How Chromosomal Correlations Form a Single Information Complex DNA Inside Living Cells?

Intermittency Informational Connections DNA

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Abstract

Are analyzed experimental data on fluorescence DNA complexes inside neutrophils and other cells in flow cytometry experiments with nanometer spatial resolution in the large populations of cells. It is shown that DNA information is packed in ultra dense fractal networks of ‘exponentially small worlds’. The exponential growth of high order’s central moments for fluctuations information in DNA fluorescence characterizes existence of intermittency in joint information complexes DNA inside living cell. Intermittency selects and ensures dominating role of corresponding correlations in DNA information. Intermittency depends on the correlation scales and order of chromosomal correlations (cooperative links). Intermittency of DNA information occurs in the coalitions of chromosomes and exists if number of correlated DNA is not small and more than one, two or three; this is the collective effect. Intermittency is observed for different, rather high orders of multiple chromosomal correlations and depends on a personal health status in given time. Strong or weak level of intermittency in information activity of correlated chromosomes also depends on the health conditions. All these facts reflect various distributions of high order's central moments for fluctuations in DNA information; oscillations, growth, decrease, switching of various functions at changes the scale, number or order of chromosomal correlations. Intermittency defines the basic natural properties of DNA activity inside cells and DNA chips.

Keywords: intermittency, self-regulation and switching information activity DNA in dense fractal networks inside cells define health status and medical diagnostics
1. Introduction

Are presented nonlinear analysis various experimental data on immunofluorescence in flow cytometry experiments with nanometer spatial resolution in the flow direction [1]. In each experiment is observed large populations~$10^4 - 10^5$ of cells, such as neutrophils in the peripheral blood and other cells for different dyes and varied excitations of fluorescence [1-5]. Oxidative activity DNA is visualized at fluorescence. In each experiment is observed fluorescence of three-dimensional (3D) DNA nanostructures in the mix of coding and non-coding DNA parts for full set chromosomes inside cells. Each cell makes a chaotic Brownian motion at chaotic rotation 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 fluorescing DNA inside each cell in large populations of cells.

In real life of all DNA inside cells is very difficult (or impossible) to select, determine and allocate an arbitrary, not abnormal, only a single separate contribution of only one non-coding and only one coding parts of separated DNA in combined correlations, synergy of joint actions of full set 46 chromosomes inside cell [1-9]. Nevertheless, almost all interests of the writers and readers are focused on various properties of various genes for lonely separated DNA, as the main values of life. Networks of oxidative and information activity of DNA, their changes, differences and non-trivial connections in this approach practically ignored or are moved, hide and depart very far into the background. Detailed analysis statistical data on 3D DNA fluorescence [1-9] shown existence very reach manifold correlations for different oxidative and information functions DNA in full set chromosomes inside living cells. DNA complexes are characterized by non-Gaussian statistics at ultra high density packing in complex multi-scale fractal networks of ‘exponentially small worlds’ [3, 5, 7, 8], at self-regulation information activity of all DNA inside cells [2, 7]. Complexity of 3D DNA activity inside living cells is much higher than statics of coding single linear fragment of DNA, their combinations, genes or biochemical schemes in standard genomic researches of lonely DNA, etc. Here exist many fundamental unsolved problems in mathematics, natural science, information theory, etc.

This paper connected with the questions about main physical, structural and statistical peculiarities in the formation and changeability of single information complex DNA in the community of all chromosomes inside living cells. It depends on health status and, therefore, defines important or (and) interesting facts for any given person and for medical diagnostics. Recording and information transfer, correlations and regulation of information activity DNA inside living cells give a good sample for future information and communication theory and technology, manifold functions cooperative networks for all living, for understanding complexity of real life and science development.

Here described a few typical peculiarities for large-scale information activity DNA inside living cells as experimental physical facts cooperative links DNA.
2. Dense fractal packing DNA information inside living cells

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 [1-6]. This is high sensitive method for diagnostics many different and complex diseases, early diagnostics of illnesses, hidden diseases [1-6]. In Figs.1 presented normalized distributions for frequency of flashes P(I) and corresponding distributions of information J(I)=lnP(I) as various functions of dimensionless intensity I, which coincides with the number of measuring channels for fluorescence intensity.

![Histograms and Information Distributions](image)

Figs. 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 N₀= 76 623; quadrate points correspond to the healthy donor, N₀= 40 109; triangle points correspond to the oncology disease, N₀= 40 752; (c) Distributions of information J(I)=−lnP(I) in the dependence on fluorescence intensity I(r=256)

Detailed descriptions experimental procedures and physical measurements in flow cytometry with nanometer spatial resolution and intercalating dyeing of DNA by ethidium bromide were presented in [1-6]. Accuracy and reproducibility of experimental results is approximately 2% for usual levels inevitable errors and fluctuations of physical and biological nature, what defines accuracy of our conclusions.

