A Study on the Nonlinear Dynamics of PR Interval Variability Using Surrogate data

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ABSTRACT

PR interval variability has been proposed as a noninvasive tool for investigating the autonomic nervous system as well as heart rate variability. The goal of this paper is to determine whether PR interval variability is generated from deterministic nonlinear dynamics. The data used in this study is a 24-hour holter ECGs of 20 healthy adults. We developed an automatic PR interval measurement algorithm, and tested it using MIT ECG Databases. The general discriminants of nonlinear dynamics, such as, correlation dimension and phase space reconstruction are used. Surrogate data is generated from simpler linear models to have similar statistical characteristics with the original data. Nonlinear discriminants are applied to both data, and compared for any significant results. It was concluded that PR interval variability shows nonlinear characteristics.

1 Introduction

Heart rate variability(HRV) has been used to estimate the activity of the autonomic nervous system(ANS) as a noninvasive method. Many studies report that HRV shows deterministic nonlinear dynamics[1]. Sympathetic and parasympathetic nervous system directly influences the SA node, and results in HRV. In the same way, two components directly influences the AV node. Therefore, AV node conduction time can be used as another noninvasive parameter to estimate the activity of ANS.

PR interval is composed of atrium activation time, AV node conduction time, and His-Purkinje condtion time. AV node conduction is much slower than others, and the dominant component of PR interval. Because it is difficult to detect AV conduction time, it is important to study PR interval variability(PRV). Since PRV is influenced by the same mechanism of HRV, it is possible that PRV has deterministic nonlinear dynamics. If it is true, it can be used as a proof of nonlinear dynamics of HRV. The purpose of this study is to determine whether PRV shows deterministic nonlinear dynamics.

First, the accurate detection of PR interval is important. In definition, PR interval is the time from the P wave start point to the R wave start point. The R wave has a relatively large amplitude, and is easily detected. But, in the case of the P wave, it is difficult to detect the starting point accurately. Therefore, we assume the P wave peak point is used to represent the PR interval instead of the P wave start point. That assumption is based on the fact that AV conduction time is what we want to see, and that AV conduction time is the major component of PRV. That asumption is also necessary to analyze 24 hour holter ECG data, because we should use computer-aid automatic detection algorithm to process a very large amount of data.

To determine nonlinear characterisitcs of PRV, correlation dimension and phase space reconstruction are calculated. Those are general methods to see nonlinear characterisitics of the data quantitatively. Embedding dimension and time delay are necessary to calculate those results, but, have not been solved to have optimum values yet. Therefore, in this study, we tried to find out the best results among various values of two parameters. Takens estimator is used to calculate the correlation dimension[2].

It was suggested to detect nonlinearty in time series using surrogate data[3]. This method is to discriminate between deterministic

nonlinear dynamics and noise from a time series. The surrogate data is generated from simpler models to have similar statistical characteristics to the original data. If the surrogate data shows the same values in the nonlinear discriminants with the original data, the original data is not supposed to be from a deterministic nonlinear dynamics.

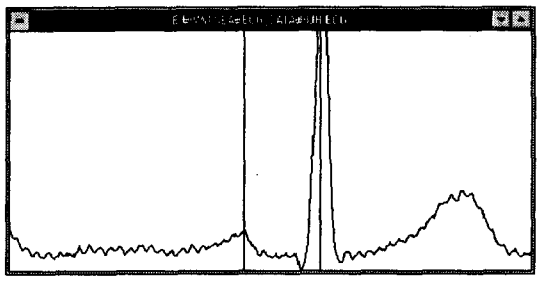

Figure 1: Automatically detected PR Interval

2 Methods

2.1 Materials and ECG preprocessing

24 hour Holter ECG data of 20 healthy adults are acquired to test nonlinearty of PRV.

We recorded data in the personal computer (486 IBM PC) through A/D converter (12 bit resolution) from Holter system. The holter system has analog output option which is 60 times faster than normal speed, and acquired ECG data at 60KHz sampling rate. In effect, we sampled the data at 1KHz. All the signal processing are processed off line.

First, QRS-complex detection is executed. For accurate detection, ECG data is low pass filtered(cufoff frequency = 11Hz) and high pass filtered (cufoff frequency = 200Hz). The algortihm to detect QRS complex is using first derivative of ECG signals, the square of that first derivative, and moving window integrations.

Second, P wave detection is executed. P waves are sometimes independent of QRS-complexes, but since the object of this study is to find out AV node conduction time's variability, it is assumed that all P waves are in front of QRS complexes. Therefore, to find P wave, we set some fixed interval in front of the QRS complex, and compare the amplitude and first derivative of the ECG signals in the interval. We tested this algorithm with MIT ECG Database, and it had been concluded that little significant errors took place.

2.2 Nonlinearity Detecting methods

correlation dimension According to Takens embedding theorem, if X_n is a discrete-time scalar cross-section across a continuous-time multidimensional system with an attractor contained in a manifold of dimension I, there will be in general an embedding dimension $J \leq 2I+1$ such that the $J-$ vectors $X_{n-1}, \ldots, X_{n-J}$ fill out a set of the same dimension with the underlying attractor.

