

ECG arrhythmia classification using time frequency distribution techniques

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Abstract In this paper, we focus on classifying cardiac arrhythmias. The MIT-BIH database is used with 14 original classes of labeling which is then mapped into 5 more general classes, using the Association for the Advancement of Medical Instrumentation standard. Three types of features were selected with a focus on the time–frequency aspects of ECG signal. After using the Wigner–Ville distribution the time–frequency plane is split into 9 windows considering the frequency bandwidth and time duration of ECG segments and peaks. The summation over these windows are employed as pseudo-energy features in classification. The “subject-oriented” scheme is used in classification, meaning the train and test sets include samples from different subjects. The subject-oriented method avoids the possible overfitting issues and guaranties the authenticity of the classification. The overall sensitivity and positive predictivity of classification is 99.67 and 98.92%, respectively, which shows a significant improvement over previous studies.

Keywords Cardiac arrhythmia · Classification · Decision tree · Ensemble learner · Time–frequency analysis · Wigner–Ville distribution

1 Introduction

Cardiac arrhythmias are group of heart conditions in which the electrical activities of the heart become irregular. Arrhythmias usually occur as a result of a malfunction in the conduction system or when a pulse is originated from where it wasn't supposed to. Some arrhythmias can be extremely dangerous and some of them can happen in an everyday life of a healthy person. However, studies show that about 80% of sudden cardiac death is the result of ventricular arrhythmias. Thus, the early and accurate detection of arrhythmias is crucial [1].

Electrocardiogram (ECG) is the recording of the electrical activity of the heart which occurs almost periodically through each heartbeat. Thus, the ECG signal is an excellent source to identify arrhythmias. Some arrhythmias don't show any persistent trace in the ECG signal and consequently a continuous monitoring of ECG is necessary for some cases. Detection and classification of different abnormalities in ECG has long been investigated by researchers in the field of biomedical signal processing. Our goal in this paper is to introduce a new prospective in cardiac arrhythmia detection and help to improve the classification process.

Notable works has been done in analyzing the time-domain features of ECG signal which include RR intervals, QT segments, QRS complexes and other morphological features [2–4]. On the other hand, the spectral domain offers a different insight and its parameters give a distinctive representation of signal which can be used for better diagnosis. Besides the subtle time-domain changes of some arrhythmias will have an evident impact on the ECG spectrum.

The most well-known tool for investigating a signal in frequency domain is the Fourier Transform (FT), which in

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spite of a detailed frequency information, provides no link to the time domain. Meaning, one wouldn't know when different frequencies of signal occur. Each arrhythmia is triggered in a specific part of the heart's conduction system and each part of the ECG signal corresponds to a specific part of depolarization or repolarization, FT can't provide the sufficient information for an accurate detection. This problem can be solved with the help of time-frequency (TF) techniques. Short-time Fourier transform (STFT) is a popular TF technique, could be used to compute the energy distribution of the ECG signal; the features are then extracted from the energy distribution and used in classification algorithms. There is a tradeoff in time and frequency resolutions in STFT, limiting authenticity of the features [5]. Wavelets resolve this issue by employing a time-scale resolution scheme for signal analysis. Papers adopting STFT and wavelet techniques for ECG signal processing and arrhythmia classifications report significant improvements compared to single domain studies [6–9].

As a supervised classification problem, many machine learning algorithms have been proposed in literature. Support vector machine (SVM) [7, 10, 11], self-organizing map (SOP) [12], artificial neural networks (ANNs) [6, 13], linear discriminant analysis (LDA) [2, 14], conditional random field (CRF) [15], decision trees [16]. Using the same dataset and exploring various features and dimensionality reduction algorithms helps in forming a fast-evolving field for ECG arrhythmia classification.

In this paper, we propose the use of time-frequency windowing for pseudo-energy feature extraction and then employ an ensemble of decision trees for classification. The results show that our proposed method is a more effective method in the analysis and classification of ECG signals.

