

MATLAB SOFTWARE FOR DETRENDED FLUCTUATION ANALYSIS OF HEART RATE VARIABILITY

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Keywords: Detrended fluctuation analysis, DFA, Heart rate variability, HRV.

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 experiment duration, which is generally not true for long-duration signals (e.g., 24-hour Holter) or signals acquired during stress tests. This paper presents a Matlab tool for detrended fluctuation analysis (DFA) of HRV signals. DFA is applicable in the context of nonstationary signals, since it involves removing fluctuation trends from the signal. The software is validated using simulated signals with different power-law characteristics, and then demonstrated using real HRV signals, obtained from three groups of subjects: healthy volunteers, individuals with Chagas disease, and individuals with mild to moderate hypertension.

1 INTRODUCTION

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 (Malik and Camm, 1995). Changes in HRV have been associated with different pathological conditions, such as hypertension, Chagas disease, hemorrhagic stroke, and septic shock. HRV is also useful as a predictor of post-infarction mortality.

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) (Malik and Camm, 1995; Anderson, 1992), frequency domain analysis (e.g., Fourier transform, auto-regressive model, Lomb-Scargle periodogram) (Malik and Camm, 1995; Anderson, 1992; Shin et al., 1994), and geometrical techniques (e.g., Poincaré plot, trend analysis) (Piskorski and Guzik, 2007; Schechtman et al., 1992). Such techniques require the signal to be stationary within the experiment duration, i.e., the variability characteristics cannot change considerably throughout the sig-

nal. This is typically an issue when analyzing long duration signals (e.g., 24-hour Holter) or stress test signals (e.g., physical tests, cold pressor, Valsalva maneuver). Alternative techniques include time-frequency approaches, using, for example, the short-time Fourier transform, the auto-regressive spectrogram, or wavelet transforms (Carvalho et al., 2003). However, means for quantifying the information extracted from these techniques have not been well established. Different computational tools have been presented for the analysis of HRV (Carvalho et al., 2002; Carvalho et al., 2003; Niskanen et al., 2004), and were important in popularizing the use of these techniques.

In 1995, Peng et al. proposed the use of detrended fluctuation analysis (DFA) for analysis of HRV (Peng et al., 1995). DFA is applicable in the context of nonstationary signals, since it involves removing fluctuation trends from the signal. The result of DFA is quantified by two coefficients (α_1 and α_2), which reflect short-term and the long-term fluctuations, respectively. Peng et al. showed that DFA coefficients are capable of discriminating healthy subjects and individuals with congestive heart failure. The HRV computational tools mentioned above do not implement this type of analysis. This contributes to its limited use by the scientific community.

In this work, we present a computational tool for

detrended fluctuation analysis of heart rate variability. The presented software is validated using simulated signals with different power-law characteristics: white noise, pink noise ($1/f$), and Brownian noise ($1/f^2$). Then, the tool is demonstrated using real HRV signals, obtained from three groups of subjects: healthy volunteers, individuals with Chagas disease, and individuals with mild to moderate hypertension. The presented tool can help popularize the use of DFA for analysis of HRV signals, making it easier to study nonstationary signals such as those from long-duration exams and from tests involving variable stress conditions.

2 THEORY

Intervals between cardiac beats vary in a complex manner, presenting exponential correlations. Detrended fluctuation analysis is a method that allows the detection of long-range correlations embedded in an irregular signal, and avoids spurious detection of apparent long-range correlations that are an artifact to the object of the analysis (Peng et al., 1995). In the context of HRV, DFA allows the distinction between complex fluctuations intrinsic to the nervous system in the command of vital actions of the human body, and those originated on the environment and that also influence the heart rate. Those fluctuations that are intrinsic to the nervous system happen to be observed throughout the signal, as opposed to the extrinsic fluctuations that present local and short-term effects. The main objective of DFA is to extract the extrinsic fluctuations in order to allow the analysis of the signal's variability associated exclusively with autonomic control (Peng et al., 1995).

The first step in the calculation of the DFA coefficients is the subtraction of the DC component of the signal (mean RR interval). The resulting signal is then integrated, as follows:

$$y(k) = \sum_{i=1}^k [RR(i) - RR_{ave}], \quad (1)$$

where $RR(i)$ is the duration of the i -th RR interval, RR_{ave} is the mean interval, and k is the current output sample time-index.

The integrated signal $y(k)$ is then segmented into multiple windows of length n . For each of these windows, a least-squares first-order approximation (a line segment) is calculated, representing the "trend" of that segment of the signal. The trend signal $y_n(k)$, formed by the line segments, is an approximation to the integrated signal $y(k)$. The detrended signal $e(k)$

is the approximation error, i.e.,

$$e(k) = y(k) - y_n(k). \quad (2)$$

Thus, the root mean squared approximation error for a particular window of length n is

$$F(n) = \sqrt{\frac{1}{N} \sum_{k=1}^N e(k)^2}, \quad (3)$$

where N is the total number of RR intervals, i.e., the length of $RR(i)$.

