Understanding the Dynamics of Heart Rate Variability in Cardiovascular Disorders using Recurrence Quantification Analysis and Radial Basis Function Neural Network

Kalpavalli Tallapragada, Sravani Singavarapu, N. Pradhan

ABSTRACT:

Heart diseases are a major health concern throughout the world. While ECG signal is of importance in diagnosis of the cardiac ailment, Heart rate variability (HRV) has been found to be of prognostic and diagnostic significance in a variety of heart conditions. HRV is derived from a large time series of ECG denoting peak to peak RR intervals. The seemingly noisy looking HRV signal is characteristically nonlinear and chaotic, therefore, a non-linear analysis method like Recurrence Plot (RP) is considered appropriate to its analysis. In this paper, we have used Recurrence Quantification Analysis (RQA) and have extracted 13 parameters i.e., recurrence rate (RR), determinism(DET), mean diagonal line length (L), maximum diagonal line length (Lmax), entropy (ENTR), Laminarity (LAM), trapping time (TT), maximum verticalline length (Vmax), recurrence time of 1st type (T1), recurrence time of 2nd type (T2), recurrence time entropy (RTE), clustering Co-efficient (Clust), transitivity (Trans) of the HRV data.

The above parameters have been subjected to a Radial Basis Probabilistic Neural Network (RBPNN) for classification and clustering of different heart disorders. The method was successful in identifying the various class of disorders with 94.2% of accuracy. This result is of importance for the development of automated diagnosis, monitoring, prognostic and predictive devices for myocardial dysfunctions. It may have utility as a warning system in critical care units.

KEY WORDS: ECG, Heart Rate Variability (HRV), Recurrence Quantification Analysis (RQA), Artificial Neural Network (ANN), Radial Basis Function Neural Network (RBFNN), Probabilistic Neural Network (PNN).

1. INTRODUCTION

HRV is significant in quantifying the health of the heart. HRV has a greater variability in a new born and becomes less variable with aging. It is of predictive value during evolution of myocardial infarction and during recovery. HRV is a noisy signal and has a 1/f like power spectrum. Therefore, it may possibly reflect a scaling behavior and chaotic property of the heart's electrical activity. A non-linear analysis such as recurrence plot may be of utility in providing hidden informations about cardiac conditions.

1.1 Recurrence Plot:

Recurrence plot (RP) measures the recurrences in the phase space of a dynamical system. It may be formally defined by a matrix called Recurrence plot, which is the basic instrument of recurrence analysis. RP allows visualization of phase space trajectories using a two-dimensional graph. The phase space matrix is constructed by time delay embedding of the HRV data and reconstructed phase space maintains the topological properties of the original system. RP is the visualization of a square matrix, in which the matrix of elements corresponds to those times at which a state of a dynamical system recurs (columns and rows corresponds then to a certain pair of times). Technically, the RP reveals all the times when the phase space trajectory of the dynamical system visits roughly the same area in phase space. [1] RP can be mathematically expressed as

$$R_{i,j} = \Theta\left(\epsilon_i - \left\| x_i - x_j \right\|\right), x_i \in R^m, i, j = 1....N,$$

Where, 'N' Number of considered states, εí a threshold distance, || · || a norm, Θ(·) the Heaviside function. The

Kalpavalli Tallapragada and Sravani Singavarapu are project interns at the National Institute of Mental Health and Neuro Sciences, Bangalore, Karnataka, India. E-mail ID: kalpavalli.tss@gmail.com, sravani_s_s@yahoo.com

structures created in RP represent the basis for recurrence quantification analysis (RQA). It is a set of parameters introduced by Zbilut and Webber (2000) [2] for the possibility of quantitative evaluations of RP. The parameters are based on diagonal lines of the structures of RP.

1.2 Recurrence Quantification Analysis (RQA):

In order to go beyond the visual impression of RPs, several measures of complexities which quantify the small scale structure in RPs have been proposed and are known as Recurrence Quantification Analysis (RQA). [2] It quantifies the number and duration of recurrences of a dynamical system presented by its phase space trajectory. RQA measures are based on the recurrence point density and the diagonal and vertical line structure of the RP. Computation of these measures in small windows (sub-matrices) of the RP moving along the line of identity (LOI) yields the time dependent behavior of these variables. Compared to other traditional methods of nonlinear analysis, RQA has the ability to capture the chaotic properties without a need of a long data series and the fact that it is relatively immune to noise and non-stationarity. One of the critical parameters of RQA is the threshold distance (εi). We focus on the application of the RQA to RPs and measure the recurrence rate (RR) or per cent recurrences from the RQA.

