Classification of cardiac abnormalities using heart rate signals

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Abstract—*The heart rate is a non-stationary signal, and its variation can contain indicators of current disease or warnings about impending cardiac diseases. The indicators can be present at all times or can occur at random, during certain intervals of the day. However, to study and pinpoint abnormalities in large quantities of data collected over several hours is strenuous and time consuming. Hence, heart rate variation measurement (instantaneous heart rate against time) has become a popular, non-invasive tool for assessing the autonomic nervous system. Computer-based analytical tools for the in-depth study and classification of data over day-long intervals can be very useful in diagnostics. The paper deals with the classification of cardiac rhythms using an artificial neural network and fuzzy relationships. The results indicate a high level of efficacy of the tools used, with an accuracy level of 80–85%*

Keywords—*Neural networks, Heart rate variability, Lyapunov exponent, Correlation function, Fuzzy equivalence relationship*

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1 Introduction

COMPUTER TECHNOLOGY has an important role in structuring biological systems. The explosive growth of high-performance computing techniques in recent years with regard to the development of good and accurate models of biological systems has contributed significantly to new approaches to fundamental problems of modelling transient behaviour of biological systems.

Electrocardiography deals with the electrical activity of the heart. The state of cardiac health is generally reflected in the shape of the ECG waveform and heart rate (SOKOLOW *et al.*, 1990). An electrocardiogram can contain important pointers to the nature of diseases afflicting the heart. However, biosignals being non-stationary, such pointers can occur at random on the time scale. Therefore, for effective diagnostics, the study of ECG patterns and heart rate variability (HRV) signals may have to be carried out over several hours.

HRV is a non-invasive measurement of cardiovascular autonomic regulation. Specifically, it is a measurement of the interaction between sympathetic and parasympathetic activity in autonomic functioning. Spectral analysis is the most popular linear technique used in the analysis of HRV signals (WEISSMAN *et al.*, 1990; AKSELROD *et al.*, 1981; POMERANZ *et al.*, 1985). Frequency-domain analysis provides for the separation of parasympathetic (high-frequency range) and sympathetic activity (low-frequency range) signals. Spectral analysis is the most popular linear technique used in the analysis of HRV signals. Spectral power in the high-frequency (HF) (0.15–0.5 Hz) band reflects respiratory sinus arrhythmia (RSA) and thus cardiac vagal activity. Low-frequency (LF) (0.04–0.15 Hz) power is related to baroreceptor control and is mediated by both vagal and sympathetic systems. Very low-frequency (VLF) (0.0033–0.04 Hz) power appears to be related to thermoregulatory and vascular mechanisms and renin-angio tensin systems (TASK FORCE, 1996).

The cardiovascular system is too complex to be linear, and treating it as a non-linear system can lead to better understanding of the system dynamics. Recently, SUN *et al.* (2000) proposed a non-linear technique for arrhythmia detection using the ECG signal. KHADRA *et al.* (1997) proposed a classification of life-threatening cardiac arrhythmias using wavelet transforms. Later, AL-FAHOUM and HOWITT (1999) combined wavelet transformation and radial basis neural networks for classifying cardiac arrhythmias. MOHAMED *et al.* (2002) used non-linear dynamic modelling in ECG arrhythmia detection and classification. DINGFIE *et al.* classified cardiac arrhythmia into six classes using autoregressive modelling (DINGFIE *et al.*, 2002).

In the present work, heart rate variability is used as the base signal for classification of cardiac abnormalities into eight classes. Three parameters extracted from the heart rate signals are used for the proposed classification.

2 Materials and method

ECG data for the analysis and classification were obtained from the MIT-BIH arrhythmia database*. Prior to recording, the

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*MIT-BIH arrhythmia database, 3rd edn, 1997, Harvard-MIT Division of Health Science Technology, Biomedical Health Centre, Cambridge, MA, USA.

ECG signals were processed to remove noise due to power-line interference, respiration, muscle tremors, spikes etc. The R peaks of the ECG were detected using the Tompkins algorithm (PAN and TOMPKINS, 1985).

The selected data set included around 1000 segments each of normal ECG, pre-ventricular contraction (PVC), complete heart block (CHB), sick sinus syndrome (SSS), left bundle branch block (LBBB), ischaemic/dilated cardiomyopathy, atrial fibrillation, and ventricular fibrillation. The sampling frequency of the data was 360 Hz.

