Application of Novel Mapping for Heart Rate Phase Space and Its Role in Cardiac Arrhythmia Diagnosis

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Abstract

The nonlinear analysis of Heart Rate Variability (HRV) is a valuable tool in both clinical practice and physiological research reflecting the ability of the cardiovascular system. Poincare plot is a geometrical representation of RR time series to demonstrate patterns of heart rate dynamics resulting from nonlinear processes. In this paper, by using Poincare plot points we introduced a novel mapping for heart rate phase space in which by analyzing the point's distribution, we could estimate a two degree polynomial equation in the form of $y = Ax^2+Bx+C$. *The useful features obtaining of this map are the coefficients A, B, and C. For evaluating them, we try to distinguish three groups of subjects using the Physionet database (Arrhythmia, Congestive Heart Failure (CHF), and Atrial Fibrillation (AF)) with Normal Sinus Rhythm (NSR). Kruskal-Wallis test was used to define the level of significance of each feature for different groups of subjects to demonstrate the usefulness of the proposed method in cardiac arrhythmia diagnosis. The results show that these features discriminate CHF from NSR subjects by p<E-4; arrhythmia from NSR by p<E-5; and AF from NSR by p<E-4.*

1. Introduction

A time series of RR interval is the time between successive R-waves and the variation in the time series of consecutive heartbeats is referred as Heart Rate Variability (HRV) [1].

Heart rate is an indicator of heart's condition [2]. Assessment of heart rate has been shown to aid clinical diagnosis and intervention strategies. It has been proved that nonlinear analysis of it might provide more valuable information for the physiological interpretation of heart rate fluctuations [3]. However, the variety of contradictory reports in this field indicates that there is a need for a more rigorous investigation of methods as aids to clinical evaluation. The nonlinear analysis of HRV is a valuable tool in both clinical practice and physiological research reflecting the ability of the cardiovascular system [4].

The Poincare plot is a tool developed by Henry Poincare for analyzing complex systems [5]. 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 quantifying HRV and proves to be quite an effective measure of this marker [6]. Poincare plot is a geometrical representation of RR time series to demonstrate patterns of heart rate dynamics resulting from nonlinear processes [7]. Poincare plot analysis of RR time series allows a beat-to-beat approach to HRV, detecting patterns associated with nonlinear processes [8]. It is a familiar method for the analysis of two-dimensional nonlinear dynamic systems [9]. Tulppo et. al. [10] fitted an ellipse to the distribution of the poincare plot and defined two standard descriptors *SD1* and *SD2* for quantification of the poincare plot geometry. These standard descriptors represent the minor axis and the major axis of the ellipse (Fig. 1) and guide the visual inspection of the distribution. In case of HRV, it reveals a useful visual pattern of the RR interval data by representing both short and long term variations of the signal [11]. But standard descriptors *SD*1 and *SD*2 are

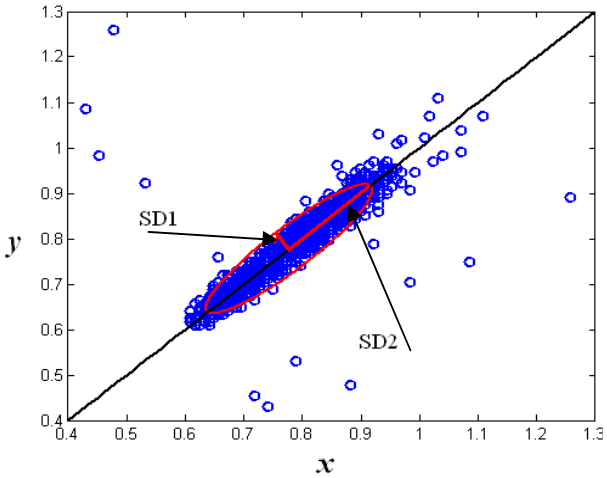

Figure 1. Poincare plot of RR intervals of a healthy person with its standard descriptors *SD1* and *SD2*

linear statistics and hence the measures do not directly quantify the nonlinear temporal variations in the time series contained in the poincare plot. Moreover, the limitations of the *SD*1/*SD*2 analysis are important to understand when attempting to investigate the physiological mechanisms in a time series, or when analyzing data where the occurrence of nonlinear behaviour may be a distinguishing feature between health and disease [11].

In this paper, we introduced a novel mapping for heart rate which we named Parabolic Phase Space Mapping (*PPSM).* Then, we measure three features in this new map to detect new aspects of poincare plot.

For evaluating these features in new map (*PPSM*), we try to use them for distinguishing four groups of subjects (Arrhythmia, Congestive Heart Failure (CHF), Atrial Fibrillation (AF) and Normal Sinus Rhythm (NSR)).