The simplest measure of the RQA is the RR or percent recurrences, which is a measure of the density of recurrence points in the RP. The recurrence rate corresponds with the probability that a specific state will recur. It is almost equal with the definition of the correlation sum, where the LOI is excluded from the computation. It is a count of the black dot in the RP and measure the density of recurrence points and corresponds to the definition of correlation sum. Parameters of RR are time delay, embedding dimension, threshold, and window size. The analysis yields 13 different RQA parameters which are described under Materials and Methods. [2]In this paper, the RQA parameters are used as the defining features of myocardial dysfunctions.

1.3 Artificial Neural Networks:

Artificial Neural Networks (ANNs) are 'trained' to produce

desired input output relationship. During the training (learning) phase, examples of data are presented to the network and using a learning algorithm, the parameters are tuned to adjust network behavior. The learning procedure employed can be either 'supervised', 'unsupervised', or both (Fig 1). The supervised learning procedure is performed with pairs of known input-output patterns while unsupervised learning consists of presenting training examples to the network input and the network organizes itself progressively to reach maximal separation between the naturally occurring classes of examples. The principal applications of ANNs have been in the area of pattern recognition.

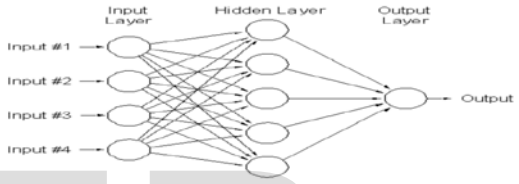

Fig 1: Diagram of Multilayer Feed-forward Network

1.4 Radial Basis Function Neural Network (RBFNN)

There are many types of networks, among which one is Radial Basis Function Neural Network (RBFNN). Its learning capacity is fast compared to other multilayer feed forward neural network. RBFN network is a particular class of multilayer networks (Poggio and Girosi, 1989) [3] in which learning occurs usually in two stages, learning in the hidden layer (usually by an unsupervised bottom-up self-organizing method such as k- means clustering), the hidden-layer of RBF unit employs a Gaussian activation function, using known centers as Gaussian function's mean, while the output units are simple linear units, followed by the output layer (a top-down supervised method such as least squares estimation). RBFN networks present two important advantages: finding the input to output map using local approximators and rapid learning which requires few examples. Another popular class of networks is the self-organizing map, or Kohonen-network (Kohonen, 1997). [4] A Kohonen network consists of two fully connected-unit layers. The output layer is generally ordered in a low-dimensional framework of units.

Radial basis networks consist of two layers: a hidden radial basis layer of *S*1 neurons and an output linear layer of *S*2

neurons (Fig 2). The || dist || box in this Fig 2 accepts the input vector **p,** the input weight matrix **IW** and produces a vector having *S*1 elements. The elements are the distances between the input vector and vectors i**IW** formed from the rows of the input weight matrix. The bias vector **b**1 and the output of || dist || are combined with the MATLAB operation, (Mathworks.inc Version 7.0, 2005), which does element-by-element multiplication.

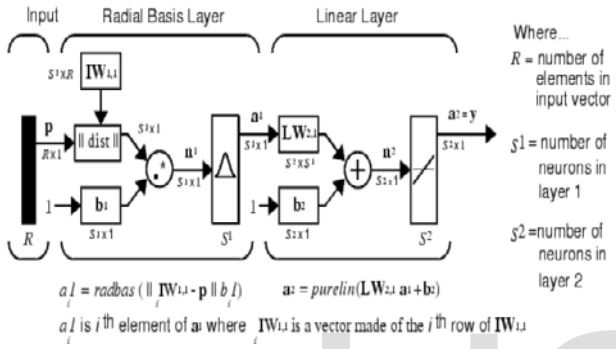

Fig 2: Architecture of Radial Basis Function Neural Network

Radial basis neurons with weight vectors quite different from the input vector **p** have outputs near zero. These small outputs have only a negligible effect on the linear output neurons. In contrast, a radial basis neuron with a weight vector close to the input vector **p** produces a value near 1. If a neuron has an output of 1, its output weights in the second layer pass their values to the linear neurons in the second layer.

In fact, if only one radial basis neuron had an output of 1 and all others had outputs of 0's (or very close to 0), the output of the linear layer would be the active neuron's output weights. This would, however, be an extreme case. Typically several neurons are always firing to varying degrees.

