AUTOMATED DIAGNOSIS OF CARDIAC HEALTH USING 
RECURRENCE QUANTIFICATION ANALYSIS

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The sum total of millions of cardiac cell depolarization potentials can be represented using an 
electrocardiogram (ECG). By inspecting the P-QRS-T wave in the ECG of a patient, the 
cardiac health can be diagnosed. Since the amplitude and duration of the ECG signal are too 
small, subtle changes in the ECG signal are very difficult to be deciphered. In this work, the 
heart rate variability (HRV) signal has been used as the base signal to observe the functioning of 
the heart. The HRV signal is non-linear and non-stationary. Recurrence quantification analysis 
(RQA) has been used to extract the important features from the heart rate signals. These 
features were fed to the fuzzy, Gaussian mixture model (GMM), and probabilistic neural net- 
work (PNN) classifiers for automated classification of cardiac bio-electrical contractile disorders. 
Receiver operating characteristics (ROC) was used to test the performance of the classifiers. In 
our work, the Fuzzy classifier performed better than the other classifiers and demonstrated an
average classification accuracy, sensitivity, specificity, and positive predictive value of more than 83%. The developed system is suitable to evaluate large datasets.

Keywords: Heart rate; RQA; fuzzy; GMM; PNN; classifier; ANOVA.

1. Introduction

The origin of the electrical activity is from the sinoatrial (SA) node of the heart. Electrical impulses are continuously generated by a group of specialized cells. These impulses spread all over the heart muscle through pathways and hence, cause the heart muscles of both the atria and ventricles to contract synchronously. This contraction induces ventricular filling and ejection of blood. For healthy people, electrical impulses of about 50 to 70 beats per minute are generated by the SA node at rest. This generation is due to the autonomic nervous system (ANS) possessing a continuous control over the output of the SA node. All internal organs of the body are involuntarily controlled by the autonomic nervous system. It consists of two branches — the sympathetic and parasympathetic (vagal) nervous systems.

A release of norepinephrine will occur when there is stimulation from the sympathetic nervous system. This release will result in an increased heart rate because of the increase in SA node discharge. The force of myocardial contraction and cardiac output will also increase due to an acceleration in the atrioventricular (AV) node conduction time. In contrast, a release of acetylcholine will occur when there is stimulation from the parasympathetic nervous system. This release will result in a decrease in the heart rate due to the decrease in the rate of SA node discharge. The cardiac output will also decrease due to a deceleration in the AV node conduction time. During the rest state, both sympathetic and parasympathetic systems are active. In order to enable optimal functioning of the heart, there must be perfect balance between them.

The external monitoring of the electrical activity of the heart, which originates at the SA node, can be carried out using the electrocardiogram (ECG). The ECG is a representative signal of the heart, where its condition can be understood by studying the shape, size, and time intervals between the various peaks of the P-QRS-T wave in the ECG. The ECG signals are recorded by placing sensors on the limb extremities of the patient. By observing the shape features of the ECG signal, the cardiac bio-electrical state of the patient can be diagnosed. It is very difficult to visually observe the subtle changes in ECG signals since they are non-stationary and non-linear in nature. Though the ECG signal changes can serve as indicators of current disease or impending diseases, it may so happen that these indicators or symptoms may occur at random in the time scale. All these factors necessitate the transformation of shape-related information contained in the ECG signal to an easy-to-handle time series data information. This is the idea behind the extraction and analysis of HRV signals from ECG signals, rather than directly analyzing ECG signals.

1.1. Heart rate variability

Heart rate variability (HRV) analysis has now developed as a widely accepted effective and non-invasive method to assess the health of the ANS. HRV signal which indicates
variations of instantaneous heart rate, are derived from the ECG signals. The RR interval is the interval between adjacent QRS complexes in ECG signal. The heart rate signal is a time series sequence of non-uniform RR intervals. The variation of RR intervals is the HRV. Decreased HRV strongly points to the increased risk of cardiovascular diseases. HRV measurements are non-invasive and easy to acquire. HRV signals have good reproducibility when acquired under standardized conditions.

HRV can be reflected using the autonomic control of the cardiac system. It is one of the indicators of the dynamic interaction and balance between the sympathetic nervous system and parasympathetic nervous system. The time domain and frequency domain analyses are the most commonly used traditional approaches to study the HRV signal.

HRV methods, which are based on statistical measures, are time domain methods, and they are simple to use. The standard deviation of the normal to normal (NN) intervals (SDNN), the standard error of the NN intervals (SENN), the standard deviation of differences between adjacent NN intervals (SDSD), the root mean square successive difference of intervals (RMSSD), and the number of successive differences of intervals that differ by more than 50 ms (pNN50%) are the statistical parameters calculated from the original heart rate signal, and can be used as time domain parameters. However, one limitation of time domain analysis is that it can be easily affected by artifacts and outliers.

