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Arrhythmia Analysis and Classification using Gaussian Mixture Model

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Abstract*— Automatic detection and classification of ECG heart beats is of high value in diagnosis and treatment of patients with life-threatening cardiac arrhythmia. Arrhythmia is an abnormal or irregular heart rhythm which reflects the bad condition of heart. Abnormal heartbeat comprises Right Bundle Branch Block (RBBB), Left Bundle Branch Block (LBBB), Atrial Premature Contraction (APC), and Ventricular Premature Contraction (VPC). ECG signal analysis includes QRS complex detection, P and T peak detection, feature selection and beat classification. In this paper, time interval features of ECG signal are extracted and Gaussian Mixture Model (GMM) is used to classify the ECG signals. The ECG signals used for the evaluation are taken from MIT-BIH arrhythmia database. The Experimental results obtained after classification are 84.99%, 96.6%, 93.08%, 94.48% and 62.83% for NORM, LBBB, RBBB, VPC and APC, respectively.

Index Terms— *Arrhythmia, ECG, GMM classifier, Peak Detection, Time interval features*

I. INTRODUCTION

ECG is the recording of the electrical activity of heart which reflects the physical condition of a patient. An Arrhythmia is an abnormal or irregular heart rhythm. Arrhythmias arise when the electrical impulse that synchronizes the heartbeats do not action properly, causing heart to beat too fast, too slow or irregularly. ECG signals are collected using one to twelve electrodes positioned on the surface of a human body. An ideal one-channel ECG comprises of five peaks namely P, Q, R, S and T as shown in the Fig.1. ECG study is an interesting task and mainly applied in medical field like ischaemic heart disease, hypertension and cardiac arrhythmias.

Heart disorder is commonly replicated in the shapes of the ECG waveform and the rate at which it beats. Almost all the ECG signal data is focused on the P wave, QRS complex and T wave. Magnitude of these waves and their time lengths such as PR interval, QRS width, ST segment are studied by the doctors to make correct diagnosis. Human heart consists of four chambers which controls the circulation of blood. Lower two chambers are termed as ventricles and upper two chambers are termed as atria. The left part consists of impure blood and right part consists of pure blood. P wave denotes atria contraction which forces blood into the ventricles. The QRS complex denotes ventricular depolarization and contraction. The PR length specifies the travel duration for the heart signal to flow from the sinus node to the ventricles. T wave denotes ventricular repolarization.

Arrhythmia analysis and classification of heart beats is of great demand in cardiovascular diagnostic system and significant in critical care. This reduces the risk of the cardiologist to identify the abnormal beats in a large amount of ECG data, to analyse cardiovascular diseases. The present work has been focused on classifying and differentiating normal (NORM) and abnormal beats. Abnormal beats comprise Ventricular Premature Contraction (VPC), Right Bundle Branch Block (RBBB), Left Bundle Branch Block (LBBB), and Atrial Premature Contraction (APC).

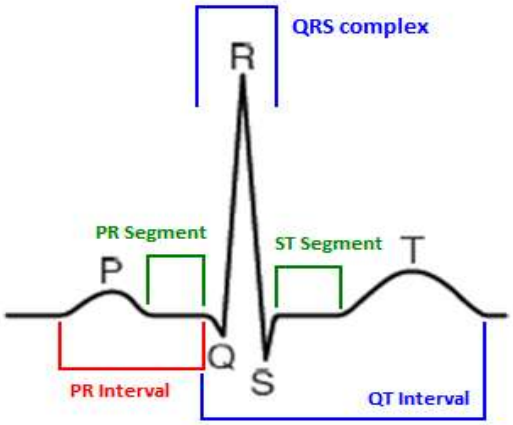

Fig. 1: Ideal ECG waveform.

