



International Journal of Advanced Research in Electrical, Electronics and Instrumentation Engineering

An ISO 3297: 2007 Certified Organization

Vol. 5, Special Issue 6, July 2016

4th National Conference on Design Innovations for 3Cs "Compute-Communicate-Control"

Organized by

Dept. of ECE, MVJ College of Engineering, Bangalore-560067, India

Analysis of ECG Signal by using TPSM Algorithm and Disease Diagnosis

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ABSTRACT: Since from the past decade in medicine field, number of heart signal monitoring systems have been built and developed different ways of representing the heart rate variability. This paper is about application of triangular phase space mapping (TPSM) algorithm which is a new way of representing heart rate variability and diagnosis of heart diseases using this algorithm. The feature extraction of the ECG signal was performed by the TPSM and the results were built forming a new database, showing the behavior of different ECG signals using MATLAB. The results are used for the disease diagnosis.

KEYWORDS: ECG, heart rate variability HRV processing, Triangular Phase Space Mapping (TPSM), Disease diagnosis.

I.INTRODUCTION

The surface ECG is the recorded potential difference between two electrodes placed on the surface of the skin at predefined points [1]. Since the ECG signal contains R wave with higher amplitude, it gives maximum information from the signal. The time interval between the R to R wave gives you the RR interval of that ECG signal. The variability in a series of RR intervals has been widely used as a measure of heart function which helps to identify patients at risk for a cardiovascular event or death [1]. The study of HRV signal provides more precious data for the biological analysis of heart rate fluctuations [1]. The importance of this signal needs more exploration of methods as backings to medical calculation. Many experiments have been done to extract various kinds of statistics from HRV signal in various ways. Time, Frequency and nonlinear analysis of this signal are the majors processing that have been done on HRV signal and the resulted features are useful tools for diagnosis different problems in heart function [1].

The Poincare plot is a tool developed by Henry Poincare for analyzing multifarious systems [2]. It has found its use in such diverse fields as physics and astronomy, geophysics, meteorology, mathematical biology and medical sciences. In the context of medical sciences, it is mainly used for enumerating HRV and proves to be quite an effective measure of this marker [3]. Poincare plot is a geometrical representation of RR time series to demonstrate patterns of heart rate dynamics resulting from nonlinear processes [4]. Poincare plot analysis of RR time series allows a beat-to-beat approach to HRV, detecting patterns associated with nonlinear processes [5]. But standard analyses of Poincare plot are linear statistics and hence the measures do not directly quantify the nonlinear temporal variations in the time series contained in the Poincare plot. Moreover, it has some limitation to investigate all the physiological mechanisms in a time series [5]. For distinguishing the behavior of different arrhythmia, accessing to more information of HRV dynamics is necessity. For obtaining this purpose, in our previous article, we introduced a novel mapping for heart rate which we named Triangle Phase Space Mapping [5]. Then, we extract geometric features in this new map to detect new aspects of HRV dynamics. For more information about this mapping refer to [5]. We found that this new mapping is so useful not only in discrimination of different arrhythmia [5], but also in detection psychological [5] and emotional response of heart. In this paper we have used TPSM algorithm to extract features of the ECG signal. We have simulated the results in MATLAB tool.

II.THE TPSM ALGORITHM

Triangle Phase Space Mapping (TPSM) was introduced in 2010.deppending on the point's distribution in this new

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space, we fetch the new geometric features such as, Area of the triangle, Angles, vertices of the triangle, the slope of the line, the length of sides perimeter of the triangle and so on which are explained further and classifying different groups of disease which is followed by results of the TPSM algorithm. To find the parameters of the triangle, RR interval values of the signal is used to generate a triangle corresponding to a particular ECG signal and the statistical analysis is used as show.