The paper is organized as follows; Sect. 2 has the background materials, in Sect. 3 we introduce our method. Section 4 provides the classification results and the paper is concluded in Sect. 5.

2 Background

2.1 Higher order statistics

The conventional lower (first and second) order statistics are well-known in the field of bio-signal processing. However, for nonlinear signals the lower order statistics are not sufficient for a proper representation. Hence the third and fourth order statistics respectively known as skewness and kurtosis are proven to be useful by many papers [9, 10, 16, 17].

For a random variable, x , the third and fourth order statistics are defined as,

$$\begin{aligned}\gamma_3 &= \frac{E\{[x - E(x)]^3\}}{\left(E\{[x - E(x)]^2\}\right)^{3/2}}, \\ \gamma_4 &= \frac{E\{[x - E(x)]^4\}}{\left(E\{[x - E(x)]^2\}\right)^2} - 3.\end{aligned}\quad (1)$$

in which E denoted the expected value. Skewness provides a measurement of the lopsidedness of the distribution and kurtosis gives a relative measurement of the signal's distribution with a Gaussian distribution of the same variance. These higher order statistics can be estimated as,

$$\begin{aligned}\hat{\gamma}_3 &= \frac{\sum_{i=1}^N (x_i - \hat{m})^3}{(N-1)\hat{\sigma}^3}, \\ \hat{\gamma}_4 &= \frac{\sum_{i=1}^N (x_i - \hat{m})^4}{(N-1)\hat{\sigma}^4} - 3,\end{aligned}\quad (2)$$

where x_i 's are realizations of the random variable x and \hat{m} and $\hat{\sigma}$ are the estimates of the mean and variance respectively.

2.2 Wigner–Ville distribution

Wigner–Ville distribution (WVD) is a simple form of the Cohen's class of bilinear time–frequency representations with a wide use in various applications. The WVD of the signal $x(t)$ with zero mean is defined as:

$$W_x(t, f) = \int x\left(t + \frac{\tau}{2}\right)x^*\left(t - \frac{\tau}{2}\right)e^{-j2\pi f\tau} d\tau \quad (3)$$

where $x^*(t)$ is the complex conjugate of $x(t)$.

In an ideal case, the WV distribution has an infinite resolution in time and frequency domains because of the absence of averaging over any finite time duration [18].

2.3 Ensemble learners

An ensemble of learners is a method for supervised classification which uses a combination of various *weak learners* to form a strong one. A weak learner is defined as a classifier which can label the results only a slightly better than a random guess. These weak learners are combined by different methods such as weighted sum or majority voting. The important issue in constructing an ensemble learner is the diversity among the weak learners, because combining same weak learners would give us no gain. The diversity can be achieved by different representations of the train set, called bagging (bootstrap aggregating) [19]. Bagging was

introduced in 1984 by Breiman [19] and is the most common bootstrap ensemble method. In order to achieve diversity in bagging, each weak learner is trained using a random subset of the main train samples. Given the train set T for our supervised classifier, bagging generates new training sets T_i by sampling uniformly from T , with replacement. These new bootstrap samples each are different from the original set, yet they resemble it in distribution and variability and are used to train the weak learners. The weak learners are then combined by voting to form the classifier [20–22].

3 Methods

In this section, we introduce the methodology used in the paper. First, we talk about our dataset and then we follow the overall processing steps as illustrated in Fig. 1. After preprocessing, which is baseline wandering removal and beat segmentation, we extract three sets of features, RR-interval, time–frequency and higher order statistical features. These features are then fed into a classifier which is the final part of the algorithm.