2. Standard descriptors of poincare plot

A standard poincare plot of RR interval is shown in figure 1. Given a time series RR = {RR_1, RR_2, …, RR_n, RR_{n+1}} the standard poincare plot is a scattergram constructed by locating points from the time series on the coordinate plane according to the pairing (x_i, y_i) in which,

$$x = \{x_1, x_2, \ldots, x_n\} = \{RR_1, RR_2, \ldots, RR_n\} \quad (1)$$

$$y = \{y_1, y_2, \ldots, y_n\} = \{RR_2, RR_3, \ldots, RR_{n+1}\} \quad (2)$$

and i = 1, 2, 3, …, n and *n* is the number of points in the poincare plot which is one less than the length of the RR time series (12).

As mentioned above, *SD1* and *SD2* are two standard descriptors of poincare plot. *SD2* is defined as the standard deviation of the projection of the poincare plot on the line of identity (*y* = *x*), and *SD1* is the standard deviation of projection of the poincare plot on the line perpendicular to the line of identity (*y* = -*x*) (6). So we may define them as:

$$SD1 = (Var(d_1))^{1/2}, \quad SD2 = (Var(d_2))^{1/2} \quad (3)$$

where Var(d) is the variance of *d*, and

$$d_1 = (x-y) / (2)^{1/2}, \quad d_2 = (x+y) / (2)^{1/2} \quad (4)$$

3. Parabolic Phase Space Mapping

In this section, first we introduced our novel mapping: Parabolic Phase space Mapping (*PPSM*). Then, base on point's distribution in this new space, we extract three new features that in the following, the theoretical development of them has been given and then they have been used for distinguishing different groups of subjects which is followed by statistical analysis.

3.1. Construction of PPSM and definition of its features

For constructing this new mapping using typical poincare plot points, we used the relations in (1) and (2). As mentioned earlier, this new phase space is based on typical Poincare plot points in relation to the mean of *RR* intervals which is defined as:

$$mean(RR) = \overline{RR} = \frac{1}{n+1}\sum_{i=1}^{n+1} RR_i \quad (5)$$

So *PPSM* consists of all the ordered pairs:

$$(x_i, (\overline{RR} - y_i)^2) \quad (6)$$

in which i = 1, 2, 3, …, n.

By evaluating the distribution of points in *PSPM* which is shown in Fig. 2, we could estimate a two degree polynomial equation in the form of $Y = Ax^2+Bx+C$, in which:

$$Y = (\overline{RR} - y_i)^2 \quad (7)$$

The useful features obtaining of this map are the coefficients of the estimated polynomial (*A*, *B*, and *C*) which fit the set of data in *PPSM*. We found them using MATLAB (2009).

4. Discrimination of heart arrhythmia

In order to validate the proposed features, coefficients *A*, *B*, and *C*, we have used them to discriminate four groups of subjects (Arrhythmia, Congestive Heart Failure (CHF), Atrial Fibrillation (AF) and Normal Sinus Rhythm (NSR)). For each groups, we calculate these features separately.

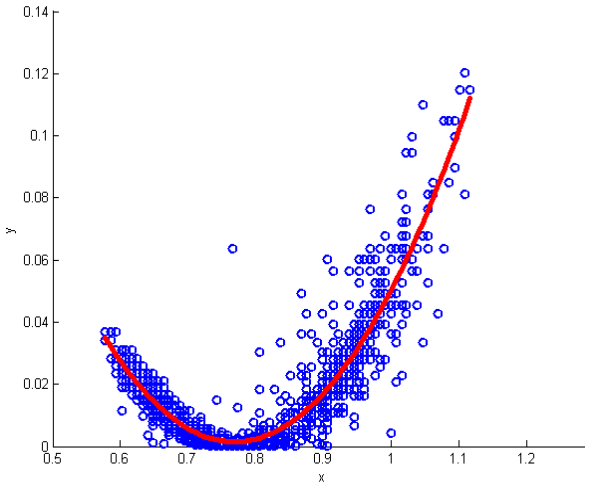

Figure 2. Points' distribution in *PSPM* and the estimation of a quadratic equation for them

The data from MIT-BIH Physionet database [13] are used in the experiment. In this study, we have used 15 long-term ECG recordings of subjects in normal sinus rhythm from Physionet Normal Sinus Rhythm database [13]. Furthermore, we have also 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 an acute myocardial infarction (MI). The database is divided into three different study groups among which we have used the Encainide (e) group data sets for our study. From that group we have chosen 15 subjects belong to subgroup baseline (no medication) [13]. 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 [13]. The original long term ECG recordings in every four groups were digitized at 128 Hz [13].

5. Results

For comparing the results and evaluate the proposed parameters, we have used statistical analysis which are explained in details in next section.

5.1. Statistical analysis

In this study, we have used Kruskal-Wallis test to define the level of significance of our proposed features.

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 assumption behind this test is that the measurements come from a continuous distribution, but not necessarily a normal distribution. The test is based on an analysis of variance using the ranks of the data values, not the data values themselves.

