Statistical Properties and Memory of Excursions in Heartbeat Intervals

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Abstract

We study the statistics of excursions, defined as the number of beats to return to a local mean value in heartbeat interval time series from healthy subjects and patients with congestive heart failure (CHF). We find that the cumulative distributions of excursions (of size τ) are consistent with a stretched exponential function of the form $G(\tau) \sim e^{a\tau^b}$ with a and b constants. Also, we study the statistics of return intervals between long excursions above certain threshold q for both groups to explore the possibility of memory in the time organization of the extreme-size excursions. The correlation method applied to the return intervals shows a weak correlation for both groups with changes as the threshold q increases. The DFA analysis confirms the presence of correlations with scaling exponents higher than the uncorrelated value ($\alpha = 0.5$).

1. Introduction

Throughout the years, many studies based on nonlinear dynamics have been applied to physiological signals [1], in particular to the interbeat time series [2]. All these studies revealed in general that the heartbeat behavior is nonstationary and long-range correlated [3,4], and important differences between healthy and diseased subjects have been reported [1, 5, 6]. Different methods to detect stationary segments in complex time series have been proposed [7], in particular to the study of nonstationary long-time interbeat records [8]. One method which is efficient and useful to detect stationary segments is the segmentation method (SM) proposed by Bernaola-Galván et. al. [9]. We recently studied the statistical properties of excursions along stationary segments, which were detected by the SM [10]. Our results reported that excursions are consistent with a stretched exponential behavior of the cumulative distribution, suggesting the presence of correlations in the excursion sequences.

On the other hand, studies based on the statistics of return intervals above certain threshold have revealed the presence of long-term correlations and clustering in different type of records such that financial indexes [11] and climate records. The return interval distributions are useful to characterize temporal properties of the events when one is interested in the time recurrence of extreme events, for example, earthquakes [12], the behavior of certain financial indexes [13], x-ray solar flares [14], climate records [15], or even long heartbeat intervals [16].

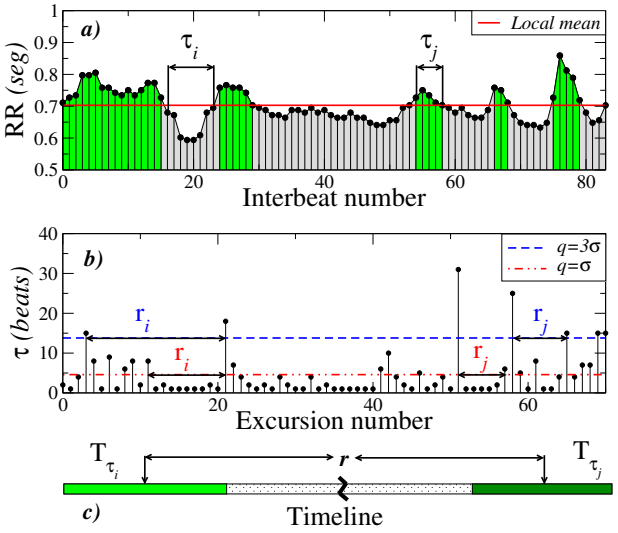

Figure 1. *a)* Representative plot of the interbeat time series (RR intervals) to illustrate the excursion identification. *b)* Representative plot to identify the return interval between two successive large excursions (above a given threshold). *c)* Time line that represents the length of the return time interval. The return time interval r will be the time between the mean time point ($T_{\tau_i}/2$) of an excursion greater than the threshold q, to the mean time point ($T_{\tau_j}/2$) of the next excursion also greater than q.

