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Detrended fluctuation analysis of EEG signals

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Abstract

Scaling properties are one of the most important quantifiers of complexity in many events, as time series (TS). To try to have a glimpse how brain is working, we need new methods of analysis. The structural characteristics of biomedical signals are often visually apparent, but not captured by conventional measures (average amplitude, Fourier analysis based methods, up to second order statistics). Biomedical signals (as LFP, ECoG, EEG) could possess a scale invariant structure. Scale invariance means that the structure repeats itself on subintervals of the signal. We know that the time series $x(t)$ are scale invariant when: $x[c \cdot n]=c^H \cdot x[n]$.

The Hurst Exponent (H) is a dimensionless estimator for the self-similarity of a time series. Presence of scaling exponents can point to an inner fractal structure of the series. The constant c represent a scaling coefficient (c > 1 - contraction, c < dilation). The power law exponent H, is the Hurst exponent and represent a particular kind of scale invariant structure in biomedical signals. Fractal analysis or moving average estimates this power law exponent H, characteristic for time series. To compare two time series is a difficult task. For biomedical signals, usually, H is time dependent. The Hurst exponent can be used to compare time series. But a best way to describe the scale invariant structure of biosignals is the use of multifractal characterization. This kind of study for the non-stationary biological signals is based on the detrended fluctuation analysis (DFA) method.

Multiple scales can be characterized through various techniques with Multifractal Spectrum (MS). Mutlifractal spectrum is a generalization of the H exponent. This paper is presenting the results of the use of detrended fluctuation analysis of multichannel EEG recordings. The main goal is the comparison of recording's fractal structure and their behavior at low and high frequency ranges. The method is proper to be used in the analysis of nonlinear and non-stationary signals.

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1. Introduction

The human body generates biological signals (biosignals). These signals are characteristic to a large scale of internal physiological events and can have proper structure for each internal event. Sometimes, the inherent structure of TS is visible during a recording process. If that internal structure has a special, visible pattern, then that structure must be analyzed to get its proper description. A structural characteristic of an event doesn't have an accepted, well known way to 'measure' it. When we investigate signals, we often chuck away some of the not so obvious dynamics and describe the remaining patterns with an average, mean value, standard deviation or median, as first order statistical descriptors. Biological signals are, in general fractal type signals. A fractal analyses method estimates the value of the power law exponent (H(t)). H has to represent the scale invariant structure of the biomedical signal. Different fractal analyzer procedures are currently used in signal processing to define the scale invariant structures of ECG, EEG and other biosignals [1, 2]. Different values and variations of H(t) exponent also can differentiate between normal and pathological conditions, and between different types of pathological symptoms. For these reasons fractal analyses are promising tools in biomedical signal processing and analysis [3].

The two basic notions, monofractal and multifractal structures are from the scale invariant structure category. The monofractal structure of biomedical signal is defined by a constant single power law exponent and then the scale invariance is independent of time, along TS. Usually, the structure of the biomedical signal has spatial (recording location) and temporal variations. These spatial and temporal variations are proper for a multifractal structure and finally are defined by a multifractal spectrum (MS) type of power law exponents and not only by a single power low exponent. Our purpose is to calculate the MS of a time series. We can state that the multifractal structure, the MS of EEG signal is able to differentiate between the neural activities of different, active task-related brain areas. Brain areas are localized by the signal recording electrodes scalp positions [7, 9].

New development in DFA proved that brain state variation, normal development, or pathological state can be detected in amplitude and/or phase modulation of cortical oscillations. It is known that DFA could also provide a significant insight into the functional organization of neuronal circuits and cell assemblies in cortical areas.

2. Methods

To begin, the concepts of self-affinity and self-similarity are presented. We must consider how the DFA algorithm represents the properties of scale-free or scale dependent variations, fluctuations. Self-affinity is a property of fractal type time series. It is a special case of self-similarity, or it is describing in which way a smaller segment (with a well defined length) of a fractal structure is similar to the whole structure. When each of the smaller parts is an exact replica of the whole, then the fractal is exact (the case for mathematical and geometrical fractals). When the self-similarity is expressed in terms of statistical properties then the fractal is a statistical fractal. This is the case when the mean and standard deviation for the segments of the fractal type signal are in a proportional relation with the mean and standard deviation of the whole TS. The isotropy property is expressed by a uniform self-similarity along all the dimensions of a fractal type signal. Self-affinity describes anisotropic scaling when statistical properties of the fractal type signal are variable along of the TS.