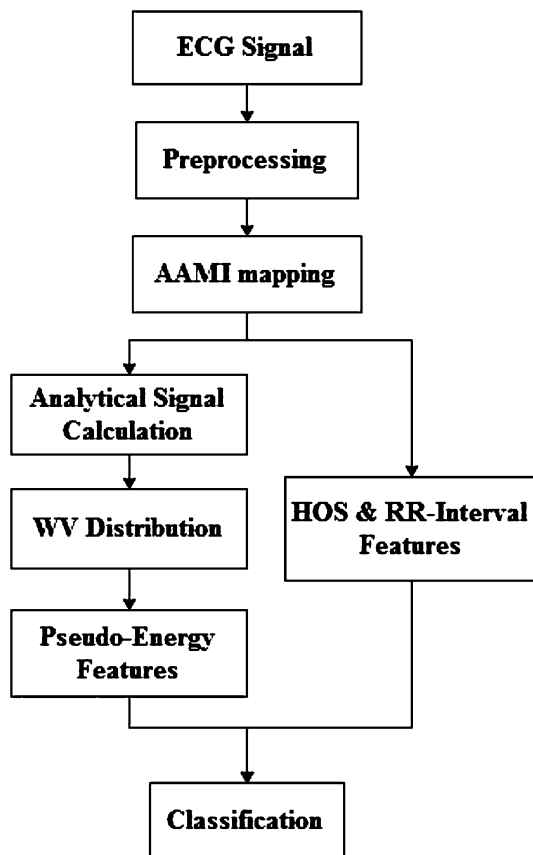


Fig. 1 Flowchart of the proposed algorithm

3.1 Dataset

We have used the MIT-BIH arrhythmia dataset [23] in our study, which includes various common and life-threatening arrhythmias. The database has 48 ECG recordings, each 30 min long, consisting two leads. For 45 recordings, the first lead is modified lead II (MLII) and for the rest it is modified lead V5. The second lead is a pericardial lead (V1 for 40 of them, V2, V4 or V5 for the others). In this paper only the first lead of the database has been used. The original labeling of the dataset has 14 classes of different rhythms listed as in Table 1. However, the Association for the Advancement of Medical Instrumentation (AAMI) [24, 25] recommends 5 more general classes of rhythms as follows. “N” beats originated from the sinus node, “S”, supraventricular ectopic beats, “V”, ventricular ectopic beats, “F”, fusion beats and “Q”, unclassified beats. This standard is adopted by many papers such as [2, 6–8, 11, 14–16, 26]. The mapping from the 14 original labels to AAMI standard labels are shown in Table 2. The heartbeat arrhythmia classification is most commonly viewed as a supervised classification problem. Thus, in random division of the train and test sets it is highly possible that the heartbeats from the same subject would appear in both sets and having correlated samples in both sets would cause overfitting and lead to promising results which are unreachable in practice. To avoid this problem a “subject-oriented” method is introduced in [2] which uses a patient-based division of the dataset, so a more realistic classifier can be trained using this scheme. The train and test sets for this method are shown respectively as DS1 and

Table 1 MIT-BIH arrhythmia database information (AAMI-approved data only)

Heartbeat type		Ann ^a	Total #
Normal rhythm	NOR	N	74,068
Left bundle branch block	LBBB	L	8066
Right bundle branch block	RBBB	R	7246
Atrial premature contraction	APC	A	2513
Premature ventricular contraction	PVC	V	6897
Aberrated atrial premature beat	AP	a	150
Ventricular flutter wave	VF	!	472
Fusion of ventricular and normal beat	VFN	F	802
Non-conducted P-wave (blocked APC)	BAP	x	193
Nodal (junctional) escape beat	NE	j	229
Ventricular escape beat	VE	E	106
Nodal (junctional) escape beat	NP	J	83
Atrial escape beat	AE	e	16
Unclassified beat	UN	Q	17
Total			100,858

^a Annotation that is used for each arrhythmia in the database

Table 2 AAMI recommended labeling with training set (DS1) and testing set (DS2) used in subject-oriented scheme

AAMI class	MIT-BIH class	Total #
N	NOR, LBBB, RBBB, AE, NE	89,625
S	APC, AP, BAP, NP	2939
V	PVC, VE, VF	7475
F	VFN	802
Q	UN	17
DS1	101, 106, 108, 109, 112, 114, 115, 116, 118, 119, 122, 124, 201, 203, 205, 207, 208, 209, 215, 220, 223, 230	
DS2	100, 103, 105, 111, 113, 117, 121, 123, 200, 202, 210, 212, 213, 214, 219, 221, 222, 228, 231, 232, 233, 234	

DS2 in Table 2. Using this scheme our results will be comparable with other arrhythmia classification algorithms such as [11, 14–16].

