The Study of Spatiotemporal Scaling Features and Correlations in Complex Biomedical Data

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***Abstract*—In this research, we demonstrate the capabilities of the normalized range method (*R*/*S* analysis) in the study of fractal patterns in biomedical data of complex living systems. The Hurst exponent allows differentiating temporal signals in the presence of minimal information about the complex system under study, depending on the nature of the correlations manifestation. The capabilities of the proposed algorithms were demonstrated by analyzing the scaling features of the temporal dynamics of the tremor rate in Parkinson's disease, the bioelectrical activity of the brain of patients with epilepsy, including those under external influences. The results can be used in computational biophysics and physics of complex systems to search for diagnostic criteria for neurological and neurodegenerative diseases, as well as to study the processes of biological aging and changes in the "physiological complexity" of the human body.**

Keywords—living systems, biomedical data, persistent and antipersistent correlations, scaling, Hurst exponent, fast and slow algorithms, localization, electroencephalograms, evoked and spontaneous brain signals

I. INTRODUCTION

Time signals, including experimental series of biomedical data, produced by complex systems, contain unique, inherent in highly organized composite objects, information about the evolution, organization, structure, as well as the nature and role of the interaction of individual components [1, 2]. The study of the unique properties of living systems: the nature of quantitative and qualitative relationships between the elements of the whole; collective phenomena of coordination and synchronization; mechanisms of self-organization and self-adjustment; power-law distributions and scale transformations, manifested in the behavior of the recorded parameters; interactions and correlations of individual components, linear and non-linear responses to external influences and excitations, becomes possible thanks to statistical methods for processing experimental data, in particular clinical and biomedical [3].

Fractal and multifractal analysis are aimed at finding an effective method for describing complex systems based on discovering their fractal nature (self-similarity) or determining simple patterns and clear laws that determine the order in the structure. It is quite simple to implement is the normalized range method or *R/S* analysis proposed in H. Hurst [4]. In the further development of this analysis, the works of B. Mandelbrot, E. Feder, and others played a significant role. At the same time, the accuracy of the calculated Hurst parameter significantly depends on the extremely individual nature of biomedical signals.

This paper shows how to improve the accuracy of calculations of the Hurst exponent, taking into account the unique nature of complex systems. The accuracy of the Hurst exponent calculated by the classical (fast) algorithm is increased by using the slow algorithm with averaging (up to 10%); by using piecewise linear approximation: in the case of a complex image of the curve log(*R*/*S*) от log(*N*); by analysis of the local Hurst exponent, which considers the peculiarities of scaling in individual sections. Thus, we mean the adaptation of the numerical algorithm in accordance with the structure of the studied time signal.

II. FAST AND SLOW ALGORITHMS IMPLEMENTING THE NORMALIZED RANGE METHOD

The research presents the basic mathematical relationships for the computer implementation of fast and slow (with averaging) algorithms for calculating the Hurst exponent.

The quick algorithm is the standard calculation of the Hurst exponent:

$$\frac{R}{S} = \left(a \cdot N\right)^H, \tag{1}$$

where a is a constant value, *N* is the number of observations *H* is the Hurst exponent, *S* is the standard deviation, *R* is the range of the deviation. At the beginning, a calculation is performed for a certain time sample of the experimental series, and the calculations are performed. Then it is increased by one discretization step τ, calculations are made, etc. An estimate of the Hurst exponent will be the slope of the *R*/*S* function of *N*, presented in double logarithmic coordinates. The slope angle tangent is determined by linear approximation.

In the case when the dependence of log(*R*/*S*) on log(*N*) has the form of a broken line, algorithm for calculating the Hurst exponent with averaging over the selected time period $N\tau$ can be used. The window $N\tau$ is shifted each time by one time series discretization step to the right (until the end of the time series). Parameter calculations are performed every time. The graph displays the logarithm of the mean *R*/*S*.

The analysis of self-similar properties in separate sections of the temporal evolution of living systems is performed using the localization procedure.

In this case, it is also possible to implement two algorithms. In the first case, the calculation is carried out by splitting the original time series into short segments of a certain size $n\tau$ and then finding the Hurst exponent for each segment. In the second case, the calculations are performed for the sample $n\tau$, each time moved by one sampling step.

