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Identification of Premature Ventricular Contraction (PVC) of Electrocardiogram using Statistical Tools and Non-Linear Analysis

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Index Terms: electrocardiogram (ECG), premature ventricular contraction (PVC), instantaneous heart rate (IHR), standard deviation(SD), central tendency measure (CTM).

I. Introduction

a) Heart and ECG

The heart is the muscular organ that pumps the blood through the circulatory system by rhythmic contraction and dilation. In vertebrate there may be up to four chambers with two atria and two ventricles. Measuring the electrical activity of heart to show whether or not it is working normally and records the heart rhythm and activity on a moving strip of paper or a line on a screen, in a word that is called ECG. Electrocardiogram (ECG) is a wave that represents an electrical event in the heart, such as atrial depolarization, atrial repolarization, ventricular depolarization, ventricular repolarization, or transmission, and so on [1-4].

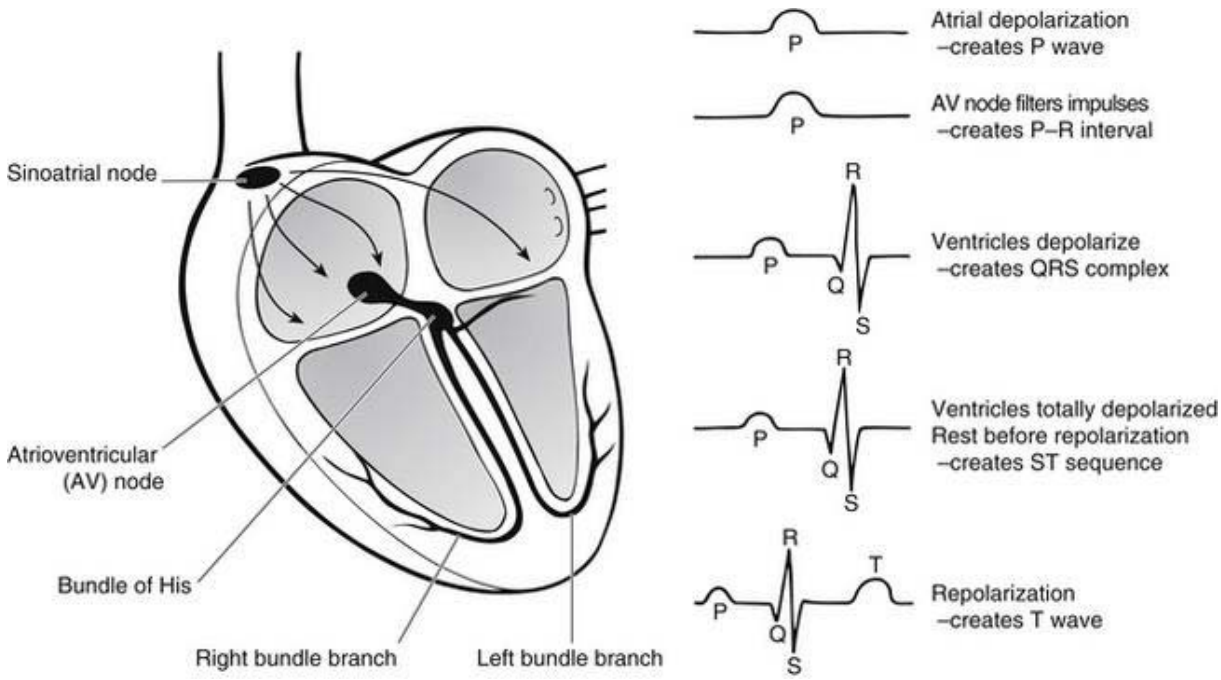

Figure: 1.1 : Anatomy of heart and ECG generation

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The electric current generated by depolarization and repolarization of the atria and ventricles is detected by electrodes, it is amplified, displayed on an oscilloscope, recorded on ECG paper, or stored in memory. The electric current generated by atrial depolarization is recorded as the P wave, and that generated by ventricular depolarization is recorded as the Q, R, and S waves: the QRS complex. Atrial repolarization is recorded as the atrial T wave (Ta), and ventricular repolarization, as the ventricular T wave, or simply, the T wave. The sections of the ECG between the waves and complexes are called segments and intervals: the PR segment, the ST segment, the TP segment, the PR interval, the QT interval, and the R-R interval. When electrical activity of the heart is not being detected, the ECG is a straight, flat line – the isoelectric line or baseline.

II. Proposed Method

This work presents heart rate variability (HRV) analysis using some non-linear methods. The ECG signal to be analyzed is first processed [5] to extract the QRS complex. From that bit-to-bit interval (BBI) is calculated. From the BBI the instantaneous heart rate (IHR) is found. On this dataset of BBI and IHR, various non-linear parameters like Poincare plot analysis (PPA), central tendency measure (CTM), phase space portrait, detrended fluctuation analysis are determined. The result is very effective to distinguish the ECG signals between the healthy person and that of the ailing person.

a) Phase space portrait

Phase space or phase diagram is such a space in which every point describes two or more states of a system variable. The number of states [6] that can be displayed in phase space is called dimension or reconstruction dimension. It is usually symbolized by the letter d or E. From the given digitized data x(1), x(2), …, x(n) of the IHR or BBI, a matrix A is obtained with its two columns given by x(1), x(2), …, x(n-τ) and x(1+ τ), x(2+ τ),.., x(n). Here τ is the time delay. The Phase space plot is constructed by plotting the data set with the time delay version of itself. The attribute of the reconstructed phase space plot depend on the choice of the value for τ. τ is measured through applying a autocorrelation function. Autocorrelation is a mathematical tool used frequently in signal processing for analyzing functions or series of values, such as time domain signals. Informally, it is a measure of how well a signal matches a with time-shifted version of itself, as a function of the amount of time shift. More precisely, it is the cross-correlation of a signal with itself. Autocorrelation is useful for finding repeating patterns in a signal, such as determining the presence of a periodic signal which has been buried under noise, or identifying the missing fundamental frequency in a signal implied by its harmonic frequencies. τ is typically chosen as the time it takes the autocorrelation function of the data to decay to 1/e or the first minimum in the graph of the average mutual information. Here we used the two dimensional phase space portrait, i.e., d = 2.