3.2 Data preprocessing

The MIT-BIH arrhythmia dataset is band-pass filtered at 0.1–100 Hz and then digitized at 360 samples per second [23]. We have removed the baseline wandering of these signals using two stages of median filtering as proposed by [27].

The MIT-BIH database also includes an annotation file associated with each sample. This file has the information about the type of the rhythms and the occurrence sample of the major local maxima for each individual heartbeat.

3.2.1 Beat segmentation

We use the annotation files as our reference in beat segmentation. The local maximums of each heartbeat (R peaks for most of cases) are extracted from the annotation files and a fixed number of samples before and after each R peak is defined for beat segmentation. While [11] uses 100 samples before R peaks and 200 samples after R peaks (total of 0.83 s), [16] selects 235 total samples (0.25 s before and 0.40 s after R peaks). Since we are using 2-dimensional time–frequency representations we choose the total amount of 256 samples (102 samples before R peaks and 153 after that) to ease the computational processes. A sample of beat segmentation is shown in Fig. 2.

3.3 Feature extraction

In this section we introduce the features we have used in classification. Time–frequency characteristics of ECG signals along with the RR interval and statistical features are extracted for classification.

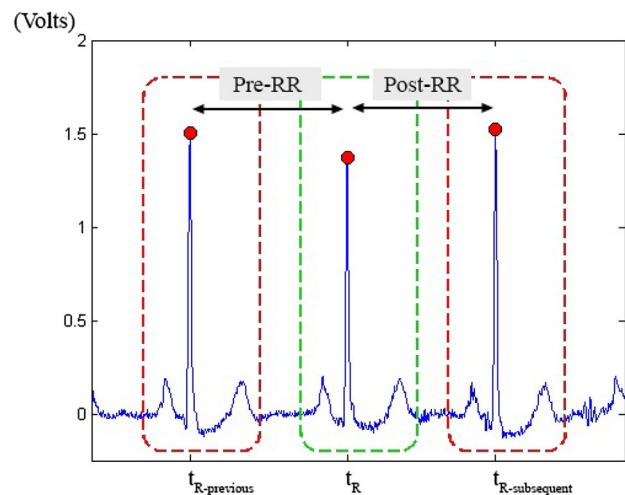


Fig. 2 Short sample from “101 m.mat” showing the beat segmentation and Pre-RR and Post-RR features

3.3.1 RR interval features

In this paper, we have used two RR-interval features as the only representatives of the time domain traits of the signal. The time distance between respective R peaks bare indispensable information about the subjects’ health and consequently the type of the rhythms. “RR variability” or “heart rate variability (HRV)” are the clinical terms used to investigate changes in the occurrence time of the R peaks which indicates the importance of these time domain features. RR based features are very popular in cardiac arrhythmia classifications and are used in various papers such as [2, 6, 8, 10–12, 14–16, 28].

Two RR based features are extracted as pre-RR and post-RR. Pre-RR is defined as the time distance between the R peak of the current heartbeat with the R peak of previous one; and the post-RR is defined as the same distance for the current and the subsequent heartbeats. Pre-RR and post-RR features are shown in Fig. 2 for a sample heartbeat.