3 Neural network classifier

Artificial neural networks (ANNs) are biologically inspired networks that are useful in application areas such as pattern recognition, classification etc. (LIPPMAN, 1989; HAYKIN, 1995). The decision making process of the ANN is holistic, based on the features of input patterns, and is suitable for classification of biomedical data. Typically, multilayer feed forward neural networks can be trained as non-linear classifiers using the generalised back propagation algorithm (BPA) (HAYKIN, 1995).

The BPA is a supervised learning algorithm, in which a mean square error function is defined, and the learning process aims to reduce the overall system error to a minimum. The connection weights are randomly assigned at the beginning and progressively modified to reduce the overall system error. The weight updating starts with the output layer and progresses backward. The weight update is in the direction of 'negative descent', to maximize the speed of error reduction (YEGNANARAYANA, 1999). The step size is chosen heuristically; in the present case, a learning constant $\eta = 0.9$ was chosen.

For effective training, it is desirable that the training data set be uniformly spread throughout the class domains. The available data can be used iteratively, until the error function is reduced to a minimum.

The ANN used for classification is shown in Fig. 1. The input layer consisted of nodes, and, in the subsequent hidden layers, process neurons with the standard sigmoid activation function were used. The output layer had three neurons, to divide the output domain into eight classes (000 to 111).

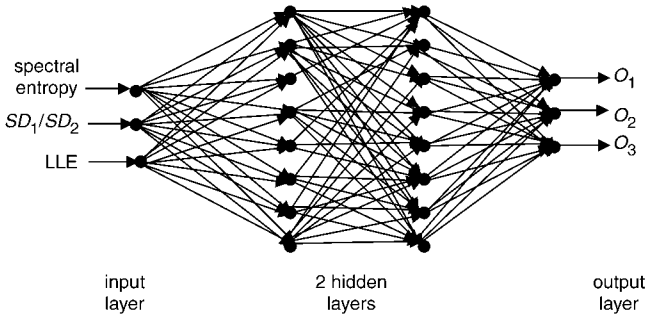

Fig. 1 *Four-layer feedforward neural network classifier*

4 Disease classification using ANN

For the purpose of this study, the cardiac disorders were classified into eight categories, namely

(i) left bundle branch block (LBBB)
(ii) normal sinus rhythm (NSR)
(iii) pre-ventricular contraction (PVC)
(iv) atrial fibrillation (AF)
(v) ventricular fibrillation(VF)
(vi) complete heart block (CHB)
(vii) ischaemic/dilated cardiomyopathy
(viii) sick sinus syndrome (SSS).

The ANN classifier was fed by three parameters derived from the heart rate signals. They were spectral entropy, Poincaré plot geometry and largest Lyapunov exponent (LLE) (Table 1).

4.1 *Spectral entropy*

Spectral entropy quantifies the spectral complexity of the time series (REZEK and ROBERTS, 1993). A variety of spectral transformations exist. Of these, the Fourier transformation (FT) is the most commonly used technique from which the power spectral density (PSD) can be obtained. The PSD represents the distribution of power as a function of frequency. Normalisation of the PSD with respect to the total spectral power yields the probability density function (PDF). Application of Shannon's channel entropy gives an estimate of the spectral entropy of the process, where entropy is given by

$$H = \sum_f p_f \log\left(\frac{1}{p_f}\right) \tag{1}$$

where p_f is the PDF value at frequency f.

Heuristically, the *entropy* is interpreted as a measure of uncertainty about the event at f. Thus entropy can be used as a measure of system complexity. The spectral entropy $H(0 \leq H \leq 1)$ describes the complexity of the HRV signal. This spectral entropy H was computed for the various types of cardiac signal.