Physiological systems are, in general, bounded systems, body temperature, blood pressure or heart rhythm are some examples where the variations are consistent with the homeostatic principle. By studding the excursions around a local mean value, we are in the position to evaluate how far a system's response goes ahead, while remaining within

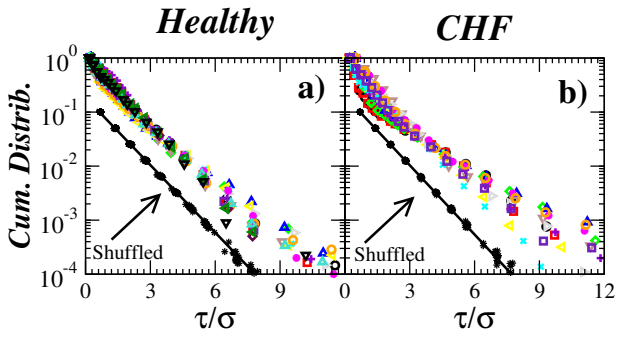

Figure 2. Cumulative distribution function of excursions τ for both groups. A slight deviation for the exponential behavior (shuffled records) is observed in original data.

a bounded region. If we connect the return intervals ideas with the excursion analysis, we may obtain additional information about the fact that the healthy systems are less bounded than disease systems due to the fact that the control mechanism are still not degradated enough to give a better response to external stimuli. In the present work, we study the statistics and correlations of the time return intervals of excursions above different thresholds.

2. Methods

Correlation Function.- Many processes in nature show a long-range correlated behavior, i.e., there is a time-dependence in the order of the events. When it happens, we say that the event has "memory". This kind of processes are characterized by an autocorrelation function $C_x(s)$ that decays as a power law,

$$C_x(s) = \frac{1}{\sigma_x^2 (L-s)} \sum_{i=1}^{L-s} (x_i - \overline{x})(x_{i+s} - \overline{x}) \sim s^{\gamma} \quad (1)$$

where σ_x denotes the standard deviation, $\overline{x}$ the mean, s the lag and γ the correlation exponent ($0 < \gamma < 1$).

The DFA method.- One method that is useful to detect correlations in nonstationary series is the detrended fluctuation analysis (DFA). To illustrate DFA method [17], we depart from an initial time series $x(i)$ (of length N), first, this series is integrated, $y(k) = \sum_{i=1}^{k} [x(i) - x_{ave}]$, the resulting series is divided into boxes of size n. For each box, a straight line is fitted to the points, $y_n(k)$. Next, the line points are subtracted from the integrated series, $y(k)$, in each box. The root mean square fluctuation of the integrated and detrended series is calculated by means of

$$F(n) = \sqrt{\frac{1}{N} \sum_{k=1}^{N} [y(k) - y_n(k)]^2}, \quad (2)$$

this process is taken over several scales (box sizes) to obtain a power law behavior of the form

$$F(n) \propto n^{\alpha}, \quad (3)$$

with α an exponent which reflects self-similar and correlation properties of the signal. It is known that $\alpha = 0.5$ corresponds to white noise (non correlated signal), $\alpha = 1$ means $1/f$ noise and $\alpha = 1.5$ represents a Brownian motion.

The segmentation method.- We use the segmentation method proposed by Bernaola-Galván et. al. [9] to detect stationary segments in the interbeat series. To apply the algorithm, first we consider a slider pointer to calculate the statistics $t = \frac{\mu_r - \mu_l}{S_D}$, where S_D is the standard deviation, μ_r and μ_l are the mean of the values on the right and left side, respectively. Next, a significance level is applied to cut the series into two new segments, as long as the means of the two new segments are significantly different from the mean of the adjacent segments. And then, the process is applied recursively until the significance value is smaller than a threshold or the length of the segment is smaller than a minimum l_0.