At the present time we do not know how extract, separate information and interpret immunofluorescence data. Let us consider some fractal peculiarities of fluorescence distributions. Range r or rank r of histogram defines scale of multistage clusters in networks with structure of bronchial tree. Range r coincides with the number of columns in histograms or number measuring channels of fluorescence intensity at given maximal value of dimensionless intensity, i.e. r=I_max. In presented experiments maximal number of channels is r=256. Variations of range r, i.e. rank r of histograms or variations the scales r, provide varied changes in irregularity and brokenness in distributions fluorescence for histograms various ranks r [1, 3, 5, 7, 8]. The quantitative measure of irregularity and brokenness for distributions of flashes P(I,r) and information J(I,r) for any
rank \( r \), in all histograms, may serve a Hurst index \( H \). Hurst exponent \( H \) [10] is determined by means of regression equation

\[
\ln(R/S) = H \times \ln k + c \quad \text{(1)}
\]

Where \( R/S \) is rescaled range (\( R=S \)), \( R \) is range or maximal deviation of \( P(I,r) \) from local mean level, \( S \) is standard deviation of \( P(I,r) \). Illustration of definition Hurst index was presented in [1,3,5,7,8]. Hurst index \( H \) for normalized frequency of flashes \( P(I,r) \) corresponds to fractal (Hausdorff) dimension \( D \) [10]

\[
D = 2 - H \quad \text{(2)}
\]

Information \( J(I)=\ln P(I) \) for an arbitrary rank \( r \) is \( J(I,r)=\ln P(I,r) \). Various examples of decreasing rank \( r \) for various histograms are presented in [1-3,5-9]. Normalized frequency of flashes \( P_I(r) \) and distributions of information \( J_I(r) \) for an arbitrary rank \( r \) are defined as

\[
P_I(r) = N_I(r)/\sum_{i=1}^{i=r} N_I(r), \quad J_I(r) = -\ln P_I(r) \quad \text{(3)}
\]

In Figs.2 presented Hurst indexes \( H(J,r) \) for distributions information in Figs.1.

The certain number \( N \) of synchronized nodes-flashes in networks of DNA fluorescence inside cells are characterized by the intensity \( I~N \), where \( N \) defines a common number of correlated nodes in network. The correlation length \( d \) depends on the network topology. Random networks with a given degree distribution may be the networks of “small worlds” if \( d \sim \ln N \) [11]. Fractal dimension \( D \) for fluorescence networks of “small worlds” is \( D(N) \sim \ln N/\ln \ln N \) [11]. In our case reduction of range \( r=I~N \) leads to the expression \( \{\ln r/D(r)\}\sim\{\ln \ln r\} \). Detailed analysis [1, 3, 5, 7, 8] shows that experimental data on DNA fluorescence correspond to correlations \( \ln \{\ln r/D(r)\}\sim\{\ln \ln r\} \) in Figs.2b. These networks with ultra dense packing in twice double logarithmic scale, denser than in networks of “small worlds”, have the name networks of “exponentially small worlds” [3].

Figs. 2: (a) Dependence of Hurst index \( H(J,r) \) on rank \( r \); initial histograms for information \( J (I) \) shown in Fig.1c: (b) Dependence of \( \ln (\ln r/D(r)) \) on double logarithm of rank \( r \) in multi-scale information networks of ‘real worlds’ for fluorescing DNA inside neutrophils; an ideal network of ‘exponentially small worlds’, without fractals (\( D=2 \)), corresponds to violet line with round dots; overall trends of \( \ln (\ln r/D(r))=A(\ln \ln r)+B \) presented here as the linear approximations in networks of ‘exponentially small worlds’; initial information distributions of \( J(I,r) \) presented in Figs. 1c.
According to Figs. 1, 2 real traffics in DNA networks always are not smooth and never can be smoothed [1, 3, 5, 7, 8].

According to Figs. 2a all multi-scale networks DNA in cell are characterized by a mix of normal D=2-H<2 and abnormal D>2 fractal dimensions that ensures very dense packing networks DNA inside cells [3, 5].

Inside living cells exist different networks of DNA activity are reflecting distributions oxidative activity, information, information entropy, etc, for DNA complex in each cell [1, 3, 5, 7, 8]. All types of DNA activity in real time packed in various networks of 'exponentially small worlds' [1, 3, 5, 7, 8]. DNA information J(J,r)=-lnP(I,r) also packed in networks of 'exponentially small worlds' [8].