VPCs are affected by an ectopic cardiac pacemaker situated in the ventricle. VPCs are categorized by premature and weirdly shaped QRS complexes. RBBB is caused by the initiation of the right ventricle is postponed as depolarization as to spread across the septum from the left ventricle. The suspended right ventricular contraction results in secondary R wave. It may cause secondary repolarization abnormalities, with T wave inversion and ST depression. LBBB is caused by septum triggered from left to right, creating minor Q waves. Sequential stimulation of ventricles instead of simultaneous movement produces a broad or notched ('M'-shaped) R wave. APCs originate from ectopic pace making tissue present in the atria. There is an irregular P wave, usually followed by a regular QRS complex.

II. LITERATURE REVIEW

Yun-Chi Yeh et al. [1] used Difference Operation Method (DOM) to detect QRS complex and Linear Discriminant Analysis (LDA) to diagnose ECG signals and heartbeat case determination. LDA is an efficient approach used in both machine learning and statistics to identify the characteristics of linear combination which can distinguish more than two classes. Aiguang Li et al. [2], [3] adopts Dynamic Time Warping (DTW) method for beat detection. Here normal and abnormal beats are characterized by templates which are carefully chosen from the training data using clustering. Time invariant DTW are used for template matching. For those the DTW distance cannot provide sharp perception, a further stage of verification is recommended. Mohamed Lamine Talbi et al. [4] distinguished the normal beats from the abnormal using the power spectrum density of the QRS Complex. FFT algorithm is applied to compute the power spectrum of each QRS complex. Finally Self-Organising Maps (SOM) neural network is used for classification that detects the mismatch in regularities and correlation. Diptangshu et al. [5] introduced Artificial Neural Network (ANN) for classifying ECG beat as normal and abnormal, where time interval features are extracted and used for training ANN with 11 inputs, 5 hidden layers and two output classes. Vinod Pathangay and Satish Prasad Rath [6] used magnitude and phase of Fourier Transform (FFT) of the ECG signal as the features to train the classifier. Here the Support Vector Machine (SVM) is used for beat classification.

In this work, ECG heartbeats are analysed using time interval features of the heart rhythm and GMM classifier is used to classify the arrhythmia or abnormal heartbeats. In the next section, database used for the evaluation is described. Signal pre-processing is one of the important methods to be followed before actual implementation of any work which is mentioned in Section IV. Algorithm for ECG peaks detection is explained in Section V. Feature extraction and classification are discussed in Section VI. Results are included in Section VII, followed by the conclusion.

III. DATABASE

There are 48 records in the MIT-BIH database [7]. The duration of each record is 30 minutes and it contains two leads; one is the modified limb lead II (MLII) and another is one among the modified leads V1, V2, V4 or V5. Here, only MLII lead signal is used for the evaluation. The ECG signals are sampled at 360 Hz and the database contains more than ten kinds of annotated beats. Annotation files contain set of labels, each of which describes beat class at a specified time in the record. Six different beat annotations of the MIT-BIH arrhythmia database are considered. We have used only Normal (N), Ventricular premature contraction (V), , Left bundle branch block (L), Right bundle branch block (R) and Atrial premature beat (A), Junctional (Nodal) escape beat (J) and Junctional (Nodal) escape beat (j) for classification. The work is concerned only for detecting NORM, LBBB, RBBB, VPC, and APC types. The annotations A, J and j together classify APC. The files (records) that comprises of very less numbers of concerned beats are not included. Therefore only 13 files each of 30 minutes duration are used as mentioned in Table I.

TABLE I. THE MIT-BIH DATABASE FILES WITH ANNOTATIONS

File name	Total beats (30-min) duration	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	-
233	3068	2230	-	-	831	7
234	2753	2700	-	-	3	50

IV. ECG SIGNAL PRE-PROCESSING

ECG signal undergoes various electrical noises at the time of capturing from the machine. Noise refers to any degradation of the ECG signal that makes it difficult to accurately detect and classify beats. Pre-processing of ECG signal involves normalization and removing of baseline drift.

A. Normalization

The input ECG signal is sampled at the sampling frequency of 360 Hz and normalized to remove the DC component present in the signal by using the equation (1).

$$Y = \frac{X - mean(X)}{\max(abs(X))} \quad (1)$$

where, X is the ECG signal and Y is the normalized output of the signal.