We may now examine the operational details of the first layer neurons. Each neuron's weighted input is the distance between the input vector and its weight vector, calculated with dist. Each neuron's net input is the element-by-element product of its weighted input with its bias, calculated with netprod. Each neuron's output is its net input passed through radbas. If a neuron's weight vector is equal to the input vector (transposed), its weighted input is 0, its net input is 0 and its output is 1. If a neuron's weight vector is a distance of spread from the input vector, its weighted input is spread, its net input is sqrt (-log (.5)) (or 0.8326), therefore its output is 0.5. In this paper, we have used RBFNN for classification and clustering of RQA parameters.

2. MATERIALS AND METHODS

A block diagram of the key stages of this work is shown in Fig 3. The methodology followed a traditional machine learning approach: (1) publicly available data were used; (2) the data were appropriately preprocessed; (3) features were selected and extracted; (4) a classifier was trained and (5) the performance of the system is evaluated. The entire process was iterated until acceptable performance results were achieved.

Fig 3: Block diagram of the Methodology

2.1 Data selection and recording:

We have downloaded the ECG signals of various heart diseases from the Physionet Atm Database. We have noted the annotations of all the signals. Basically, we focused on the cardiac arrhythmia, which may result out of Ischemic heart diseases. The sets were selected from ECG records after purifying artifacts. 40 recordings available in from the PhysioNet Challenge were analyzed in this investigation.

The ECG recordings were typically of ~2 min duration and all the signals were recorded for at least 30 s. The present investigation first normalized the ECG signals into the unit range and collected a segment of 4000 data points starting from the first *R*-peak. Then the data are further resample to 2000 data points to reduce the RQA computational efforts. These two preprocessing steps can also ensure that the resulted recurrence plots are aligned uniformly from the *R*-peak and reduce the biases from misalignments.

2.2 Recurrence Quantification Analysis:

It is a method of non linear data analysis to determine the recurrence rate of HRV data. In this study, the embedding dimension (m), time delay (Ƭ), threshold (εί), window size and window shift values are obtained to find recurrence

rate. The 'm' and 'τ' are found based on standard method like false nearest neighbor (for m) and average mutual information (for τ) which avoid autocorrelation effects. Threshold value (εί) is one of the most critical parameter. Even a small change can dramatically affect the result of RQA. Threshold value (εί) is obtained with the help of Dr.Marwan (2003) [5] recommended principle that is normalize the data and then use a fraction of the standard deviation as the value of threshold parameter. The window size (W) short windows focus on small-scale recurrences, whereas long windows focus on large-scale recurrences. The window shift value (WS) is the first five numbers after the data series. Time delay or log (τ) is determined from the average mutual information (AMI) criteria.

$$AMI(\tau) = \sum_{s(n),s(n+1)} P[s(n), s(n+1)] \log_2 \left\{ \frac{p[s(n), s(n+\tau)]}{p[s(n)]p[s(n+\tau)]} \right\}$$

The HRV time series of each window is delayed in step and the average mutual information is calculated at each delay. The delay at which the mutual information reaches its first minimum is chosen as the optimum delay 'τ' for embedding. The maximum embedding dimension'd' is determined using false nearest neighbor approach.

$$R_d(n)^2 = \sum_{m=1}^{d} [s(n+\tau(m-1)) - s^{NN}(n+\tau(m-1))]^2$$

Where n is the current index of the discrete signal (in this case (n)) and FNN is the nearest neighbor (NN) of s(n). The square of the Euclidian distance in dimension d+1 becomes:

$$R_{d+1}(n)^2 = \sum_{m=1}^{d+1} \left[s(n+\tau(m-1)) - s^{NN}(n+\tau(m-1)) \right]^2$$
$$= R_d(n)^2 + (s(n+\tau d)) - s^{NN}(n+\tau D)^2$$

The dimension'd' is increased in step until the amount of false nearest neighbor approach is zero. For some natural process the amount of false neighbor may not be zero. In that case the value of d at which the amount of false neighbor remains constant even if the dimension is increased is chosen as the maximum embedding dimension. [6]

From the reconstructed phase space matrix a symmetric matrix of distance (e.g., Euclidean distances) is constructed by computing distance between all pairs of embedded vectors. The corresponding recurrence matrix is obtained using an appropriate threshold (radius) in terms of 1's and 0's. The recurrence plot is obtained from the recurrence matrix where a black dot corresponds to a 1 and white dot corresponds to a 0. The recurrence rate is obtained which gives an idea of how many times the state of system re-occurs.

$$RR = \frac{1}{N^2} \sum_{i,j=1}^{N} R(i, j)$$

RR which is a measure of the density of recurrence points in the RP. Furthermore, in the limit $N \to \infty$, RR is the probability that a state recurs to its ε-neighborhood in phase space.

