MULTI DETRENDED FLUCTUATION ANALYSIS IN HEART RATE VARIABILITY OF EARLY INFANTS

PHÂN TÍCH BIẾN ĐỘNG TÍN HIỆU LOẠN NHỊP TIM ĐA TRỊ Ở TRẺ NHỎ

Chu Duc Hoang, Nguyen Duc Thuan, Nguyen Thanh Linh

School of Electronics and Telecommunications, Hanoi University of Science and Technology;
Email: hoang.chuduc@hust.edu.vn, thuan.nguyenduc@hust.edu.vn, linhnt.bme@gmail.com

Abstract - The analysis of heart rate variability (HRV) is an important tool for the assessment of the autonomic regulation of circulatory function. HRV analysis is usually performed using methods that are based on the assumption that the signal is stationary within the RR interval duration (up to 24 hour per patient), which is generally not true for long duration signals. Analysis and evaluation of Electrocardiography(ECG) arrhythmia data can be processed by the method of time methods, frequency methods and nonlinear methods. Detrended fluctuation analysis (DFA), afractal analysis method which is widely used in heart rate variability studies, is used to analyze the scaling behavior of RR interval series of preterm neonates. In this paper, we improve the DFA algorithm to MDFA (MultiDetrended fluctuation analysis) to evaluate the possibility of arrhythmias RR intervals detail for each period of 20 minutes in entire RR intervals. Evaluation results are shown graphically intuitive with three levels of basic arrhythmia arrhythmia is high, medium and low arrhythmia.

Key words - multi detrended fluctuation analysis; MDFA; heart rate variability; HRV; Early Infant.

Tóm tắt - Phân tích tín hiệu loạn nhịp tim (HRV) là một công cụ quan trọng trong việc đánh giá các chức năng tuần hoàn của hệ thần kinh thực vật. Phân tích HRV thường được thực hiện bằng cách sử dụng phương pháp dựa trên giả định rằng các tín hiệu RR (lên tới 24 giờ) có liên quan với nhau trong quá trình thu nhận. Phân tích và đánh giá dữ liệu điện tim loạn nhịp có thể được xử lý bằng các phương pháp thời gian, phương pháp tần số và phương pháp phi tuyến. Trong các phương pháp phân tích HRV, phương pháp phân tích động tín hiệu động đa trị được sử dụng rộng rãi, đặc biệt là trong việc đánh giá các thông số loạn nhịp RR của trẻ sơ sinh. Trong bài báo này, chúng tôi cải thiện thuật toán DFA thành MDFA để đánh giá khả năng rối loạn nhịp một cách chi tiết cho từng khoảng thời gian 20 phút. Kết quả đánh giá được biểu diễn bằng đồ thị trực quan với ba mức độ loạn nhịp cơ bản là loạn nhịp cao, loạn nhịp vừa và không loạn nhịp.

Từ khóa - phân tích động tín hiệu đông đa trị; MDFA; loạn nhịp tim; HRV; trẻ sơ sinh.

1. Introduction

Heart rate variability (HRV) is the physiological phenomenon of variation in the time interval between heartbeats. It is measured by the variation in the beat-to-beat interval. Other terms used include: "cycle length variability", "RR variability" (where R is a point corresponding to the peak of thethree of the graphical deflections seen on a typical ECG (QRS); and RR is the interval between successive Rs), and "heart period variability". Methods used to detect beats include: ECG, blood pressure, ballistocardiograms,[1][2] and the pulse wave signal derived from a photoplethysmograph (PPG). ECG is considered superior because it provides a clear waveform, which makes it easier to exclude heartbeats not originating in the senatorial node. The term "NN" is used in place of RR to emphasize the fact that the processed beats are "normal" beats.