4.2 *Poincaré plot geometry*

Poincaré plot geometry, a technique taken from non-linear dynamics, portrays the nature of R-R interval fluctuations. It is a graph of each R-R interval plotted against the next interval. Poincaré plot analysis is an emerging quantitative-visual technique whereby the shape of the plot is categorised into functional classes that indicate the degree of heart failure in a subject (WOO *et al.*, 1992). The plot provides summary information as well as detailed beat-to-beat information on the behaviour of the heart (KAMEN *et al.*, 1996). The Poincaré plot can be analysed quantitatively by calculating the standard deviations of the distances of the $R\text{-}R(i)$ to the lines $y = x$ and $y = -x + 2{*}R\text{-}R_m$, where $R\text{-}R_m$ is the mean of all $R\text{-}R(i)$ (TULPPO *et al.*, 1996). The standard deviations are referred to as SD_1 and SD_2, respectively. SD_1 related to the fast beat-to-beat variability in

Table 1 Range of input parameters to ANN classification model

Class	Spectral entropy	SD_1/SD_2	LLE
LBBB	1.24 ± 0.047	0.70 ± 0.20	0.47 ± 0.044
Normal	1.63 ± 0.025	0.80 ± 0.16	0.50 ± 0.058
PVC	1.14 ± 0.057	1.42 ± 0.54	0.62 ± 0.003
AF	1.20 ± 0.037	2.98 ± 1.56	0.56 ± 0.112
VF	1.06 ± 0.003	1.13 ± 0.47	0.42 ± 0.036
Complete heart block	0.86 ± 0.054	0.64 ± 0.024	0.078 ± 0.114
Ischaemic/dilated cardiomyopathy	1.12 ± 0.11	0.59 ± 0.37	0.193 ± 0.066
SSS	1.27 ± 0.135	0.96 ± 0.32	0.82 ± 0.102

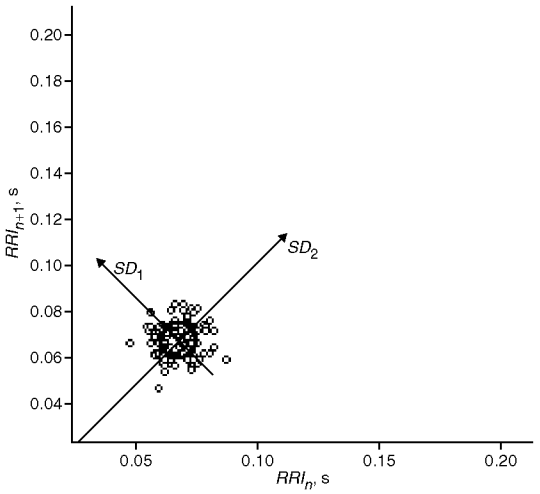

Fig. 2 *Poincaré plot of a normal subject*

the data, and SD_2 described the longer-term variability of R-$R(i)$ (TULPPO *et al.*, 1996). The ratio SD_1/SD_2 can also be computed to describe the relationship between these components. Fig. 2 shows the Poincaré plot of a normal subject.

4.3 *Largest Lyapunov exponent*

The Lyapunov exponent λ is a measure of the rate at which the trajectories separate one from another (WOLF *et al.*, 1985; METIN, 2001; WEST, 2000). A negative exponent implies that the orbits approach a common fixed point. A zero exponent means the orbits maintain their relative positions; they are on a stable attractor. Finally, a positive exponent implies that the orbits are on a chaotic attractor.

For two points in a space X_0 and $X_0 + \Delta x_0$, that are function of time and each of which will generate an orbit in that space using some equations or system of equations, then the separation between the two orbits Δx will also be a function of time. This separation is also a function of the location of the initial value and has the form $\Delta x\,(X_0,t)$. For a chaotic data set, the function $\Delta x\,(X_0,t)$ will behave erratically. The mean exponential rate of divergence of two initially close orbits is characterised by

$$\lambda = \lim_{t \to \alpha} \frac{1}{t} \ln \frac{|\Delta x(X_0,t)|}{|\Delta X_0|} \tag{2}$$

The Lyapunov exponent λ is useful for distinguishing various orbits.