In our study, this test has been used to evaluate the hypothesis for each feature separately. The p values obtained from Kruskal-Wallis analysis are shown in Table 1 for coefficients *A*, *B* and *C*.

In case of $p < 0.05$ to be considered as significant, we can see that *PSPM* features would show the significant difference between groups which p value is shown in Table 1.

Table 1. *p-Value Results for PSPM Features*

Groups	*PSPM* Features		
	Coefficient A	Coefficient B	Coefficient C
NSR, CHF	0.0001	0.0002	0.1826
NSR, CAST	1.029E-5	0.0058	0.5503
NSR, AF	0.0003	0.0002	0.0006

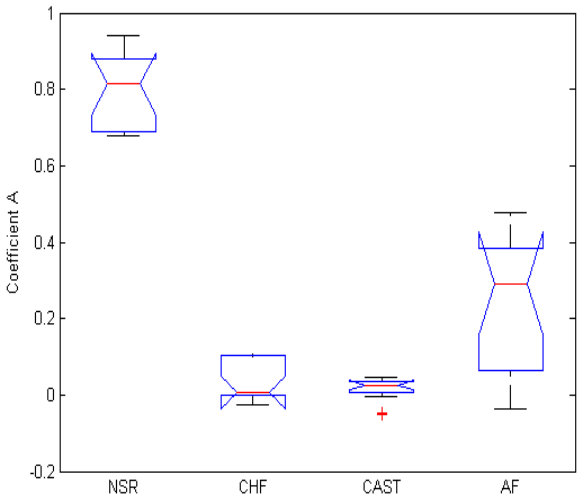

Figure 3. Box-Whiskers Plot of *A* coefficient for four groups of subjects

The results show that coefficient *A* has the best results and doesn't depend on the type of arrhythmia (Fig. 3). It discriminate CHF from NSR by $p<E-4$; AF from NSR by $p<3E-4$; and arrhythmia from NSR by $p<E-5$.

6. Discussion

In this novel method, we have used the function between current data of time series and the following one. Hence, it seems that this kind of mapping and the resulted quadratic equation has the capability of being used as a prediction method for some kinds of cardiac arrhythmia. So this method would be evaluated in most cases and compared with clinical results to detect its more advantages in cardiac arrhythmia diagnosis.

References

[1] McLernon D, Dabanloo N, Ayatollahi A, Majd V, Zhang H. A new nonlinear model for generating RR tachograms. Computers in Cardiology, 2004. 2004:481-4.

[2] Dabanloo N, McLernon D, Ayatollahi A, Majd V, editors. A nonlinear signal processing approach to model heart rate variability2004.

[3] Hnatkova K, Copie X, Staunton A, Malik M. Numeric processing of Lorenz plots of RR intervals from long-term ECGs*:: Comparison with time-domain measures of heart rate variability for risk stratification after myocardial infarction. Journal of Electrocardiology. 1995;28:74-80.

[4] Karmakar C, Khandoker A, Gubbi J, Palaniswami M. Defining asymmetry in heart rate variability signals using a Poincaré plot. Physiological measurement. 2009;30:1227.

[5] Kamen P, Krum H, Tonkin A. Poincare plot of heart rate variability allows quantitative display of parasympathetic nervous activity in humans. Clinical science. 1996;91:201-8.
[6] Piskorski J, Guzik P. Filtering Poincaré plots. Computational methods in science and technology. 2005;11(1):39-48.
[7] Schechtman V, Raetz S, Harper R, Garfinkel A, Wilson A, Southall D, et al. Dynamic analysis of cardiac RR intervals in normal infants and in infants who subsequently succumbed to the sudden infant death syndrome. Pediatric research. 1992;31(6):606.
[8] Woo M, Stevenson W, Moser D, Trelease R, Harper R. Patterns of beat-to-beat heart rate variability in advanced heart failure* 1. American Heart Journal. 1992;123(3):704-10.
[9] Brennan M, Palaniswami M, Kamen P. Do existing measures of Poincaré Plot geometry reflect nonlinear features of Heart Rate Variability? IEEE transactions on biomedical engineering. 2001;48(11):1342-7.
[10] Tulppo M, Makikallio T, Takala T, Seppanen T, Huikuri H. Quantitative beat-to-beat analysis of heart rate dynamics during exercise. American Journal of Physiology- Heart and Circulatory Physiology. 1996;271(1):H244.
[11] Karmakar C, Khandoker A, Gubbi J, Palaniswami M. Complex Correlation Measure: a novel descriptor for Poincaré plot. BioMedical Engineering OnLine. 2009;8(1):17.
[12] Piskorski J, Guzik P. Geometry of the Poincaré plot of RR intervals and its asymmetry in healthy adults. Physiological measurement. 2007;28:287.
[13] Goldberger A, Amaral L, Glass L, Hausdorff J, Ivanov P, Mark R, et al. PhysioBank, PhysioToolkit, and PhysioNet: Components of a new research resource for complex physiologic signals. Circulation. 2000;101(23):e215.

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