The 13 RQA parameters are computed (extracted) from each RP by implementing a sliding window design, each of those parameters is computed multiple times creating 13 new derivative dynamical systems expressed in terms of recurrence rate (RR), determinism(DET), mean diagonal line length (L), maximum diagonal line length (Lmax), entropy (ENTR), Laminarity (LAM), trapping time (TT), maximum verticalline length (Vmax), recurrence time of 1st type (T1), recurrence time of 2nd type (T2), recurrence time entropy (RTE), clustering Co-efficient (Clust), transitivity (Trans) of the HRV data. Alignment of those variables (outputs) with the original time series (input) (adjusting for the embedding dimension 'm' might reveal details not obvious in the 1- dimensional input data. These 13 RQA parameters are subjected to RBFNN in clustering and classification.

2.2.1 RQA PARAMETERS:

The first recurrence parameter is recurrence (REC). It quantifies the percentage of recurrence points falling within the specified radius and this variable can range from 0% (no recurrence points) to 100% (all points recurrence). The recurrence rate corresponds with the probability that a specific state will recur. It is almost equal with the definition of the correlation sum, where the LOI is excluded from the computation.

$$\mathrm{RR} = \frac{1}{N^2} \sum_{i,j=1}^{N} \mathbf{R}(i,j).$$

The second and third recurrence parameter are determinism (DET) and length (ℓ), which measures the proportion of recurrence points forming diagonal line structures. The name determinism came from repeating or deterministic patterns in the dynamics. Periodic signals (e.g. sine waves) will give very long diagonal lines, chaotic signals will give very short diagonal lines and stochastic signals will give no diagonal lines at all.

$$\mathrm{DET} = \frac{\sum_{\ell=\ell_{\min}}^{N} \ell\, P(\ell)}{\sum_{i,j=1}^{N} R(i,j)},$$

Where $P(\ell)$ is the frequency distribution of the lengths ℓ of the diagonal lines. This measure is called determinism and is related with the predictability of the dynamical system, because white noise has a recurrence plot with almost only single dots and very few diagonal lines, whereas a deterministic process has a recurrence plot with very few single dots but many long diagonal lines.

The fourth recurrence parameter is linemax (LMAX), which is simply the length of the longest diagonal line segment in the plot, excluding the main diagonal line of identity .The amount of recurrence points which form vertical lines can be quantified in the same way:

$$\mathrm{LAM} = \frac{\sum_{v=v_{\min}}^{N} vP(v)}{\sum_{v=1}^{N} vP(v)},$$

Where $P(v)$ is the frequency distribution of the lengths v of the vertical lines, which have at least a length of $v_{\min}$. This measure is called laminarity and is related with the amount of laminar phases in the system.

The lengths of the diagonal and vertical lines can be measured as well. The averaged diagonal line length is related with the predictability time of the dynamical system and the trapping time, measuring the average length of the vertical lines.

$$\mathrm{L} = \frac{\sum_{\ell=\ell_{\min}}^{N} \ell\, P(\ell)}{\sum_{\ell=\ell_{\min}}^{N} P(\ell)}$$

And the trapping time, measuring the average length of the vertical lines is related with the laminarity time of the dynamical system, i.e. how long the system remains in a specific state.

$$TT = \frac{\sum_{v=v_{\min}}^{N} vP(v)}{\sum_{v=v_{\min}}^{N} P(v)}$$

The fifth and sixth recurrence parameters are entropy (ENT) and Recurrence Time Entropy (RTE), which is the Shannon information entropy of all diagonal line lengths distributed over integer bins in a histogram. ENT is a measure of signal complexity and is calibrated in units of bits/bin. Individual histogram bin probabilities (Pbin) are computed for each non-zero bin and reflect the complexity of the deterministic structure in the system. However, this entropy depends sensitively on the bin number and thus, may differ for different realizations of the same process, as well as for different data preparations.

$$\mathrm{ENTR} = -\sum_{\ell=\ell_{\min}}^{N} p(\ell) \ln p(\ell),$$

The seventh and eighth recurrence parameters, laminarity (LAM) and trapping time (TT), were introduced by Marwan, Wessel. [7] LAM is analogous to DET except that it measures the percentage of recurrent point comprising of vertical line structures rather than diagonal line structures. The line parameter still governs the minimum length of vertical lines for the Recurrence quantification. It is strongly dependent on the sequential organization of the time series or data string. By contrast, the standard statistical measures such as mean and standard deviation are sequence independent.