The largest Lyapunov exponent (LLE) quantifies sensitivity of the system to initial conditions and gives a measure of predictability. The presence of a positive Lyapunov exponent indicates chaos. Even though an m dimensional system has m Lyapunov exponents, in most applications it is sufficient to compute only the LLE. We made use of the method proposed by ROSENSTIEN *et al.* (1993), which is robust with data length. This method looks for the nearest neighbour of each point in phase-space and tracks their separation over a certain time evolution. The LLE is estimated using a least squares fit to an average line defined by

$$y(n) = \frac{1}{\Delta t}\langle In(d_i(n))\rangle \tag{3}$$

where $d_i(n)$ is the distance between the i^{th} phase-space point and its nearest neighbour at the n^{th} time step, and $\langle\cdot\rangle$ denotes the average overall phase-space points. This last averaging step is the main feature that allows an accurate evaluation of the LLE, even when we have short and noisy data. The results of the classification are shown in Table 2.

5 Fuzzy classifier

A more efficient classifier is developed using a fuzzy equivalence relationship. The process of classification involves obtaining a fuzzy *equivalence relationship* matrix for each class of datum and then comparing a fresh input with each group for classification (KLIR and YUAN, 1995).

The fuzzy *equivalence relationship* requires the properties of reflexivity, symmetry and transitivity to be satisfied. If it satisfies only the first two the reflexivity and symmetry properties, it is termed a fuzzy compatible relationship. Although it is usually difficult to identify an equivalence relationship directly, it is possible to identify a compatible relationship in terms of an appropriate 'distance function' of the Minkowski class. The general expression used for the distance function (Minkowski class) is

$$R(x_i,x_j) = 1 - \delta\left(\sum_{l=1}^{n} |x_{il} - x_{jl}|^q\right)^{1/q} \tag{4}$$

where $n \rightarrow$ total dimensionality of the input data point; $l \rightarrow$ dimensionality index of the input data $(1,2,\ldots,n)$; $p \rightarrow$ size of the input data set; $i,j \rightarrow$ input index $i,\ j \in [1\ldots p]$; $q \rightarrow$ distance function parameter; and $\delta \rightarrow$ normalising factor to ensure the resultant $R(x_i,x_j) \in [0,1]$.

Variable n represents the total dimensions of the data, and each dimension refers to the components of the input data. For example, from Table 1, the input data (HRV signal) are represented by three components (HR (average), Lyapunov, correlation function), and hence, $n = 3$ here.

The Minkowski relationship can be evaluated for integer values of q for $q = 1$, the 'distance function' happens to be the Hamming distance; for $q = 2$, it is the Euclidean distance etc. The normalising factor δ is taken as the inverse of the largest distance between the data pairs.

As indicated above, for our purposes, the input data (HRV signal) was represented using the three parameters used for ANN classification earlier (Table 1). Thus the data had three components ($n = 3$). The size of the training data set (defined by $P_k k \in [1\ldots 4]$) was different for each class i. The size of the entire data set was given by p.

Table 2 Training and testing data sets

Class	Number of data set used for training	Number of data set used for testing	Percentage of correct classification (10 000 iterations)
LBBB	28	14	85.7
Normal	60	30	90.0
PVC	45	25	88.0
AF	30	20	85.0
VF	28	21	81.0
Complete heart block	28	21	81.0
Ischaemic/dilated cardiomyopathy	30	18	83.3
SSS	30	18	88.9

In the present case, the Euclidean distance *function* of the Minkowski class ($q = 2$) was used as the basis to define a mutual relationship among the input data belonging to a particular class. Thus (4) reduces to

$$R(x_i, x_j) = 1 - \delta\left(\sum_{l=1}^{3} |x_{il} - x_{jl}|^2\right)^{1/2} \quad (5)$$

The value of δ was taken to be equal to $1/n^{1/2}$, where n was the number dimensionality of the input data points, which was three in our case.

The result of the above evaluation could be listed in the form of a symmetrical $p \times p$ matrix, which satisfied both the reflexivity and symmetry conditions. The compatibility relationship thus formed was converted to an equivalence relationship by performance of the transitive closure operation. The processing algorithm is described in the following discussion. First, a few definitions are necessary.

For a relationship R, we write $R(u,v)$ if the pair $\langle u,v \rangle$ is a member of the set.

Given a relationship R, its transitive closure R^* can be determined as follows.

R is transitive if $(a, b) \in R \wedge (b, c) \in R \wedge (a, c) \in R$. We can add elements to a relationship R and create a new relationship that is the transitive closure of R. However, the procedure requires an iterative process. We find the transitive closure by examining every pair of elements of R where the second element of the first pair matches the first element of the second pair.