3.4 HOS features

We have used three higher order statistical (HOS) features because they have proven to be less sensitive to the

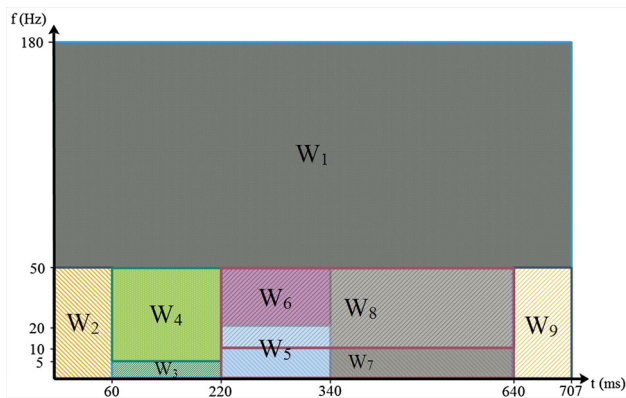


Fig. 3 Time–frequency windowing for feature extraction

morphological changes of signal [29]. In addition, the nonlinear nature of these features can help in better highlighting the dynamic aspects of ECG signal [30]. Skewness, kurtosis and 5th order moment of each signal is extracted and put into the feature vector.

3.5 Time–frequency features

We have used Wigner–Ville distribution to get a time–frequency representation of signal and extract pseudo-energy features. Each signal is represented as a 256×256 matrix after using Eq. (3) and is summed over 9 windows as shown in Fig. 3. W_1 covers the high frequency i.e. frequencies higher than 50 Hz. W_2 is over the beginning part of the signal before the potential PR segment; W_2 is a window of 62 ms width over frequencies lower than 50 Hz. W_3 and W_4 lie on the PR segment with 160 ms width and frequencies lower than 5 Hz and mid-frequency between 5 and 50 Hz. P and T waves have most of their