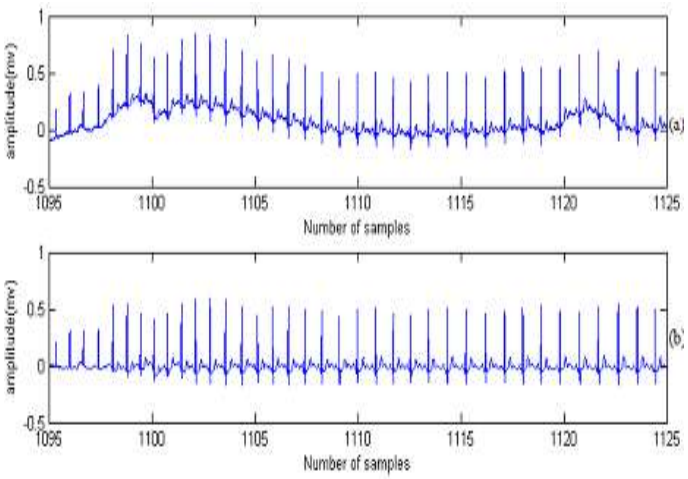

Fig. 2: (a) Original ECG signal, (b) Baseline removed using BPF and Normalization

B. Baseline Drift Removing

The baseline drift in a raw ECG signal wander at the frequency range below 0.5 Hz. Band pass filter helps to reduce the influence of muscle noise, 60 Hz power-line inference. Therefore, here a Butterworth band-pass filter with 0.5 Hz lower cut-off frequency and 50 Hz higher cut-off frequency has been used. Fig. 2 shows the result of baseline removed using Butterworth filter.

V. QRS EXTRACTION AND PEAK DETECTION

The QRS complexes are extracted from the band-pass filtered signal using window based threshold technique. A normal window of length 1.4s is applied to reduce the discontinuities. Then the P and T peaks are detected using two moving averages. Fig. 3 shows the algorithm used for P and T peak detection.

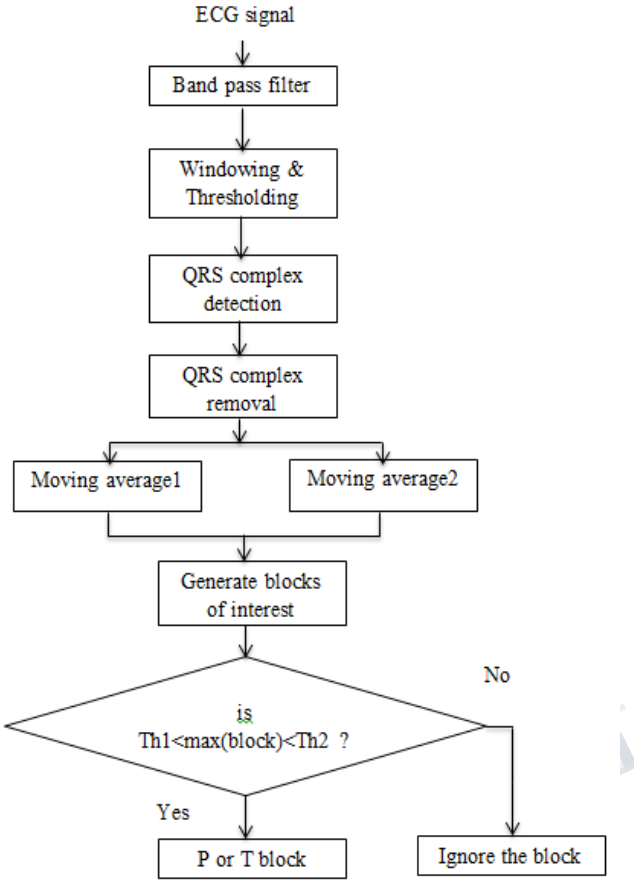

Fig. 3 Block diagram of Peak detection

To make the P and T waves the dominant feature of the signal, QRS complexes must be removed. This can be done by setting the QRS complex duration to zero in all the beats as shown the Fig. 4 and is used for further processing. As given in the equation (2), y[n] is the QRS complex removed signal and x[n] is the band-pass filtered signal.

