Nonlinear Analysis of Heart Rate Variability and Plethysmogram in Subjects with Normal and Abnormal Cardiovascular Function

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Abstract—We used nonlinear methods of Detrended Fluctuation Analysis (DFA) and Recurrence Quantification Analysis (RQA) to analysis of plethysmograms and their peak intervals in subjects with normal and pathological cardiovascular functions. Our results on HRV using DFA showed that scaling exponent indicated quantitatively differentiations among normal and pathologies. The measures of RQA were found to provide an unambiguous and quantitatively characterization of the plethysmogram time series in different cases. Accordingly, the integrations of these two analyses had the ability to identify and quantify normal and pathological cases, implying a possible clinical application.

I. INTRODUCTION

It has been argued that the mechanisms underlying heart rate variability (HRV) and finger plethysmograms are nonlinear [1][2]. Although nonlinear dynamics was widely used in recent years to characterize the behavior of a physiological system in analysis of electrocardiogram (ECG) and electroencephalogram (EEG) [3][4], there are seldom investigations using recent developed nonlinear techniques to study time series from plethysmograms and their peak intervals in both healthy conditions and various pathologies. Methods of Detrended Fluctuation Analysis (DFA) and Recurrence Quantification Analysis (RQA) have developed recently and broadly applied in analysis of physiological/psychological data [1]-[4]. Important advantages of the methods are that they can measure the complexity of short and non-stationary signals with noise and can capture subtle nonlinear aspects.

In this paper, we used the nonlinear analysis of methods of DFA and RQA to study subjects with normal and pathological cardiovascular functions in the cases of Essential Hyper Tension (HT), Angina Pectoris (AP), Atrial Fibrillation (AF), Diabetes Mellitus (DM), and Old Myocardial Infarction (OM). Our aim is to explore the ability to identify and quantify the cardiovascular functions in normal and pathologies by using of the advanced nonlinear analysis of plethysmogram and its derived peak intervals.

There are two reasons to deal with plethysmography peak intervals along with plethysmograms. First, we demonstrated that R-R intervals of electrocardiogram (ECG) were equally derived from peak to peak intervals of plethysmogram waveforms [5]. Thus, it is convenient to give a HRV analysis using the variability within plethysmography peak intervals. Second, beside of the fact that HRV can reveal underlying autonomous activities, the dynamics from plethysmogram waveforms reflects both autonomic and central neural influences [5]. Therefore, the nonlinear analysis of both plethysmogram and its peaks (or HRV) can give additional and complementary physiological information, leading a better understanding of cardiovascular functions.

The method of measurements and recordings of finger plethysmogram is noninvasive, easily installed, inducing no uncomfortable to the subject. Then this study, by making use of the advantage, may have practical implications for the designing a convenient clinical and diagnosis system.

In sec. II, we explain experiment and data acquisition. Sec. III describes DFA and RQA methods. In Sec. IV and V, we give results and our conclusions.

II. THE EXPERIMENTATION

The Cardiovascular Institute Hospital Committee approved this investigation. All participants gave informed consent to all experimental procedures.

A. Participants

The healthy subjects were with normal cardiovascular function. They were eligible if they did not report persistent fatigue and had normal findings on routine medical tests. They were ten subjects (called NM; n =10; 2 women and 8 men) with age 33-63 yr. (mean 53 ± 9 yr.). The subjects with pathologies and abnormal cardiovascular function were those patients selected according to definition criteria of The Cardiovascular Institute Hospital. They were categorized to five groups: Essential Hyper Tension (called HT; n =19; 5 women and 14 men; age 45-73 yr; mean 62 ± 7 yr.), Angina Pectoris (called AP; n =14; 3 women and 11 men; age 42-80 yr; mean 66 ± 9 yr.), Atrial Fibrillation (called AF; n =7; 2 women and 5 men; age 53-78 yr; mean 66 ± 8 yr.), Diabetes Mellitus (called DM; n =8; 0 women and 8 men; age 56-71 yr; mean, 65 ± 6 yr.), Old Myocardial Infarction (called OM; n =8; 1 women and 7 men; age 54-78 yr; mean 69 ± 7 yr.).
**B. Apparatus and Signal Acquisition**

Each subject was given at least 5 minutes to become accustomed to the surroundings in a room. They sit comfortably in a chair in a relaxed manner. The arm was supported horizontally at heart level at all times during the experiment. The hand was held in a relaxed semi-open position, with the palm turned downward. A photoelectric sensor of the plethysmography was placed on the distal phalanx of second finger. Finger plethysmogram was recorded continuously for 5min by the instrument (BACS2000-sp; CCI). The signals were digitized with a 200Hz sampling rate with resolution 12 bits, and transferred via an A/D converter to a PC for data processing.