The analysis of heart rate variability (HRV) is an important tool to the assessment of the autonomic regulation of circulatory function. HRV is especially useful for assessing sympathovagal balance [3]. HRV is typically studied by analyzing the variability of the intervals between two consecutive heartbeats. Most commonly, these are calculated by measuring the RR intervals, i.e., the interval between two consecutive R waves in the electrocardiogram. The most popular techniques for analysis of HRV include time domain analysis (e.g., coefficient of variation, pNN50, RMSSD) [4], frequency domain analysis (e.g., Fourier transform, auto-regressive model, Lomb-Scargle periodogram) [5], and geometrical techniques (e.g.,Poincar´ e plot, trend analysis) [6]. Given the complexity of the mechanisms regulating heart rate, it is reasonable to assume that applying HRV analysis based on methods of non-linear dynamics will yield valuable information. Although chaotic behavior has been assumed, more rigorous testing has shown that heart rate variability cannot be described as a chaotic process [7]. The most commonly used non-linear method of analyzing heart rate variability is the Poincaré plot. Each data point represents a pair of successive beats, the x-axis is the current RR interval, while the y-axis is the previous RR interval. HRV is quantified by fitting mathematically defined geometric shapes to the data [8]. Other methods used are the correlation dimension, nonlinear predictability [7], pointwise correlation dimension and approximate entropy [9]. Detrended fluctuation analysis (DFA), a method that characterizes power-law scaling in the time domain, is widely used in HRV analysis since it is considered to be robust and to correctly identify long range correlations in certain types of non-stationary time series [10]. The scaling exponent's α obtained with DFA are reported to have diagnostic and prognostic value for patients with various types of cardiac diseases. A recent study, on a small group of patients, suggests that the DFA scaling exponents allow the discrimination of normal neonates from neonates having experienced an apparent life threatening event (ALTE), which are considered to be at increased risk for sudden infant death syndrome (SIDS) [11]. The main goal of the present paper is to contribute to the understanding of the performance of DFA and its interactions with physiological signals [12]. Although the results are based on the analysis of neonatal heart rate data, the methodologies and findings are also useful for the interpretation of the DFA results obtained from other signals [13].

2. Methods

2.1. Heart rate data in RR matrix

This case-control study included 10 newborn very low birth weight infants with intraventricular hemorrhage (5 grade IV, 4 grade III, and 1 grade II) and 14 control infants without intraventricular hemorrhage. Heart rhythm data from the first day of life before the development of intraventricular hemorrhage were evaluated. The infants' medical charts were reviewed and the following data were recorded: birth weight, gestational age, race, gender, date and time of birth, cranial ultrasound findings, maternal demographics, delivery route, obstetrical history, maternal medications, labor and delivery complications, details of newborn stabilization, neonatal complications, type of ventilator and settings, and timing and number of surfactant doses. The length of each RR matrix was between 90000 and 135000 RR intervals. It can be noted that the mean heart rate of neonates is approximately 150 bpm (2.5 Hz), corresponding to a mean RR interval of 0.4 s, which is higher than in adults.

2.2. Multi Detrended Fluctuation Analysis (MDFA)

The MDFA is a well-established method for determining the scaling of long-term correlation in presence of trends without knowing their origin and shape. In general the MDFA procedure consists of three steps:

(**Step 1**) Split RR matrix into smaller matrices, each matrix element RR satisfying some conditions the total time of the matrix RR = 1200 seconds.

$$Y = \sum Y(t) \tag{1}$$

Where:

$$|Y(t)| = \sum_{i=1}^{n} RRi = 1200 \tag{2}$$

(**Step 2**) Determine the aggregated or *profile function*:

$$Y(t) = \sum \sum_{k=1}^{t} \omega(k) = \sum \sum_{k=1}^{t} [y(i) - \langle y(i) \rangle_{\mathrm{mod}\,\phi}] \tag{3}$$

of the deseasoned record $\omega(t)$ of length N.

(**Step 3**) Divide the $Y(t)$ time series into non overlapping segments $[N_s = \mathrm{int}(N/s)]$ of equal length *s*. In each of these υ segments $(1 \le \upsilon \le N/s)$, determine the local polynomial trend of order *n*, $Pol_{n,s}(t,\upsilon)$by a least-square fitting. I.e., $Pol_{n,s}(t,\upsilon)$, $\upsilon = 1, 2, ..., N/s$, consist of concatenated polynomials of order *n* which are calculated separately for each of the segments. The interpolating curve represents the *local trend* in the υ*th*-segment.The order of the polynomial can be varied in order to eliminate *linear (n=1), quadratic (n=2), cubic (n=3)* or higher order trends in the profile function. Compute for each segment υ the detrended series:

$$Z_{n,s}(t,\upsilon) = Y(t) - Pol_{n,s}(t,\upsilon) \tag{4}$$
$$\textbf{with} \quad (\upsilon - 1)s + 1 \le t \le \upsilon s$$