Using that theorem, Grassberger and Procaccia suggested correlation dimension, and estimated it by a procedure based on nearest-neighbor distances[4]. Most of the literature about the dimension estimation are based on this procedure because of its ease of estimation.
Suppose the observations $Y_n, 1 \leq n \leq N$ are independent, identically distributed $p-$ vectors with twice continuously differentiable density f. Let $D_{mn} = ||Y_m - Y_n||$, and,

$$C(r) = \Pr\{D_{mn} < r\} = ar^p\{1 + br^r + 0(r^r)\} \quad (1)$$

where, a and b are constants and, $C(r)$ is the correlation integral. Assume $N(N-1)/2$ D's are independent, and

$$C(r) = ar^p, r < \epsilon \quad (2)$$

for some small (assumed known) ϵ, and, p is the correlation dimension.

Suppose that we order the D's as $D_1 \leq D_2 \leq \ldots \leq D_{N(N-1)/2}$ and that the first M of these are less than ϵ. Takens maximum likelihood estimation is

$$\hat{p} = \frac{M}{\sum_{j=1}^{M} \log(\frac{\epsilon}{D_j})} \quad (3)$$

And the mean squared error(MSE), or the sum of squared bias and variance, is :

$$MSE \approx (\frac{2pb}{p+2})^2 \epsilon^4 + \frac{2p^2}{N^2 a \epsilon^p} \quad (4)$$

The sample size which is needed to calculate the p value grows exponentially with p. But being dependent on the MSE value, the sample size can be decreased, provided the MSE value is increased[5].

Phase space reconstruction It is very useful to make a time delay reconstruction of a phase space to represent the nonlinear dynamics visually. Many methods are suggested to determine time delay and embedding dimension, But currently it is not clear in real data. Those methods include first zero-crossing of the autocorrelation function, mutual information, and false nearest neighbors, etc.

We followed *false nearest neighbors* algorithm, because that algorithm gives better results than others that were tried[6].

2.3 Surrogate data

Surrogate data is an ensemble of data sets similar to the observed data, but consistent with the null hypothesis. There are some possibilities to select null hypothesis to generate surrogate data. The algorithm used in this study is based on the null hypothesis that the data come from a linear gaussian process. The surrogate data is generated to have the same Fourier spectrum as the original data.

To achieve this goal, Fourier transform of the original data is computed. Second, randomize the coefficients by multiply $e^{i\phi[t]}$, where $\phi[t]$ is uniformly distributed in $[0, 2\Pi]$. We symmetrize the phases $\pi(f) = -\pi(-f)$. Finally, the inverse fourier transform calculated is the surrogate data. Note that by the symmetry of the phases, the resulting time series are real.

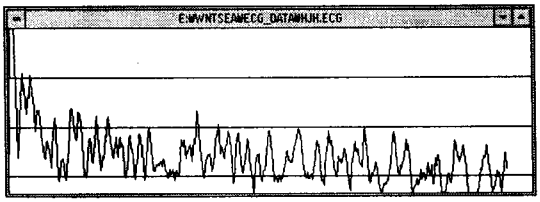

Figure 2: Power Spectrum of the PRV

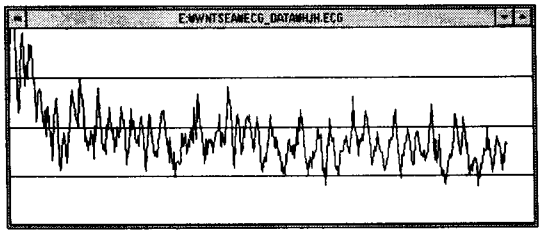

Figure 3: Power Spectrum of the Surrogate Data

3 results

Figure 1 shows the automatically detected PR interval of ECG data.

Figure 2 shows the power spectrum of the PRV data, and figure 3 shows the power spectrum of the surrogate data.

Figure 4 shows the time series of the PRV data, and figure 5 shows the time series of the surrogate data.

From the figure 2 - 5, we see that the surrogate data follows the powerspectrum of the original PRV data, but is generated from the lineary correlated models.

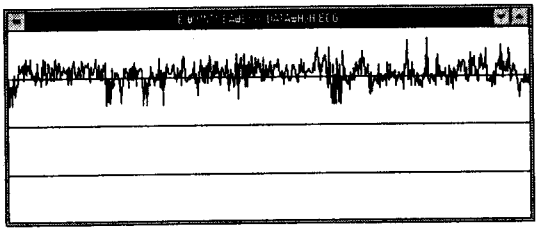

Figure 4: Time series of the PRV

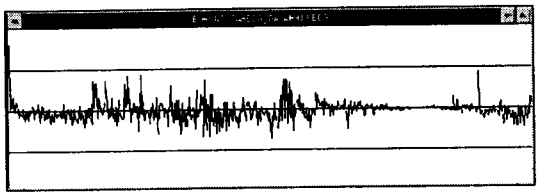

Figure 5: Time series of the Surrogate data

Table 1 shows the means and variances of the correlation dimensions of the original PR interval and its surrogate data. The correlation dimension of the original data is different from that of the surrogate data.

We can conclude that at least PRV is not generated from the linearly correlated models.

Table 1: Mean and S.D of correlation dimensions between PRV and surrogate data

	Mean	S.D.
PRV data	2.1	0.35
Surrogate data	1.7	0.41

4 conclusion and discussion

We have concluded that the PRV shows nonlinear characteristics. It means that AV node conduction time has nonlinearty, and is determined by the deterministic interaction of sympathetic and parasympathetic nervous system. Therefore, we hope that combined with HRV, PRV can be used as a indicator to show heart's states.

It is clear that at least PRV can not be generated from linear correlated models from the study of the surrogate data.

More discriminants, such as Lyapunov exponent, prediction error, are needed to reveal the nonlinearty accurately. A further study of theoretical background about nonlinear discriminants' parameters for the biological signals are necessary.

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