All signals were checked for artifacts and noise effects. Data was band filtered at 0.2-10Hz. A middle segment of 3min of the plethysmogram data was taken for extracting sequences of peak to peak intervals in order for HRV analysis. The location of waveform peaks of plethysmography pulses was determined with resolution of 5ms. The intervals between consecutive peaks determined in this way were assumed to agree with R-R intervals obtained from ECG. The time series of the intervals was thus used to analysis of HRV.

Whereas only a segment of 26s taken from the plethysmogram data put for RQA analysis. For suppressing the effects of low-frequency noise and increasing signal-to-noise ratio, we differentiated the signal twice using a Savitzky-Golay filtering method and obtained acceleration plethysmogram that was for a nonlinear RQA analysis.

**III. THE THEORY**

Two mathematical methods were applied to time series of plethysmogram and peak intervals. DFA method was applied to peak intervals to perform HRV analysis. RQA was used for analysis of dynamics of plethysmograms.

**A. Detrended fluctuation analysis (DFA)**

Advantages of DFA over conventional methods are that it permits detection of long-range correlations embedded in non-stationary time series, and avoids spurious measurements. Briefly, the DFA method involves the following steps [1][6]. First, the signal time series is integrated to "mimic" a random walk after the mean value of the signal is subtracted. Next, the integrated time series \( y(n) \) is divided into boxes of equal length \( n \). Then in each box, a least-squares linear fit to the data, representing the trend in that box, is calculated. Subsequently, the integrated time series is detrended by subtracting the local trend in each box. Finally, the above computation is repeated over all time scales (box size \( n \)) to provide a relationship between \( F(n) \) and box size \( n \) (i.e., the observation window). A power-law relation between the average root-mean-square fluctuation function \( F(n) \) and the observation window size indicates the presence of so-called scaling, i.e., the fluctuation correlations can be characterized by a scaling exponent \( \alpha \) as

\[
F(n) \propto n^\alpha
\]  

We calculated the fluctuation function by increasing \( n \) beats (peaks). Two different regimes of scaling were characterized respectively by scaling exponent \( \alpha_1 \) and \( \alpha_2 \). Of those, only \( \alpha_1 \) estimated for range 2-11 beats (peaks) was emphasized in our studies in evaluation of scaling behavior of HRV.

**B. Recurrence quantitative analysis (RQA)**

Recurrence plots proposed originally by Eckmann et al, describe the recurrence feature of a deterministic dynamics system by visualizing the time dependent behavior of orbits in a phase space [7]. Assume a dynamical system governed by \( \dot{x} = F(x) \), \( x \in R^n \). \( N \) discrete points recorded in time are \( x(i), i = 1, \ldots, N \). A threshold recurrence plot is constructed by forming the matrix

\[
R_{ij} = \Theta(\epsilon - ||x(i) - x(j)||)
\]  

where \( \epsilon \) is a threshold parameter and \( || \cdot || \) takes Euclidean norm of the m-dimensional distance vector. \( \Theta(\cdot) \) is Heaviside function. The values of \( R_{ij} \) are 1 or 0 depending on whether the distance between points \( i \) and \( j \) is less than or greater than \( \epsilon \). The binary values of \( R_{ij} \) can be simply visualized with black (1) and white (0). Thereby the visualized plots can be considered as an inspection of a high-dimensional phase space trajectory.

Based on a single measured variable \( u(i) \), the phase space vector \( x(i) \) can be reconstructed by using the Taken's time delay method as

\[
x(i) = (u(i), u(i + \tau), \ldots, u(i + (m - 1)\tau))
\]  

with time delay \( \tau \) and embedding dimension \( m \).

The recurrence quantitative analysis (RQA) was proposed in [8][9] to measure the visualized recurrence plots of \( R_{ij} \). We used three important measures: determinism (DET), average diagonal line length (<I>l<>, and entropy (ENTR).

If the frequency distribution of the lengths \( l \) of the diagonal lines in recurrence plots is \( P(l) \), then the ratio of recurrence points on the diagonal lines to all recurrence points is called DET defined by

\[
DET = \frac{\sum_{l=l_{\text{min}}}^N lP(l)}{\sum_{l}^N R_{ij}}
\]  

where \( l_{\text{min}} = 2 \) in this paper. Processes with stochastic
behavior cause non or very short diagonals, whereas
deterministic ones cause longer diagonals and less single,
iso late recurrence points.