Here in this project, phase space analysis has been used on IHR time series and the results are analyzed to see if any significant difference is found between normal and abnormal data series.

Following are the portraits obtained using phase space portrait on IHR. They are presented along with the IHR plot against each sample.

b) Poincare plot Analysis

The most commonly used non-linear method of analyzing heart rate variability is the Poincare plot. The Poincare plot analysis (PPA) [7] is a quantitative visual technique, whereby the shape of the plot is categorized into functional classes and provides detailed beat-to-beat information on the behaviour of the heart. Poincare plots are applied for a two-dimensional graphical and quantitative representation where RR_j is plotted against $RRj+1$.Most commonly, three indices are calculated from Poincare plots: the standard deviation of the short-term RR-interval variability (SD1), the standard deviation of the long-term RR-interval variability (SD2) and the axes ratio (SD1/SD2) [8].

The standard deviation of the point's is perpendicular to the line-of identity denoted by SD1 describes short-term variability which is mainly caused by RSA. It can be shown that SD1 is related to the time-domain measure SDSD by,

$$SD12 = 1/2\ SDSD2 \quad \text{..... (2.1)}$$

The standard deviation along the line-of-identity denoted by SD2, on the other hand, describes long-term variability and has been shown to be related to time-domain measures SDNN and SDSD by,

$$SD22 = 2SDNN2\text{-}1/2\ SDSD2 \quad \text{..... (2.2)}$$

The standard Poincare plot can be considered to be of the first order. For the healthy heart, PPA shows a cigar-shaped cloud of points oriented along the line of identity.

In Poincare plot analysis here is the record of seven normal person's and seven abnormal person's ECG and analysis SD, MEAN VALUE, VAREANCE, RMSSD, SDSD.

Data table for SD, MEAN, VARIANCE, RMSSD & SDSD:

Table 2.1 : For normal patients

Patients name	SD	MEAN	VARIANCE	RMSSD	SDSD
107	5.6302	71.3858	31.6986	71.6073	6.2638
111	3.9393	70.7966	15.5179	70.9061	3.9646
112	2.5849	84.4500	6.6817	84.4895	2.3993
117	2.3313	51.0788	5.4351	51.1320	1.998
121	6.2172	62.3587	38.6533	62.6677	3.5439
122	4.5251	82.5183	20.4762	82.6422	2.2118
124	6.1893	54.3189	38.3076	54.6701	7.0596
AVERAGE	4.4881	68.1295	22.3957	68.3021	3.9202

Table 2.2: For Abnormal patients

Patients name	SD	MEAN	VARIANCE	RMSSD	SDSD
106	27.25	75.228	742.65	80.00	43.31
119	22.521	72.091	507.20	75.52	39.9055
208	19.397	101.93	376.244	103.75	30.7995
213	15.796	108.307	33.5941	108.462	8.8309
221	22.890	86.448	523.992	89.426	35.141
223	15.254	88.874	232.689	90.1735	25.6777
233	29.43	109.10	866.2365	113.001	50.6858
AVERAGE	21.79	91.711	468.9451	94.3464	33.4788

c) Detrended Fluctuation Analysis

Detrended Fluctuation Analysis is an interesting method for scaling the long-term autocorrelation of non-stationary signals [9-12]. It quantifies the complexity of signals using the fractal property. This method is a modified root mean square method for the random walk. Mean square distance of the signal from the local trend line is analyzed as a function of scale parameter. There is usually power-law dependence and interesting parameter is the exponent.

Detrended fluctuation analysis (DFA) measures the correlation within the signal. The correlation is extracted for different time scales. First, the RR interval time series is integrated,

$$(k) = \Sigma\,(RR_{j\,kj=1} - \overline{RR})\ \text{k=1,....N} \qquad \ldots\ldots(2.3)$$

Where $\overline{RR}$ is the average RR interval. Next, the integrated series is divided into segments of equal length n. Within each segment, a least squares line is fitted into the data. Let $y(k)$ denote these regression lines. Next the integrated series (k) is detrended by subtracting the local trend within each segment and the root-mean-square fluctuation of this integrated and detrended time series is calculated by,

$$F(n) = \sqrt{\frac{1}{N}\sum_{k=1}^{N}[y(k) - y_n(k)]^2} \qquad (2.4)$$

This computation is repeated over different segment lengths to yield the index (n) as a function of segment length n. Typically$F(n)$ increases with segment length. A linear relationship on a double log graph indicates presence of fractal scaling and the fluctuations can be characterized by scaling exponent **α** slope of the regression line relating log $(n)$to log n.

In the DFA method, the fractal-like signal (1/f noise) results in exponent value **α** =1.0, the white noise results in value 0.5, and the Brownian noise in value 1.5. White noise indicates a simulated uncorrelated random time series. The white noise is the value at one instant that does not correlate with any previous value, and the Brownian noise is the integration of the white noise. The 1/f noise can be interpreted as a "compromise" between the complete unpredictability of white noise and the much smoother "landscape" of Brownian noise.