Excursions and Return Intervals.- Once we get the time series segmented, we proceed to identify an excursion with size τ if $x_j > \overline{x}$ and $x_{j+\tau} > \overline{x}$ while $x_i > \overline{x}$ for $j < i < j + \tau$ or conversely $x_j < \overline{x}$ and $x_{j+\tau} < \overline{x}$ while $x_i < \overline{x}$ for $j < i < j + \tau$ (see Fig. 1*a*), where $\overline{x}$ represents the local mean of a given segment. Next, we define a return interval as the elapsed time between two excursions above some large threshold q (see Fig. 1*b*), for example, proportional to the standard deviation σ_τ of the excursions. For a detailed explanation of the return time see Fig. 1*c*.

$$r = \frac{T_{\tau_i}}{2} + \sum_{k=i}^{j} T_{\tau_k} + \frac{T_{\tau_j}}{2} \quad (4)$$

3. Results

In a previous work [10] we reported that the distribution of excursions follows a stretched exponential function to consider for the cumulative distribution function given by $g(x) \sim e^{-a\tau^b}$, with $a = 1.09 \pm 0.15$ (mean value $\pm$ SD) and $b = 0.91 \pm 0.11$ for healthy subjects and $a = 1.31 \pm 0.23$ and $b = 0.77 \pm 0.13$ for CHF patients. In Fig. 2*a* and 2*b* we observe that, for shuffled data, the distribution of excursions becomes exponential for both groups, which suggest the presence of correlations [10].

Next, we study the return intervals defined in the previous section. In Fig. 3*a* and 3*b* we show the cumulative distributions of the return intervals for both groups of individ-

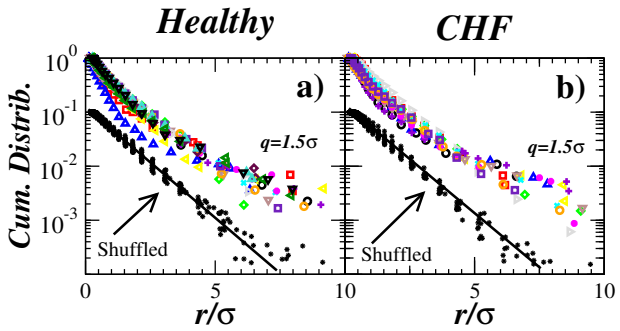

Figure 3. Distributions of the return intervals r for both groups for a given threshold $q = 1.5\sigma$. In *a)* and *b)*, a comparison among all the individuals of the group is made, and also, the shuffled of the original data of every record is shown.

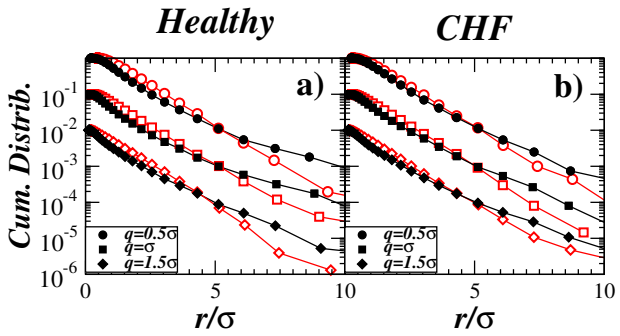

Figure 4. Distributions of the return intervals r for both groups for several thresholds. In *a)* and *b)*, the shuffled data are represented with open symbols and scaled together with their own original data for a better observation. Also, in *a)* and *b)* each point represents the average value of all the individuals of the group for each value of lag s.

uals. We found that they also follow a stretched exponential function with parameters given by $a = 1.34 \pm 0.36$ and $b = 0.75 \pm 0.16$ for healthy subjects and $a = 1.38 \pm 0.37$ and $b = 0.73 \pm 0.16$ for CHF patients (for a threshold $q = 1.5\sigma_\tau$). In the two cases, the results for shuffled records are also shown. We notice that all the individuals have a common behavior under normalization, suggesting that we can pool all the individual data to improve the statistics. Figures 4*a* and 4*b* show the distribution of return intervals in the case of three different thresholds (filled symbols), together with their corresponding shuffled version (open symbols). For the three thresholds cases, both groups shows a slight different behavior to the one for the uncorrelated shuffled data. Therefore, to evaluate the presence of correlations in the return interval series, we perform two proofs: Correlation function and DFA analysis.