The ninth recurrence parameter is Maximum verticalline length (Vmax). It is important when extracting quantitative features from recurrence plots, but exerts no effect on the recurrence matrix itself. If the length of a recurrence feature is shorter than the Vmax parameter, that feature is rejected during the quantitative analysis.

The tenth recurrence parameter, clustering coefficient of a graph is the average clustering coefficient of all nodes in the graph. Slightly different definitions of clustering exist in the literature but irrespective of the precise nature of these definitions, their values are always higher for real networks in comparison to random graphs with a similar number of vertices and edges.

$$c = \sum_{i-1}^{N} \frac{\sum_{j}^{N}, k = 1 R_{i,j}^{m,e} R_{j,k}^{m,e} R_{k,i}^{m,e}}{RR_i}$$

With $RR_i = \sum_{j=1}^{N} R_{i,j}^{m,e}$ the local recurrence rate

The eleventh recurrence parameter is Transitivity (Trans):

$$c = \frac{\sum_{i,j,k=1}^{N} R_{i,j}^{m,e} R_{j,k}^{m,e} R_{k,i}^{m,e}}{\sum_{i,j,k=1}^{N} R_{i,j}^{m,e} R_{k,i}^{m,e}}$$

The twelfth recurrence parameter is Recurrence time of 1st type (T_1):

$$T_j^1 = \left| \left\{ i, j : \vec{x}_{\bar{1}}, \vec{x}_j \in R_i \right\} \right|$$

The thirteenth recurrence parameter is Recurrence time of 2nd^t type (T_2):

$$T_j^2 = \left| \left\{ i, j : \vec{x}_{\bar{1}}, \vec{x}_j \in R_i ; \vec{x}_{j-1} \notin R_i \right\} \right|$$

where R_i are the recurrence points which belong to the state $\vec{x}_i$.

2.3 Radial Basis Function Neural Network:

Probabilistic neural networks (PNN) are to be known to converse faster than the back propagation network. Radial basis function (RBF) networks typically have three layers: an input layer, a hidden layer with a non-linear RBF activation function and a linear output layer. The input can be modeled as a vector of real numbers $x \in R^n$. The output of the network is then a scalar function of the input vector, $\varphi : R^n \to R$, and is given by

$$\varphi(x) = \sum_{i=1}^{N} a_i \, p(\|x - c_i\|)$$

Where N is the number of neurons in the hidden layer, $\mathbf{c}_i$ is the center vector for neuron i, and a_i is the weight of neuron 'i' in the linear output neuron. Functions that depend only on the distance from a center vector are radially symmetric about that vector hence it is named as radial basis function. In the basic form all inputs are connected to each hidden neuron. The norm is typically taken to be the Euclidean distance (although the Mahalanobis distance appears to perform better in general) and the radial basis function is commonly taken to be Gaussian.

$$p(\|x - c_i\|) = \exp\left[-\beta \|x - c_i\|^2 \right]$$

The Gaussian basis functions are local to the center vector in the sense

$$\lim_{\|x\| \to \infty} p(\|x - c_i\|) = 0$$

i.e. changing parameters of one neuron has only a small effect for input values that are far away from the center of that neuron. Given certain mild conditions on the shape of the activation function, RBF networks are universal approximators on a compact subset of R^n. This means that an RBF network with enough hidden neurons can approximate any continuous function with arbitrary precision.

RBF networks are typically trained by a two-step algorithm. In the first step, the center vectors c_i of the RBF functions in the hidden layer are chosen. This step can be performed in several ways; centers can be randomly sampled from some set of examples, or they can be determined using k-means clustering. The second step simply fits a linear model with coefficients w_i to the hidden layer's outputs with respect to some objective function. A common objective function, at least for regression/function estimation, is the least squares function.

$$K(w) \overset{def}{=} \sum_{t=1}^{\infty} K_t(w)$$

Where,

$$K_t(w) \stackrel{def}{=} [y(t) - \varphi(x(t), w)]^2$$

To reduce the bias and over fitting of classification performance evaluation, both *K*-fold cross-validation and random sub sampling methods were employed in this investigation. *K*-fold cross-validation totally conducts *K* experiments, in each of which*K*−1 folds are used for the training purpose and the rest one fold for testing. The true performance estimate is obtained as the average of those randomly separate error rates on testing samples repeated from twofold to tenfold for the identification of MI subjects in the database. The classification results are evaluated based on two performance statistics, namely, sensitivity and specificity from the testing dataset. Sensitivity measures the proportion of actual positives, which are correctly identified as such, and the specificity measures the proportion of negatives, which are correctly identified. In other words, sensitivity is the indictor, which gives the percentage of MI subjects that are identified as having the condition and specificity is the percentage of healthy control cases that are identified as not having the condition.