In recent years the DFA method has become a used technique to determine the fractal scaling properties and the detection of long-range correlations in noisy and non-stationary time series. Detrended fluctuation analysis is a simple mathematical method but very efficient to investigate the power-law of long-term correlations of non-stationary time series. It is necessary to obtain the characteristics of the local fluctuations at different time-scales. Many recordings do not exhibit a simple monofractal scaling behavior, defined by a single scaling Hurst exponent only. There are cases where, different parts of the TS ask for different scaling exponents. Multifractal analysis must be applied for a full description of scaling behavior (important to consider H(t) as a function of time). We have used a DFA analysis method, able to estimate the multifractal spectrum of power law exponents from biomedical time series (EEG) and able to compare (by giving a kind of measure of similarity) the trends in different, recorded TS. Multifractality should be due to a 'special' probability density function (PDF) for the values of the TS or due to

different time related correlations of the small and large fluctuations within TS [10]. In any case, the TS must be considered a stochastic sequence of values.

3. Discussion

The multifractal detrended fluctuation analysis procedure consists of five steps described in the literature [5, 10]. A basic element of the method is choosing the order of fitting polynomial in time segments for the detrending procedure, important in eliminating the trends in TS and in obtaining the cumulate fluctuation function. The main steps in multifractal detrended fluctuation analysis are [6, 10]:

- Creating the random walk like variation in a time series (cumulate TS)
- Computing the root-mean-square variation (RMS) of TS (global and local)
- Finding local detrending of the time series
- Computing multifractal detrending, q-order RMS (qRMS)
- Computing q-order Hurst exponent (Hq) and q-order mass exponent (tq),
- Computing q-order singularity exponent (hq), q-order singularity dimension (Dq)
- Computing Multifractal Spectrum, the main goal of DFA

The Hurst exponent (H) defined by the monofractal DFA represents the average fractal structure of the time series. The deviation from average fractal structure for segments with large and small events (fluctuations) is represented by the MS width. The shape of the multifractal spectrum usually is not symmetric.

The multifractal spectrum can also have either a right or a left truncation. This can have its roots on the q-order Hurst exponent for negative or positive q-values. We have used the q-order, the integer values of [-5 5] interval. If the Hq has a constant shape, then q-order Hurst exponent reflects that the qRMS is not depending on the amplitude of the local fluctuations (2^{nd} order RMS (2RMS) is widely used) [10]. The new concept, the local Hurst exponent (Ht), in relation with the fluctuations of small and large amplitudes in TS, is correlated with the q-order Hurst exponent Hq (calculated for negative and positive q, integer values). It is also important to calculate a temporal variation of local Hurst exponent (Ht). Ht can be summarized in a histogram representing the probability distribution (Ph).

The distribution Ph and the multifractal spectrum MS of biomedical time series might reflect important properties of physiological processes. Using q-order singularity exponent (hq) and q-order singularity dimension (Dq) we get the Multifractal Spectrum (MS). Details of multifractal spectrum can provide insight of the time-scale behaviour of a biosignal.

These are the theoretical considerations from the literature how to interpret the multifractal spectrum. We used these concepts to analyze (to compare) our EEG signal recordings. We used the method to compare the internal behaviour of four EEG signals recorded at four different channels. It was mentioned that EEG signals, in general, are nonlinear and non-stationary signals. Our recordings were performed with 7 pairs (left and right hemisphere) of electrodes positioned using the 10-20 international standard. The following figures from this paper are representing the results of main steps to obtain MS. The goal of this paper is not to give an exhaustive analysis of EEG signals from a biological point of view, but to test the accuracy of the steps toward MS, with the sequence of the main figures plotted.

The first sequence of figures is considering our KN-51-49 recordings (17.12.2010) from FC6-FC5, T8-T7 recording electrode positions (10-20 standard) and the second sequence of figures is related to KN-48-35 recordings (17.12.2010) from the P8-P7, T8-T7 EEG positions.

On Fig.1, the blue signals are the recordings (FC5, FC6, T7, T8 electrodes positions, in order from top to bottom) from the first sequence. The sampling frequency for each recording is Fs = 256 Hz. The length of the recordings is 100 s. The red signal in top of the recordings is the calculated random walk like variation in each time series. This random walk is a normalized cumulate sum of the signal (after removing the mean value of it). This is the starting signal for the DFA analysis. This is not an average of the signal but is reflecting the cumulate time course of the recording. In general, the recorded signals are contaminated by different type of noises. An about 30s sequence of

eyeball moving task was repeated (3.5 cycles) during recordings. A blue-cyan (FC5-FC6) and red-magenta (T7-T8) color cod is used along each of figures.