Here DFA1 & DFA2 for the normal patients and abnormal patients are taken and plotted them.

Table 2.3 : Detrended fluctuation analysis α1 and α2 for normal patients

Patients name	107	111	112	117	121	122	124	AVERAGE
α1	0.835	0.789	0.603	0.845	1.143	1.140	0.406	0.823
α2	0.55	0.75	1.21	1.115	1.38	1.05	1.05	1.0270

Table 2.4 : Detrended fluctuation analysis α1 and α2 for abnormal patients

Patients name	106	119	208	213	221	223	233	AVERAGE
α1	0.321	0.216	0.200	0.404	0.342	0.265	0.245	0.2847
α2	0.776	0.359	0.619	0.207	0.674	0.457	0.233	0.4750

d) Central Tendency Measure

Central tendency measure (CTM) is used to quantify the degree of variability in the second order difference plot [13- 15]. It is calculated by selecting a circular region of radius r, around the origin, counting the number of points that fall within the radius, and dividing by the total number of points. If t = total number of points, and r = radius of central area.
Then,

$$n = \frac{[\sum_{i=1}^{t-2} \delta(di)]}{t-2} \qquad (2.5)$$

Where,

$$\delta(di) = 1, \text{ if } [(a_{i+2} - a_{i+1})^2 + (a_{i+1} - a_i)^2]^{0.5} < r \quad (2.6)$$

$$= 0, \text{ otherwise}$$

In this paper, the data set from BBI and IHR are used to measure the CTM. In first step, the optimum radius is determined for the circular region.

It is determined the central tendency measures (CTM) with the variation of standard deviation (4 & 6) which varies from 10% to 100% for normal and abnormal patients. This is shown in table 2.5 to 2.8.

Table 2.5 : CTM value for SD-4 varies from 10% to 100% obtained from IHR of normal rhythm

PATIENT NAME(CTM VALUE 0F SD)	107	111	112	117	121	122	124
10%	0.0084	0.0085	0.0197	0.0464	0.0361	0.0182	0.0260
20%	0.0436	0.0349	0.0868	0.1522	0.1659	0.0724	0.0959
30%	0.1072	0.0797	0.1759	0.2926	0.3561	0.1505	0.1975
40%	0.2013	0.1452	0.2892	0.4592	0.5334	0.2447	0.3038
50%	0.2921	0.2301	0.4158	0.6166	0.6920	0.3515	0.4016
60%	0.4003	0.3215	0.5250	0.7511	0.7953	0.4773	0.5043
70%	0.4939	0.4130	0.6355	0.8589	0.8766	0.5769	0.5947
80%	0.6011	0.5064	0.7239	0.9286	0.9294	0.6764	0.6863
90%	0.7065	0.5908	0.7893	0.9589	0.9542	0.7540	0.7550
100%	0.7804	0.6671	0.8430	0.9765	0.9725	0.8131	0.8137

Table 2.6 : CTM value for SD-4 varies from 10% to 100% obtained from IHR of abnormal rhythm

PATIENT NAME(CTM VALUE 0F SD)	106	119	208	213	221	223	233
10%	0.0015	0.0050	0	0.0037	0	0.0073	0.0006
20%	0.0109	0.0181	0.0017	0.0246	0	0.0288	0.0072
30%	0.0247	0.0378	0.0615	0.0058	0.0003	0.0550	0.0156
40%	0.0400	0.0615	0.0095	0.0748	0.0004	0.0915	0.0231
50%	0.0647	0.0958	0.0136	0.1152	0.0012	0.1307	0.0322
60%	0.0954	0.1285	0.0221	0.1577	0.0025	0.1745	0.0494
70%	0.1215	0.1522	0.0283	0.2057	0.0029	0.2345	0.0605
80%	0.1546	0.1830	0.0337	0.2519	0.0054	0.2899	0.0778
90%	0.1873	0.2172	0.0426	0.3021	0.0066	0.3148	0.0888
100%	0.2184	0.2394	0.0525	0.3548	0.0083	0.3902	0.0996

Table 2.7 : CTM value for SD-6 varies from 10% to 100% obtained from IHR of normal rhythm

PATIENT NAME(CTM VALUE OF SD	107	111	112	117	121	122	124
10	0.0197	0.0174	0.0387	0.0875	0.0857	0.0372	0.0514
205	0.1072	0.0797	0.1759	0.2926	0.3561	0.1505	0.1074
30%	0.2486	0.1858	0.3511	0.5382	0.6212	0.3034	0.3558
40%	0.4003	0.3215	0.5250	0.7511	0.7953	0.4773	0.5043
50%	0.5473	0.4611	0.6864	0.9007	0.9052	0.6290	0.6380
60%	0.7065	0.5908	0.7893	0.9589	0.9542	0.7540	0.7550
70%	0.8076	0.6959	0.8682	0.9837	0.9795	0.8394	0.8385
80%	0.8680	0.7751	0.9219	0.9902	0.9881	0.9049	0.8868
90%	0.8904	0.8501	0.9598	0.9922	0.9919	0.9442	0.9202
100%	0.8951	0.9043	0.9795	0.9941	0.9919	0.9672	0.9375

Table 2.8 : CTM value for SD-6 varies from 10% to 100% obtained from IHR of abnormal rhythm