Instead a polynomial, a linear fit (i.e., $n = 1$) is normally used. In each of the segments determine the mean squared fluctuation or spread $F^2_{n,s}(\upsilon)$ around the *local trend* $[Pol_{n,s}(t,\upsilon)]$

$$F^2_{n,s}(\upsilon) = \frac{1}{s} \sum_{t=(\upsilon-1)s+1}^{\upsilon s} [Z_{n,s}(t,\upsilon)]^2 \tag{5}$$

(**Step 4**) At last determine the *fluctuation function* or the square root of the average over all segments of length *s* (*Ns*)

$$F_n(s) = [F_n^2(s)]^{1/2} = \left[\frac{1}{N_s} \sum_{\upsilon=1}^{N_s} F^2_{n,s}(\upsilon) \right]^{1/2} \tag{6}$$

For different detrending orders *n* one obtains different fluctuation functions $F_n(s)$. We are interested in the s-dependence of $F_n(s)$.

(Step 5) Repeat the above procedure for a broad range of segment lengths *s*. According to recommendation made by Peng CK[10],, the following range $s_{\min} \approx 5$ and $s_{\max} \approx N/4$ may be selected. It is apparent, that the fluctuation functionill increase with increasing the segments length "*s"* (duration). If data (*Y(t)*) are long-range correlated without deterministic trend, a power-law behavior for the fluctuation function $F_n(s)$ is observed

$$F_n(s) \approx s^{\alpha_n} \tag{7}$$

where α_n is the scaling exponent.RR matrix Y can calculate from Y(t) as array of αn:

$$\mathrm{Y1} = \sum F_1(s) \approx s^{\alpha_1} \tag{8}$$

$$\mathrm{Y2} = \sum F_2(s) \approx s^{\alpha 2} \tag{9}$$

We focus on α1 and α2 to concentration to assess the correlation of type 1 (linear), level 2 (parabolic) chain of ECG arrhythmia 20 minutes. The values of α1 and α2 show the correlation values in RRmatrix. The degree of this correlation will reflect the possibility of cardiac arrhythmias. Table 1 below shows the ability to detect ECG arrhythmias depending on the value calculated.

(Step 6) Performing matrix Y1 and Y2 over time and compared with the threshold of 0.5 and 1 will determine the extent and timing of arrhythmia occurs. Location arrhythmias are computed at time step 20 minutes from the start of the track.

Table 1*. Correlation of type 1 and type 2.*

No.	TYPE 1 AND TYPE 2		
	Values	***Correlation status***	***HRV status***
1	0.5 <α1 and α2 <1	High	Low
2	0 <α1 and α2 <0.5	Nomal	Nomal
3	1 <α1 and α2	Low	High
4	α1 and α2 = 1	Noises	Noises
5	α1 and α2 = 1.5		
6	α1 and α2 = 0.5		

3. Results

The process of calculation is used with patients with follow-up time of about 23 hours. The calculated parameters were calculated arrhythmias through the Kubios HRV tool. This heart rate variability (HRV) analysis software is developed by the Biosignal Analysis and Medical Imaging Group (BSAMIG) at the Department of Applied Physics, University of Eastern Finland, Kuopio, Finland. HRV parameters using Kubio tools is user to calculate the single α1 and α2 as the Table 2 below:

***Table 2**. HRV Parameter by using Kubios tools.*

No.	HRV PARAMETER		
	Parameter	***Values***	***Unit***
1	Poincare plot, SD1	925.76	Ms
2	Poincare plot, SD2	929.32	Ms
3	Recurrence plot, Lmean	94.296	beats
4	Recurrence plot, Lmax	528.60	beats
5	Recurrence plot, REC	84.848	%
6	Recurrence plot, DET	99.942	%
7	Recurrence plot, ShanEn	4.3053	
8	**DFA, α1**	**0.65235**	
9	**DFA, α2**	**0.59586**	
10	ApEn	0.35554	
11	SampEn	0.30910	
12	Correlation dimension, D2	0.74620	
13	Recurrence plot, Lmax	528.60	beats

As the HRV parameter α1 and α2 are 0.65235 and 0.59586. When we implement algorithms MDFA of patients with the same RR matrix, the number value ofα1 and α2 are more than about 80 α1 and α2 values.The set of values α1 through MDFA calculations are shown in Fig. 1 below. This data set is divided into 3 different values range from 0 to 0.5, from 0.5 to 1 and greater than 1. α1 ratio values are approximately corresponding to the value of 3 is shown in Table 3.