$F(n)$ is calculated for several different window lengths. As the window length increases, the approximation error typically increases. Thus, $F(n)$ is generally a monotonically increasing function. By analyzing the relationship between window length and approximation error, it is possible to verify the presence of fractal characteristics in the signal. If $F(n)$ is an exponential function of n , then a linear relation is observed in log-log scale. When this is the case, it can be said that the signal presents a scale-invariant (fractal) correlation property. Under such conditions, HRV fluctuations can be characterized by a coefficient α , which corresponds to the slope of the line relating $\log(F(n))$ to $\log(n)$.

Although DFA is of great utility in the detection and classification of different pathologies in long duration signals, it is important to provide the possibility of analyzing short duration signals, as those typically used in classical HRV analysis (e.g., 5 minute segments). Typically, short duration HRV signals display different correlation properties for short windows ($n \leq 16$) and for long windows ($n > 16$) (Peng et al., 1995). This cross-over phenomenon is typically observed in the log-log plot of $F(n)$ as a curve that can be clearly modeled by two different slopes, one for small values of n , and one for large values of n . Thus, we calculate two different values of α , i.e., two DFA coefficients: α_1 and α_2 , which reflect short-term and long-term fluctuations, respectively (Peng et al., 1995).

3 METHODS AND RESULTS

3.1 Matlab Software for DFA of HRV

The proposed computational tool was developed in Matlab 6.5 (The MathWorks, Inc., Natick, MA, USA). It implements a graphical interface in which each of the DFA calculation steps discussed above is graphically displayed, so as to improve user understanding of the entire process. The interface is divided in four subplots (Figure 1). The first subplot, in

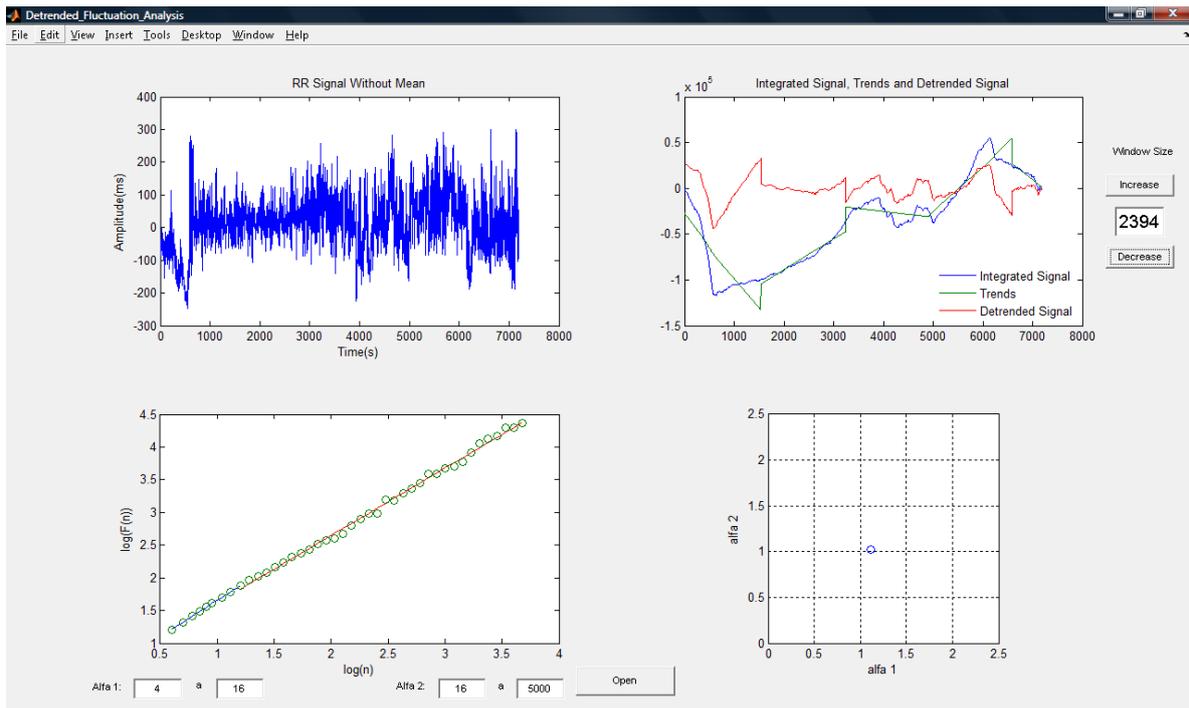


Figure 1: Graphical user interface for detrended fluctuation analysis of HRV.