PATIENT NAME(CTM VALUE 0F SD)	106	119	208	213	221	223	233
10%	0.0069	0.0111	0.0110	0.0166	0	0.0135	0.0036
20%	0.0247	0.0378	0.0058	0.0431	0.0020	0.0550	0.0156
30%	0.0514	0.0776	0.0116	0.1006	0.0022	0.1100	0.0280
40%	0.0954	0.1285	0.0221	0.1577	0.0025	0.1745	0.0495
50%	0.1383	0.1673	0.0327	0.2270	0.0045	0.2645	0.0687
60%	0.1873	0.2172	0.0426	0.3021	0.0066	0.3418	0.0888
70%	0.2372	0.2505	0.0565	0.3831	0.0091	0.4118	0.1048
80%	0.2737	0.2853	0.0725	0.4675	0.0140	0.4721	0.1185
90%	0.3162	0.3100	0.0831	0.5417	0.0173	0.5152	0.1305
100%	0.3523	0.3221	0.0954	0.6070	0.0277	0.5417	0.1354

III. Simulation Result and Analysis

a) Simulation Result of Phase Space Portrait

i. *Simulation Results for normal patient*

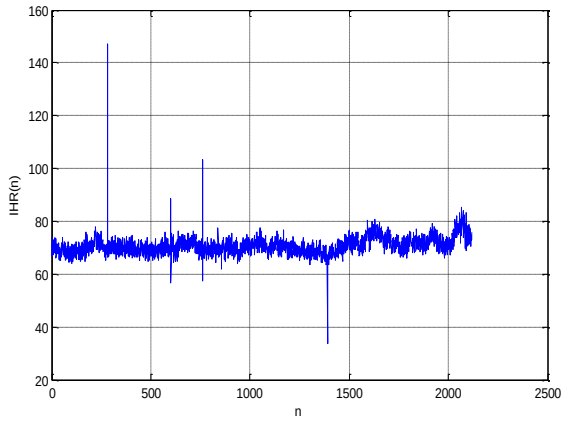

Figure 3.1 : n vs RR interval

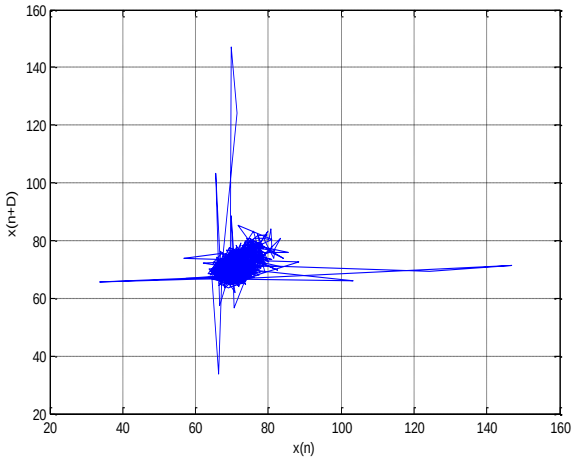

Figure 3.2 : X(n) vs X(n-1)

ii. *Simulation Results for abnormal patient*

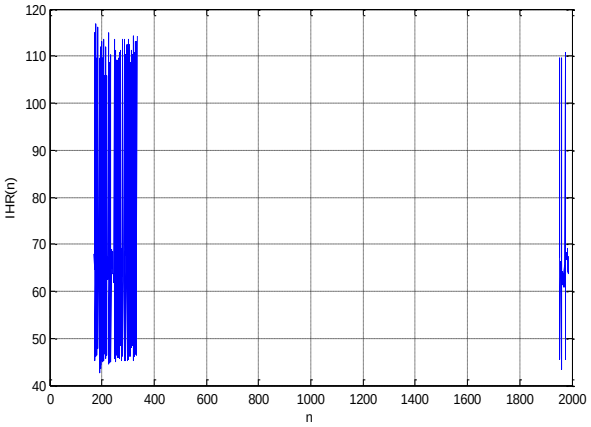

Figure 3.3 : n vs RR interval

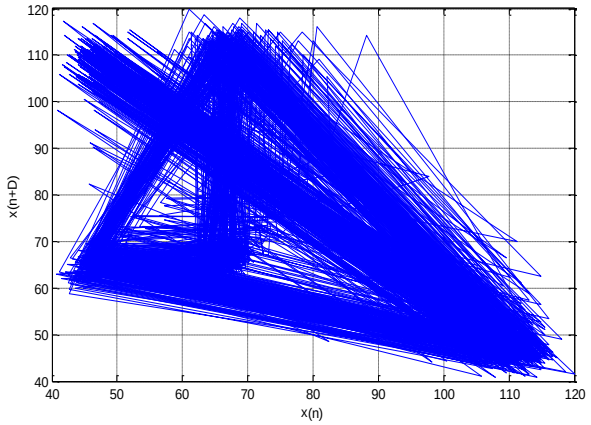

Figure 3.4 : X(n) vs X(n-1)

From the phase space plot for IHR, there lies significant difference between normal and abnormal rhythms. For the normal rhythm, there is normal attractor which forms a slope of almost 45 degree with the axes and there is slight dispersion around that attractor. For the abnormal rhythm, it is seen that their phase space portrait fill more space in the plane and there is random attractor present in the plot.