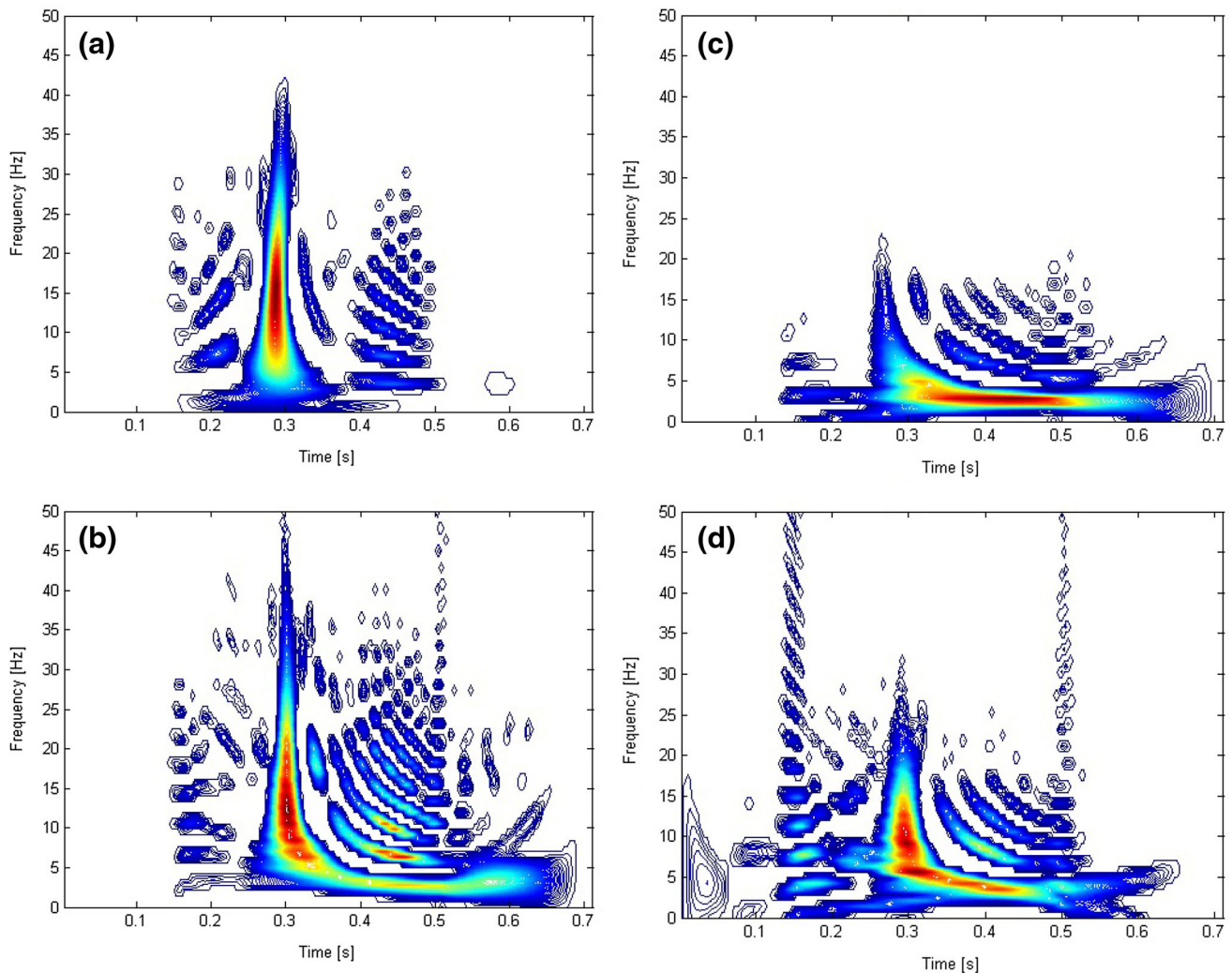


Fig. 4 Wigner–Ville distribution for a sample first lead (lead II) of **a** class N, **b** class S and **c** class V

energies over the frequency band lower than 5 Hz and that is why we have considered two windows over this time period. W_5 and W_6 cover the potential occurrence time of the QRS complex with 120 ms width and with frequencies lower and higher than 20 Hz. W_7 and W_8 are over the QT segment with 420 ms long and frequency margin of 10 Hz. Finally, W_9 covers the part after the potential QT segment with frequencies lower than 50 Hz. Figure 4 illustrates three samples of WVD for each class of “N”, “S” and “V” with frequencies lower than 50 Hz.

The summation over each window provides a measure of energy during that time within the specific frequency range and can be a good feature for differentiating arrhythmias. Figure 5 shows the mean energy density for all 9 windows of four main rhymes in our trainset. Although the Wigner–Ville distribution is criticized for producing cross terms, the computational advantages it offers over the other methods such as Choi-Williams distribution are critical specially in a big database as MIT-BIH.

It should be mentioned that in order to reduce the computational costs and avoid the cross terms between positive and negative frequencies the original signals are not used in WV distribution. First the analytical signals are calculated for each heartbeat then the WVD is used. Analytical signals have the same spectrum for positive frequencies and zero spectrum for the negative frequencies can be calculated as in Eq. (4)

$$x_a(t) = x(t) + j\mathcal{H}[x(t)] = x(t) + j\left[\frac{1}{\pi t} * x(t)\right] \quad (4)$$

where $x_a(t)$ is the analytical signal, $\mathcal{H}(\cdot)$ is the Hilbert transform and $*$ is the convolution symbol.

