

Detrended Fluctuation Analysis (DFA) and R-R Interval Variability: A New Linear Segmentation Algorithm

JC Peretto¹, A Ruiz², C D'Attellis³

¹Biomedical Engineering Institute - University of Buenos Aires, Argentina

²Fernandez Hospital, Buenos Aires, Argentina

³University of Favaloro, Buenos Aires, Argentina

Abstract

The detrended fluctuation analysis (DFA) [1] method is used to quantify the fractal-like scaling properties of the variability of cardiac parameters, i.e. R-R interval data.

DFA has proved to be a useful index in predicting survival in heart failure. Several authors have proposed to break the numerical series in two zones with linear slopes. The breakpoint between segments is empirically situated at $\log n$ equals 1,1.

We have used the DFA method to process records of passive head up tilt (H.U.T.) test done to patients who have suffered one or more faint episodes.

Slopes of numerical series obtained from real signals neither change at a specific point, nor have only one breakpoint, especially if they correspond to pathological records. On the contrary some of them present abrupt changes in slope. This fact could be hidden in the traditional computation if changes in slope have different sign, but are detected in our approach.

A method that tracks the DFA function, detect breakpoints, and obtain a continuous set of lines between them, and their corresponding slopes, is proposed.

1. Introduction

Detrended Fluctuation Analysis had allowed applying fractal and complexity to non stationary series. DFA was used with RR Interval variability [2] to discriminate between normal and congestive heart failure using very long series (24 hours)[1] [3]. More recently it was used in shorter series between 300 to 500 heart beats [4] [6].

DFA method requires to do a cumulative summing to the original time series. Then the series is cut into several segments and the degree of dispersion from a local trend is measured. This is done to each segment and repeated with different segment lengths.

In equations:

$$F_n = \sqrt{1/N \cdot \sum_{k=1}^N [y(k) - y_n(k)]^2}$$

where

$$y(k) = \sum_{i=1}^k (R(i) - \bar{R})$$

y_n is the local trend and n is the box size.

We obtain the average fluctuation F_n as a function of the box size n . A linear relationship on a double log graph reveals a scaling factor between those magnitudes. If the points are aligned the slope of this line represents a scaling exponent α . An α of 0.5 corresponds to white noise, $\alpha = 1$ represents 1/f noise and $\alpha = 1.5$ indicates Brownian noise or random walk. A good linear fit on the entire range of n corresponds to a the single exponent α describing the correlation properties of the heart rate data. This α is known as the fractal dimension and has been presented as a useful value for diagnostic purpose. Scaling exponent α , calculated from healthy subjects use to be around the unity; disclosure from this value is a marker of pathology. However in some cases, several authors have found that the DFA plot was not strictly linear but rather consisted of two distinct regions of different slopes [3] [4] α_1 α_2 representing short and long time correlations. The frontier between the two zones has been empirically set at n equals 11 beats [5]. Other values like 12, 13 and 16 beats [6] [7] [4] [1] are also recommended. Both slopes estimations are affected by the election of one or another breakpoint, although the $\log(n)$ partially hides the differences. These slopes, which are the estimation of α_1 and α_2 , are altered in disease, therefore, a different pattern with one or more breakpoints could be expected. If we miss one breakpoint from a pathologic study the slope probably don't differ much from a normal case. Our approach is to detect these breakpoints directly from the data series, as the points where the dynamics changes without taking into account any assumption a priori.