The high frequency power spectrum (HFPS), the low frequency power spectrum (LFPS), and the very low frequency power spectrum (VLFPS) are the three main frequency regions in a typical power spectrum of the heart rate signal. HFPS exists in the 0.15 Hz to 0.4 Hz range. It reflects the parasympathetic (vagal) tone and fluctuations caused by the spontaneous respiration known as respiratory sinus arrhythmia (RSA). Next, LFPS exists in the band of 0.04 Hz to 0.15 Hz, and reflects both the sympathetic and parasympathetic systems. The band of 0.0033 Hz to 0.04 Hz represents the VLFPS. It indicates the sympathetic tone and slower humoral and thermoregulatory effects during long recordings. VLFPS can also help in the detection of various negative emotions, worries, rumination, etc. during shorter recordings. The disadvantage of the Fourier domain method is that the reliability of the spectral measurements reduces with the reduction of signal power and signal-to-noise power.

The human cardiovascular system is non-linear in nature. There are evidences which suggest that heart is not a periodic oscillator under normal physiological conditions. Generally, all bio-signals (ECG and HRV) are non-stationary, non-linear, highly irregular, and exhibits typically complex dynamics. For handling such signals, traditional time domain and frequency domain methods are not sufficient.

In the past, many linear and non-linear methods have been used for the detection of alcoholic, epileptic, and sleep stages. Faust et al. have used time-frequency analysis and spatial filling index to calculate Renyi’s entropy from the input HRV signals. Wavelets also provide time-frequency information. Patil et al. used discrete wavelet transform (DWT) to classify QRS complexes of ECG waveforms as normal
or myocardial ischaemic. Techniques like principal component analysis (PCA) and linear predictive coding (LPC) have been used for analyzing ECG waveform for the classification of ventricular ectopic beats (VEBs).16

Higher order spectrum (HOS) which provides very good noise immunity, is another method to extract information from non-linear signals. Phase entropies and bispectrum invariant features, which come under HOS features, were used to study cardiac arrhythmia using heart rate as base signal.17 Different bicoherence and bispectrum plots that classified normal and other four other classes with an average classification accuracy of above 85% were also proposed. Chua et al.18,19 used HOS to extract nonlinear information from EEG signals for classifying them to normal, preictal (background), and epileptic categories.

The second option is to adopt an entirely different method of non-linear analysis. The biological time series analysis is a very recognized area of non-linear analysis. The non-linear dynamical methods are based on the concept of chaos. The chaos theory has been employed to detect cardiac arrhythmia such as ventricular fibrillation and to predict the onset events such as ventricular tachycardia for the purpose of detecting congestive heart failure situations by analyzing HRV signals in the 1990s.20,21 Hence, nonlinear techniques, which extract and analyze the nonlinear features from HRV signals, are widely used to unveil the “hidden information” in the signals instead of linear methods.16,22–24 Recently, recurrence quantification analysis (RQA) was applied to automatically detect normal, interictal, and epileptic EEG signals.25 In another study, to analyze eight types of cardiac classes such as atrial fibrillation, complete heart block, pre-ventricular contraction, normal, left bundle branch block, ventricular fibrillation, ischemic/dilated cardiomyopathy, and sick sinus syndrome, different non-linear and linear methods were applied.26 Different ranges of values for different linear and non-linear parameters were proposed. These values are considered to be clinically significant as they have p-value of less than 0.001. Using non-linear and artificial intelligence techniques in their study, the authors reported a classification accuracy of 85%. Furthermore, RQA was used for the classification of normal, interictal, and epileptic EEG signals with an accuracy of more than 95%,25 with proposed unique recurrence plots of three classes.

In order to extract non-linear fluctuations in heart rates which are not obvious, new dynamic methods of HRV quantification were applied. Correlation dimension, lyapunov exponents, 1/f slope, detrended fluctuation analysis, and approximate entropy (ApEn) are among the several methods which have been proposed in the literature.27–31 The range over which these parameter values fall gives an indication about the presence or absence of cardiac problems.

Classification of normal sinus rhythm (NSR) and other cardiac arrhythmia namely atrial premature contraction (APC), premature ventricular contraction (PVC), supraventricular tachycardia (SVT), ventricular tachycardia (VT), and ventricular fibrillation (VF) was done using the autoregressive modeling (AR) technique.5 Classification accuracy between 93.2% and 100% was achieved using
generalized linear model (GLM)-based classification algorithm while trying to classify NSR, APC, PVC, SVT, VT, and VF.

In this paper, the features derived from RQA were used for automated classification of cardiac bio-electrical contractile disorders using the Gaussian mixture model (GMM) and probabilistic neural network (PNN) classifiers. The methodology used for the automatic identification of the cardiac diseases is presented in this paper. The layout of this paper is as follows. The data acquisition process and preprocessing of the raw cardiac signals is presented in Sec. 2. The Description of the following techniques — RQA, statistical analysis (ANOVA), GMM, and PNN — is given in Sec. 3. The results of this work are shown in Sec. 4. The discussion about the data analysis presented in the work is given in Sec. 5. Finally, the paper is concluded in Sec. 6.

2. Data Acquisition Process

Kasturba Medical Hospital, Manipal, India provided the ECG data used in this study. Consequently, the permission for ECG signal recording was obtained from the concerned hospital authorities. When the patient was lying down in a comfortable position, the Holter was used to store the patient’s 15 min of ECG recording. A sampling frequency of 320 samples/s was used to digitize the analog data. A typical heart rate signal of a patient with normal sinus rhythm is shown in Fig. 1.