The PNN scheme consists 4 layers; input layer, pattern layer, summation layer, output layer. The architecture of PNN is based on straightforward approach with 23 inputs belonging to 9 different classes. Then the validation is performed. The training and the testing of all the 23 vectors are done and based on this the percentage of accuracy, sensitivity and specificity were found. The results using PNN were encouraging. The program was run several times with different spread values and the matching and mismatching between the training and the testing results were found.

The recurrence analysis of signals effectively captures the system transient, intermittent, and steady behaviors. Recurrence method yields a better overall accurate classification rate (>5.5%) compared to human expertise or other standard methods.

3 RESULTS and DISCUSSIONS

It is challenging to characterize and identify the ECG signals in pathological conditions like MI using automated computer methods or human expertise. The complexities arise due to the various nidus locations and different degrees of myocardium damages.

Additionally, various noise levels contaminate the signals at the recording stage. It is known that a complex biological system like heart is highly nonlinear and non-stationary in nature. Not only the different MI conditions but also the inherent complexities from the living organisms pose remarkable difficulties for the MI identification, which also defy the conventional time-domain analysis and other statistical methods including spectral measures. In this study, we have used RQA analysis in conjunction with RBFN network in understanding different types of myocardial dysfunctions.

We have represented a sample signals in Fig 4.A, B, C, D. The original ECG signals are given in 4.A and 4.B. The filtered signals for 1000 samples of 4.A and 4.B are given in 4.C and 4.D. A special algorithm has been devised to detect the RR intervals (HRV signals). The HRV signals are primarily used for RQA analysis. The significance of RQA analysis in characterizing non linear chaotic processes is known in literature. In recent days RQA analysis has found extensive applications in bio-medical signal processing. The RQA analysis begins with the recurrence plot which is based on the principle of Phase space reconstruction of a dynamical system. We have shown the short length HRV signal in Fig 4.E which is used as a window in RQA analysis. We also have displayed the total length of the HRV signal of one subject AHADB in Fig 4.F which is included in the Table 1. An example of the mutual information with lags is given in Fig 5.A, B, C, D. The lowest of the mutual information is determined as 101 to 119 in 2 different examples shown in this figures.

The table represents two channels of data for different RQA parameters and the classification category belongs to class 3 which is AHADB. American Heart Association Data Base (AHADB) is used for evaluation of ventricular arrhythmia (arising out of cardiac ischemia). However, the analysis has been conducted for 9 different classes of myocardial dysfunctions. We have only represented one table in this paper.

The results are highly promising that the RBFNN using RQA parameters is able to detect the various cardiac anomalies with 94.2% accuracy. The testing was performed

10 times with different spread values and then the matching and mismatching is done, on the basis of results.

Total Test Sets=14*10=140, Total Match=132, Total Mismatching=8

4. CONCLUSION

It is now established that all biological systems have nonlinear properties. Hence, nonlinear dynamics is an emerging new approach to biological systems and in the ECG signals. The nonlinear dynamic analysis is superior to the traditional method of time-domain or spectral methods in revealing hidden structures in time series. It has given rise to a fundamentally different approach to ECG analysis. The present study has clinical implication for visual and quantitative ECG interpretation in normal and pathological state. The technique employed in this project gives an indication about the dynamics of the system (heart) during any threat in the form of distribution of RR across the heart and the early diagnosis and prognosis of any disease with the help of probabilistic neural network with 94.2% accuracy. However, limited by the overall classification rate in a particular approach, researchers can either improve the sensitivity at the expense of specificity or sacrifice the sensitivity to improve the specificity. This investigation shows that the ECG features extracted using RQA analysis is useful indicators of the cardiovascular conditions. This research has great potential for the development of automated MI and Ischemic Heart Disease classification and warning system, which can dramatically reduce the healthcare cost and promote the preventive medicine.

In addition, the results from this study can also be applied in the understanding of the recurrence dynamics and non-stationary patterns of other physiological and engineering systems.

