Extended Triangle Phase Space Mapping: Novel Method for Representation of Heart Rate Variability Signals

Sadaf Moharreri[1], Nader Jafarnia Dabanloo[1], Gholamreza Attarodi[1], Saman Parvaneh[1], Ali M Nasrabadi

[1] Department of Biomedical Engineering, Science and Research Branch, Islamic Azad University, Tehran, Iran
[2] Shahed University, Tehran, Iran

Abstract

In this paper, we have introduce new features in the Extended Triangle Phase space mapping (ETPSM), a novel method for representation of heart rate which is obtaining by using RR interval time series signal to plot the Triangle mapping consist of all the ordered pairs: (RR_i, abs ($\overline{RR} - RR_{i+1}$)), $i = 1, \dots, N$ where $\overline{RR}$ is the mean of RR intervals. We obtained a triangle from the distribution of these points and introduced three new features in this mapping by counting the points in, on and out of the triangle. These features were evaluated in distinguishing four groups of subjects (Arrhythmia, Congestive Heart Failure (CHF), Atrial Fibrillation (AF) and Normal Sinus Rhythm (NSR)) obtained of Physionet database. The results show that these features discriminate arrhythmia from NSR subjects by p<1E-6; CHF from NSR by p<2E-3; AF from NSR by p<4E-4; CHF from arrhythmia by p<1E-2; CHF from AF by p<5E-4; and arrhythmia from AF by p<2E-3.

1. Introduction

The Poincare plot is a tool developed by Henry Poincare for analyzing complex systems (1). 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 (2). Poincare plot is a geometrical representation of RR time series to demonstrate patterns of heart rate dynamics resulting from nonlinear processes (3). Poincare plot analysis of RR time series allows a beat-to-beat approach to HRV, detecting patterns associated with nonlinear processes (4).

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 (6). Then, we extract geometric features in this new map to detect new aspects of HRV dynamics. For more information about this mapping refer to (6). We found that this new mapping is so useful not only in discrimination of different arrhythmia (6), but also in detection psychological (7) and emotional (8) response of heart to color stimulation.

In this paper, we have extended this map and introduce new features in this novel extended mapping.

For evaluating these features in new map (*ETPSM*), 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

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,

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

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

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 (9), (10) (Figure 1).

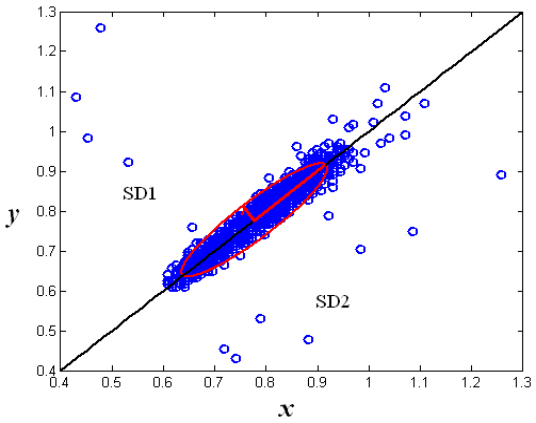

Figure 1. Poincare plot of RR intervals of a healthy person with its standard descriptors *SD1* and *SD2*

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 ($y = -x$) (2). So we may define them as:

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

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

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

3. Extended triangle phase space mapping

In this section, first we introduced our novel mapping: Extended Triangle Phase space Mapping (*ETPSM*). 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 ETPSM 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:

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

So *ETPSM* consists of all the ordered pairs:

$$\left(x_i, abs(\overline{RR} - y_i)\right) \qquad (6)$$

in which i = 1, 2, 3, …, n.

By analyzing the point's distribution in this new map, we could obtain a triangle which for the all kinds of HRV has special features. This triangle is shown in Fig. 3.

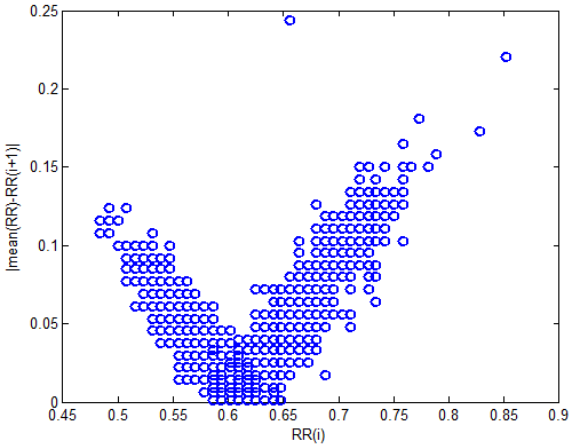

Figure 2. The distribution of points in *ETPSM*

For all kinds of HRV data, normal or abnormal, the obtained triangle is a right angled triangle. Because its interior angle *C* is 90°. Also the slope of the sides *a* and *b* is respectively *1* and *-1* (6).

In this mapping, we have all the features which we introduce in TPSM (6), further more three new feature that will mentioned in the following. The first step in geometrical analysis of *TPSM* is finding the coordination of three vertices of the triangle. The methods for measuring the features of TPSM are explained in details in (6, 7). After finding the coordinates of three vertices, we find the slope of the sides which as mentioned before, it's enough to find the slope of side *c* (m_c) (6).

