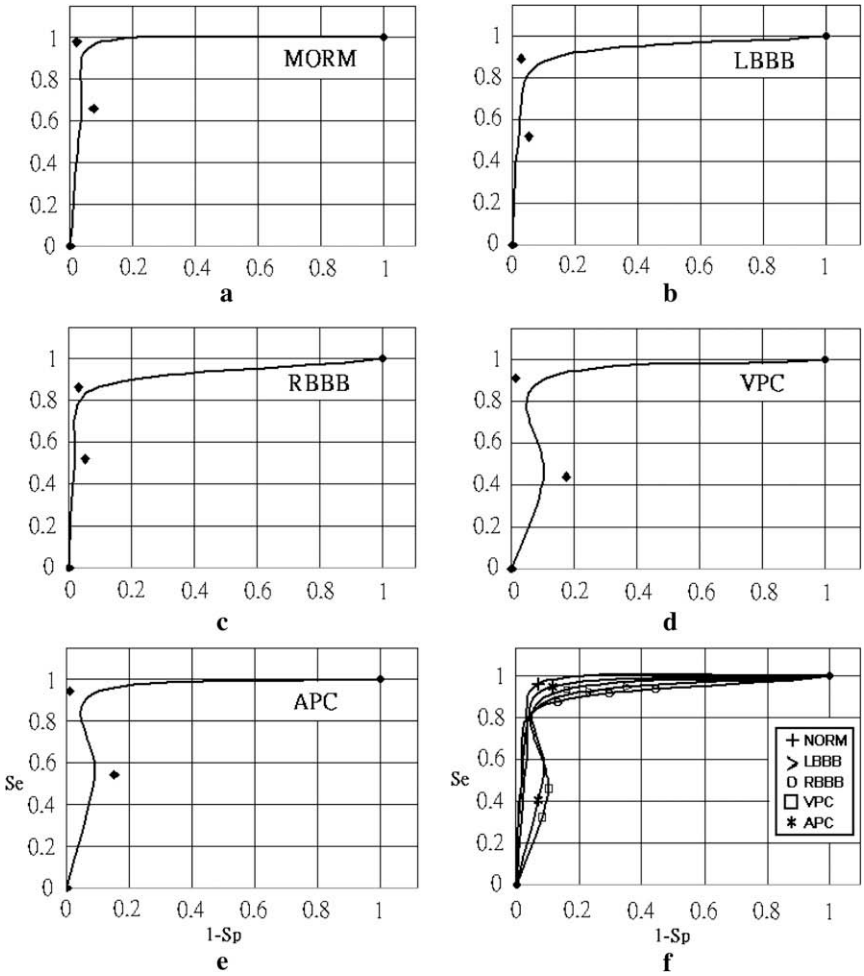

Fig. 18. ROC curves of the cluster analysis (CA) method.

5.2. The second experiment: cluster analysis (CA) method

CA is a data classification method that has been widely adopted in many applications, including speech recognition, image retrieval and pattern recognition. For instance, consider K pattern classes and assume that they are represented by prototype patterns $x_1, x_2, \ldots, x_k$. The Mahalanobis distance D_i between an arbitrary pattern vector y and the ith prototype is given by (Johnson & Wichern, 2007).

$$D_i = (y - \overline{X_i})' S^{-1} (y - \overline{X_i}); \quad \text{for } i = 1, 2, \ldots, k \tag{11}$$

In Eq. (11), S denotes the covariance matrix of a pattern population, and $\overline{X_i}$ denotes the mean vector for the ith class. A minimum-distance classifier calculates the distance from a pattern y to the prototype of each class, and the pattern y is assigned to class j if its Mahalanobis distance has the lowest value among prototype class i ($i = 1, 2, \ldots, k$). Fig. 17 shows a flowchart of the CA method, which consists of three main stages: (i) QRS extraction stage for detecting QRS waveform using the Difference Operation Method (DOM) method proposed in Yeh and Wang (2008); (ii) qualitative features stage for qualitative feature selection on ECG signals and (iii) classification stage for determining patient's heartbeat cases. The ECG signals in the MIT-BIH arrhythmia database are adopted as the reference data for accomplishing the first two stages, and the CA method is used to determine the heartbeat cases for the patient.

Results of the second experiment indicate that the four qualitative features are the best choice for discriminating each heartbeat case using CA method. The verification procedure is described as follows. First, four qualitative features (QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′, see Fig. 14) are selected. In these experiments, the sensitivities were 98.28%, 90.35%, 86.97%, 92.19% and 94.86% for NORM, LBBB, RBBB, VPC and APC, respectively (see Table 13). The TCA was about 93.57%. Second, five disjoint features are selected from four qualitative features (QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′, see Fig. 14) and one feature from Table 6. The experimental results are similar to Table 13. Third, any three qualitative features, for example, QRS-dur, QTP-int, and Area-R′ST were selected. Fig. 18 shows the ROC curves for this experiment, and indicates that the best choice is again one using four qualitative features (QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′) to discriminate each heartbeat case.

6. Conclusion

This study proposes a simple, fast and reliable method called "Range-Overlaps Method" for effective feature selection. The Range-Overlaps Method has the following advantages: (1) good detection results (high-reliability): the average failure rate for processing 10-min long records of ECG signals is 0.19% by DOM (Yeh & Wang, 2008); (2) it does not need complex mathematics computations (such as cross-correlation and Fourier transformation); (3) hi-speed and low memory space: the average time required to process 10-min long of ECG data is less than 1 min, and the maximum memory requirement is only about 1.5 MB for a 30-min long (about 2100 beats) recording with 16-bit sampling points, and (4) the time complexity for this method is $O(n)$, where n denotes the number of sampling vectors. After performing the Procedure QFS (qualitative feature selection), four qualitative features (QRS-dur, QTP-int, Ratio-RR, and Area-R′ST′) were selected from the original PQRST features. In these experiments, the total classification accuracy was about 93.57% for cluster analysis, and 93.17% for fuzzy logic. Experimental results indicate that the proposed algorithm provides an efficient, simple and fast method for feature selection on ECG signals.

Acknowledgment

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