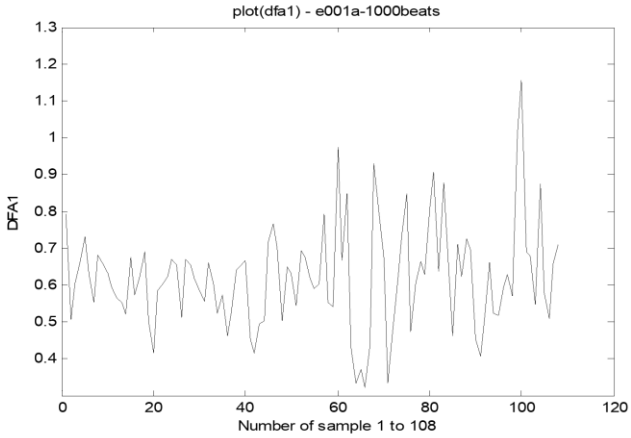

***Figure 1.** α1 array in MDFA results*

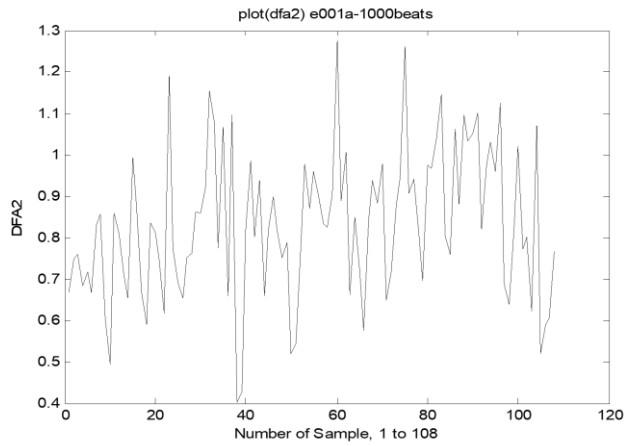

***Figure 2**. A2 array in MDFA results*

The set of values α2 through MDFA calculations are shown in Fig. 2 below. This data set is divided into 3 different values range from 0 to 0.5, from 0.5 to 1 and greater than 1. α2 ratio values are approximately corresponding to the value of 3 is shown in Table 3.

***Table 3**. Correlation of type 1 and type 2*

No.	TYPE 1 AND TYPE 2		
	Values	***α1***	***α2***
1	0.5 <α1 and α2 <1	84%	79%
2	0 <α1 and α2 <0.5	15%	3%
3	1 <α1 and α2	1%	18%
4	α1 and α2 = 1	0%	0%
5	α1 and α2 = 1.5		
6	α1 and α2 = 0.5		

Table 3 shows the percentage $\alpha 1\ and\ \alpha 2$ values calculated by the method MDFA. This result is mainly concentrated in the range of 0.5 to 1. The threshold of less than 0.5 and greater than 1 accounted for the low rate, and no value is in 0.5 or 1 or 1.5 corresponding to different types of noise.

With 84% and 79% of the data are calculated in the range from 0.5 to 1, the degree of correlation between the values in the matrix is large. This is equivalent to the possibility of ECG arrhythmia is low. This advantage is more prominent than the DFA method of Peng CK. This result allows eliminating most about ECG little noise or no noise.

Each pair of *α1 and α2* values outside the range 0.5 to 1.0 will show an average arrhythmia (0 < *α1 and α2 < 0,5)*, high arrhythmias $(1 < \alpha 1\ and\ \alpha 2)$ or noise ($\alpha 1\ and\ \alpha 2 = 1.0$ or $\alpha 1\ and\ \alpha 2 = 0.5$ or $\alpha 1\ and\ \alpha 2 = 1.5$). Besides, the order of the pairs in the value chain α1 and α2 calculated results also reflect the time of the ECG arrhythmia.