In this work, the cardiac data are classified into the following five classes: complete heart block (CHB), atrial fibrillation (AF), ischemic/dilated cardiomyopathy (ISCH), sick sinus syndrome (SSS), and normal sinus rhythm (NSR). Brief descriptions of these classes are given below.

**Complete heart block (CHB)**

CHB occurs when the electric signals in the heart are unable to flow from the upper to the lower chambers due to a disease of the electrical system of the heart. The conduction of the impulses generated from the sinus node in the right atrium does not occur to the ventricles, which will cause them to contract and pump blood at a slower rate. Therefore, the result is a reduction in the heart rate, which can be as low as 30 beats per minute. There is no normal relationship between the P and the QRS waves in ECG for patients diagnosed with CHB.

![Fig. 1. Typical heart rate signal of patient with normal sinus rhythm.](image-url)
Atrial fibrillation (AF)
AF occurs when multiple patterns of electrical impulses are travelling randomly through the atria. Random activation of different parts of the atria at different times is the cause of AF in patients. In such cases, observations from the ECG indicate the absence of P waves and an irregularity of the R–R interval which may be due to the irregular conduction of impulses to the ventricles from the atria. Patients with AF have heart rate ranging from 100 to 175 beats per minute.

Ischemic/dilated cardiomyopathy (ISCH)
ISCH is the weakness of the heart muscles and coronary artery disease is the most common cause of ISCH. It is caused by an inadequate amount of oxygen being delivered to the myocardium. Irregular heartbeats can be observed in a patient with ISCH due to the inability of the ventricles to pump out blood to the normal degree. Patients with ISCH also have low HRV.

Sick sinus syndrome (SSS)
SSS occurs when there is a group of symptoms which indicate that the SA node is dysfunctioning. It can cause a patient to experience alternating slow and rapid heart rates, a sinus arrest, or persistently slow heart rate. The heart rate can vary rhythmically in bradycardia and tachycardia patterns.

Normal sinus rhythm (NSR)
NSR usually occurs in a healthy person. The sinus node will generate the rhythm which will travel in a normal fashion in the heart. In the ECG, the P wave will be observed first. After the occurrence of the P wave and a brief pause, the QRS complex will appear, and finally the T wave will appear. The P wave morphology and axis are normal. The PR interval will range between 120 ms to 200 ms. A patient with heart rate of any value between 60–100 bpm is usually a characteristic of NSR. Table 1 presents the number of datasets collected in each class in this study.

2.1. Preprocessing
There are four steps involved in the preprocessing of the ECG signals:

(1) A low-pass filter with a cut-off frequency of 35 Hz is applied to the ECG signal in order to remove the presence of unwanted high frequencies in the data;
(2) Next, a high-pass filter with a cut-off frequency of 0.3 Hz is used to suppress the baseline wander which is present in the signal;

<table>
<thead>
<tr>
<th>Class</th>
<th>CHB</th>
<th>AF</th>
<th>ISCH</th>
<th>SSS</th>
<th>NSR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of datasets</td>
<td>27</td>
<td>30</td>
<td>32</td>
<td>36</td>
<td>162</td>
</tr>
</tbody>
</table>
(3) After removing the unwanted high frequencies and baseline wander from the ECG signal, a band-stop filter with cut-off frequencies of 50 or 60 Hz is used to suppress the power-line interference noise; and

(4) Finally, a median filter is used in order to extract the baseline wander from the processed ECG signal. By subtracting it from the processed ECG signal, this process will effectively remove all the baseline wanders from the ECG.

To detect the R peaks of the ECG signal, the Tompkins algorithm was applied on the ECG data.\textsuperscript{32,33} The heart rate (beats/min) was calculated using Eq. (1). The RR interval \((t_{r-r} \text{ seconds})\) is an interval which exists between two successive QRS complexes:

\[
HR = 60t_{r-r}. \tag{1}
\]

3. Methodology

The HRV signals were analyzed using RQA. In this work, RQA was used to extract 10 features from the HRV signal. These features were used as input to the classifiers (GMM and PNN). Fig. 2 below shows the proposed system used in this work.

3.1. Recurrence quantification analysis (RQA)

RQA is one of the methods used for non-linear data analysis. In a state space trajectory of a dynamical system, RQA can be used to quantify its number and duration of recurrences. A cross recurrence plot (CRP) reveals all the times at which the phase space trajectory of the first dynamical system visits approximately the same area in the phase space where the phase space trajectory of the second dynamical system is located. It can be a non-square CRP matrix if the data length of both the systems is different. Figure 4 shows the CRPs of the five classes of HR signals. The diagonal structures in the recurrence plots represent the deterministic dynamics of the signal. The cyclicity of recurrence can be revealed from the distance between the diagonal structures.