$$y[n] = QRS\,\mathrm{Re}moval(x[n]) \qquad (2)$$

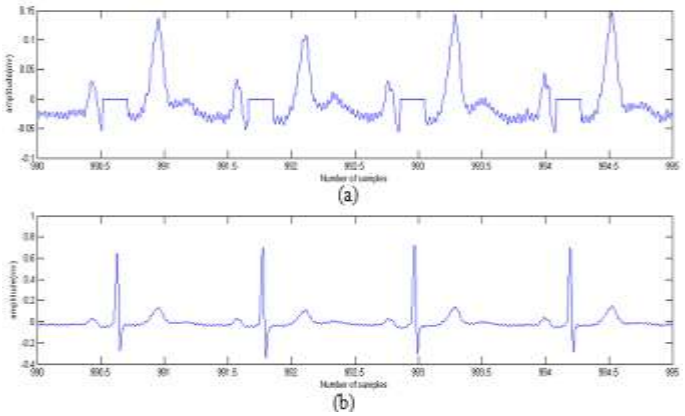

Fig. 4 (a) QRS removed from ECG signal (b) ECG signal

Detection of P and T waves will depend on two moving averages. First moving average integration is used to define P and T waves, while the second moving average acts as the threshold for first moving average. The window widths W_1 and W_2 are selected randomly, but the width of W_2 must be twice the W_1. Each moving average integrations generates a signal using the equations (3) and (4),

$$MA_1[n] = \frac{1}{W_1}(y[n-(W_1-1)/2] + ... + y[n] + ... \\ ... + y[n+(W_1-1)/2]) \quad (3)$$

$$MA_2[n] = \frac{1}{W_2}(y[n-(W_2-1)/2] + ... + y[n] + ... \\ .. + y[n+(W_2-1)/2]) \quad (4)$$

MA_1 corresponds to the output of first moving average integration and MA_2 corresponds to the output of second moving average integration. A block is generated when the amplitude of signal generated by MA_1 is greater than the amplitude of signal generated by MA_2 for the throughout QRS removed signal. Fig. 5 shows the block generated by comparing the outputs of two moving averages.

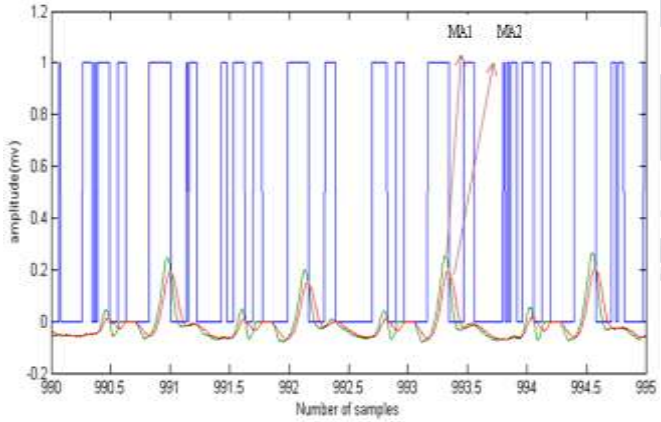

Fig. 5: Blocks generated by comparing moving averages

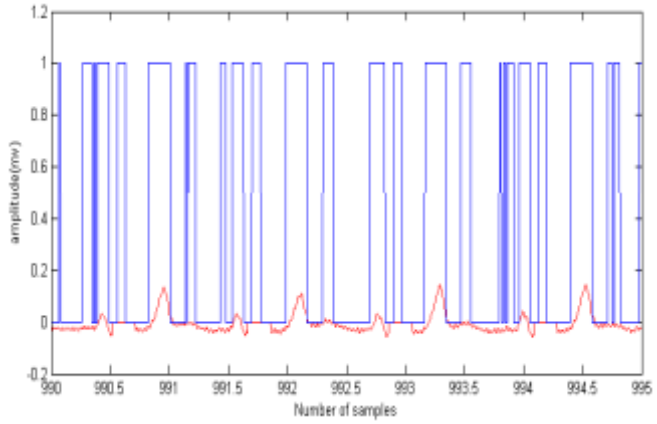

Fig. 6: Comparison of block generated with QRS removed signal

QRS removed signal corresponding to the block generated is shown in Fig. 6. Maximum over the block generated towards right and left of the QRS complex detects the P and T waves. The overall peak detection of the ECG signal is shown in Fig. 7.