Other useful features in TPSM are the length of the

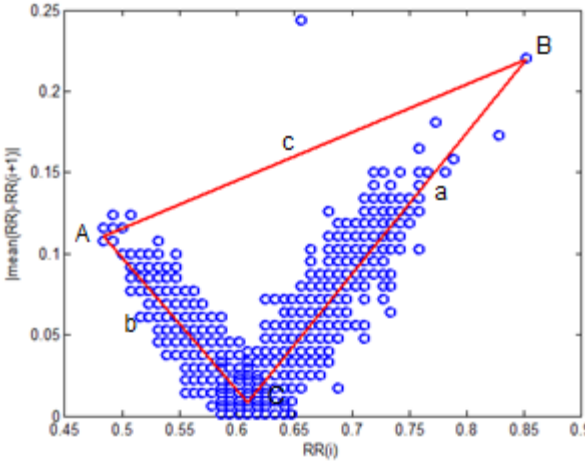

Figure 3. Points' distribution in *ETPSM* and the estimation of a triangle for them

sides which is measure by the distance between two points. Now, by knowing the lengths of all three sides of triangle, the three internal angles can be calculated. Of course, because the angle *C* is 90°, the angles *A* and *B* are complementary. It means that $A+B = 90°$. So it's sufficient to just measure angle *A*.

The others geometric features extracted from *TPSM* are the perimeter, area and the quality of the triangle which are explained more in (6).

Now, in this extended version of ETPSM, we introduce three new features that are exactly related to the distribution of points in relation to the estimated triangle. For this purpose, we divided the points in three groups (figure 4):

- Points which are in the triangle (I)
- Points which are on the triangle (T)
- Points which are out of the triangle (O)

By measuring the features of TPSM, we have the equation of each side of the triangle as follow:

$$\begin{cases} a: y = m_a x + b_a \\ b: y = m_b x + b_b \\ c: y = m_c x + b_c \end{cases} \qquad (7)$$

in which *m* is the slope of the line and *b* determines the point at which the line crosses the y-axis.

Now, the decision about a point as to whether it belongs to one of the above three classes are made based on the point's location in related to each side of the triangle, that means:

- $if \begin{cases} y_i - m_a x_i - b_a > 0 \\ y_i - m_b x_i - b_b > 0 \\ y_i - m_c x_i - b_c < 0 \end{cases} \Rightarrow p_i \in I$

- $if \begin{cases} y_i - m_a x_i - b_a < 0 \\ y_i - m_b x_i - b_b < 0 \\ y_i - m_c x_i - b_c > 0 \end{cases} \Rightarrow p_i \in O$

- $if \begin{cases} y_i - m_a x_i - b_a = 0 \\ y_i - m_b x_i - b_b = 0 \\ y_i - m_c x_i - b_c = 0 \end{cases} \Rightarrow p_i \in T$

In which $p_i(x_i,y_i)$ is each point in the mapping and $i = 1, 2, \ldots, n$. Note that for $p_i \in I$, all the three constraints should be true. It means that there is logical *AND* between constraints. But for $p_i \in O$ and $p_i \in T$, it's enough to have one of the constraints. It means that there is logical *OR* between constraints.

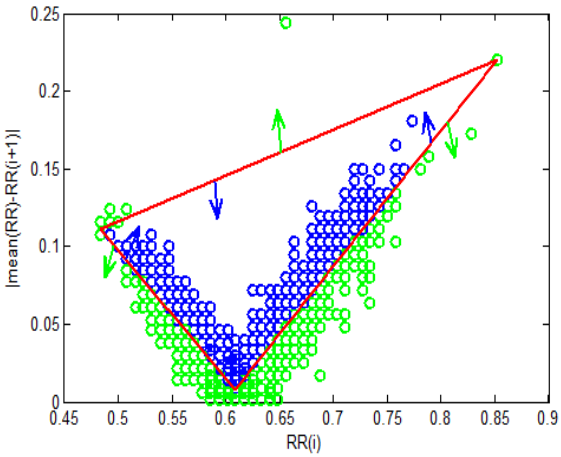

Figure 4. Modified classes in ETPSM

These modified classes are shown in Fig. 4. After defining the classes of all the points, we counted the members of each class for constructing our new features: N_I, N_O and N_T.

N_I is the number of points in class *I* that means the number of points which are in the estimated triangle, N_O is the number of points in class *O* that means the number of points which are out the estimated triangle, and N_T is the number of points in class *T* that means the number of points which are on the estimated triangle.

4. Discrimination of heart arrhythmia

In order to validate the proposed features, N_I, N_O and N_T, 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.

The data from MIT-BIH Physionet database (11) 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 (11). 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) (11). 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 (11). The original long term ECG recordings in every four groups

were digitized at 128 Hz (11).

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 N_I, N_O and N_T.

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

The results show that N_I and N_T have the best results and don't depend on the type of arrhythmia (Table 1). It discriminate CHF from NSR by *p<2E-3*; AF from NSR by *p<3E-4*; arrhythmia from NSR by *p<2E-6*, CHF from arrhythmia by p<1E-2; CHF from AF by p<5E-4; and arrhythmia from AF by p<2E-3.

Table 1. p-Value Results for ETPSM Features

Groups	*ETPSM* Features		
	N_I	N_O	N_T
NSR, CHF	0.002	0.1826	0.05
NSR, CAST	1.03E-6	0.5503	0.008
NSR, AF	0.0003	0.02	0.0004
CHF, CAST	0.032	0.0846	0.01
CHF, AF	0.0012	0.034	0.0005
CAST, AF	0.0041	0.061	0.002

6. Discussion

In this novel method, we have used the function between continuous data of time series in relation to the mean of whole data. It was shown that this new mapping was able to differentiate four groups of subjects significantly. The triangle model of it enable the user to test different geometric analysis on it and extract different features which each one may reflect different aspects of HRV behavior. Furthermore, the extended mapping, make it possible to follow the dynamic of HRV points in Poincare plots more precisely.

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Address for correspondence:

Nader Jafarnia Dabanloo
Islamic Azad University, Science and research Branch, School of Biomedical Engineering, Golzare1 Ave., Sardare Jangal Ave., Tehran, Iran
n_jafarnia@yahoo.com