That is, $(a, b) \in R$ and $(b, c) \in R$.

Transitivity requires that (a, c) must also be an element of R. If it is not, then we must add it to the new relationship that we are building into the transitive closure. Let us call the new relationship R'. (Initially, $R' = R$, and, when the process of adding edges is over, $R' = R^*$). After we have examined all such pairs of members of R and added the required edges to R' where needed, we must then begin the same process again.

The resultant R^* is the transitive closure of R.

After computing the transitive closure and having satisfied the properties of reflexivity, symmetry and transitivity, the fuzzy equivalence relationship matrix so obtained can now be used for classification of fresh data. The data to be classified are appended to the already classified data, and the fuzzy equivalence relationship is found. At the end, the class to which the unknown data belong is the one with whom they have the maximum degree of closeness. The formal algorithm is as follows, and the results of the classification are listed in Table 3:

Step 1: Initialisation phase:

1.1 Read classified data from an input file
$[input\_data]_{i,j}$ $[classes]_k \leftarrow$ Buffer
i: 1 to m (number of data)
j: 1 to n (number of attributes)
k: 1 to i; where there are 'o' classes

1.2 Read unclassified data from test file
$[unclassified]_{i,j} \leftarrow$ Buffer
i: 1 to p (number of data)
j: 1 to n (number of attributes)

Step 2: Pre-processing phase:

2.1 Append unclassified_data onto input_data
$[\text{input\_data}]_{l,j} \leftarrow [\text{input\_data}]_{i,j} \Downarrow [\text{unclassified\_data}]_{k,j}$
l: 1 to $(m+p)$
i: $m+1$ to $m+p$
k: 1 to p
j: 1 to n

2.2 Normalise the data matrix attribute wise selecting the maximum in each attribute
$[input\_data]_{l,j} \leftarrow \frac{[input\_data]_{l,j}}{\max\{[input\_data]\}_j}$
l: 1 to $(m+p)$
j: 1 to n

Step 3: Compute the fuzzy equivalence relationship:

3.1 Find the compatibility relationship between the data using distance function of Minkowski class
$R_c(x_i,x_j) = 1 - \delta(\sum_{l=1}^{n}(x_{il} - x_{jl})^2))^{1/2}$
i, j: 1 to $(m+p)$
where $\delta = 1/n^{1/2}$

3.2 Find the transitive closure of R_c using algorithm given below

3.2.1 $R' = R_c(R_c \bullet R_c)$
$\cup$ = Max operator
$\bullet$ = Max-Min composition
where $R \bullet R = r_{ij} = \max_k \min(r_{ik}, r_{kj})$
i, j, k: 1 to $(m+p)$

3.2.2 If $R' = R_c$ then stop. Else make $R_c = R'$ go to step 3.2.1.

3.2.3 $R_t = R'$; R_t is the transitive closure matrix $(m+p) \times (m+p)$

Step 4: Prediction phase:
Beginning from row $m+1$ search for the maximum membership degree until column m and store the corresponding index in matrix *Max_membership*
$[Max\_membership]_i = \max[R_t]_{i,j}$;
i: $m+1$ to $(m+p)$
j: 1 to m
corresponding to each unclassified datum, the class to which it belongs is given by $[classes]_{[Max\_membership]i}$; i: 1 to p

6 Conclusion

The HRV signal can be used as a reliable indicator of heart diseases. In this paper, both the neural network classifier and the fuzzy classifier are presented as diagnostic tools to aid the physician in the analysis of heart diseases. However, these tools

Table 3 Results of fuzzy classifier

Class	Number of data set used for training	Number of data set used for testing	Percentage of correct classification (10 000 iterations)
LBBB	28	18	88.9
Normal	60	40	92.5
PVC	45	30	90.0
AF	30	25	88.0
VF	28	25	84.0
Complete heart block	28	25	88.0
Ischaemic/dilated cardiomyopathy	30	22	86.4
SSS	30	22	90.9

generally do not yield results with 100% accuracy. The accuracy of the tools depends on several factors, such as the size and quality of the training set, the rigour of the training imparted and also the parameters chosen to represent the input. However, from the analysis of the results listed in Tables 2 and 3, it is evident that the classifiers presented are effective with about 80–85% accuracy.

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