5. REFERENCES

[1] J.P.Eckmann, S.O. Kamphorst, and D.Ruelle, Recurrence Plots of Dynamical Systems, Europhysics Letters, 5 (1987) 973–977.

[2] J.P.Zbilut, A.Giuliani,C.L.Webber Jr , Recurrence quantification analysis as an empirical test to distinguish deterministic versus random number series, Phys Lett A, 267 (2000) 174-178.

[3] Poggio.T, Girosi.F, A theory of networks for approximation and learning. AI Memo No. 1140, MIT, Artificial Intelligence Laboratory, 1989

[4] Kohenen.T, Self organizing maps, Second edition, Berlin, Springer-Verlag, 1997

[5] N.Marwan., Encounters With Neighbours - Current Developments Of Concepts Based On Recurrence Plots And Their Applications, Ph.D. Thesis, University of Potsdam, http://www.recurrence-plot.tk, ISBN 3-00-012347-4(2003).

[6] Ashish Kaul Sahib, N.Pradhan, Understanding Coupling and Synchronization in EEG Of Epileptic Discharge Using Recurrence Plots with Varying Threshold

[7] N. Marwan, N. Wessel, U. Meyerfeldt, A. Schirdewan, and J. Kurths, "Recurrence plot based measures of complexity and their application to heart-rate-variability data," Phys. Rev. E, vol. 66, p. 026702, Aug. 2002

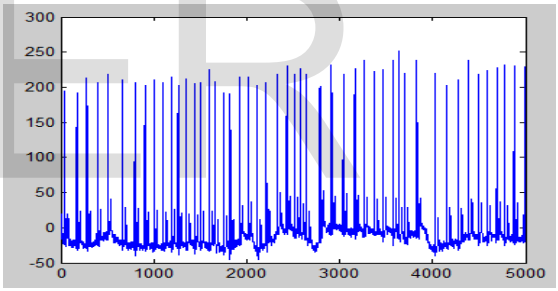

Fig 4. A. Original Signal (channel2)

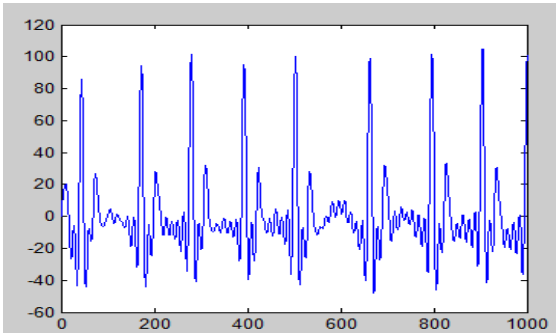

Fig 4. B. Filtered Signal (channel1)

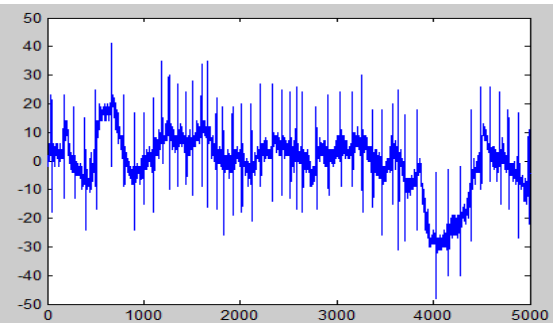

Fig 4. C Original Signal (channel2)

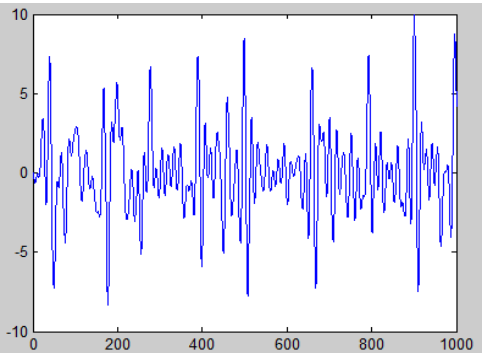

Fig 4. D Filtered Signal (channel2)

