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ScienceDirect

IERI Procedia 10 (2014) 25 – 31

Procedia IERI

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2014 International Conference on Future Information Engineering

Dense Patterns, Switching, Stability and Self-Regulation in Information Networks DNA inside Living Cells

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Abstract

Are analyzed varied experimental data on DNA fluorescence inside neutrophils and other aerobic cells in flow cytometry with nanometer spatial resolution, in the large populations of cells. Analysis of fluorescence distributions for histograms various ranks shows that exist two classes of Good and Bad networks for DNA activity, for a good and bad health of different people, with two classes of 'n' or 's' shaped curves for fractal correlations densely packed in twice double logarithmic scale, Here reflected two types of positive and negative trends in changes fractal dimension and stability of information distributions. All types of DNA activity packed in networks of 'exponentially small worlds'. In all cells exists invariance (homeostasis) for total Shannon entropy and self-regulation of distributions of noises entropy for support informational homeostasis. Information networks DNA in living cells are a sample for future information engineering.

Selection and peer review under responsibility of Information Engineering Research Institute

Keywords: Abnormal and normal fractals, manifold complex networks of information activity of DNA for full set chromosomes in cells

1. Introduction

We present results of novel nonlinear analysis of experiments flow cytometry on immunofluorescence with nanometer spatial resolution in the flow direction [1] for large populations~10^4 -10^5 of neutrophils in the peripheral blood and for other cells of human and chickens, for different dyes and varied excitations of

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Selection and peer review under responsibility of Information Engineering Research Institute
doi:10.1016/j.ieri.2014.09.066

fluorescence [1-5]. Oxidative activity of DNA is visualized at fluorescence. In each experiment is observed fluorescence of three-dimensional (3D) DNA nanostructures of all non-coding and coding parts of DNA in full set of chromosomes inside cells. Each cell makes a chaotic Brownian motion at chaotic rotations in the jet of blood, flowing through the laser beam, during measurements. Therefore, each fluorescence histogram defines a representative statistics for various two dimensional (2D) projections on the photomultiplier all possible detailed spatial images of fluorescing 3D DNA in large populations of cells.

In real life of all DNA in the group of cells cannot select, determine and allocate only a single separate contribution of only non-coding and only coding parts of separated DNA in combined correlations, synergy of joint actions of full set chromosomes inside cell. Detailed analysis statistical data on 3D DNA fluorescence inside neutrophils [1-4] shows that actual correlations and topology stochastic coils of complex networks DNA for full set of chromosomes in living cells are characterized by non-Gaussian statistics, very high dense packing in networks DNA consisting from a mix of normal and abnormal fractal structures, changeability and flexibility in self-regulation of information and entropyentropy, which provide high adaptability DNA inside cells for real life. Complexity real life 3D DNA inside living cells is much higher than statics coding single linear fragment of DNA, their combinations, gene networks or biochemical schemes in textbooks, in standard genomic researches lonely DNA, *etc*. Here exist many unsolved problems in mathematics, natural science, *etc*

However, there are some overall patterns, universal features and switching in networks DNA which allow classify different types of correlations and information networks DNA inside cells for any given donor in given time [1-6]. New physical and mathematical patterns information activity 3D DNA define new opportunities in medical diagnostics and classification basic types of health and immunity. Information networks DNA inside living cells give a good sample for future networks in information engineering.

2. Main fractal networks DNA inside living cells; large-scale correlations

Three original histograms are shown in Figs.1 for illustrations fluorescing neutrophils in the blood different healthy and unhealthy men. Detailed descriptions experimental procedures for physical measurements and dyeing DNA by ethidium bromide, *etc* presented in [1-5]. This is high sensitive method for diagnostics many different and complex diseases, early diagnostics of illnesses, hidden diseases [1-5]. In Figs.1 presented normalized distributions for frequency of fluorescence flashes P(I) , of information J(I)=-lnP(I) and information entropy E(J(I))=p(I)J(I), based on normalized distribution of information (see eqns. (3),(4)) [1-6].

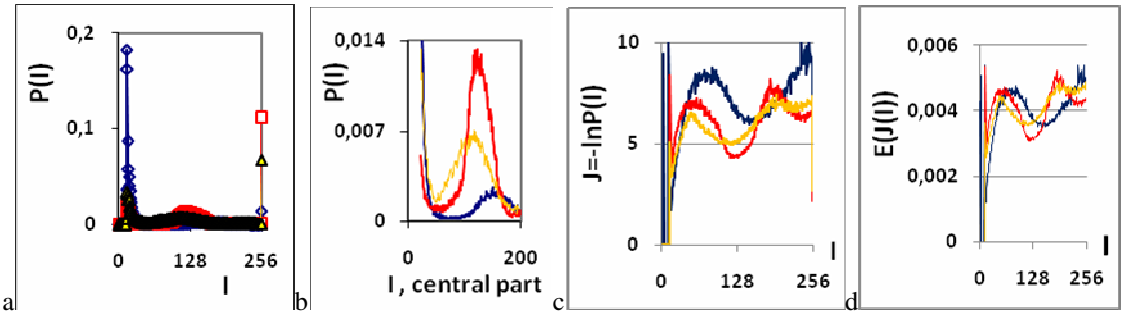

Fig. 1 (a) Normalized dependence frequency of flashes P(I) on their intensity I(r=256) for fluorescing DNA in neutrophils; (b) only central part of histogram (a); rhombuses points correspond to bronchial asthma. Total number of flashes is N_0= 76 623; quadrate points correspond to the healthy donor, N_0= 40 109; triangle points correspond to the oncology disease, N_0= 40 752. 2 (c) Logarithmic dependence LnP(I) frequency of flashes P(I) on their intensity I(r=256); (d) Normalized distributions of information entropy E(J(I)) in the dependence on fluorescence intensity I(r=256)