Mean of the RR interval is calculated as [6]

$$\overline{RR} = \frac{1}{N} \sum_{i=1}^{N} RRi$$

The vertices of the triangle are given as [6]

$$A(\min(RRi), |\overline{RR} - \min(RRi)|)$$

 $B(\max(RRi), |\overline{RR} - \max(RRi)|)$
 $C(RRc, \min(|\overline{RR} - RRc|))$

The sides of the triangle ABC are [6]

$$a = \sqrt{(Xb - Xc)^2 + (Yb - Yc)^2}$$

$$b = \sqrt{(Xa - Xc)^2 + (Ya - Yc)^2}$$

$$c = \sqrt{(Xa - Xb)^2 + (Ya - Yb)^2}$$

The slope of the side c is m_c [6]

$$mc = \frac{Yb - Ya}{Xb - Xa}$$

The angles of the triangle are given by [6]

$$A = \cos^{-1}\{(b^2 + c^2 - a^2)/2bc\}$$

$$B = \cos^{-1}\{(a^2 + c^2 - b^2)/2ac\}$$

$$C = \cos^{-1}\{(a^2 + b^2 - c^2)/2ab\} = 90^{\circ}$$

The perimeter, the area and the quality of the triangle is given by respectively [6]

$$p = a + b + c$$

$$S = \frac{1}{2} |(Xa - Xc)(Yb - Ya) + (Xa - Xb)(Yc - Ya)|$$

$$q = \frac{4\sqrt{3}S}{a^2 + b^2 + c^2}$$

The parameters A, B, C, a, b, c, mc, S, p and q are further discussed for the disease diagnosis.

III.DISEASE DIAGNOSIS USING TPSM

In this paper we have introduced new Fig.1. shows the disease diagnosis system using TPSM algorithm. The RR interval is calculated from the ECG signal. The series of RR differences are fed to the TPSM algorithm. Before you begin the feature extraction first check the peak values of the R waves to calculate the threshold value of the peak. The results of some of the samples from the MIT-BIH Arrhythmia Database Directory (Records) is shown in Table 1.

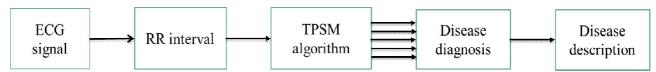


Fig. 1. Disease diagnosis system using TPSM algorithm.

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According to MIT-BIH database and records, the signal characteristics which signifies the disease symptoms are seen in the Table 1. The area of the triangle, the perimeter, sides of the triangle, slope of the side c and the angle C in the triangle are suspicious to the disease diagnosis. The results give the behavior of the signals. The following are some of the important observations that are found while experimenting the signals in MATLAB:

- 1) Slope m_c is negative when there is an axial shift in the ECG signal (it may be either upper shift or lower shift).
- 2) RR_{avg} , RR_{max} and RR_{min} values signifies the missing beats or change in duration in the ECG signal. Which implies there must be a missing beat along with the shift in the axis
- 3) The area of triangle S and perimeter of the triangle P signifies that the RR_{max} and RR_{min} separations are causing a drastic change in the signal peak values as well as the missed peaks or abnormalities.

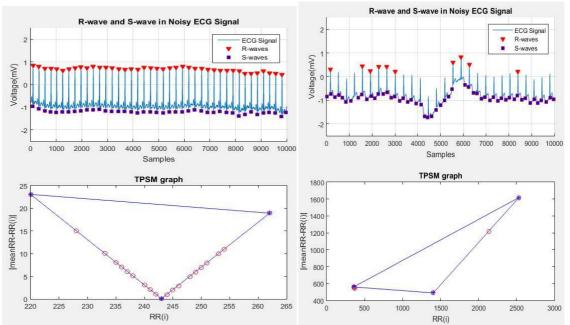


Fig. 2. TPSM results for patient No 100 from MIT-BIH.Fig. 3. TPSM results for patient No 121 from MIT-BIH.