Next, the average diagonal line length is

\[ <L> = \frac{\sum_{l=1}^{N} lP(l)}{\sum_{l=1}^{N} P(l)} \]  

This length gives a hint about the divergence of the
trajectory segments. Many studies suggested that the diagonal
line length could estimate the largest positive Lyapunov
exponent.

Finally, \( \text{ENTR} \) refers to the Shannon entropy of the
frequency distribution of the diagonal line lengths as

\[
\text{ENTR} = -\sum_{l=1}^{N} p(l) \ln p(l) \quad \text{with} \quad p(l) = \frac{P(l)}{\sum_{l=1}^{N} P(l)}
\]

\( \text{ENTR} \) is a complexity measure of a deterministic structure
in dynamical system.

C. Statistical analysis

A nonparametric Mann-Whitney \( U \)-test with
\( p \)-significance performed to compare two groups. \( p \)-value of
0.05 or less was accepted as statistically significant.

IV. RESULTS

A. Results of DFA

By applying DFA to time series of peak intervals obtained
from finger plethysmograms, we analyzed HRV in subjects
under healthy and pathological conditions in HT, AP, AF,
DM, and OM.

Fig. 1 shows a typical time series of peak intervals obtained
from a healthy individual. Detrended fluctuation analysis of
the data is illustrated in Fig.2, where dividing point is \( n=11 \)
beats (peaks) giving rise to an initial slope (exponent) of
\( \alpha_1 = 1.01 \) for \( n < 11 \) and another slope of \( \alpha_2 = 0.93 \) for \( n > 11 \).

Here we focus only the value of \( \alpha_1 \).

Fig.3 shows the results of \( \alpha_1 \) for all groups: normal (NM)
and pathologies. A box plot representation is used in Fig.3
and Figs.5-7. Boxes of the box plot contain 50\% of values
falling between the 25th and 75th percentiles. The horizontal
line within the box represents the median value. The
'whiskers' are lines that extend from the box to the highest and
lowest values, excluding outliers.

U-test performed to compare two groups. As shown in
Fig.3 and summarized in TABLE I with mean ±SD, NM has
the exponent \( \alpha_1 \) of value 0.94 ±0.11, which is significantly
higher than AF (0.55 ±0.05, \( p < 0.0005 \)), DM (0.67 ±0.15, \( p < 0.001 \)), and OM (0.73 ±0.21, \( p < 0.05 \)). Also HT (0.84 ±0.19) and AP (0.89 ±0.21) are lower than NM. Reference [6]
evidenced a healthy HRV if \( \alpha_1 \) near 1.0 (1/f) and a

pathological HRV if \( \alpha_1 \) less 1.0 and near to 0.5 (white noise,
i.e., no correlation). Consequently, our results show that AF
is most close to "white noise" or "no correlation", DM and
OM are secondly decreased correlation, and HT and AP are
least. Therefore \( \alpha_1 \) provides quantitatively and clearly
differentiations among normal and pathologies.
### TABLE I
DFA RESULTS OF MEAN±SD

<table>
<thead>
<tr>
<th></th>
<th>NM</th>
<th>HT</th>
<th>AP</th>
<th>AF</th>
<th>DM</th>
<th>OM</th>
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<tr>
<td>(n=10)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α_1</td>
<td>0.94±0.11</td>
<td>0.84±0.19</td>
<td>0.89±0.21</td>
<td>0.55±0.05</td>
<td>0.67±0.15</td>
<td>0.73±0.21</td>
</tr>
</tbody>
</table>

**B. Results of RQA**

We calculated three measures of RQA, namely DET, <L>, and ENTR, to analyze the data of plethysmograms. The embedding dimension to reconstruct phase space of plethysmogram was found to be about 4 for all subjects according to a method of FNN (false nearest neighbors) [10] [11], then the parameter of dimension in computation of RQA was taken as an over-embedding one of 7. Time delay was in a range of 16± 4 determined by initial minimum points in mutual information function. The parameter of threshold ε was 5% of the maximum phase space diameter to make recurrence point density approximately 1%[12]. In order to suppress noise in time series of plethysmograms, we filtered the time series using Savitzky-Golay differentiation filter, and down sampled to 50Hz in calculations.

To give a visually reviews at first, Figs.4 (a)-4(f) show respective time series of plethysmogram, along with their three-dimensional view of phase space trajectory (chaotic attractor), and unthresholded recurrence plot, for a typically normal (NM) and pathological cases (HT, AP, AF, DM, OM). To help understanding phase space trajectory structure, instead of plotting binary representation (black and white), we display unthresholded plot in which the distance between x(i) and x(j) is plotted for an increasing changed threshold ε.

