Heart Variability Analysis by using Non-Linear Techniques and their Comparison

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ABSTRACT
An electrocardiogram (ECG) provides information about individual cardiac health. Aside from directly analyzing the ECG signals, researchers and doctors also extract other indirect measurements from the ECG signals and one of the most popular measurements is heart rate variability (HRV). Heart Rate Variability (HRV) measurements analyze how the RR intervals of an ECG signal, which show the variation between consecutive heartbeats, change over time. Heart rate (HR) is a non-stationary signal and its variation may contain indicators of current disease, or warnings about impending cardiac diseases. Hence, HR variation analysis (instantaneous HR against time axis) has become a popular noninvasive tool for assessing the activities of the autonomic nervous system. Computer based analytical tools for in-depth study of data over daylong intervals can be very useful in diagnostics [2]. Therefore, in this paper two non linear techniques Poincare and Recurrence Quantification Analysis are implemented by using Matlab for HRV analysis. Three parameters SD1, SD2 and % REC are taken into consideration for doing the comparison between both the techniques.

General Terms
Heart rate variability, RR intervals.

Keywords
ECG, HRV, Poincare, Recurrence, RQA, SD1, SD2, % REC.

1. INTRODUCTION
The Electrocardiograph (ECG) signal is basically the measure of electrical activity associated with the heart. This electrical activity is recorded and analyzed. The deviations from the normal electrical patterns are due to cardiac disorders. Heart rate variability (HRV) is a reliable reflection of the many physiological factors modulating the normal rhythm of the heart. In fact, they provide a powerful means of observing the interplay between the sympathetic and parasympathetic nervous systems. It shows that the structure generating the signal is not only simply linear, but also involves nonlinear contributions. Hence, HR variation analysis (instantaneous HR against time axis) has become a popular tool for assessing the activities of the autonomic nervous system. Therefore, the HRV signal parameters, extracted and analyzed using computers, are highly useful in diagnostics.

There are different methods of HRV analysis. One of the methods is time domain analysis. This method extracts a few special measures using only the temporal RR interval signals. Another method is spectral analysis. This method interpolates the RR interval at a certain rate and transforms this interval into the frequency domain. Other methods are non-linear methods which are used in this paper to do HRV analysis [1].

Our aim is to differentiate healthy and patient subjects by doing their HRV analysis so that HR variation can be used as indicator or warning for disease and to find which technique is more suitable. In order to do this we applied these two techniques on RR intervals extracted from ECG signals of healthy and patient subjects taken from fantasia database and the comparison between results obtained by two techniques is done.

2. NON LINEAR TECHNIQUES
Non-linear techniques are certainly involved in the genesis of HRV. It has been speculated that analysis of HRV based on the non-linear methods might elicit valuable information for the physiological interpretation of HRV and for the assessment of the risk of disease. At present, the non-linear methods represent potentially promising tools for HRV assessment, but standards are lacking and the full scope of these methods cannot be assessed. Advances in technology and the interpretation of the results of non-linear methods are needed before these methods are ready for physiological and clinical studies [1] [2].

2.1 Poincare Plot Analysis
The Poincare plot analysis is a geometrical and non-linear method to assess the dynamics of heart rate variability (HRV). The Poincare plot is a representation of a time series into a phase space, where the values of each pair of successive elements of the time series define a point in the plot. The theoretical background that supports the use of a phase space is the Takens theorem (Takens, 1981). According to Takens, it is possible to reconstruct the attractor of a dynamical system by mapping a scalar measurement into a phase space using a given time delay and embedding dimension. The Poincare plot is a very simplified phase space with dimension two and delay or lag of one beat (i.e. each R-R interval is plotted as a function of the previous R-R interval). The 'true' attractor of HRV is certainly not displayed by the Poincare plot as the HRV has a higher estimated dimension than two [7].