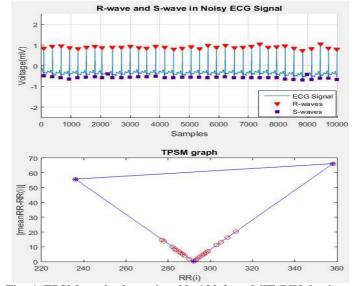


Fig. 4. TPSM results for patient No 122 from MIT-BIH database

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IV.RESULTS

Table 1. TPSM Results of the experiment

Patient	A	В	С	A	В	С	Mc	P	S	Q
No.										
100	49.6718	41.8612	90.2114	93.3381	78.9053	122.4435	0.0853	294.6869	3734.5000	0.8644
101	46.1193	43.1578	91.4203	35.3553	33.1301	49.0476	0.0441	117.5331	586.5645	0.8550
102	47.8080	42.4774	90.9285	29.6985	26.4450	40.0848	0.0652	96.2283	395.2424	0.8589
103	60.1070	33.8326	92.0673	34.1458	18.3848	39.3602	0.2699	91.8908	375.2258	0.8515
104	32.7183	52.8398	90.5100	28.0358	43.8406	52.2483	-	124.1248	676.9706	0.8625
							0.2226			
105	45.0183	44.9110	90.1318	149.9066	149.5630	212.0006	0.0023	511.4702	11210.00	0.8650
106	45.1932	44.0286	91.0759	97.1873	94.7523	137.0006	0.0031	328.9402	4604.20	0.8577
107	14.8701	70.3641	92.1500	25.9160	176.7767	179.6257	-	382.3184	7979.9000	0.8613
							0.7457			
109	87.1725	22.9715	90.0710	998.6123	48.0833	999.8288	0.9059	2046.5000	249880.0000	0.8660
111	46.4832	42.8824	91.4742	26.8701	24.8254	37.0489	0.0514	88.7444	334.3710	0.8545

In this analysis, we have used Kruskal-Wallis test to define the level of significance of proposed features [6]. Kruskal-Wallis test is a nonparametric version of the classical one-way ANOVA, and an extension of the Wilcoxon rank sum test to more than two groups. The supposition behind this test is that the extents come from a incessant distribution, but not inevitably a normal distribution. The experiment is based on an analysis of variance using the ranks of the data values, not the data values themselves [1] [6]. In our study, this test has been used to evaluate the hypothesis for each feature separately. In case of p < 0.05 to be considered as significant [6], we can see that TPSM features would show the significant difference between groups which p value is shown in the Table 1.

In order to validate the proposed features, measurements A, B, and C, we have used them to distinguish four groups of subjects (Arrhythmia, Congestive Heart Failure (CHF), Atrial Fibrillation (AF) and Normal Sinus Rhythm (NSR)). For each groups, we analyze these features distinctly. The data from MIT-BIH Physionet database [7] are used in the research. In this study, we have used 15 long-term ECG recordings of patients in normal sinus rhythm from Phytsionet Normal Sinus Rhythm database [7]. Also, we have used NHLBI sponsored Cardiac Arrhythmia Suppression Trial (CAST) RR-Interval Sub-study database for the arrhythmia data set from Physionet. Subjects of CAST database had a critical myocardial infarction (MI). The database is distributed into three different study groups among which we have used the Encainide (e) group data sets for our study. From Encainide (e) group we have selected 15 subjects belong to subgroup baseline (no medication) [8]. Also, we have used 15 long-term ECG recordings of subjects with CHF from Physionet Congestive Heart Failure database along with 15 ECG recordings of subjects with Atrial Fibrillation from Physionet Atrial Fibrillation database. The original long term ECG recordings were digitized at 128 Hz[8].

V.CONCLUSION

In this paper, the main moto is to introduce a new methodology that is helpful in diagnosing the heart and find the problems present in it, using the TPSM features extraction. The TPSM algorithm enables the user to check diverse geometric analysis on ECG signal and extract the features which each one may reflect different phases of HRV activities. Using this algorithm, in future, a medical instrument can be developed such that the patients can be able to see the results of their heart test or behavior of HRV signal without consulting any doctor. This may change the course of the system in the future of medicine field.

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