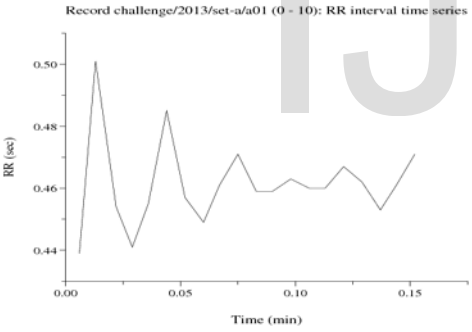

Fig 4 .E HRV signal

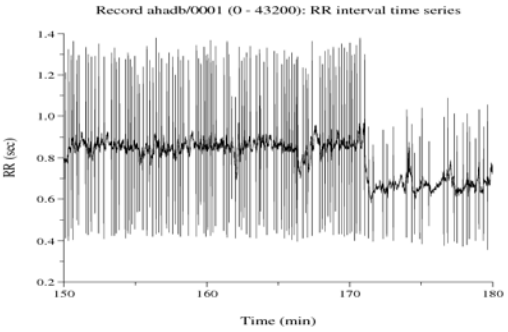

Fig 4. F HRV signal – AHADB

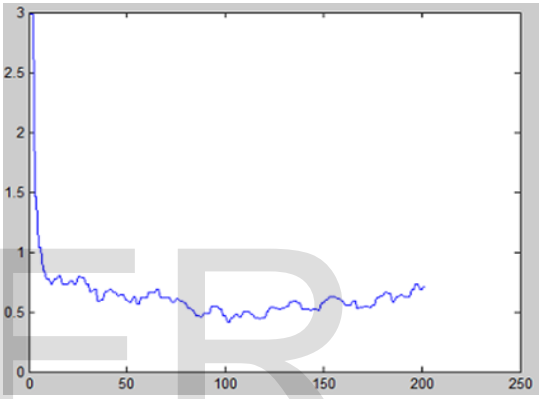

Fig 5. A Mutual Information (channel1, lag 101)

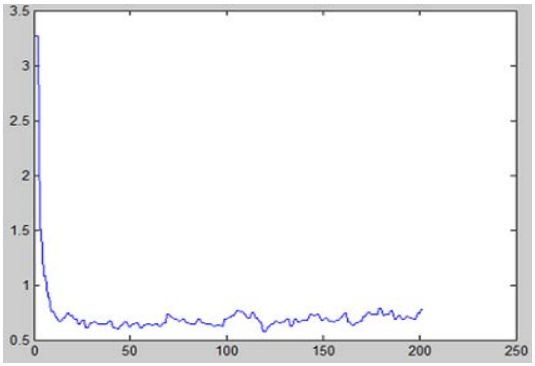

Fig 5. B Mutual Information (channel2, lag 119)

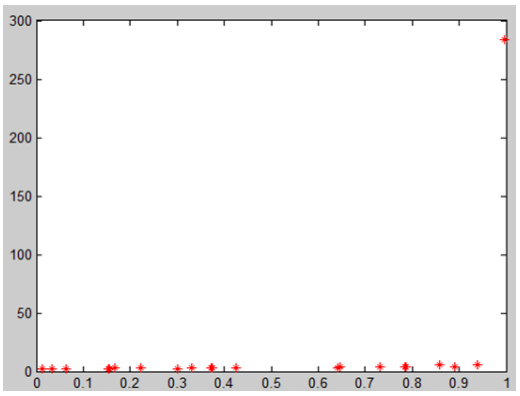

Fig 5. C Training Result of PNN with 23 Inputs

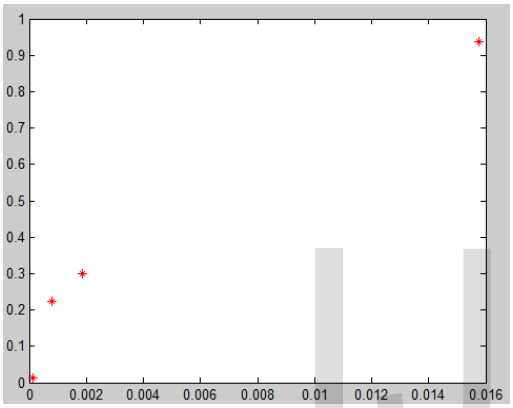

Fig 5. D Testing Result of PNN with 4 inputs

Table 1: AHADB

Class - 3

AHADB														
Channles	**RR**	**DET**	**<L>**	**Lmax**	**ENTR**	**LAM**	**TT**	**Vmax**	**T1**	**T2**	**RTE**	**Clust**	**Trans**	**class**
ch1	0.00186	0.300902	2.617172	25	0.018285	0.3611484	2.296905	7	537.602	675.3085	0.098385	NaN	0.500705	3
ch2	0.00186	0.300902	2.617172	25	0.018285	0.3611484	2.296905	7	537.602	675.3085	0.098385	NaN	0.500705	3