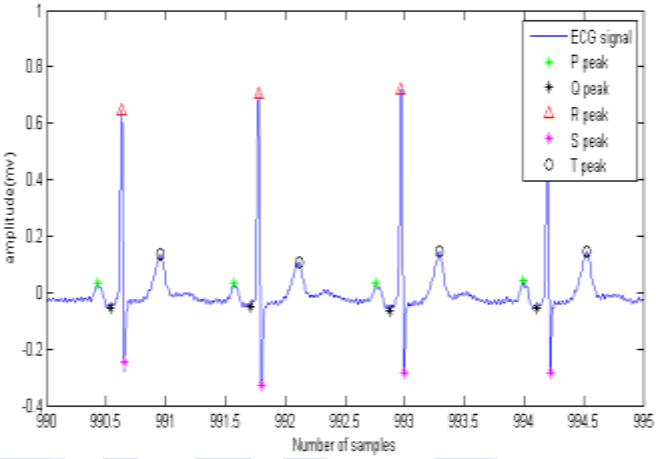

Fig. 7: Peak detection in an ECG signal

VI. FEATURE EXTRACTION

The features extracted in an ECG signal correspond to location, amplitude and shape of the waves. The peaks detected in the ECG signal are used for the extraction of time interval features.

TABLE II. SIX FEATURES USED IN THE PRESENT WORK

Feature No.	Feature Symbol	Feature Description
1	QRS-dur	The time interval between Q and S in QRS complex
2	QT-int	The time interval between Q and T peak
3	A-QR	The amplitude between Q and R in QRS Complex
4	A-RS	The amplitude between R and S in QRS complex
5	Area-QRS	The area of QRS complex

The five features used in the present work are QRS-duration (QRS-dur), QT-interval (QT-int), Amplitude of QR segment (A-QR), Amplitude of RS segment (A-RS), and Area of QRS complex (Area-QRS) is as shown in Fig. 7 and their description is given in the Table II.

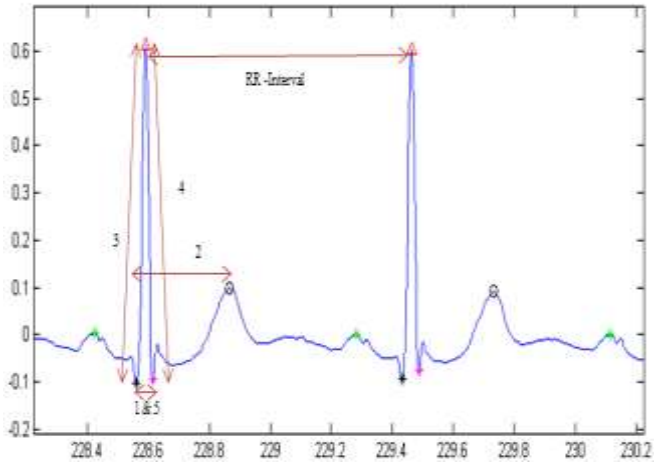

Fig. 7: Extracted ECG signal features: (1) F_1: QRS-duration, (2) F_2: QT-interval, (3) F_3: Amplitude of QR segment (4) F_4: Amplitude of RS segment (5) F_5: Area of QRS complex.

VII. GMM CLASSIFIER

A GMM classifier is used in this work for the classification of ECG beats, where the acoustic models are obtaining by training with the number of mixtures varying from 5 to 11. GMM is a supervised learning based on the Maximum Likelihood (ML) estimation using Expectation Maximization (EM).