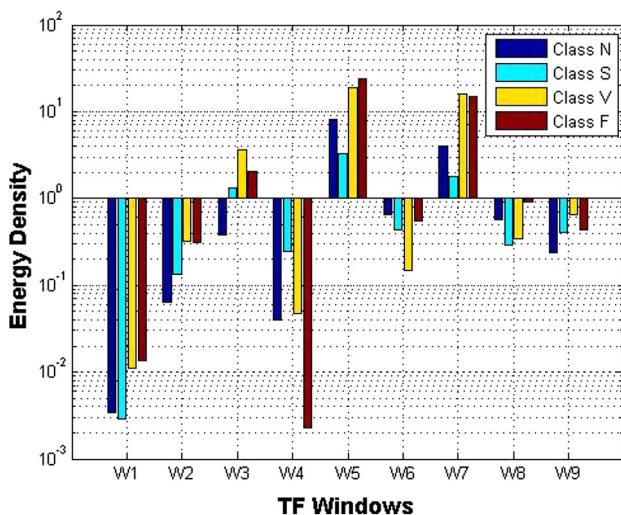


Fig. 5 Mean of energy density for 4 windows and three main arrhythmia classes

4 Classification results

As shown in Table 3 the total number of 100,858 heartbeats from five different AAMI-recommended groups of arrhythmia are used in classification. The test and train sets are selected as in Table 2, proposed by [2]. 14 extracted features are normalized and put into the feature vector for a supervised classification. An ensemble of 100 decision trees are combined in bagging scheme to form a stable and accurate classifier. By reducing the variance, bagging avoids overfitting problems. The prior probability for each class is set to 0.2; of course, better results can be achieved by setting prior probabilities proportional to the population of each class or unbalancing the misclassification cost in favor of life threatening arrhythmias. However, we didn't want to involve any knowledge of class populations in the classification procedures.

4.1 Performance metrics

Various approaches are adopted in literature to evaluate the classification results. In this paper, we have considered sensitivity and positive predictivity to compare the algorithm with previous studies. Sensitivity (Se) can be defined as the measure of successfully classified positive samples,

$$Se = \frac{TP}{TP + FN} \times 100, \quad (5)$$

in which FN is the total number of misclassified positive samples and TP is the total number of correctly classified positive samples. Positive predictivity (Pp) measures

Table 3 Results of classification

Class	Total #	Train	Test	Se (%)	Pp (%)
N	89,625	45,807	43,818	99.79	99.14
S	2939	999	1940	94.28	95.96
V	7475	4257	3218	95.37	94.14
F	802	414	388	12.11	51.09
Q	17	8	9	100	100
Total	100,858	51,485	49,373	99.67	98.92

Table 4 Confusion matrix for the results

Reference	Predicted results				
	N	S	V	F	Q
N	43,726	42	6	44	0
S	41	1829	70	0	0
V	120	28	3069	1	0
F	219	7	115	47	0
Q	0	0	0	0	9

Table 5 Comparative results of subject-oriented classification

Method	N		S		V	
	Se	Pp	Se	Pp	Se	Pp
Llamedo and Martinez [14]	95	98	77	39	81	87
Ye et al. [11]	88.6	97.5	60.8	52.3	81.5	63.1
de Chazal et al. [2]	87.1	99.2	75.9	38.5	77.7	81.6
Ghorbani Afkhami et al. [16]	97.4	98.4	86.5	90.9	96.0	77.6
Proposed	99.8	99.1	94.3	96.0	95.4	94.1

success rate among samples classified as positive and can be defined as,

$$Pp = \frac{TP}{TP + FP} \times 100, \quad (6)$$

where FP is the total number of falsely classified negative samples.

4.2 Results

The results of classification are shown in Table 3 which has the total sensitivity and positive predictivity of 99.67 and 98.92%. The Table 4 illustrates the confusion matrix, the high amount of misclassified samples for class “F” is evident. However, there are only 693 misclassified beats in total which is 1.4% of the test set. Table 5 shows the overall results of our method compared with previous works. Only the results for three main classes of “N”, “S” and “V” are mentioned in papers so the Se and Pp are compared for these classes. The proposed method shows a significant improvement of classification accuracy over our previous work [16] and other papers with same database, indicating the importance of TF role in ECG analysis.

5 Conclusion

In this paper, we have proposed a new algorithm based on time–frequency representation to extract features for cardiac arrhythmia classification. Considering the normal time duration of QRS complex, PR interval and QT interval and the normal bandwidth of each P wave, T wave and QRS complex, 9 TF windows are selected. The summation over these windows along with RR-interval and HOS features are used in classification. An ensemble of decision trees is used with subject-oriented scheme. The results show extremely high accuracy in the three main classes of “N”, “S” and “V”, which contain over 99% of the database. The “F” class on the other hand has many misclassified samples as it is the case in other papers too. The TF features as a measure of energy are proven to be effective for heartbeat classification.

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