A large set of Bio-Signals

\[
\begin{array}{c}
\text{RQA} \\
\text{Normalized Features} \\
\text{ANOVA} \\
\text{Normalized Features} \\
\text{Classifiers} \\
\text{AF} \hspace{1cm} \text{CHB} \hspace{1cm} \text{NSR} \hspace{1cm} \text{SSS} \hspace{1cm} \text{ISCH}
\end{array}
\]

Fig. 2. The proposed system.
Zbilut and Webber Jr.\textsuperscript{34,35} developed a quantification of recurrence plots. Marwan \textit{et al.}\textsuperscript{36} extended the quantification of recurrence plots with new measures of complexity. The new measures include recurrence rate (RR), determinism (DET), laminarity (LAM), averaged diagonal line length ($< L >$), trapping time (TT), longest diagonal line ($L_{\text{max}}$), longest vertical line ($V_{\text{max}}$), entropy (ENTR), and recurrence time of 1st type (T1) and 2nd type (T2). These measures are defined subsequently. In the equations shown below, $N$ represents the number of points on the phase space trajectory, $N_v$ represents the number of vertical lines in the recurrence plot, $N_l$ represents the number of diagonal lines in the recurrence plot, while $P(l)$ and $P(v)$ represent the histogram of the line lengths of the diagonal and vertical lines, respectively.

RR is the percentage or density of the recurrence points in a recurrence plot and it corresponds to the correlation sum. It is given by Eq. (2).

$$RR = \frac{1}{N^2} \sum_{i,j=0}^{N} R_{i,j}.$$  \hspace{1cm} (2)

DET is the percentage or fraction which forms diagonal lines and $P(l)$ is the histogram of the length $l$ of the diagonal lines. Equation (3) gives the determinism:

$$DET = \frac{\sum_{l=l_{\text{min}}}^{l_{\text{max}}} lP(l)}{\sum_{i,j} R_{i,j}}.$$  \hspace{1cm} (3)

LAM is the percentage or fraction which forms vertical lines and $P(v)$ is the histogram of the length $v$ of the vertical lines. Equation (4) gives the laminarity:

$$LAM = \frac{\sum_{v=v_{\text{min}}}^{v_{\text{max}}} vP(v)}{\sum_{i=1}^{N} P(v)}.$$  \hspace{1cm} (4)

$< L >$ is the average or mean length of the diagonal lines. Equation (5) gives the average diagonal line length:

$$< L > = \frac{\sum_{l=l_{\text{min}}}^{l_{\text{max}}} lP(l)}{\sum_{i=1}^{N} P(l)}.$$  \hspace{1cm} (5)

TT, depicted by Eq. (6), is the average or mean length of the vertical lines:

$$TT = \frac{\sum_{v=v_{\text{min}}}^{v_{\text{max}}} vP(v)}{\sum_{i=1}^{N} P(v)}.$$  \hspace{1cm} (6)

$L_{\text{max}}$ is the length of the longest diagonal line. Equation (7) gives the longest diagonal line:

$$L_{\text{max}} = \max(\{l_i; i = 1 \ldots N_l\}).$$  \hspace{1cm} (7)

$V_{\text{max}}$ is the length of the longest vertical line. Equation (8) gives the longest vertical line:

$$V_{\text{max}} = \max(\{v_i; i = 1 \ldots N_v\}).$$  \hspace{1cm} (8)
ENTR refers to the Shannon entropy of the probability distribution of the diagonal line lengths \( P(l) \). Equation (9) gives the entropy:

\[
ENTR = - \sum_{l=l_{\min}}^{N} P(l) \ln P(l).
\] (9)

Equations (10) and (11) depict the recurrence times of the 1st and 2nd Poincare recurrence points, respectively:

\[
T_1(i) = t_{i+1} - t_i, \quad t = 1, 2, K \quad \text{and} \quad T_2(i) = t_{i+1} - t_i, \quad t = 1, 2, K.
\] (10) (11)

In this work, measures obtained after performing RQA on the HRV, the signals will be used as the extracted features that are input to the classifiers for classification studies.

### 3.2. Statistical analysis

In this work, analysis of variance (ANOVA) was used to determine whether the means of all the features described above are different. Variances are used by the statistical method, ANOVA, to determine whether the means are different. Although ANOVA is closely related to the \( t \)-test, there is still a distinct difference between them. The \( t \)-test measures the differences between the means of two groups, while ANOVA tests the differences between the means of more than two groups.

### 3.3. Gaussian mixture model (GMM)

One of the probabilistic models that perform density estimation using mixture distribution is the Gaussian mixture model (GMM). The clustering method or unsupervised learning is often used by the mixture model. Since GMM is considered to be a type of pattern recognition system, it is widely used as a classification tool. GMM is a parametric statistical model which contains a number of Gaussian functions. GMM can be used to approximate the continuous probability density function of a multidimensional set. The linear superposition of Gaussian is described by Eq. (12):

\[
p(x) = \sum_{k=1}^{K} \pi_k N\left(x | \mu_k, \sum_k \right),
\] (12)

where \( \mu_k \), \( \pi_k \), and \( \sum_k \) represent mean, mixing coefficients, and covariance respectively. Maximizing the likelihood function with respect to the given parameters is the objective of GMM. Several steps are involved in the expectation–maximization (EM) algorithm. They include initializing the covariances \( \sum_k \), mixing coefficients \( \pi_k \), and means \( \mu_k \). Next, the initial value of the log likelihood is evaluated. Equation (13) shows the current parameter values which will be used to evaluate the responsibilities.
for the expectation (E) step:

\[
\gamma(z_{nk}) = \frac{\pi_k N(x_n | \mu_k, \sum_k)}{\sum_{j=1}^{K} \pi_j N(x_n | \mu_j, \sum_j)}.
\]