The mathematical implementation of all the presented algorithms is presented in the extended version of the work.

The capabilities of the proposed algorithms were demonstrated by analyzing the scaling features of the temporal dynamics of the tremor rate in Parkinson's disease, the bioelectrical activity of the brain of patients with epilepsy, including those under external influences.

III. Experimental data

The study considers three types of biomedical data:

1. Pathological index finger tremor velocity signals of 16 patients with Parkinson's disease (Fig. 1). Registration was performed in the absence of medical interventions, under the influence of deep brain stimulation and drugs (8 conditions in total) [5].

2. Electroencephalograms (EEG) of patients with epilepsy. Recordings included periods before, during and after an epileptic seizure. The C_4 electrode was located in the central part of the head (Fig. 2) [6].

3. Visually evoked EEG from patients with epilepsy. Registration was carried out by means of an O_1 electrode located in the occipital region of the head (Fig. 2) [6].

The results of processing the second and third data arrays, and the study of the local behavior of the Hurst exponent are presented in an extended version of the work.

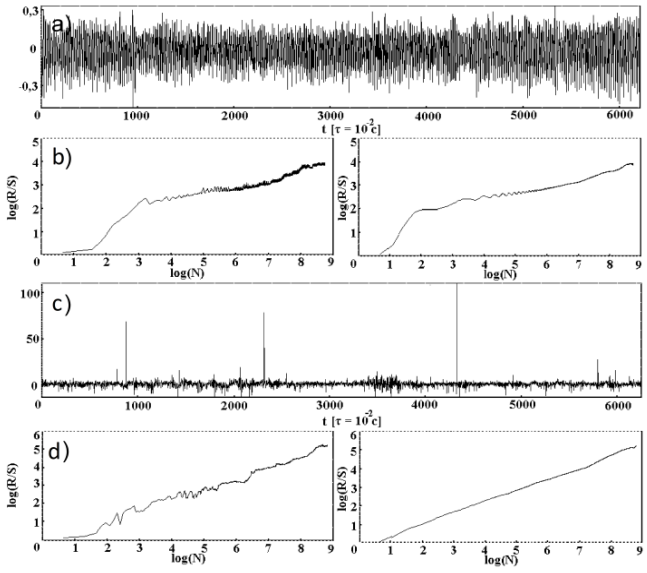

Fig. 1. The graphs show the speed of oscillations of the index finger of a patient with Parkinson's syndrome: (a) – without treatment (H=0.514, H=0.519), (c) – after treatment (H=0.599, H=0.604). b), d) – plots of log(R/S) and log(N) dependences for the studied signals: «quick» algorithm – on the left, algorithm with averaging – on the right

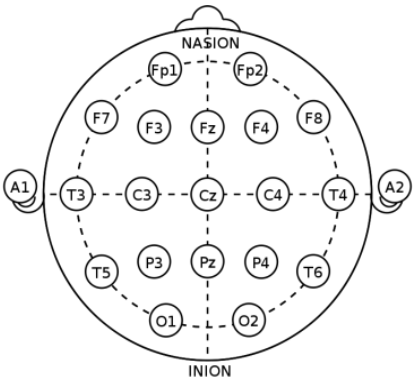

Fig. 2. International scheme of layout of electrodes «10-20»

IV. Conclusions

To study the features of spatiotemporal scaling and correlations in complex biomedical data, various implementations of the normalized range method are proposed: a fast algorithm and a slow algorithm with window-time averaging followed by a linear approximation. The study of the local behavior of the Hurst exponent is performed based on the localization procedure presented in two implementations [7].

In the frameworks of the R/S analysis an increase in the persistent nature of correlations was found in the case of a therapeutic effect on a patient with Parkinson's disease. A reversal (decline-rise) nature of the dynamics of correlations was found during a tonic seizure in a person with epilepsy. It has been established that the dynamics of visually evoked human EEG signals is characterized by a high level of correlation. An analysis of the temporal (local) behavior of the Hurst exponent $H(t)$ allowed revealing the alternation of persistent and antipersistent correlations in certain areas of the EEG signal of a person during a tonic seizure.

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