Beyond the qualitative description in Fig.4, RQA gives a quantitatively description for these normal and abnormal cases. Fig. 5 shows box plot of RQA results for the measure DET. In comparison with NM (normal), DET value of AF is significantly lower (p <0.01), indicating a decrease in determinism. Whereas the value of DM is significantly higher (p <0.05), and one of OM is higher too, both indicating increases in determinism and recurrences. HT and AP are slightly lower than NM.

Fig.6 shows results of <L>. In relation to NM, AF is significantly lower (p <0.005), DM and OM are significantly higher with respective p <0.01 and p <0.05. Owing to the possible reciprocal relationship between <L> and Lyapunov exponent [7][11], our results imply that there is a largely loss of dynamical complexity (divergence) in DM and OM, whereas there is a significantly increased complexity for AF, when comparing with NM. HT and AP are not apparent.

Fig. 7 shows box plot of the third measure: ENTR. Similar to Figs.5-6, ENTR of AF is significantly lower (p<0.05) than NM, one of DM is significantly higher (p<0.005), and one of OM is higher too. Perhaps, HT and AP show a decreasing tendency.

All of these results are summarized in TABLE II, where results of DET, <L>, and ENTR for normal and abnormal groups are given for all 66 subjects. Obviously, measures of RQA provided quantitatively characterizations and identifications for the groups.
(continued)

(d) AF

(e) DM

(f) OM

Fig. 4(a)-(f). For a typically normal (a) NM and pathological cases of (b) HT, (c) AP, (d) AF, (e) DM, and (f) OM, we display respective plethysmogram time series, their three-dimensional view of phase space trajectory (chaotic attractor), and unthresholded recurrence plot.

Fig. 5. Box plot representation of values of $DET$

Fig. 6. Box plot representation of values of $\langle L \rangle$

Fig. 7. Box plot representation of values of $ENTR$
TABLE II

<table>
<thead>
<tr>
<th></th>
<th>NM</th>
<th>HT</th>
<th>AP</th>
<th>AF</th>
<th>DM</th>
<th>OM</th>
</tr>
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<tbody>
<tr>
<td>DET</td>
<td>0.90 ±0.05</td>
<td>0.87 ±0.09</td>
<td>0.88 ±0.06</td>
<td>0.76 ±0.13</td>
<td>0.95 ±0.02</td>
<td>0.94 ±0.05</td>
</tr>
<tr>
<td>&lt;L&gt;</td>
<td>7.66 ±1.85</td>
<td>7.78 ±3.05</td>
<td>6.63 ±2.02</td>
<td>4.43 ±1.13</td>
<td>10.29 ±1.62</td>
<td>11.06 ±3.97</td>
</tr>
<tr>
<td>ENTR</td>
<td>2.25 ±0.38</td>
<td>2.23 ±0.57</td>
<td>2.14 ±0.48</td>
<td>1.62 ±0.55</td>
<td>2.81 ±0.27</td>
<td>2.68 ±0.59</td>
</tr>
</tbody>
</table>

V. CONCLUSION

We used nonlinear methods of DFA and RQA in this study, owing to that the methods can discover some important properties in the time series that are unrevealed by linear methods. We performed analysis of plethysmograms and their peak intervals in subjects with normal and pathological cardiovascular functions.

Our results on HRV using DFA showed that scaling exponent $\alpha_1$ of AF was most close to "white noise (i.e., no correlation)", DM and OM were secondly, and HT and AP were least.

The measures of RQA applied to plethysmograms were found to provide an unambiguous and quantitatively characterization of the plethysmogram time series in different cases. Values of $\text{DET}$, $<\text{L}>$, and $\text{ENTR}$ were quite distinct and characteristic among NM, AF, DM, and OM, and showed a possible tendency for HT and AP. Especially we showed a largely decreased determinism and increased uncontrollable "noise" in AF, whereas significantly increased determinism and loss of complexity in DM and OM, when comparing with NM. Accordingly we conclude that the integrations of these two analyses is capable of identifying and quantifying normal and pathologies.

Due to the measurement method of finger plethysmogram and its peaks is noninvasive, easily installed, inducing no uncomfortable to the subject, the results of our study may have implications for helping to design of potentially valuable and easily accessed clinical and diagnosis system in practice.

ACKNOWLEDGMENT

The partial support of Yazaki Co., Ltd. is gratefully acknowledged.

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