the upper-left quadrant, provides a visualization of the original RR time-series, $RR(i)$. The second subplot, in the upper-right quadrant, presents three signals: the integrated signal, $y(k)$; the trend signal, $y_n(k)$; and the approximation error (detrended signal), $e(k)$. On this subplot, it is possible to change the window-length for visualization (Figure 2). This, however, does not affect the calculation of the $F(n)$ log-log plot, displayed on the lower-left quadrant. The range of values of n associated with coefficients α_1 and α_2 are manually defined by the user, on a set of text-edit boxes, located below the log-log subplot. Finally, the values of the coefficients α_1 and α_2 are plotted in a Cartesian coordinate system on the fourth subplot (lower-right quadrant).

3.2 Validation

In order to validate the software, we used simulated signals with different power-law correlation characteristics. Specifically, we used three different kinds of noise: white noise, pink noise ($1/f$), and Brownian noise ($1/f^2$). The α coefficient associated with each of these types of noise is 0.5, 1 and 1.5, respectively (Peng et al., 1995). The smoother the signal, the larger the value of α , as discussed next.

Theoretically, white noise presents constant power spectral density amplitude for all frequencies (f), and an auto-correlation equal to the Dirac delta function.

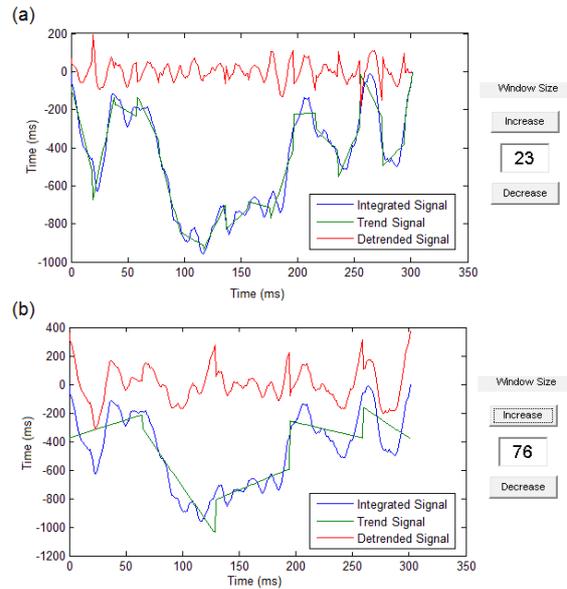


Figure 2: Subplot for visualization of the detrending process, where the integrated signal $y(k)$, the trend signal $y_n(k)$, and the approximation error (detrended signal) $e(k)$, are displayed for a specific window length (n). The value of n can be manually changed by the user, using the interface shown on the right. (a) $n = 23$ samples; (b) $n = 76$ samples. Note that the approximation error increases for longer windows.

This type of noise can be compared to a HRV signal that presents low long-term correlation, and sharp

variations. Integrated white noise corresponds to a random walk, and therefore $\alpha = 0.5$. Pink noise has power spectral density amplitude inversely proportional to f , i.e., proportional to $1/f$. Its associated value of α is 1, which represents a boundary between sharp and smooth variations. Brownian noise corresponds to the integration of white noise. Thus, it presents smoother variations than white and pink noises, and its associated α value is 1.5.

The white noise signals used in this validation were created using the `rand` function in Matlab. Pink noise signals were generated by weighting the discrete Fourier transform of each white noise signal by $f^{1/2}$ and then taking the inverse Fourier transform. Brownian noise signals, $b(i)$, were obtained by integrating the white noise signals, $x(i)$, using the following difference equation: $b(i) = b(i-1) + x(i)$.

The simulated signals were processed using the presented software. The results of this experiment are presented in Figure 3. The measured coefficients show good agreement with the theoretical values.

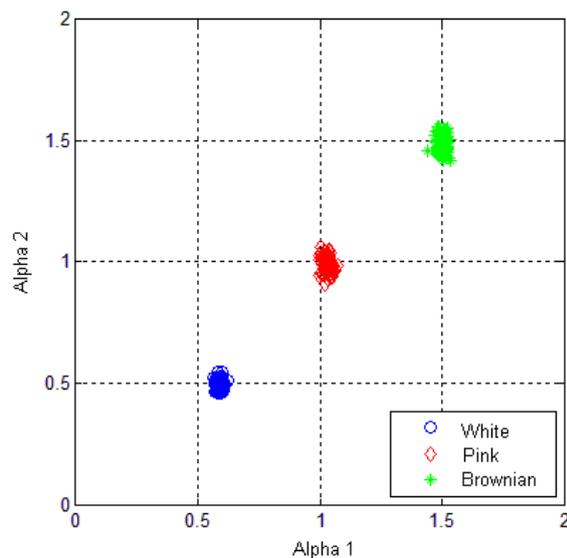


Figure 3: Validation of the software, using different types of noise signals.