b) Simulation Result of Poincare plot Analysis

i. *Comparison of simulation results between normal & abnormal patients*

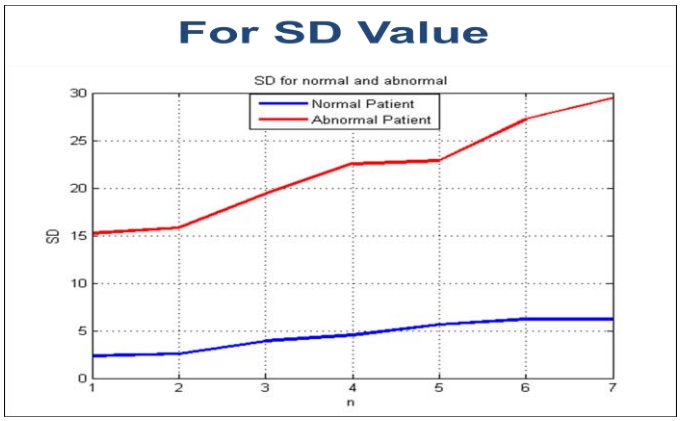

Figure 3.5 : SD Value for normal & abnormal patient

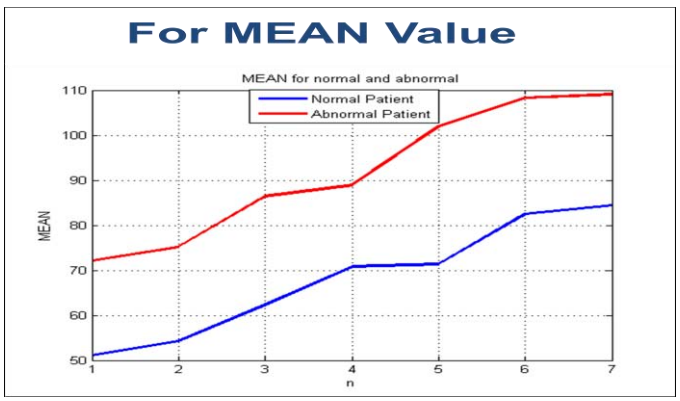

Figure 3.6 : MEAN Value for normal & abnormal patient

Here from the Fig it is seen that the abnormal patients SD is higher than the normal patients. Similarly the abnormal patients MEAN VALUE, VAREANCE, RMSSD, SDSD, is more than the normal patients

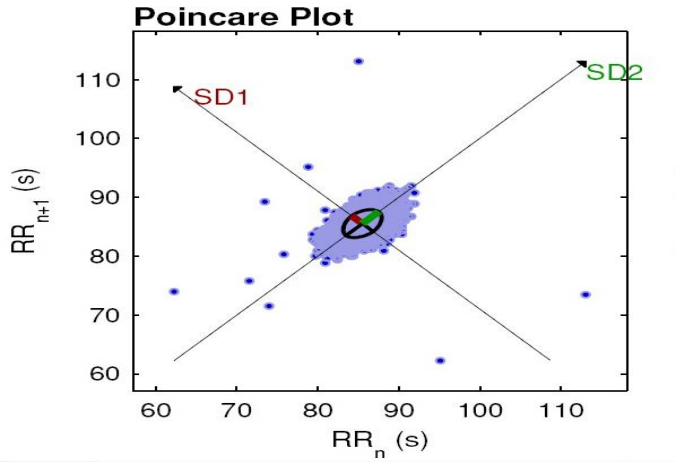

Figure 3.7 : Poincare plot for normal patient [16]

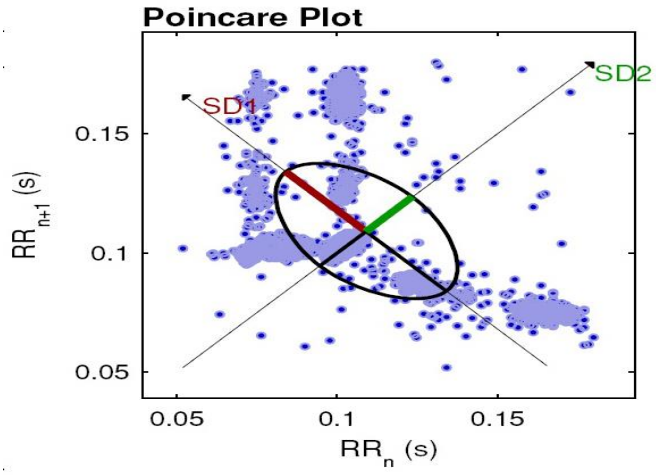

Figure 3.8 : Poincare plot for abnormal patient [16].

Here from the figure it is seen that the all data of the normal patients is close to center. But for the abnormal patients the data scatter from the center as a result the area fill-up by the abnormal patients is more than the area fill-up by the normal patients.