Equation (14) shows the current responsibilities which will be used to re-estimate the parameters for the maximization (M) step:

\[
\mu_k^{new} = \frac{1}{N_k} \sum_{n=1}^{N} \gamma(z_{nk}) x_n,
\]

where

\[
\sum_{k}^{new} = \frac{1}{N_k} \sum_{n=1}^{N} \gamma(z_{nk})(x_n - \mu_k^{new})(x_n - \mu_k^{new})^T,
\]

\[
\pi_k^{new} = \frac{N_k}{N}, \quad \text{and}
\]

\[
N_k = \sum_{n=1}^{N} \gamma(z_{nk}).
\]

Equation (15) shows the log likelihood of parameters which will be checked for convergence after the log likelihood is evaluated:

\[
\ln p(X | \mu, \sum, \pi) = \sum_{n=1}^{N} \ln \left\{ \sum_{k=1}^{K} \pi_k N \left( x_n | \mu_k, \sum_k \right) \right\}.
\]

In the case where the convergence criterion is not met, it will return to the estimation step. Hence, more iteration is required for the EM algorithm to reach its convergence. Instead of the full covariance matrix, the diagonal covariance matrix is usually used. The diagonal covariance matrix was not only more computationally efficient, but also had better performance than the full covariance matrix.

### 3.4. Probabilistic neural network (PNN)

One of the neural networks based on a direct continuation of the work on Bayes classifiers is the probabilistic neural network (PNN). By using the approach, which is related to Bayes probabilistic rule, PNN, a special type of neural network, gives solutions for classification problems. It learns to approximate the probability density function (pdf) of the training data. The typical structure of a PNN consists of four layers: input layer, hidden layer, pattern layer, and decision layer. Figure 3 shows the structure of the PNN used in this work. It has 10 neurons in the input layer corresponding to 10 features that were extracted from the data and five neurons in the pattern layer/summation layer since the classifier is trained using five classes of data.

In the input layer, there is one neuron for each feature extracted from the data. Subtracting the median and dividing by the interquartile range, the range of values...
will be standardized by the input neurons. The values will be fed by the input neurons to each of the neurons in the hidden layer. In the hidden layer, there is one neuron for each case in the training dataset. The values of the features for the case along with the target value are stored by the neuron. A hidden neuron will compute the Euclidean distance of the \( \mathbf{x} \) vector of the input values from the input layer with respect to the center point of the neuron. The PNN kernel function using the sigma value(s) is then applied. After the result value is obtained, it is passed to the neurons in the pattern layer.

In the pattern layer/summation layer, there is one pattern neuron for each category of the target variable. Each hidden neuron stores the actual target category of each training case. The weighted value from the hidden neuron will be fed to the pattern neuron which corresponds to the hidden neuron’s category. The weighted value is passed through an activation function which is shown in Eq. (16):

\[
\exp\left[\frac{(X^T W_{ki} - 1)}{s^2}\right].
\]

Then, the pattern neurons add the values for the class they represent (therefore, it will be a weighted vote for that category). This is shown in Eq. (17):

\[
S_{i-1}^{N_k} \exp\left[\frac{(X^T W_{ki} - 1)}{s^2}\right].
\]

Finally, the decision layer will compare the weighted votes for each target category accumulated in the pattern layer. The largest vote will be used to predict the target category. The output nodes are binary neurons that produce the classification decision as shown in Eq. (18):

\[
S_{i-1}^{N_k} \exp\left[\frac{(X^T W_{ki} - 1)}{s^2}\right] > S_{i-1}^{N_j} \exp\left[\frac{(X^T W_{kj} - 1)}{s^2}\right].
\]

The output produced by PNN is an integer. In this work, there are five classes of HRV signals. Hence, the output will be one of the following integers: 1, 3, 6, 20, 21.

Fig. 3. Structure of the probabilistic neural network (PNN) structure used in this work.
3.5. Fuzzy classifier

Fuzzy logic is multi-valued logic derived from fuzzy set theory to deal with reasoning that may be approximate which may not be precise with binary values of true or false. Nowadays this fuzzy logic has used widely in control theory, artificial intelligence, medical diagnosis. In this work, a fuzzy inference system (FIS) was generated with the help of subtractive clustering technique which is used to estimate the number of clusters and the cluster centres in the test data. The FIS consists of inputs, outputs, and a set of rules explaining the behaviour of the fuzzy system. Each input and output has the number of input and output membership functions equal to the number of clusters chosen by the clustering technique. Radius parameter is used to specify the cluster centre’s range of influence in each of the data dimensions. After the training, FIS structure will have a set of fuzzy rules to cover the feature space and it is used to perform fuzzy inference calculations of the test data.

4. Results

The CRPs of the five classes are shown in Fig. 4. Table 2 shows the range of 10 features (RR, DET, $< L >$, $L_{\text{max}}$, ENTR, LAM, TT, $V_{\text{max}}$, T1, T2) for the five classes.