The Poincare plot gives a useful visual contact to the R-R data by representing both short and long-term variations included in the recording. Analysis of Poincare plots can be performed by a simple visual inspection of the shape of the attractor (like torpedo or butterfly shape), which has been used to classify the signal. In chronic renal failure (CRF) patients this approach has proved to be useful to evaluate the survival prognosis in the presence of coronary disease. However, the assessment and standardization of these qualitative

classifications are difficult because they are highly subjective. A quantitative analysis of the HRV attractor displayed by the Poincare plot can be made by adjusting it to an ellipse. For the performance analysis, the SD1 (Standard Deviation1), SD2 (Standard Deviation 2) and Area of ellipse are used as evaluation parameters. These evaluation parameters have taken different definitions in different research reports [7]. The most acceptable definitions are given below:

2.1.1. SD1: Standard Deviation1

It is the standard deviation (SD) of the instantaneous (short term) beat-to-beat R-R interval variability (minor axis of the ellipse or SD1)[7].

2.1.2. SD2: Standard Deviation 2

It is the standard deviation (SD) of the long term R-R interval variability (major axis of the ellipse or SD2)[7].

2.1.3. Area of Ellipse

It is the amount of area covered by the ellipse. It is calculated by doing the product of π , SD1 and SD2.

2.2 Recurrence Quantification Analysis

RQA was first introduced to the physical sciences by Eckmann, Kamphorst and Ruelle in 1987 as a purely graphical technique which they called "recurrence plot" (RP), to detect patterns of recurrence in the data, which are one of the most important characteristics of dynamic systems. This techniques is based on the "Time Delay Method". However being a tool of a visual and qualitative nature, its results are not always conclusive and so it ended up being considered a minor technique. Zbilut and Webber (1992) and Webber and Zbilut (1994) recognized this drawback and tried to overcome it through what they called Recurrence Quantification Analysis (RQA)[8].

The RQA considers that it is possible to quantify the information supplied by the RP by using certain simple pattern recognition algorithms. This technique is of great interest because it allows us to obtain more objective information than that which could be derived from a purely visual analysis which helps us to interpret information more rigorously[8]. The starting point of the RQA is the following function:

$$d_{ij} = \begin{Bmatrix} 1, if \parallel x(i) - x(j) \parallel, \langle r \\ 0, if \parallel x(i) - x(j) \} \parallel, \geq r \end{Bmatrix} \quad [1]$$

Clearly, the points of the Recurrence Plot correspond to the values of $d_{ij} = 1$. Therefore, this indicator function collects the information given by the RP in a binary symmetric *n* x *n* matrix (which we will call "recurrence matrix", RM), with *n* being the number of vectors of the embedding. The main features of the structure of the RP may be quantified from this matrix and transformed into analytical indicators. Finally, considering that the RM is symmetric, the analytical indicators introduced by the RQA are obtained in practice using the upper (or lower) triangular part of the RM excluding the main diagonal [8]. The various statistics proposed by the RQA are the following:

2.2.1. %REC: Percent Recurrence

It is the percentage of recurrent points (% REC) in the upper triangle without including main diagonal. It is a measure of the density of recurrent points, and is analogous to the "recurrence rate". Mathematically it is defined as

$$\%REC = 100 \times \frac{NREC}{NP}$$

Where NREC is the number of recurrent points or number of ones of the TRM and NP is the total elements of the TRM[8].

2.2.2. %DET: Percent of determinism

It is the number of points on lines parallel to the main diagonal, considering that a line is formed with a minimum of at least two adjacent points. Determinism (DET) is calculated by dividing the number of recurrent points in diagonal line structures (in the upper triangle) by the total number of recurrent points (in upper triangle).

$$\%DET = 100 \times \frac{NPD}{NREC}$$

Where *NPD* is the number of points on lines parallel to the main diagonal, considering that a line is formed with a minimum of at least two adjacent points [8].

2.2.3. ENT: Entropy

Entropy is a measure of the average information contained in the line-segment distribution. This statistic gives information about the diversity of lines parallel to the main diagonal. Hence it can also be an indicator of the deterministic or stochastic nature of the series.

2.3. Results and Discussions

2.3.1. Poincare Plot Analysis

The Poincare Plot Analysis has been done on the RR intervals extracted from ECG signals taken from fantasia database of various normal and patient persons. Poincare Plot analysis has provided us both the quantitative and qualitative analysis of ECG signals by using non linear methodology.