Figure Fig.2 is presenting the values of average RMS (colored dots) in case of using a sequence of time-scales (compulsory time windows (scales) of power of two sample lengths, Fs=256Hz sampling frequency of the recordings). For each of used time-scale and for each of recordings we have the RMS value. The average of these values of RMS, in case of a scale, has a representation with a color coded dot in the figure Fig. 2. It is very important, that within each time-scale it was calculated a trend (linear or not linear), and before calculating the RMS value for each time-scale, the approximate trend value is removed from the signal value (detrending procedure).

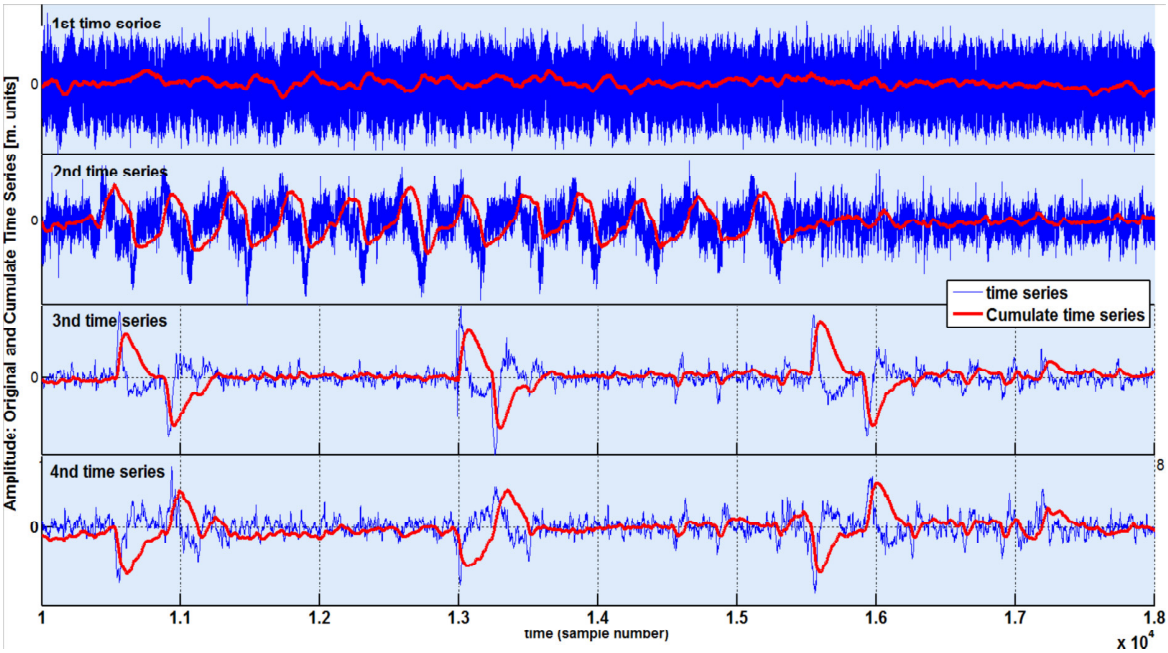

Fig. 1. Recorded time series are the blue signals. The red signals are the cumulate TS. (3.12s segment of the original regordings)

In each specific time series, for the calculated RMS values (dots of corresponding colour), a linear approximate (Fig. 2) slope is the so called average Hurst exponent. Two remarks are important with these approximations. Firstly it shows that the linear approximation is not the best possible method. In case of the time series, at short time-scales (4 to 16) and long time-scales (256 to 512) the fitting is not so good. Short time-scales are proper for higher frequency components of the TS, longer time-scales for lower frequency components. This aspect is suggesting that different frequency components of the signal are not linearly distributed within the signals.