Fig. 4. CRPs for heart rate signals. (a) atrial fibrillation (AF), (b) complete heart block (CHB), (c) ischemic/dilated cardiomyopathy (ISCH), (d) sick sinus syndrome (SSS), and (e) normal sinus rhythm (NSR).
Fig. 4. (Continued)

Automated Diagnosis of Cardiac Health Using Recurrence Quantification Analysis
Fig. 4. (Continued)
Table 2. Results of RQA features for CHB, AF, ischemic/dilated cardiomyopathy, SSS, and NSR.

<table>
<thead>
<tr>
<th>Features</th>
<th>CHB</th>
<th>AF</th>
<th>ISCH</th>
<th>SSS</th>
<th>NSR</th>
<th>( p )-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>RR</td>
<td>0.25870 ± 0.102</td>
<td>(8.29900 ± 3.688) ( \times 10^{-2} )</td>
<td>(0.13250 ± 3.615) ( \times 10^{-2} )</td>
<td>(0.16810 ± 6.079) ( \times 10^{-2} )</td>
<td>(9.55318 ± 5.230) ( \times 10^{-2} )</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>DET</td>
<td>0.50998 ± 0.131</td>
<td>0.33329 ± 0.195</td>
<td>0.2450 ± 0.182 ( \times 10^{-2} )</td>
<td>0.53646 ± 0.160</td>
<td>0.27800 ± 0.139</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>( &lt; L &gt; )</td>
<td>2.6203 ± 0.305</td>
<td>2.5546 ± 0.557</td>
<td>2.3994 ± 0.189</td>
<td>3.4322 ± 0.959</td>
<td>2.2399 ± 0.196</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>( L_{\text{max}} )</td>
<td>95.519 ± 95.8</td>
<td>13.167 ± 12.1</td>
<td>8.4062 ± 3.08</td>
<td>58.972 ± 66.4</td>
<td>13.494 ± 38.8</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>ENTR</td>
<td>0.99360 ± 0.292</td>
<td>0.83793 ± 0.490</td>
<td>0.80844 ± 0.216</td>
<td>1.4531 ± 0.501</td>
<td>0.55129 ± 0.251</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>LAM</td>
<td>0.63752 ± 0.122</td>
<td>0.41717 ± 0.222</td>
<td>0.54468 ± 0.104</td>
<td>0.49967 ± 0.247</td>
<td>0.35838 ± 0.177</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>( TT )</td>
<td>3.1526 ± 0.709</td>
<td>2.8470 ± 0.887</td>
<td>2.7240 ± 0.422</td>
<td>4.2849 ± 1.54</td>
<td>2.3466 ± 0.396</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>( V_{\text{max}} )</td>
<td>10.667 ± 8.07</td>
<td>12.167 ± 10.7</td>
<td>6.8750 ± 2.42</td>
<td>29.139 ± 21.3</td>
<td>5.5247 ± 4.67</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>T1</td>
<td>4.3945 ± 2.01</td>
<td>11.604 ± 3.93</td>
<td>7.1902 ± 2.64</td>
<td>5.8548 ± 1.39</td>
<td>11.618 ± 4.98</td>
<td>(&lt; 0.0001)</td>
</tr>
<tr>
<td>T2</td>
<td>7.5532 ± 1.88</td>
<td>16.049 ± 2.93</td>
<td>10.841 ± 2.65</td>
<td>10.231 ± 1.77</td>
<td>14.366 ± 4.82</td>
<td>(&lt; 0.0001)</td>
</tr>
</tbody>
</table>
Figure 5 shows the distribution of the 10 features for the five classes. The result of ANOVA with features obtained from RQA for normal cardiac condition and the various kinds of cardiac diseases is listed in Table 2. These classes of values are clinically significant since the $p$-values are low ($< 0.0001$).

Heart rate will vary continuously between 60 beats per minute and 80 beats per minute for NSR. Since there is higher variation in the heart rate, the features (T1, T2) appear to be high in Table 2. The means values of features (RR, DET, $<L>$, $L_{\text{max}}$, ENTR, LAM, $TT$, $V_{\text{max}}$, T1, and T2) are 0.096, 0.279, 2.240, 13.494, 0.551, 0.358, 2.347, 5.525, 11.618, and 14.366, respectively. Due to a possibility of a relationship between these values and the rate of breathing and its harmonics, the modulating effect on the HRV due to the breathing pattern has to be taken into consideration. In order to meet higher body demands, the heart is required to work more and this will result in a high HRV. Figure 4(e) shows the cross recurrence plot of the NSR. There is no particular pattern in this figure because heart rate is random in nature.

For patients with CHB, HRV will be low since the AV node is unable to send electrical signals rhythmically to the ventricles. Compared to NSR, there is a reduced beat to beat variation for CHB as indicated in Table 2 for the mean values of features (T1, T2). The means values of features (RR, DET, $<L>$, $L_{\text{max}}$, ENTR, LAM, $TT$, $V_{\text{max}}$, T1, and T2) are 0.259, 0.510, 2.62, 95.519, 0.994, 0.638, 3.153, 10.667, 4.395, and 7.553, respectively. Figure 4(b) shows the CRP of the CHB. There is uniform pattern in this figure due to the slow uniform change in the heart rate.