ii. *Comparison based on Poincare plot*

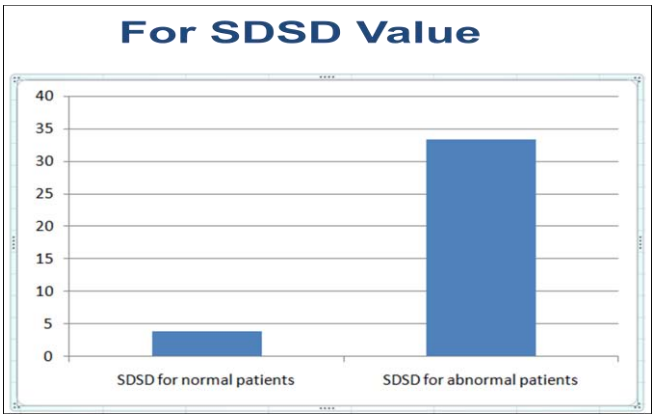

Figure 3.9 : SDSD for normal & abnormal patient

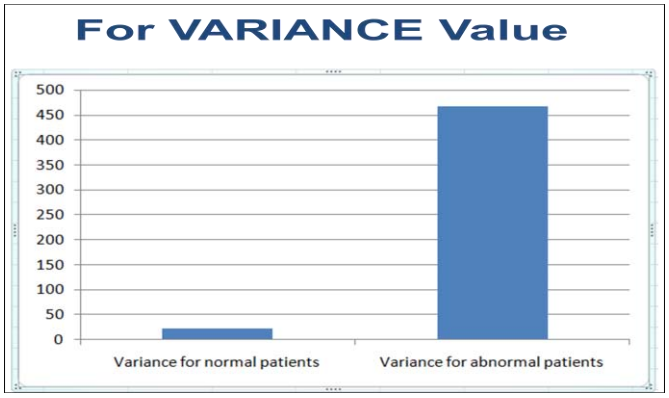

Figure 3.10 : VARIANCE for normal & abnormal patient

From the above figure is seen that the SDSD VALUE for normal patients is 3.92 and for abnormal patients is 33.47.Theoretically for normal patient value of SDSD should be less than 5 and for abnormal patient value of SD should be less than 5.where correct value is achieved and clearly detect the abnormal patients. Similarly for VARIANCE perfect value is achieved to detect the normal and abnormal patients.

c) Simulation Result of Detrended Fluctuation Analysis

i. *Comparison between normal and abnormal patients for DFA*

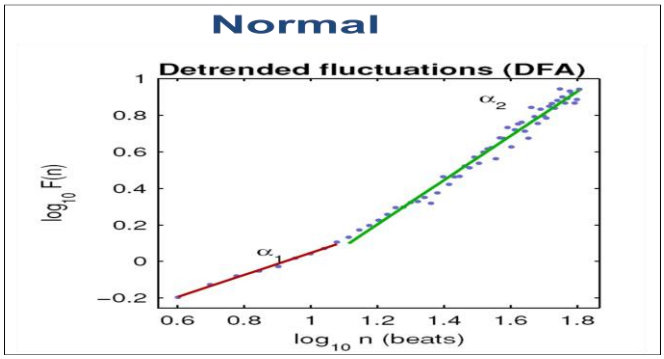

Figure 3.11 : DFA for normal patients

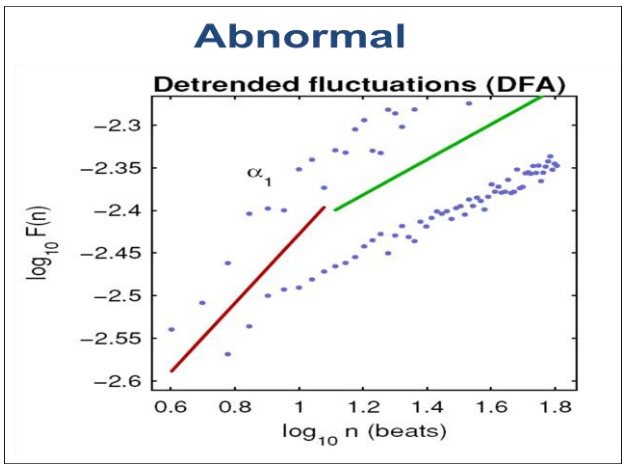

Figure 3.12 : DFA for abnormal patients

Using the DFA method it can be distinguished healthy from unhealthy subjects. Also can be determined which signal is more regular and less complex – useful for analyzing biomedical signals. It's concluded that using non- linear dynamics methods like DFA method is a quantitatively and qualitatively study of physiological signals.

ii. *Comparison based on AREA for Detrended Fluctuation Analysis*

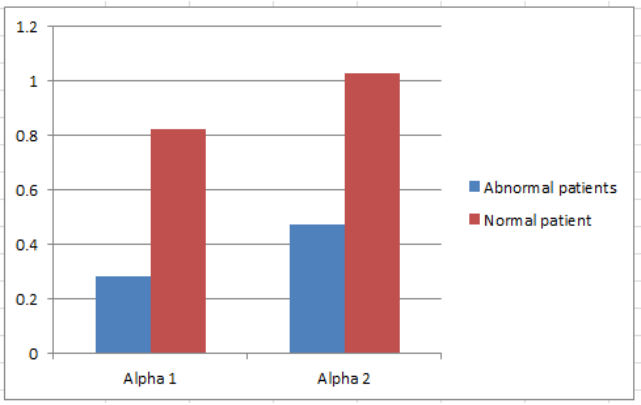

Figure 3.13 : Comparison of AREA between normal & abnormal patients.

From Fig it is seen that Alpha1&2 for normal patients is more than the abnormal patients.

So, if here compare the four techniques it is used namely phase space portrait, Poincare plot DFA and the central tendency measure with the following facts should came out . Phase space portrait only gives us a visual observation of the ECG signals, whether they are from normal or abnormal rhythms. Poincare plot & DFA is more complex to find the normal and abnormal rhythms. On the contrary, central tendency measure quantifies the abnormality levels present in the ECG signals. Moreover, it roughly gives an idea about the abnormality type as observed in our work.

d) Simulation Result of Central Tendency Measure

i. *Simulation Result for both SD-4 and SD-6*

CTM value for SD 10% :