2. Materials and Methods

2.1. Algorithm Description

Our method finds the minimal number of linear segments that fits a cloud of points with a given tolerance. Each point is defined by its coordinates (x_i, y_i) .

$$x=[x_1.....x_i.....x_n]$$

$$y=[y_1.....y_i.....y_n]$$

Beginning with the first pair of points we computes the tangent

$$\theta_1 = \frac{(y_2 - y_1)}{(x_2 - x_1)} \quad \theta_i = \frac{(y_{i+1} - y_i)}{(x_{i+1} - x_i)}$$

$$\theta = [\theta_1..... \theta_i..... \theta_{n-1}]$$

if $(\theta_i - \theta_{i-1}) < \text{threshold}$ (x_{i+1}, y_{i+1}) is accepted
 else x_{i+1}, y_{i+1} is a new breakpoint

Then we continue with the second and third points, and so on, to finish with a tangent series related to angle information. If all of the points correspond strictly to a linear segments they must share the same angle. For each element we then check that the difference between adjacent values, which corresponds to a measure of misalignment, is lower than a certain threshold we had previously established. If a point does not fulfill this condition, a break point is included and the point is rejected. The last is now the first point of a new linear segment. And the process continues till the last point is evaluated.

Each segment is formed with points that are aligned and now a linear regression is done to each of them. For each segment a slope and the norm of residuals are obtained.

If data is truly linear, our algorithm does not break it, but if it is not, several breakpoints can be included. If the last is true a better fitting can be expected.

2.2 Data and preprocessing

To evaluate our algorithm, we use records from normal controls and from subjects that suffers faint episodes.

To study the adaptation mechanisms in their cardiovascular system we use a procedure named tilt

tests. With the aid of a tilt bed a passive tilt of the patient, head up, in angles between sixty to eighty degrees is reached. This maneuver leads to hypotension and eventually to a syncope, in this case we refer to it as a positive Tilt Test (TT+), if not as a negative Tilt test (TT-). Signal acquisition during tilt test includes electrocardiogram (ECG) and continuous blood pressure curve (CBPC).

Two signals are then available as digital data for computer processing: beat to beat interval and beat to beat systolic and diastolic BP. They are obtained respectively from ECG and CBPC. This implies detection of R wave on ECG to compute intervals between them and determination of maximum and minimum BP for every heart beat on CBPC.

An automatic method for the detection of R wave on ECG is applied to the data. A posteriori manual editing of the marks of occurrence of the R waves is performed by experts. The intervals between them were used to form the RR event series in function of beat number.

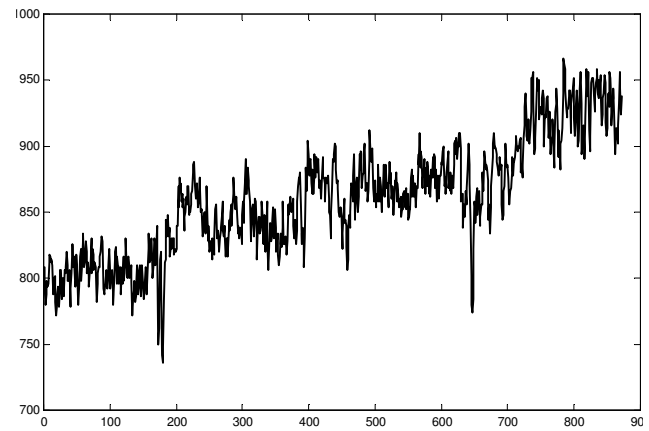


Fig. 1 - RR Interval from a normal control. We can see also that the series is not stationary

3. Results

We then compute the DFA and apply our method to find the natural breakpoints and slopes. The result corresponding to the example in Fig 1. can be observed in figure 2. In this example, the first breakpoint is located at a value of $\log(n) < 1$, and the slope at the intermediate zone a_2 , is very close to one, as expected since it belongs to a normal subject. Close to each segment the corresponding slope and the norm of the residuals are annotated. In the top of the chart, the slope that results using all the points, is shown.

We can see that local slopes are different from that value. The notable reduction in the residuals indicate a

better adjust using our algorithm and confirm our previous hypothesis.