For patients with AF, random activation of different parts of the atria occurs at different times. Compared to NSR, the mean values of features (DET, $<L>$, ENTR, LAM, $TT$, $V_{\text{max}}$, T2) are of higher amplitudes for AF in Table 2. The means values of features (RR, DET, $<L>$, $L_{\text{max}}$, ENTR, LAM, $TT$, $V_{\text{max}}$, T1, and T2) are 0.083, 0.333, 2.555, 13.167, 0.838, 0.417, 2.847, 12.167, 11.604 and 16.049, respectively. Figure 4(a) shows the CRP of the AF. There is a particular pattern in this figure because the heart rate is varying abruptly with an underlying pattern in it.

For patients with ISCH, the heart rate variation will be low like patients with CHB due to the inability of the ventricles to pump out blood to a normal degree. Compared to NSR, the mean values of features (RR, DET, $<L>$, ENTR, LAM, $TT$, $V_{\text{max}}$) are of higher amplitudes for SSS in Table 2. The means values of features (RR, DET, $<L>$, $L_{\text{max}}$, ENTR, LAM, $TT$, $V_{\text{max}}$, T1, and T2) are 0.133, 0.425, 2.4, 8.406, 0.808, 0.545, 2.724, 6.875, 7.190, and 10.841, respectively. Figure 4(c) shows the CRP of the ischemic/dilated cardiomyopathy. There are particular pattern of patches in this figure indicating hidden rhythmicity in the cardiac signal.

For patients with SSS, there will be a continuous variation in heart rate in tachycardia and bradycardia patterns. Compared to NSR, the mean values of features (RR, DET, $<L>$, $L_{\text{max}}$, ENTR, LAM, $TT$, $V_{\text{max}}$) are of higher amplitudes for SSS in Table 2. The means values of features (RR, DET, $<L>$, $L_{\text{max}}$, ENTR, LAM, $TT$, $V_{\text{max}}$, T1, and T2) are 0.168, 0.536, 3.342, 58.972, 1.453, 0.5, 4.285, 29.139, 5.855, and 10.321, respectively. Figure 4(d) shows the cross recurrence plot of the SSS. There are small and long dark patches indicating continuous bradycardia and tachycardia variation in this figure.
Ten-fold stratified cross validation method was used to test all classifiers. The whole dataset was split into 10 equal parts. Two parts of the data (training set) were used for classifier development and the built classifier was evaluated using the remaining one part (testing data) (258 data was used training and 29 data for testing each time). This procedure was repeated 10 times using a different part for testing in each case. Then the average of all the 10 results is evaluated to get the accuracy, sensitivity, specificity, and positive predictive accuracy. This procedure is repeated for all classifiers.

Figure 5 shows the distributions of the RQA features. Table 3 presents the classification accuracy, specificity, sensitivity, and positive predictive value obtained using the fuzzy, GMM, and PNN classifiers, respectively. The results indicate that the proposed method has the ability to allow classification of the unknown cardiac class with an average classification rate, specificity, sensitivity, and positive predictive value.
Fig. 5. (Continued)
of more than 79% as indicated in Table 3. Figure 6 shows the ROC plot of the three classifiers. ROC curve is a plot of sensitivity against (100−specificity). When the disease is present, the probability of a positive test result is represented by sensitivity. Since the area under the ROC curve (AUC) determines the overall classification accuracy for the three classifiers, it is also considered as an important parameter. The AUC of PNN is 0.829, GMM is 0.798, while the AUC of fuzzy is 0.861. Since the AUC for fuzzy is larger than the AUC for GMM and PNN, it shows that fuzzy provides a higher rate of classification than GMM and PNN.

### Table 3. Results of True Negatives (TN), False Positives (FP), True Positives (TP), and False Negatives (FN), classification accuracy, specificity, sensitivity, positive predictive value (PPV), and area under curve (AUC) for fuzzy, GMM, and PNN classifiers.

<table>
<thead>
<tr>
<th>Classifier</th>
<th>TN</th>
<th>FN</th>
<th>TP</th>
<th>FP</th>
<th>Accuracy (%)</th>
<th>PPV (%)</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
<th>AUC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fuzzy</td>
<td>14</td>
<td>2</td>
<td>11</td>
<td>2</td>
<td>83.1</td>
<td>83.1</td>
<td>83</td>
<td>86.4</td>
<td>0.861</td>
</tr>
<tr>
<td>GMM</td>
<td>12</td>
<td>4</td>
<td>12</td>
<td>1</td>
<td>81.4</td>
<td>88.5</td>
<td>75.4</td>
<td>89.2</td>
<td>0.837</td>
</tr>
<tr>
<td>PNN</td>
<td>13</td>
<td>3</td>
<td>11</td>
<td>2</td>
<td>80</td>
<td>82.3</td>
<td>79.3</td>
<td>85.3</td>
<td>0.829</td>
</tr>
</tbody>
</table>

### Fig. 6. ROC plots of fuzzy, GMM, and PNN.

5. Discussion

Over the years, many different non-linear methods have been applied to try to classify the cardiac classes through the use of heart rate signals. Fractal dimension (FD), detrended fluctuation analysis, Lyapunov exponent, approximate entropy, Hurst exponent, and correlation dimension are different non-linear parameters used in these studies to identify an unknown cardiac class using the heart rate signal.
Acharya et al.\textsuperscript{43} used FD and wavelet transformation methods for analyzing cardiac health. It was observed that FD showed a better performance and provided more than 90% confidence interval in classifying cardiac data. Acharya et al.\textsuperscript{1} presented the calculated ranges of linear and non-linear parameters with a confidence level of more than 90% for classifying cardiac abnormalities to eight categories. Acharya et al.\textsuperscript{44} found that the ranges of the correlation dimension (CD) and DFA parameters fall in distinct ranges for the different states or diseases of the heart such as NSR, SSS, and CHB.