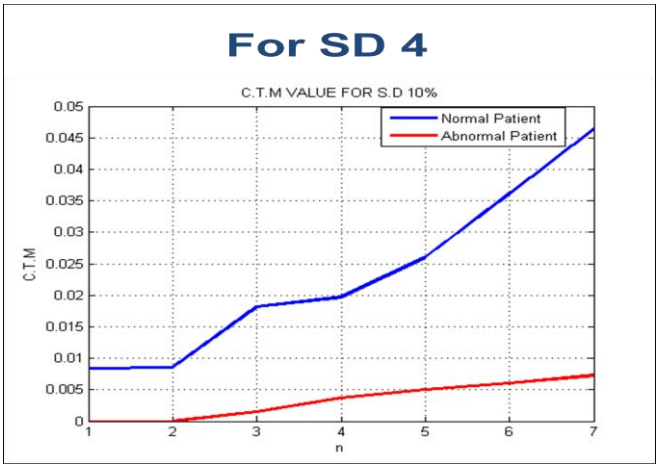

Figure 3.14 : CTM for normal & abnormal patient

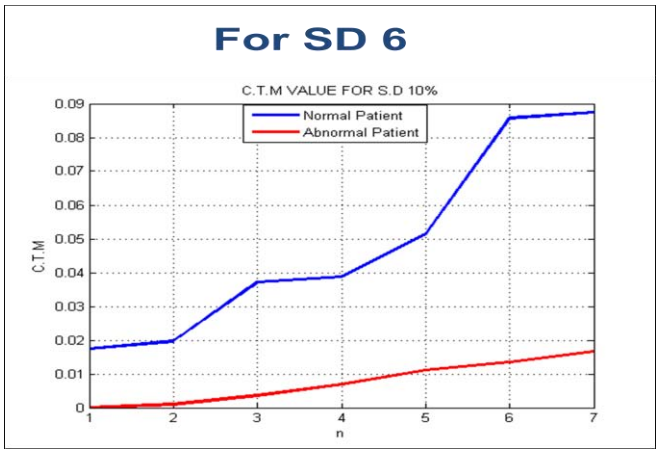

Figure 3.15 : CTM for normal & abnormal patient

CTM value for SD 100% :

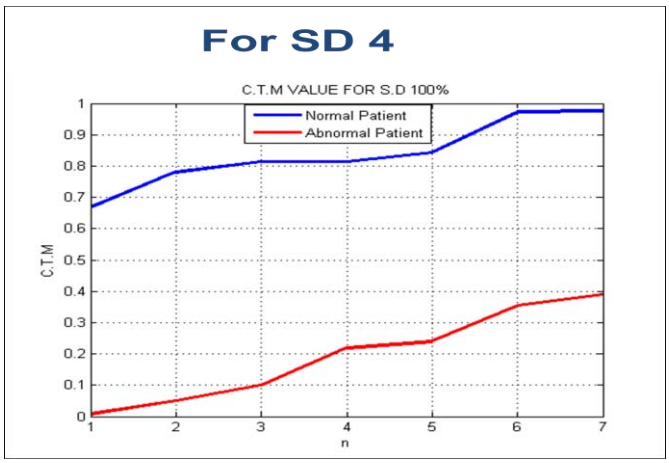

Figure 3.16 : CTM for normal & abnormal patient

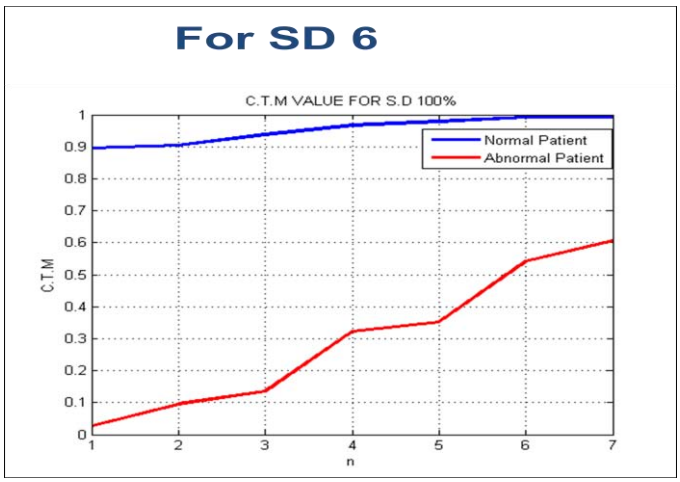

Figure 3.17 : CTM for normal & abnormal patient

Average CTM form 10% to 100% :