3.3 Demonstration

In order to demonstrate the ability of this tool of discriminating between normal and pathological individuals, an experiment using real HRV signals was conducted. We used a database of 58 RR interval time-series, of approximately 5 minutes each, composed of 32 signals from healthy subjects (Jesus, 1996; Correia Filho, 2000), 13 signals from individuals with organic Chagas disease (cardiac or digestive forms) (Correia Filho, 2000), and 13 signals from individuals with ar-

terial hypertension (mild or moderate) (Junqueira Jr et al., 2001). The signals in this database were acquired by the faculty and staff of the Cardiovascular Laboratory of the School of Medicine of the University of Brasília. The experimental protocols are described in detail in (Jesus, 1996; Correia Filho, 2000; Junqueira Jr et al., 2001).

The results of this experiment are shown in Figure 4. The DFA tool was capable of satisfactorily discriminating the group of healthy subjects from the group of Chagas disease individuals. The group of individuals with hypertension show some overlap with a portion of the group of healthy volunteers. This is explained by the fact that the hypertension level in this group was from mild to moderate. Nevertheless, individuals in this group seem to present a higher α_1 value than that of the healthy subjects, in average.

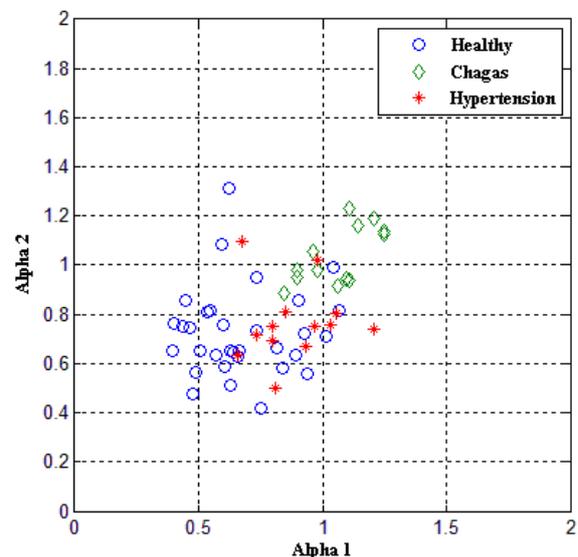


Figure 4: DFA coefficients for a group composed of three different types of subjects: healthy volunteers, individuals with Chagas disease (cardiac or digestive), and individuals with arterial hypertension (mild or moderate).

Based on the results above, the characteristics of each group of individuals can be compared with the characteristics of the noise signals discussed in the previous section. Based on the average value of α for healthy volunteers, it can be said that the power-law characteristics of such signals are closer to those of white noise ($\alpha = 0.5$). Therefore, despite the dispersion of the measured coefficients, the results suggest that normal individuals present small long-term correlations. On the other hand, the group of individuals with Chagas disease presents an average value of α approximately equal to 1, what makes it possible to compare the power-law characteristics of this group

to those of pink noise, indicating a smoother RR signal, with stronger long-term correlations. Finally, the group of individuals with hypertension presents RR signals with moderate smoothness. Arterial hypertension is associated with reduced variability of cardiac frequency, specially that associated with parasympathetic activities, what can partially explain the observed results.

4 CONCLUSIONS

A new tool for analysis of HRV was presented. The presented software implemented detrended fluctuation analysis, and may facilitate the study of pathologies on long duration examinations or during exams involving variable stress conditions, since DFA does not make assumptions about signal stationarity. The output of DFA analysis is a pair of numerical coefficients, what could make the statistical analysis of such signals simple and practical. DFA could be combined with pattern classification methods based on neural networks, for a potentially powerful diagnosis tool.

The presented software was first validated with a set of simulated signals, and then applied to real RR signals, which demonstrated its utility for the analysis of HRV. The DFA tool was capable of satisfactorily discriminating the group of healthy subjects from the group of Chagas disease individuals. The group of individuals with mild to moderate hypertension showed some overlap with a portion of the group of healthy volunteers, but seemed to present higher α_1 values than that of the healthy subjects, in average.

The presented tool may help popularizing the use of DFA among the HRV scientific community. The software is open source, and is available upon request.

ACKNOWLEDGEMENTS

The authors thank Prof. Luiz Fernando Junqueira Jr. and the faculty, staff and alumni of the Cardiovascular Laboratory of the University of Brasília for providing the HRV signals used in this work. The authors also thank Mr. Pandelis Perakakis for motivating this work, and for useful discussions.

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