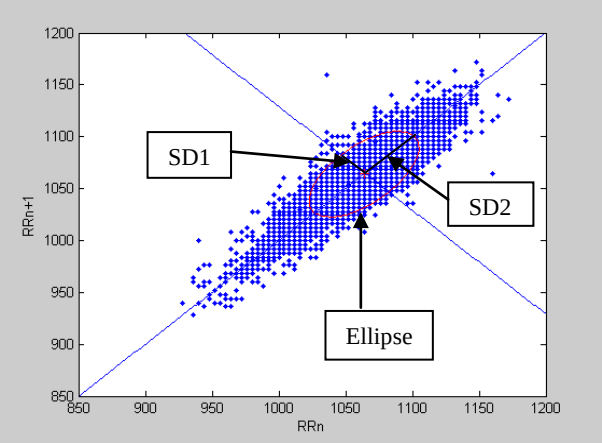

Fig 1: Poincare Plot of RR intervals of a patient person with its standard descriptor SD1 and SD2

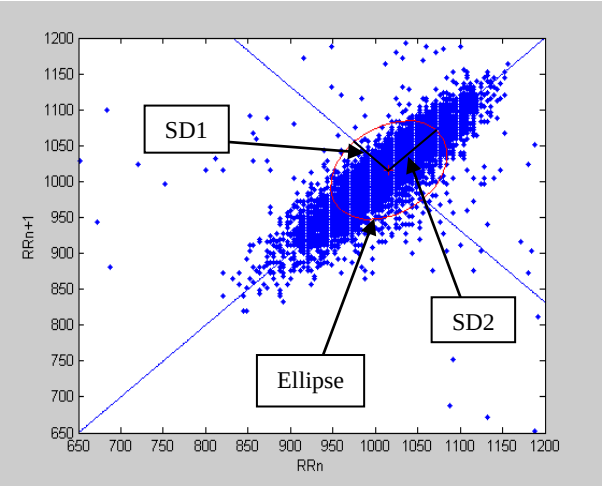

Fig 2: Poincare Plot of RR intervals of an another patient person with its standard descriptor SD1 and SD2

If we see the Poincare plots of persons suffering from disease as shown in Fig 1 and Fig 2 it can be observed clearly that majority of RR intervals lies within a small region and are not dispersed throughout the plot. This shows that the variation which is the difference between RR intervals is less which further results in smaller values for SD1, SD2 and area of ellipse.

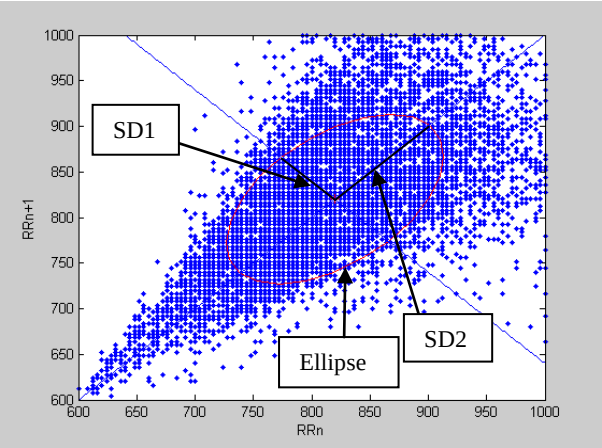

Fig 3: Poincare Plot of RR intervals of a normal person with its standard descriptor SD1 and SD2

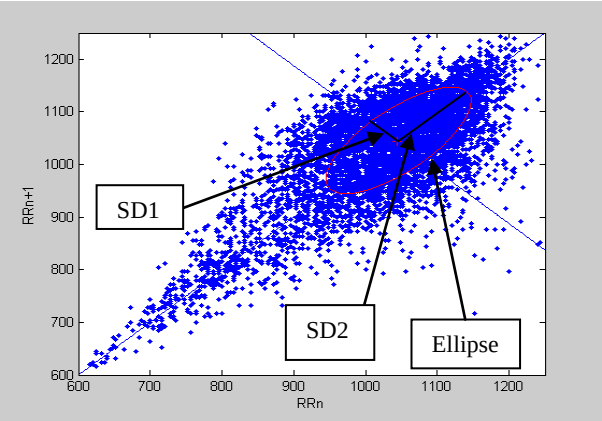

Fig 4: Poincare Plot of RR intervals of an another normal person with its standard descriptor SD1 and SD2

If we see the Poincare plots of normal persons not suffering from any disease as shown in Fig 3 and Fig 4 it can be observed clearly that majority of RR intervals are well dispersed throughout the plot which shows that variation in RR intervals is more which results in larger values of SD1, SD2 and area of ellipse.