A. Finite Mixture Models

Consider a data set $D = \{\underline{x}_1, \ldots, \underline{x}_N\}$ where $\underline{x}_i$ is a d-dimensional vector measurement. Data points are generated in an IID (invariant independent) fashion from an underlying density $p(\underline{x})$. $p(\underline{x})$ is defined as a finite mixture model with K components.

$$p(\underline{x} \mid \Theta) = \sum_{k=1}^{K} \alpha_k \, p(\underline{x} \mid z_k, \theta_k) \tag{5}$$

where $p_k(\underline{x} \mid z_k, \theta_k)$ are mixture components. z is a K-array random variable representing the identity of the mixture component that generated $\underline{x}$. $\alpha_k = p(z_k)$ are the mixture weights, representing the probability that a randomly selected $\underline{x}$ was generated by component k, where $\sum_{k=1}^{K} \alpha_k = 1$.

The Complete set of parameters for a mixture model with K components is $\Theta = \{\alpha_1, \ldots, \alpha_k, \theta_1, \ldots, \theta_k\}$

Membership weights are generated by using the Bayes rule over data points $\underline{x}_i$ in cluster k with given parameters Θ as in the equation (6),

$$w_{ik} = p(z_{ik} = 1 \mid \underline{x}_i, \Theta) = \frac{p_k(\underline{x}_i \mid z_k, \theta_k).\alpha_k}{\sum_{m=1}^{K} p_m(\underline{x}_i \mid z_{m,} \theta_m).\alpha_m}, \tag{6}$$

$$1 \le k \le K, 1 \le i \le N$$

Multivariate Gaussian density is given by,

$$p_k(\underline{x} \mid \theta_k) = \frac{1}{(2\pi)^{d/2} \mid \sum_k \mid^{1/2}} e^{-\frac{1}{2}(\underline{x}-\underline{\mu}_k)^t \sum_k^{-1} (\underline{x}-\underline{\mu}_k)} \tag{7}$$

with its own parameters $\theta_k = \{\underline{\mu}_k, \sum_k\}$.

B. EM algorithm for Gaussian Mixture Models

The algorithm is an iterative process that starts from some initial estimate of Θ (random) and then proceeds to iteratively update Θ until convergence is detected. Each iteration consists of an E-step and M-step.

i. E-step:
Current parameter values are denoted by Θ. Membership weights w_{ik} are computed for all data points $\underline{x}_i$, $1 \le i \le N$ and all the mixture components, $1 \le k \le K$. For each data point $\underline{x}_i$ the membership weights are defined such that, $\sum_{k=1}^{K} w_{ik} = 1$. This yields an N X K matrix of membership weights, where each of the rows sums to 1.

ii. M-step:
Here the membership weights and the data set are used to compute the new parameter values. Let, $N_k = \sum_{i=1}^{N} w_{ik}$ i.e., the sum of the membership weights for the k^{th} component.

Mean, covariance and mixture weights are updated using the previous membership weights and the data as in the equation (8), (9) & (10),

$$\alpha_k^{new} = \frac{N_k}{N}, 1 \le k \le K \tag{8}$$

$$\underline{\mu}_k^{new} = \frac{1}{N_k} \sum_{i=1}^{N} w_{ik} . \underline{x}_i, 1 \le k \le K \tag{9}$$

$$\sum_k^{new} = \frac{1}{N_k} \sum_{i=1}^{N} w_{ik} . (\underline{x}_i - \underline{\mu}_k^{new})(\underline{x}_i - \underline{\mu}_k^{new})^t, 1 \le k \le K \tag{10}$$

C. Initialization and convergence in EM algorithm

The initial parameters or weights are chosen randomly by selecting *K* random data points as initial means and selecting the covariance matrix of the whole data set as the initial K covariance matrices. Convergence is generally detected by computing the value of the log-likelihood after each iteration and halting when it appears not to be changing in a significant manner from one iteration to the next. The Maximum log-likelihood is computed by the equation (11),

$$\log l(\Theta) = \sum_{i=1}^{N} \log p(\underline{x_i} \mid \Theta) = \sum_{i=1}^{N} \left(\log \sum_{k=1}^{K} \alpha_k p_k (\underline{x_i} \mid z_k, \theta_k) \right) \quad (11)$$

Where, $p_k(\underline{x_i} \mid z_k, \theta_k)$ is the Gaussian density for the k^{th} mixture component.