3. Invariance of total Shannon entropy. Self-regulation of information activity DNA inside living cells

How to estimate quality, quantity and changeability of DNA communications in oxidative metabolism and DNA information transfer in the life of given person? What need for comparison various data on informational activity of DNA inside cells for one human at various times and for different people? Let us consider hierarchy multi-scale distributions of fluorescence, for frequency of flashes P(I,r), information J(P(I,r)) and information entropy.

Let us introduce two types of Shannon entropy for distributions of flashes P(I,r) and information p(I,r). Normalized frequency of information $p_i(r)$ for reduced distribution on information $J(I,r)=-\text{ln}P_i(r)$ at reduction of range r is

$$p_i(r) = J_i(r) / \sum J_i(r)$$

Distribution of Shannon entropy $S_i(P,r)$ , based on various distributions of flashes P(I,r), for an arbitrary rank r is

$$S_i(P,r) = -p_i(r) \text{ln} p_i(r)$$

Distribution of Shannon entropy $E_i(J,r)$ , based on various distributions of information, for an arbitrary rank r is

$$E_i(J,r) = -p_i(r) \text{ln} p_i(r)$$

Two types of Shannon entropy $S_i(P,r)$ and $E_i(J,r)$ define oxidative and information activity DNA. Total Shannon entropy $S(P,r)=\sum S_i(P,r)=<I(P(I,r)>$ characterizes Shannon-Weaver biodiversity DNA inside cells. Total Shannon entropy $E(J,r)=\sum E_i(J,r)=<I(p(I,r)>$ characterizes Shannon-Weaver biodiversity for information DNA inside cells. The entropies $S(P,r)$ and $E(J,r)$ are shown in Figs. 3.
Figs. 3 (a) Total Shannon information entropy $E(J,r) = \ln r$ and (b) Shannon-Weaver biodiversity of neutrophils $S(P,r)$ in the dependence on rank $r$; initial histograms at range $r=256$ are shown in Figs.1.

Comparison Figs.3a and 3b shows that biodiversity for DNA information in cell is more than biodiversity for oxidative activity DNA in cell; $E(J,r) > S(P,r)$ [2].

Detailed analysis experimental data [2,5] shown that total entropy $E(J,r) = \langle J(p(I,r)) \rangle = -\langle \ln p(I,r) \rangle$ is invariant, identical for given $r$ in all cells [2]. Dependence of $E(J,r)$ on rank $r$, as it is illustrated in Fig.3a, is logarithmic

$$E(J,r) = - \langle \ln p_i(r) \rangle = - \sum_{i=1}^{\ell(r)} p_i \ln p_i = \ln r$$

(7)

This empirical invariant defines informational homeostasis of oxidative activity of 3D DNA in full set chromosomes inside living cells. Total entropy $E(J,r) = \ln r$ conserves invariance for any Shannon-Weaver index of biodiversity $S(P,r) = \langle J(P(I,r)) \rangle = -\langle \ln p(I,r) \rangle$ in any cell and in all cells, at any state of health for any, different and all aerobic beings [2]. Invariance of total entropy $E(r) = \ln r$ defines special role local distribution of Shannon entropy $E_k(r)$, as for all functions associated with the conservation laws, as the main dominant variable to describe the states and dynamics of informational activity of DNA in cells. Informational invariant $E(r) = \ln r$ difficult to compare with conservation laws of mass, energy, etc. Each rank $r$ corresponds to the certain constant values of total entropy $E(r) = \ln r$ for all cells varied aerobic organisms, i.e. defines universality entropy scale. There are many values, but not one and the same values of energy, mass, etc, for all beings and varied cells, but exists only one overall, unified value of total information entropy for oxidative activity of DNA in all living cells at identical values of rank $r$, i.e. for identical scales $r$ of clusters for Shannon entropy $E(J(I),r)$. Therefore each cell exists among other cells in given body and among other cells and bodies at universal self-regulation of information equilibrium for total entropy $E(r) = \ln r$, what ensures stability of cell life during eating, sleeping, at division, at illness and treatment, in communicating with communities of different cells, many bodies.
and various individualities, continuity at transportation, in life and adaptation in changeable environment. Thus, all aerobic cells live in a single information space.