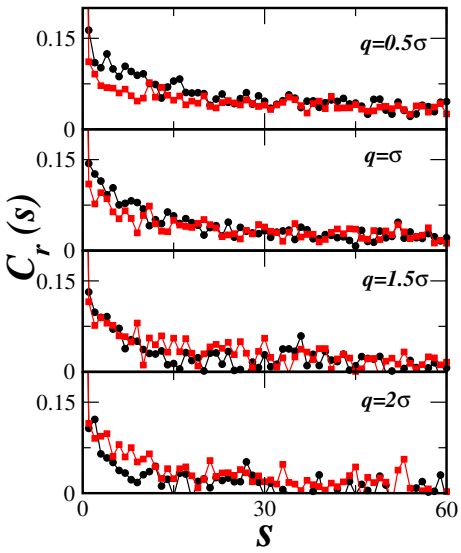

Figure 5. Correlation function for the return intervals for different values of threshold q. Results for the healthy group (circles) and CHF patients (squares) are shown. Each point presented in the graphics represents the average value of all the individuals of the group.

The correlation proof is performed by means of the correlation coefficient for a given lag s. Specifically, Fig. 5 shows the results of correlation proof for different values of threshold q. The correlation function shows a slight difference between healthy and CHF groups. At short lag s, the correlation function from healthy data is slightly higher than CHF records, whereas the opposite behavior is observed when the threshold is increased.

Referring to the DFA analysis (see Fig. 6), our calculations shows that the scaling exponents become closer as the threshold size q increases. For small values of the threshold ($q = 0.5\sigma$), healthy data is characterized by the scaling exponent $\alpha = 0.66 \pm 0.06$. This average value tends to decrease as the threshold increases. For CHF patients, we observe $\alpha = 0.60 \pm 0.05$ when $q = 0.5\sigma$ and this value remains almost constant as q increases. We remark that the scaling exponent becomes closer as the threshold size q increases.

4. Discussion and conclusions

We have analyzed excursion sequences and return intervals from stationary segments detected in hearbeat interval series. Our study reveals that healthy and CHF excursion sequences and return intervals are characterized by stretched exponential distributions with different fitting parameters. When the correlation proof is applied we found that, for short thresholds, the healthy dynamics exhibits higher correlation in the return time series of large excur-

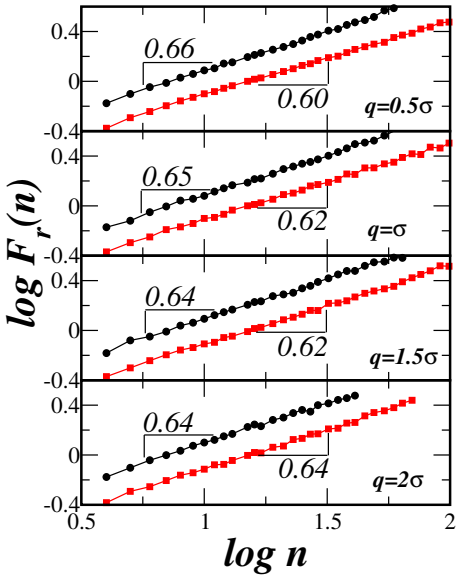

Figure 6. DFA proof for the return intervals for different values of threshold q. Results for the healthy group (circles) and CHF patients (squares) are shown. Each point presented in the graphics represents the average value of all the individuals of the group.

sions.

By means of DFA analysis, we confirm the presence of long-term correlations in return time sequences from healthy and pathological data. The DFA analysis shows that the scaling exponent for healthy data is slightly higher than the CHF group for small values of q, and they tend to be close each other as the threshold increases. These findings suggest that there exist some kind of long range correlations in the return interval series due to the fact that the scaling exponents for both groups differ from white noise.

Acknowledgments

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