The GMM classifier verifies the similarity of time interval features between the training beats and the test beats by creating mixture of Gaussians based on EM and Maximum likelihood algorithm. Finally in the present work, it classifies a candidate record into five number of class.

VIII. RESULTS

The method used in this work is tested against MIT-BIH arrhythmia database which are corresponding to normal heartbeat and 4 types of arrhythmia. The work is concerned only for detecting NORM, LBBB, RBBB, VPC, and APC types, so records that contain very small numbers of concerned beats are excluded. Therefore only thirteen records are used for evaluation as mentioned in Table I. Number of beats (R-peaks) detected when a common threshold is used is tabulated in Table III. Similarly the beats detected using window based threshold technique is given in Table IV where some beats are inserted because of the sliding window passing through an unknown R considering it as an R peak.

TABLE III. ACCURACY OF BEATS DETECTED USING COMMON THRESHOLD TECHNIQUE

File Name	Total number of beats	No. of beats detected	Accuracy (%)	No. of beats deleted	No. of beats inserted
103	2085	2070	99.51	10	-
111	2124	1497	70.48	627	-
113	1795	1795	100	-	-
118	2278	2259	99.16	19	-
123	1518	1518	100	-	-
200	2599	1322	50.87	1277	-
212	2748	2720	98.98	28	-
214	2258	2203	97.56	55	-
221	2427	2264	93.28	163	-
222	2483	1084	43.66	1399	-
231	1571	1565	99.62	6	-
233	3068	3049	99.38	19	-
234	2753	2747	99.78	6	-

The performance of the detection of heartbeats has improved in the window based technique compared to common threshold technique. Among detected beats, number of beats used for training and testing are tabulated in Table V. Table VI shows the accuracy of test beats detected as NORM, LBBB, RBBB, VPC and APC using GMM classifier.

TABLE IV. ACCURACY OF BEATS DETECTED USING WINDOW BASED THRESHOLD TECHNIQUE

File Name	Total number of beats	No. of beats detected	Accuracy (%)	No. of beats deleted	No. of beats inserted
103	2085	2073	99.66	7	-
111	2124	1759	82.82	365	-
113	1795	1788	99.61	7	-
118	2278	2237	98.2	41	-
123	1518	1514	99.74	4	-
200	2599	2410	92.73	189	-
212	2748	2701	98.29	47	-
214	2258	2082	92.21	176	-
221	2427	2289	94.31	138	-
222	2483	1741	70.12	742	-
231	1571	1623	96.69	-	52
233	3068	2830	92.24	238	-
234	2753	2830	99.56	12	-

TABLE V. LIST OF TRAINING AND TEST SAMPLES

Sl.no	Classes	Number of training samples	Number of testing samples
1	NORM	10421	6926
2	LBBB	2470	1646
3	RBBB	3140	2098
4	VPC	1250	834
5	APC	336	226

TABLE VI. ACCURACY OF TEST BEATS CLASSIFICATION

Class	NORM	LBBB	RBBB	VPC	APC	Accuracy (%)
NORM	5838	269	19	56	741	84.99
LBBB	13	1590	0	6	37	96.6
RBBB	11	0	1953	15	119	93.08
VPC	8	4	18	788	16	94.48
APC	42	22	27	3	142	62.83

CONCLUSION

This work proposes a new method based on GMM classification to analyze ECG signal for diagnosis of cardiac arrhythmias. Thirteen files from MIT-BIH arrhythmia database are used for evaluation. The proposed method can easily differentiate normal and abnormal beats. Abnormal beats include left bundle branch block (LBBB), right bundle branch block (RBBB), ventricular premature contraction (VPC) and atrial premature contraction (APC). This gives an

accuracy of 84.99%, 96.6%, 93.08%, 94.48% and 62.83% for NORM, LBBB, RBBB, VPC and APC, respectively.

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