

The 7<sup>th</sup> International Conference Interdisciplinarity in Engineering (INTER-ENG 2013)

## 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. Formally, 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,  $c < 1$  - 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,  $H=H(t)$  where  $t$  is the independent time variable, is usable to compare different time series. Multifractal characterization of non-stationary biological signals is based on a generalization of the detrended fluctuation analysis (DFA).

Multiple scales can be characterized through various techniques with Multifractal Spectrum (MS). Multifractal spectrum is a measure of strength 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 recordings 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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Selection and peer-review under responsibility of Department of Electrical and Computer Engineering, Faculty of Engineering, "PetruMaiorescu" University of Tirgu Mures.

**Keywords:** Nonlinearity, non-stationary signals, Fractal property, DFA – detrended fluctuation analysis;

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## 1. Introduction

The human body can generate biological signals (biosignals). These signals are characteristic to a very large scale of internal physiological events and could have a 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 has not an accepted, well known conventional measure. When we are investigating signals, we often discard some of not so obvious dynamics and describe the remaining patterns with an average, a mean standard deviation or median, as first order statistical descriptors. Biological signals are, in general fractal type signals. A usual fractal analysis 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 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 conditions. Fractal analyses are therefore promising tools in biomedical signal processing and analysis [3].

The two basic notions, monofractal and multifractal structures are scale invariant structures. Most commonly, the monofractal structure of biomedical signals are defined by a single power law exponent and the scale invariance is independent of time and space. It is usual that in the structure of the biomedical signal often appear spatial and temporal variations. These spatial and temporal variations indicate a multifractal structure and it is finally defined by a multifractal spectrum (MS) of power law exponents. Our purpose is to calculate the MS of a time series. We can state that the multifractal structure, the MS of EEG signals is able to differentiate between the neural activities of different, active task-related brain areas [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 provide a significant insight into the functional organization of neuronal circuits and cell assemblies in cortical areas.

## 2. Methods

For the beginning, the concepts of self-affinity and stationarity 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 part 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 to the mean and standard deviation of the whole TS. The self-similarity property is uniform along all the dimensions of a fractal type signal (isotropy property). Self-affinity describes anisotropic scaling where 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 but very efficient method for investigating 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  $t$ ). The method is able to avoid the detection of fluctuations that are artifacts as a consequence of non-stationarities. 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 the recognized trends in different, measured 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].

### 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 the choosing of the order of fitting polynomial in segments for the detrending procedure, important in eliminating the trends in TS and in obtaining the 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 that originate from the q-order Hurst exponent for negative or positive q-order, respectively. We have used the q-order, the integer values of [-5 5] interval. The leveling of q-order Hurst exponent reflects that the q-order RMS is insensitive to the amplitude of the local fluctuations (2<sup>nd</sup> order RMS is widely used) [10]. The local Hurst exponent (H(t)), in relation with fluctuations of small and large amplitudes, 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) of Ht.

The distribution Ph and the multifractal spectrum Dh 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). Multifractal spectrum can provide insight of the time-scale behaviour of a biosignal.

These are the theoretical steps from the literature, to get the Multifractal Spectrum. We have used these steps to analyze (to compare) our EEG signal recordings. We have used the method to compare the behaviour of four different channel linked EEG biosignals. It is known 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 figures from this paper, with explanations follow the described 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 steps toward MS, with a sequence of the main figures plotted at the end of each basic step.

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 about KN-48-35 recordings (17.12.2010) from the P8-P7, T8-T7 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  $F_s = 256$  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 samples,  $F_s=256$ Hz sampling frequency). 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).

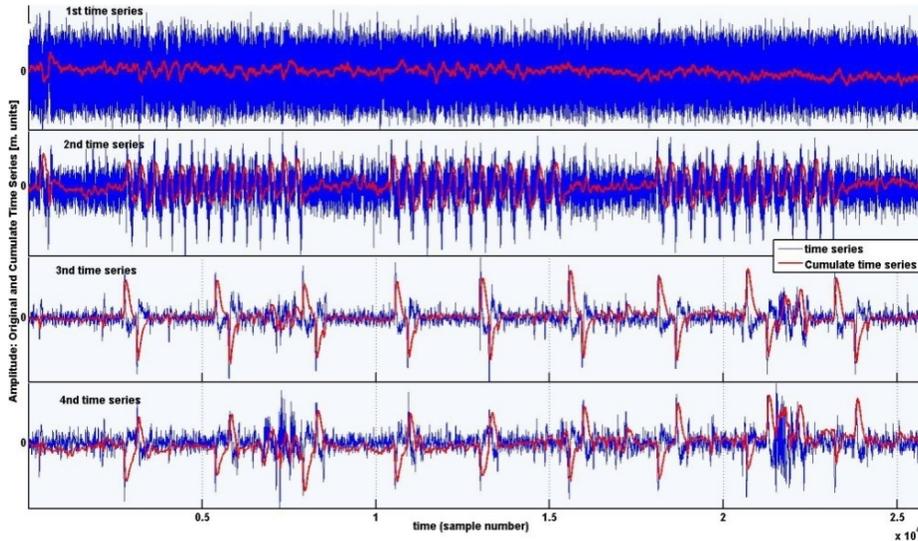


Fig. 1. Recorded time series are the blue signals. The red signals are the cumulate TS.