Poincare plot geometry, largest Lyapunov exponent, and spectral entropy are the non-linear parameters that were fed to an artificial neural network (ANN) and fuzzy classifiers for automatic classification.\textsuperscript{20} An average classification accuracy of 95% was achieved for four classes, and 85.36% accuracy for eight classes.\textsuperscript{9} A classification accuracy of 94% was achieved for 10 cardiac classes by using the same non-linear features and adaptive neuro-fuzzy inference system (ANFIS) classifier.\textsuperscript{40} Acharya et al.\textsuperscript{3} used features obtained from fast fourier transform (FFT), and auto-regressive (AR), auto-regressive moving average (ARMA), and moving average (MA) modeling techniques to classify nine classes. The input to the neural network classifier consisted of the first three peak amplitudes and corresponding frequencies. Compared to the other modeling methods, the ARMA modeling technique performed better with a classification accuracy of 83.83%.

Using AR modeling coefficients and the GLM classification algorithm, six different cardiac classes were classified correctly with accuracy between 93.2% and 100%.\textsuperscript{5} In a recent study by Chua et al.,\textsuperscript{16} the classification of five classes of heart rate signals was carried out using HOS features and support vector machine (SVM) classifier. An accuracy of 85% was reported. A comparison of the results of the various arrhythmia classification studies is presented in Table 4.

These heart rate signals and patient information can be interleaved within the images with the different error correcting codes in a noisy environment without affecting the hidden information.\textsuperscript{45,46}

In our present work, we obtained features of HRV using RQA. Next, we used fuzzy, GMM, and PNN classifiers to classify the features into five classes of HRV signals and obtained an accuracy of approximately 80%. This classification accuracy may be further increased by obtaining better features of HRV and more robust training of the classifiers and diverse data. The novelty of this work is RQA parameters can be easily extracted from the heart rate signals and hence, the

<table>
<thead>
<tr>
<th>Authors</th>
<th>Method</th>
<th>No. of class</th>
<th>accuracy (%)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acharya et al.\textsuperscript{22}</td>
<td>Non-linear features — ANN-fuzzy</td>
<td>4</td>
<td>95</td>
<td>22</td>
</tr>
<tr>
<td>Acharya et al.\textsuperscript{9}</td>
<td>Non-linear — ANN-fuzzy</td>
<td>8</td>
<td>85.36</td>
<td>9</td>
</tr>
<tr>
<td>Kannathal et al.\textsuperscript{40}</td>
<td>Non-linear — ANFIS</td>
<td>10</td>
<td>94.09</td>
<td>40</td>
</tr>
<tr>
<td>Acharya et al.\textsuperscript{3}</td>
<td>Modeling — ANN</td>
<td>9</td>
<td>83.38</td>
<td>3</td>
</tr>
<tr>
<td>Chua et al.\textsuperscript{17}</td>
<td>HOS — SVM</td>
<td>5</td>
<td>85.7</td>
<td>17</td>
</tr>
<tr>
<td>Ge et al.\textsuperscript{5}</td>
<td>HOS — SVM</td>
<td>6</td>
<td>93.2–100</td>
<td>5</td>
</tr>
</tbody>
</table>
computation time can be done in a very short time. The proposed recurrence plots for various classes are unique.

6. Conclusion

One of the reliable indicators of the cardiac diseases is heart rate. The novelty of this work is the application of RQA parameters for the detection of cardiac diseases. Also, we have proposed unique recurrence plots for five cardiac classes. RQA features are extracted and fed to the fuzzy, GMM, and PNN classifiers to automatically identify five cardiac classes. Our proposed system is able to identify the unknown cardiac class with average classification accuracy, sensitivity, specificity, and positive predictive value of approximately 83%, respectively, using the fuzzy classifier. The accuracy of this classification can be improved further by using more diverse heart rate signals and better classifiers. Different kinds of cardiac diseases can be identified simply by inspecting the recurrence plots and they can be used to check the efficacy of the drug.

Appendix

Figure A.1 shows the snap shot of the graphical user interface of our proposed automated cardiac class detection. There is a push button called “Browse” is
provided to upload the heart rate file to be analyzed. The cardiac signal to be analyzed is displayed at the “Original signal” window. Then we can select the length of the data to be analyzed by entering the initial and final length. In our present example it is 1 to 500. Then we need to click on the push button Obtain “RP plot for area of interest”. Then the heart rate signal and the corresponding RP will be displayed in the “Recurrence plot” section of the display. Click on the push button “Obtain the Features” in the region “Recurrence Quantification Analysis” will display various values of the features. Click on the “Diagnosis” push button will display the outcome of the analysis. And it is Atrial Fibrillation in this example. “Clear All” push button is provided to clear the present textboxes.

References