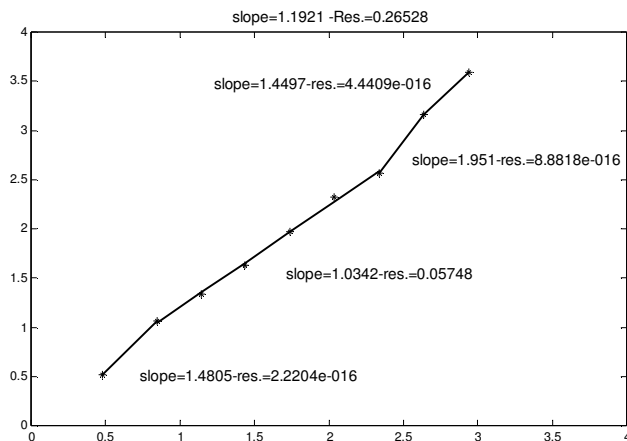


Fig. 2- DFA and our segmentation algorithm on normal control. The slope that results from using all the points is =1,1921 and the norm of the residuals= 0.28. $\alpha_1 = 1,4805$ and $\alpha_2= 1.032$ and the residuals = 0,057 five times lower approximately

Now we turn to a subject that has done a TT+ with autonomic origin

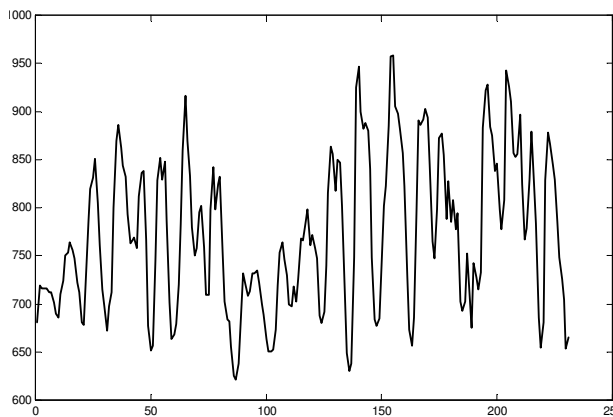


Fig. 3- RR Interval record from a subject with TT+. Comparing with Fig 1. 'high frequency' components are missing.

And the corresponding DFA followed by our segmentation algorithm results in the following figure. In this case the first breakpoint is also < 1.

The slope in the intermediate zone is far from the unit, revealing a pathologic case.

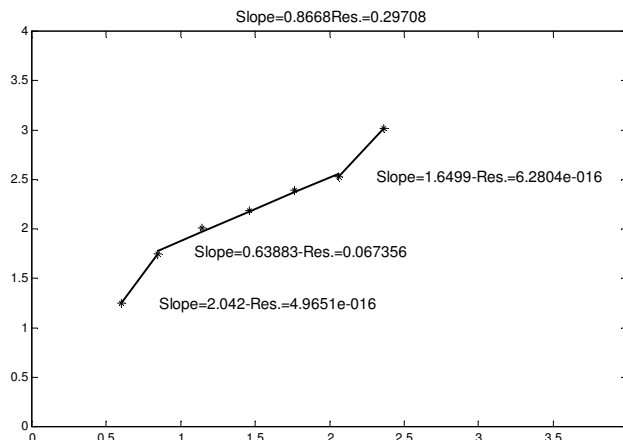


Fig. 4- DFA and our segmentation algorithm -TT+. The slope that results from using all the points is=0,86 and the norm of the residuals= 0.297. $\alpha_1 = 2,042$ and $\alpha_2= 0.638$ and the residuals = 0,067

4. Discussion and conclusions

We are not into confronting with others authors, but to prevent using DFA in a mechanical manner, without taking into account the real nature of the data. Our method brings a methodological improvement when trying to fit the model to the data and not the other way around.

Our algorithm is very simple, but capable of detecting natural breakpoints and bringing us the real slope in the different interest zones. It can be applied to normal, but to pathological series also.

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Address for correspondence

Name: Juan Carlos Perfetto

Full postal address: Paseo Colon 850- 5° Piso Instituto de Ingeniería Biomédica

E-mail address : jperfet@fi.uba.ar