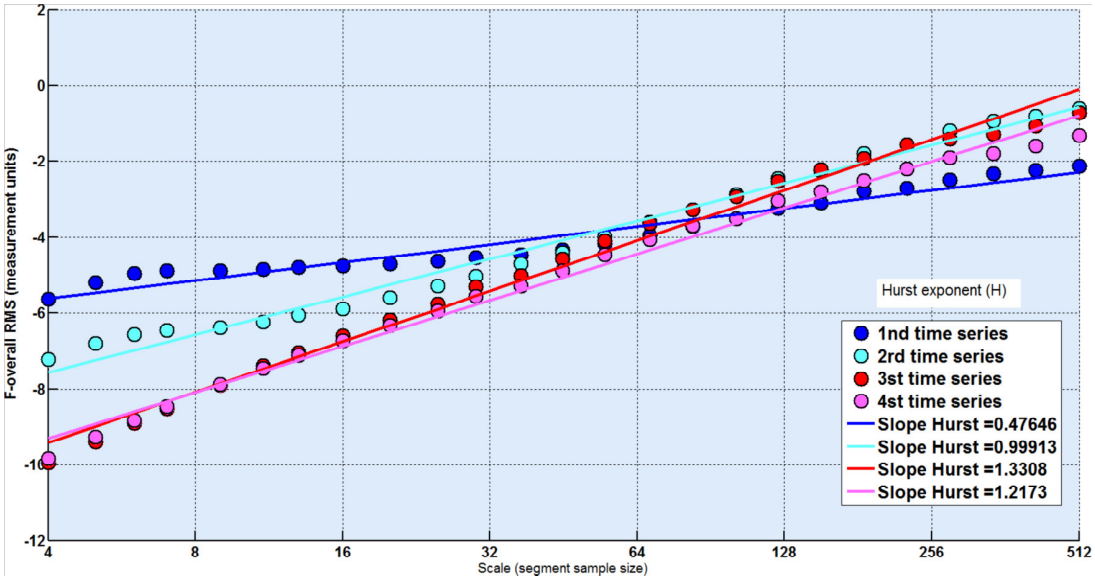

Fig. 2. Plot of average RMS versus the time-scale size (scale in log-coordinates). A scale relation is indicated by the slope of the regression lines (Hurst coefficient, a power law exponent). The error of fitting are visible at low and high time-scales.

In any case, this linear approximation is only an average of time-scale dependence of the signal.

The second observation is regarding the Hurst exponent. This exponent (H), is the value of the slope of the best fitting linear approximation of the average RMS for each signal, when we have used not overlapping windows. If the slope is 0, then the fitting line is horizontal, and the signal can be considered a noise. In this case, the length of the time-scales have no influence upon the average RMSs. We can see that the 1st signal with Hurst exponent 0.47 should be considered as a white noise signal. The range of Hurst exponents defines a continuum of fractal structures as white noise like ($H < 0.5$), pink noise like ($H < 1$), random walk like ($H > 1$). Signals with $H > 0.7$ can be considered as multifractal signals, in other case they are called monofractal TS.

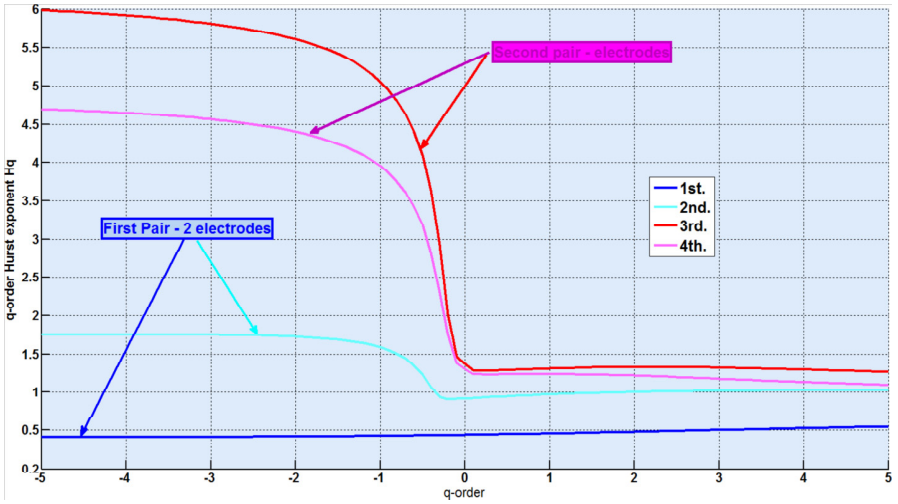

Fig. 3.The q-order Hurst exponent. The blue and cyan lines can be considered from noise category ($H < 1$) for each q-order.