Table1. SD1 and SD2 of Patient Persons

Age Group	SD1	SD2	Area of Ellipse (π*SD1*SD2)
Patient-1	25.2745	52.9018	4198.38895
Patient-2	23.2662	66.9031	4887.66404
Patient-3	32.9287	120.0742	12415.2062
Patient-4	21.3007	33.9414	2270.14332
Patient-5	57.2607	79.0343	14210.2563
Patient-6	21.8979	61.7105	4243.17732
Patient-7	15.7004	79.8127	3934.70673

Table2. SD1 and SD2 of Normal Persons

Age Group	SD1	SD2	Area of Ellipse (π*SD1*SD2)
Normal-1	52.8311	133.4969	22145.75455
Normal-2	24.4095	89.8919	6889.83928
Normal-3	78.8477	159.1354	39399.02527
Normal-4	39.0706	138.8992	17040.38776
Normal-5	96.0846	268.1668	80907.43709
Normal-6	36.8274	126.5634	14635.54300
Normal-7	45.4924	117.4879	16782.69254

The evaluation parameters as shown in Table 1 and Table 2 are obtained by applying Poincare Plot analysis on RR intervals of various patient and normal persons.

2.3.2. Recurrence Quantification Analysis

The Recurrence Quantification Analysis has been done on the same RR intervals that are used in Poincare Plot Analysis. Recurrence Quantification Analysis has provided us the quantitative analysis of ECG signals by using non linear methodology.

Table3. % REC of Patient Persons

Age Group	% REC
Patient-1	97.16372
Patient-2	68.62068
Patient-3	93.643
Patient-4	98.77217
Patient-5	63.50069
Patient-6	90.3994
Patient-7	78.20291

Table4. % REC of Normal Persons

Age Group	% REC
Normal-1	53.39009
Normal-2	48.96373
Normal-3	86.86449
Normal-4	88.82684
Normal-5	51.02709
Normal-6	35.63875
Normal-7	39.58099

The RQA statistics values shown in Table 3 and Table 4 are obtained by applying Recurrence Quantification Analysis on RR intervals of various patient and normal persons. It can be observed from the values of % REC in Table 3 and Table 4 that % Recurrence is more in case of patient persons in comparison to normal person which means less variation in RR intervals of patient persons and more variation in case normal persons.

2.3.3. Comparison of Poincare Plot and RQA

Table 5. Poincare and RQA evaluation parameters of patient person

Age Group	% REC	SD1	SD2
Patient-1	97.16372	25.2745	52.9018
Patient-2	68.62068	23.2662	66.9031
Patient-3	93.643	32.9287	120.0742
Patient-4	98.77217	21.3007	33.9414
Patient-5	63.50069	57.2607	79.0343
Patient-6	90.3994	21.8979	61.7105
Patient-7	78.20291	15.7004	79.8127

Table 6. Poincare and RQA evaluation parameters of normal person

Age Group	% REC	SD1	SD2
Normal-1	53.39009	52.8311	133.4969
Normal-2	48.96373	24.4095	89.8919
Normal-3	86.86449	78.8477	159.1354
Normal-4	88.82684	39.0706	138.8992
Normal-5	51.02709	96.0846	268.1668
Normal-6	35.63875	36.8274	126.5634
Normal-7	39.58099	45.4924	117.4879

Evaluation parameters obtained from Poincare Plot and RQA are combined in Table 5 and Table 6 to do the comparison of these non linear techniques. By doing the comparison it has been observed that in case of patient persons the value of SD1, SD2, and Area of ellipse will be less but % REC will be more whereas in case of normal persons the value of SD1, SD2, and Area of ellipse will be more but % REC will be less.

2.4. Conclusion

It can be concluded that by using evaluation parameters of Poincare and Recurrence Quantification Analysis we can differentiate healthy and patient persons and these parameters can be used as an early indicators for the disease detection. It can also be concluded that the results obtained by both the techniques are same but Poincare Analysis is easy to implement and interpret in comparison to RQA .In future these methods can be used in developing technology that can have significant potential for advancing personal health care and telemedicine.

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