4. Conclusions

MDFA results of our calculations allow assessment of the correlation matrix more detailed and specificthan DFA method of Peng CK [10].With the original data matrix of about 100000 RR heart rate, we can calculate the value of 80 pairs α1 and α2 different from specific classification level in accordance with the arrhythmia low level (0.5 < α1 and α2 < 1), middle average(0 < α1 and α2 < 0.5) or higher (1 < α1 and α2). Besides, comparing the order of calculation and DFA2 DFA1 value pairs will allow a period determined arrhythmia occurs (correct up to 20 minutes). The process of calculating the data also give similar results with the ability to remove over 54% of the RR data matrix stability and help researchers can focus detecting arrhythmias level with remaining data.

REFERENCES

[1] Brüser, Christoph; Stadlthanner, Kurt; de Waele, Stijn; Leonhardt, Steffen (2011). "Adaptive Beat-to-Beat Heart Rate Estimation in Ballistocardiograms". IEEE Transactions on Information Technology in Biomedicine (IEEE) 15 (5): 778–786

[2] Brüser, Christoph; Winter, Stefan; Leonhardt, Steffen (2012). "Unsupervised Heart Rate Variability Estimation from Ballistocardiograms". 7th International Workshop on Biosignal

Interpretation (BSI 2012), Como, Italy.

[3] Anderson, S. (1992). Advanced Electrocardiography (Biophysical Measurement Series). Spacelabs Medical,Inc., Redmond, WA.

[4] Carvalho, J. L. A., da Rocha, A. F., Junqueira Jr, L. F., Souza Neto, J., Santos, I., and Nascimento, F. A. O. (2003). A tool for time-frequency analysis of heart rate variability. In EMBC'03, 25th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, volume 3, pages 2574–2577.

[5] Carvalho, J. L. A., da Rocha, A. F., Nascimento, F. A. O., Souza Neto, J., and Junqueira Jr, L. F. (2002). Development of a Matlab software for analysis of heart rate variability. In ICSP'02, 6th International Conferenceon Signal Processing, volume 2, pages 1488–1491.

[6] Correia Filho, D. (2000). Avaliac¸ ˜ao Cl´ınico-Funcional, Bioqu´ımica e Imunol ´ ogica do Sistema Nervoso Aut ˆ onomo em Residentes em´ Area Endˆ emica da Doenc¸a de Chagas. PhD thesis, Universidade Federal de Minas Gerais (UFMG), Belo Horizonte–MG,Brazil.

[7] Kanters JK, Holstein-Rathlou NH, Agner E (1994). "Lack of evidence for low-dimensional chaos in heart rate variability". Journal of Cardiovascular Electrophysiology 5 (7): 591–601.

[8] Brennan M,Palaniswami M, Kamen P. Do existing measures of Poincaré plot geometry reflect non-linear features of heart rate variability? Biomedical Engineering, IEEE Transactions on, Proc. IEEE Transactions on Biomedical Engineering, 2001, 48, 1342-1347

[9] Storella RJ, Wood HW, Mills KM et al. (1994). "Approximate entropy and point correlation dimension of heart rate variability in healthy subjects". Integrative Physiological & Behavioral Science 33 (4): 315–20.

[10] C. Peng, S. Havlin, H. Stanley, and A. Goldberger, "Quantification of scaling exponents and crossover phenomena in nonstationary heartbeat time series,"Chaos,vol. 5, no. 1, pp. 82–87, 1995.

[11] G. Morren, Advanced signal processing applied to invivo spectroscopy and heart rate variability. PhD thesis, K.U.Leuven, 2004.

[12] Alvarez-Ramirez J., Rodriguez E. and Echeverria J.C. (2005). Detrending fluctuation analysis based on moving average filtering. Physica A, 354, 199-219.

[13] J.W. Kantelhardt, St. A. Zschiegner, E. Koscielny-Bunde, Sh. Havlin, A. Bunde, H.E. Stanley: Multifractal detrended Fuctuation analysis of nonstationary time series Physica A 316 (2002) 87-114.

(The Board of Editors received the paper on 05/05/2014, its review was completed on 17/06/2014)