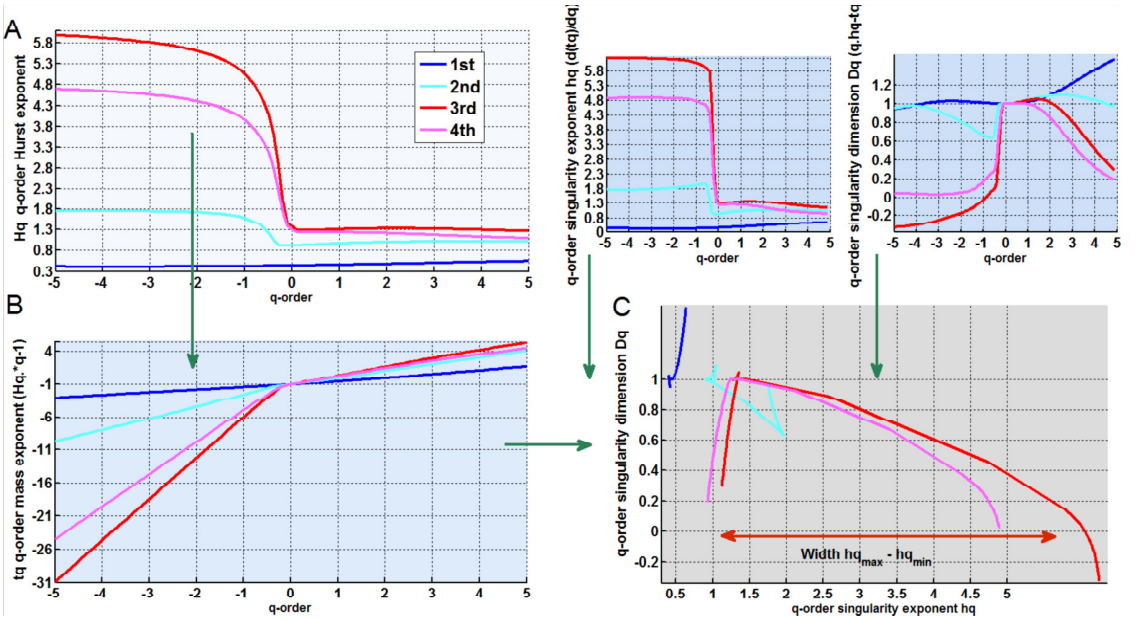

Fig. 4. (A) the Hq curves of the four signals (see also Fig.3.). (B) The tq mass exponent computed from Hq. TheMultifractal Spectrum (MS) is the plotting of Dq and hq against each other. The constant Hq (noise type) TS leads to almost linear tq that further leads to almost constant hq and Dq that, finally, are joined to become almost small arcs in as MS.

The structure of a multifractal and monofractal TS is different even if they have similar average RMSs and Hurst exponent values (linear fitting slope). Multifractal TSs have local fluctuations with small and large amplitudes (For a biosignal, to be considered significant, at least one of its frequency component (with biological significance), must have a large amplitude).

The 2nd order statistics (mean, variance) are enough to describe oscillations where fluctuations of large and small amplitudes are not significant. In the multifractal time series, local fluctuation, will be of large amplitude for segments within time periods of large fluctuations and of small amplitude for segments within the time periods of small fluctuations. Usually, it is considered that q-orders within the interval [-5 5] influence the segments with large and small fluctuations. For positive q, the segments with large fluctuations are influenced, for negative q, segments with small amplitude of fluctuations are influenced. For the value q = 0, we must use special considerations. Using these ideas, we can calculate the qRMS (the q-order RMS). The values of qRMS (and corresponding H(q)=Hq) are presented in Fig.4 - A (Fig. 3). This Hq variation is only one of different types of scaling exponents. At first this Hq variation is transformed to the q-order mass exponent tq (see Fig. 4 - B). This tq mass exponent is transformed into q-order singularity exponent hq and q-order singularity dimension Dq. The plot of hq versus Dq is the Multifractal Spectrum (MS) (see Fig.4 - C) [10]. The MS is composed from different arcs. The multifractal spectrum must have a long left tail in case the time series have a multifractal structure that is almost invariant to the local fluctuations with insignificant amplitudes. In other case, when the multifractal spectrum has a long right tail (Fig.4 -C (red, magenta)) then the TS have a multifractal structure almost invariant to the local fluctuations with significant amplitudes.