For a time series, for the calculated RMS values, a linear approximate (Fig. 2) slope is the so called average Hurst exponent. Two remarks are important in case of these approximations. First, it is visible that the linear approximation is not the best possible. 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.

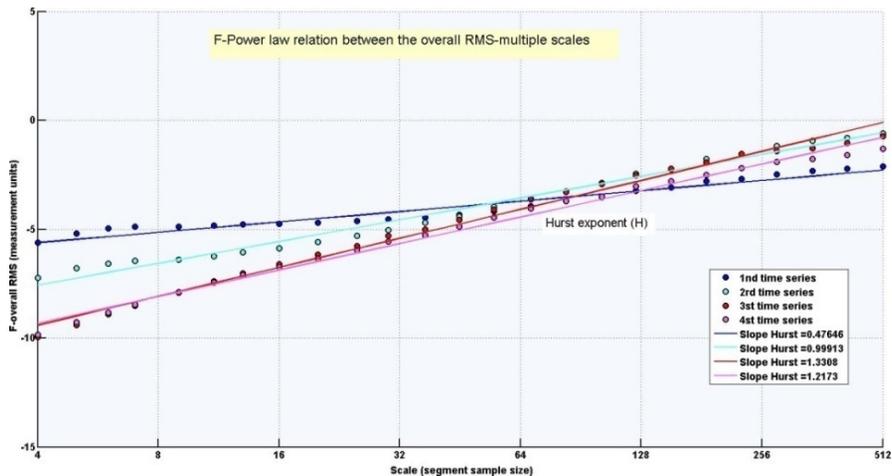


Fig. 2. Plot of average RMS versus the time-scale size (scale in log-coordinates). A scale relation is indicated by the slope of the regression lines (Hurst coefficient, a power law exponent). The error of fitting are visible at low and high time-scales.

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

The second observation is relative to 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 not overlapping windows are used. If the slope is 0, then the fitting line is horizontal, and the signal is a noise. In this case, the length of the time-scales have no influence upon the average RMSs. We can see that the 1<sup>st</sup> 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.

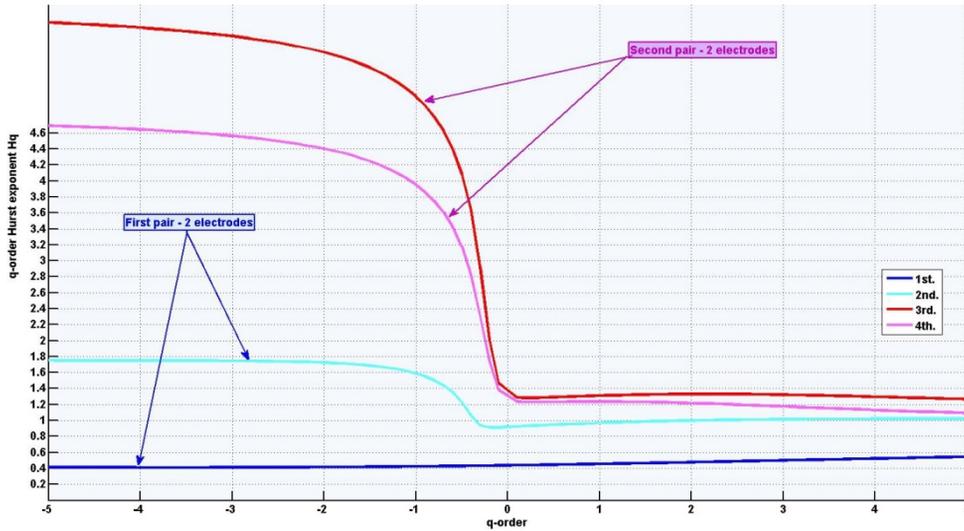


Fig. 3. The q-order Hurst exponent. The blue and cyan lines can be considered from noise category ( $H < 1$ ) for each q-order.