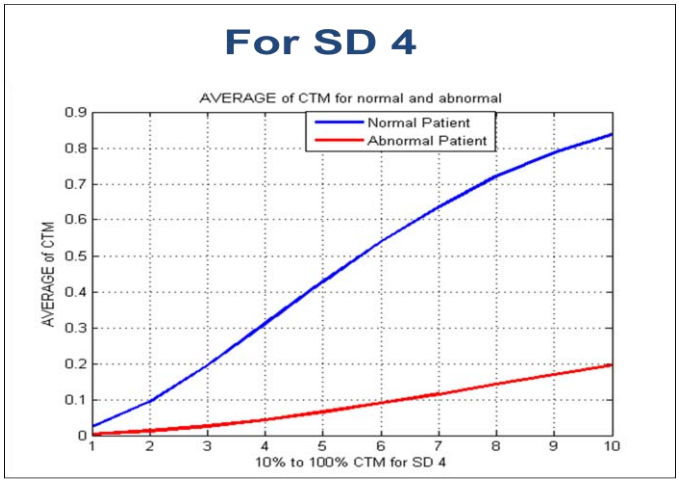

Figure 3.18 : Avg CTM for normal & abnormal patient

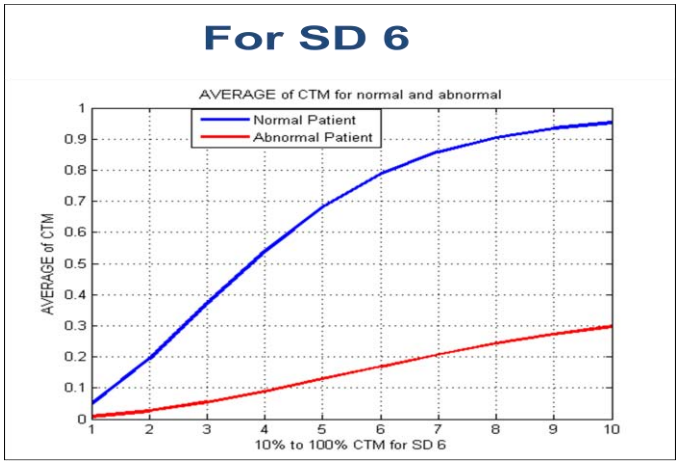

Figure 3.19 : Avg CTM for normal & abnormal patient

Here from the Figure 3.14 to 3.19 it is seen that central tendency is gradually increased with respect to the standard deviation than the normal patients. At the same way for the abnormal patients central tendency is not sharply increased with respect to standard deviation and the CTM values is always lower than 0.5 for abnormal patients. The normal patients's CTM value is similarly increased with respect to SD increase from 10% to 100 %. But for abnormal patients CTM values is increased gradually with respect to SD increase from 10% to 100. The normal patients's CTM value's is much higher than both abnormal patients's so it can be perfectly said that the normal patients's is much more healthy than other normal patients.

ii. *Comparison based on CTM*

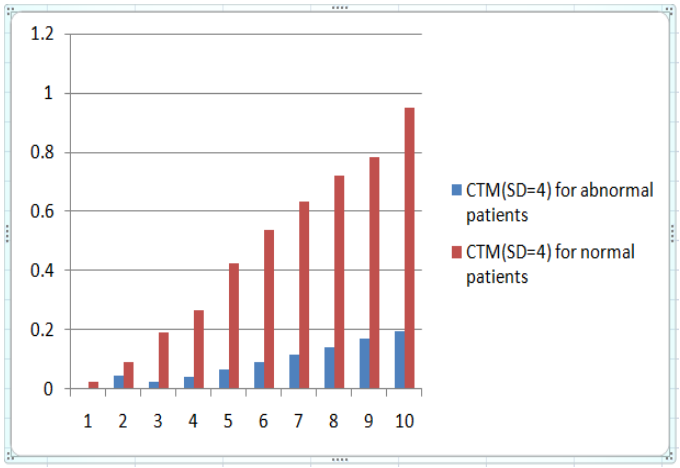

Figure 3.20 : Comparison between normal & abnormal patients (SD-4)

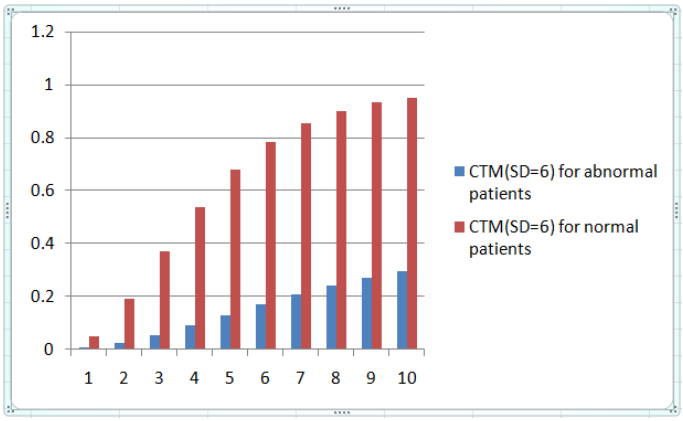

Figure 3.21 : Comparison between normal & abnormal patients (SD-6)

From this Figure 3.20 when the SD = 4 then the average value of CTM for normal patients is more than the CTM of abnormal patients. From this Fig 3.20 it is found that when the SD = 6 then the average value of CTM for normal patients is more than the CTM of abnormal patients. But when SD=6 is used it provides more clear data than SD = 4.

So, here comparing the four techniques namely phase space portrait, Poincare plot DFA and the central tendency measure, it can come out with the following facts. Phase space portrait only gives us a visual observation of the ECG signals, whether they are from normal or abnormal rhythms. Poincare plot & DFA is more complex to find the normal and abnormal rhythms. On the contrary, central tendency measure quantifies the abnormality level presented in the ECG signals. CTM is simpler and give a clear idea than the other techniques. Moreover it roughly gives an idea about the abnormality type as observed in this work.

IV. Conclusion and Future Work

In this work PVC in ECG data set have been identified. The whole work is based on the fact that R-R intervals for normal rhythm data set tend to invariant and for the abnormal rhythm data set tend to vary a lot. This work describes the application of phase space portrait, Poincare Plot, DFA and CTM. Phase Space Portrait is a visible technique. From Poincare Plot a significant difference between normal and abnormal rhythm have been achieved. DFA determine the fluctuation of RR interval from the Slope. For normal rhythm value of CTM is more than the abnormal rhythm. Here clear difference for the normal and abnormal rhythm and high level of accuracy between them has been achieved. So it can be said that it is better to use CTM for classifying the ECG as normal or abnormal. In this paper abnormality of ECG signal have been detected specially in PVC cases. In future several frequency domain methods (i.e cross entropy analysis, Lyapunov Exponents, Support Vector Machine (SVM), Discrete Cosine Transform (DCT)) will be added to detect the abnormalities of heart. Future

work may also include working with more number of abnormal records to generalize the detection of beat abnormality type.

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