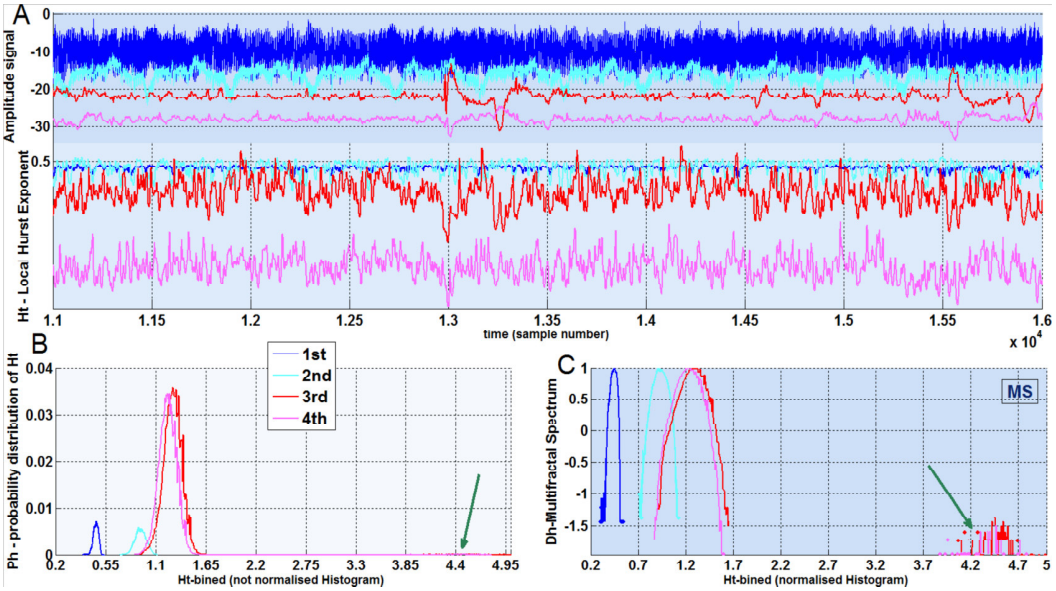

Fig.5. (A) The four time series (upper panel) and their local Hurst exponents (Ht) (lower panel). The large amplitude of local variation contains the smallest Ht when local fluctuation of smallest amplitude contains the maximum of Ht. tis is about 2 second segment of the original recordings (B) The probability distribution Ph of the local Hurst exponents Ht estimated as histograms. (C) The multifractal spectrum Dh estimated from distribution Ph. The arrows are indicating extreme fluctuations within the four Ts = 1 / Fs.

Now we represent th local Hurst exponent (Ht). The calculation of local Hurst exponent is an other way to get a multifractal spectrum, as a measure of the fractal structure of a biosignal. A local Hurst exponent can be defined directly from, qRMS, for each time instant. The local Hurst exponent is estimated for a multifractal time series with fluctuation in time (see Fig.5 - A). The local characteristic of Ht is because it is able to identify the thime moment when a fractal type of changing has happened.

The temporal variation of the local Hurst exponent can be turned into a probability like density function (see Fig.5 - B) and finally into the multifractal spectrum. This MS is the normalized probability distribution in log coordinates (see Fig.5 - C). The width and shape of the multifractal spectrum reflect the temporal variation of the local Hurst exponent, the basic characteristics of each analyzed TS.

4. Conclusions

The multifractal spectrum (MS) reflects the variation in the fluctuation structure of the biomedical time series, nonlinear non-stationary signals [8,11]. The methods to calculate MS are simply based on the computation of local RMS for multiple segment sizes. MS indicates the trends from TS after removing the general trends of variation. With short and long scale, q-order analyses we can get an inside to a neural assembly at the origin of the analyzed signal. From one point of view DFA should be employed to ensure that the biomedical time series has a noise like structure. Recent studies have reported that DFA exponents of neuronal oscillations are independent of oscillation power for a given frequency band. Most studies found the DFA a very useful instrument to study neuronal dynamics in a healthy and cortical sikness. DFA is a recognized method to analyze the scaling properties of non-stationary signals and allows a characterization of multifractal non-stationary TS (where a q dependent procedure is required). These results indicate that the DFA can be used as a robust measure of oscillatory dynamics, which captures also other features of brain activity than those seen in classical analysis such as spectral analysis. In corroboration with spatial and temporal considerations of recording electrodes positions, the relative shape and position of calculated MSs are determinant for physiological events identification and for their interrelation.

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