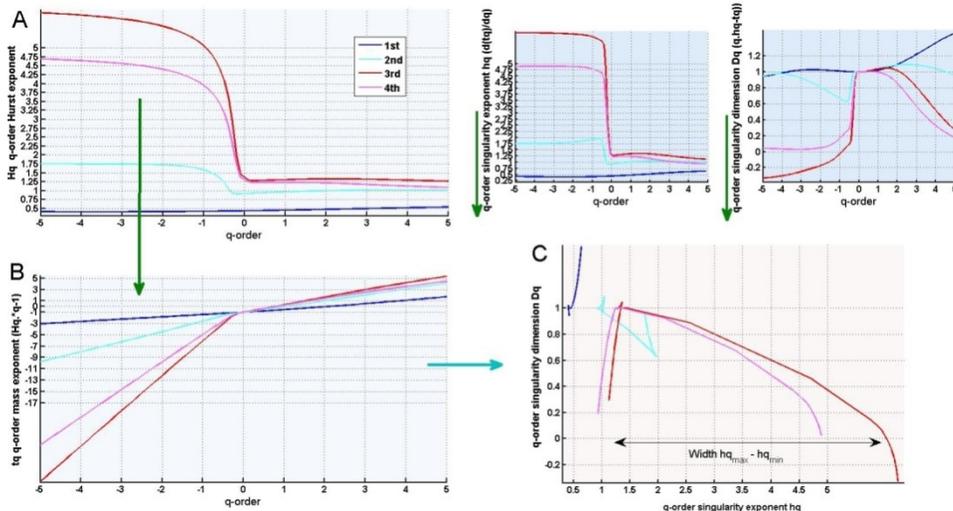


Fig. 4. (A) the Hq curves of the four signals (see also Fig.3.). (B) The tq mass exponent computed from Hq. The Multifractal Spectrum (MS) is the plotting of Dq and hq against each other. The constant Hq (noise type) TS leads to almost linear tq that further leads to almost constant hq and Dq that, finally,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

The structure of a multifractal and monofractal TS are 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, from biological point of view, must have a large amplitude).

The 2<sup>nd</sup> order statistics (mean, variance) is enough to describe oscillations where fluctuations of large and small amplitudes are missing. 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  $q$ -orders within the interval  $[-5, 5]$  to 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  $q$ RMS (the  $q$ -order RMS). The values of  $q$ RMS (and corresponding  $H(q)=Hq$ ) are presented in Fig.4 - A. 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). 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.

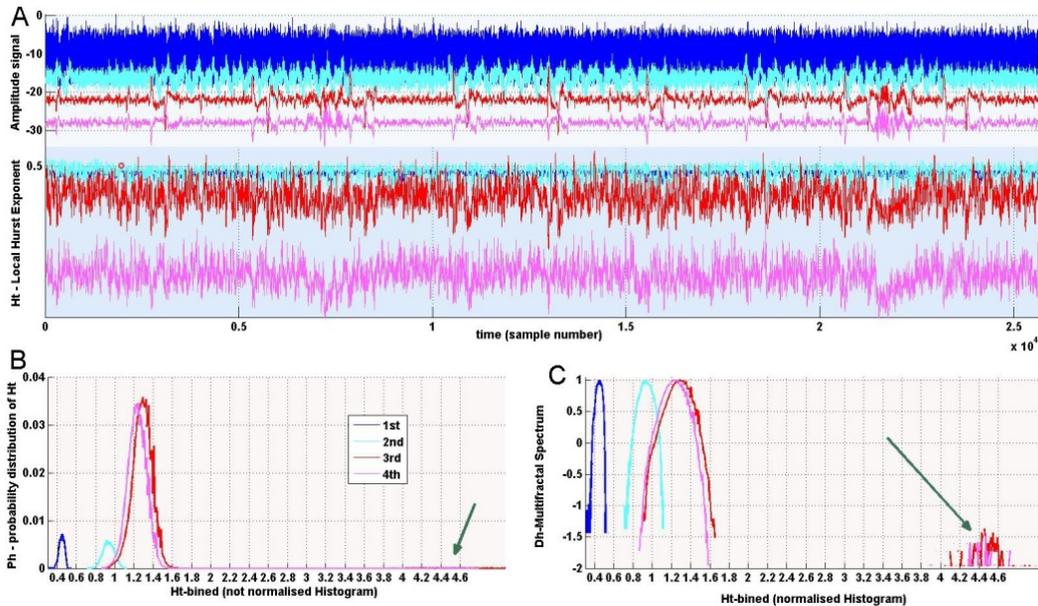


Fig.5. (A) The four time series (upper panel) and their local Hurst exponents (Ht) (lower panel). The large amplitude of local variation contains the smallest Ht when local fluctuation of smallest amplitude contains the maximum of Ht. (B) The probability distribution Ph of the local Hurst exponents Ht estimated as histograms. (C) The multifractal spectrum Dh estimated from distribution Ph. The arrows are indicating extreme fluctuations within the four  $T_s=1/F_s$ .

A new notion is the local Hurst exponent. 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,  $q$ RMS, for each time instant. The local Hurst exponent is an estimated for a multifractal time series with fluctuation in time (see Fig.5 - A).

The temporal variation of the local Hurst exponent can be summarized in a probability distribution function (see Fig.5 - B) and finally in 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 health and disease. DFA is recognized being a 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 different 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.

#### Acknowledgements

Project funded by the Romanian National Authority for Scientific Research, No.347/23.08.2011.

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