Information transforms at DNA activity inside cells at variations of inner and external conditions ensure stability, adaptability and vitality cell at self-regulation of informational homeostasis [2, 5, 7]. This self-regulation is defined by the local noises or fluctuations near homeostasis level of total information entropy

$$E(J, r) = \ln r$$

$$e_i(r) = E_i(r) / E(J, r) - 1 / r, \quad E_i(r) = - p_i(r) \ln p_i(r)$$

(8)

Analyses of average characteristics for individual distributions noise $e_i(r)$, such as central moments and Hölder’s averages, in varied blood samples shown that stability of homeostasis is supported only at participation of all 46 chromosomes inside cells [2, 5, 7]; saturation of Hölder averages occurs at $m=46$. We need all 46 chromosomes in cells for support stable level of information activity DNA [2, 5, 7].

Local distributions of noises $e_i(r)$ depend on health status given person in real time. The same results are typical for all cells of blood such as neutrophils, lymphocytes, all leukocytes of human and chicken erythrocytes for various dyes, colors and various excitations of fluorescence [2].

Varied fluctuations in DNA activity, as and self-regulation of informational homeostasis, are associated with cell life in the body as in the open system, for stability support of vitality conditions at varied perturbations of different origin. Both functions for oxidation and information in DNA activity unite in Shannon entropy $E_k(j, r) \propto \ln P_k(r) \times \ln p_k(r)$ . This means that informational homeostasis $E(r) = \ln r$ provides non-local feedback between distributions of oxidation and information, i.e. between distributions of $P(I, r)$ and $p(I, r)$, in the local distributions of Shannon entropy, at invariance of average information $<J(p(I, r))>=\ln r$. Entropy’s noises $e_k(r)$ form main signal for self-regulation of homeostasis $E(r) = \ln r$ for any cells of any aerobic beings in the cases of any local disorders of any origin, i.e. inner diseases, infections, traumas, etc [7]. This self-regulation determines the defensive response and immunity during reconstruction of fractals and complex information networks DNA for homeostasis support in all cells, living inside us [2, 5, 7, 8]. Thank self-regulation.

4. Intermittency in information activity DNA inside living cells

Next approach and more detailed types of classification systematic differences in histograms of fluorescence are connected with distributions of central moments for varied fluctuations. We use the centered random variables and their central moments for all procedures on any step. This approach is needed for exception of uncontrollable and systematic errors in experimental data, instabilities of algorithmic procedures and corresponding drift of averages. Distribution frequency of flashes $P_j(r)$ at reduced rank $r$ is defined in equation (3). Local deviations of information $J_i(r)=-\ln P_i(r)$ from average value $<J>$ for given $i$’ channel with the number $i=1,2,\ldots,r$ is $j_i(r)$,
where symbol \(<...>\) denotes statistical average for distributions \(P_i(r)\). Central moments \(<j^m_i(r)>\) the order of \(m\) are defined as

\[<j^m_i(r)> = M_i(j_1(r), m) = M_{m}(j(r)) = \sum_{i=1}^{r} j^m_i(r) \times P_i(r)\]  

Random variable \(j_i(r)\) characterizes various local fluctuations information for corresponding distributions frequency of flashes \(P_i(r)\) fluorescing DNA. Total Shannon entropy \(S(P(r)) = <\ln P(r)>\) defines the ‘center of gravity’ as the zero level for stochastic motions of local fluctuations \(j_i(r)\). This ‘center of gravity’ for information \(S(P(r)) = <\ln P(r)>\) coincides with index of Shannon-Weaver biodiversity for population fluorescing DNA inside cells [2].

Statistical peculiarities of any distribution \(j_i(r)\) at given rank \(r\) are characterized by corresponding distributions of central moments \(<j^m(r)> = M_m(j(r))\). Distributions \(M_m(j(r))\) are individual for given person in given time with individual dependences on \(m\) and \(r\), as it is shown in Figs.4 [12]

Figs.4 Distributions central moments \(M(j(r=256),m)\) (b),(c),(d) and Hölder’s averages \(H_{m}=H(r=256,m)=[M(j(r=256),m)]^{1/m}\) (a) in the dependence on number \(m\) at rank \(r=256\) for full set chromosomes inside cells; (a) ragged positive and negative branches of Hölder’s averages; (b) only positive values of \(M>0\) for any health status; (c) quadrate and round points correspond to \(M>0\) and \(M<0\) for healthy men; (d) triangle and round points reflect \(M<0\) and \(M>0\) at oncology

According to Fig.4a Hölder’s averages \(H_{m}= H(r=256,m)=[M(j(r=256),m)]^{1/m}\) for fluctuations information during oxidative activity DNA near average level may be positive and negative in the absence of a direct link between even or odd numbers \(m\), as and the sign of the moments \(M_m(j(r))\). At asthma disease in Figs.4a,b are observed only positive values of \(M_m>0\) and \(H_m>0\) for all even and odd \(m\). In Figs.
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4a,c, observed more complex and asymmetric situation when the negative moments $M_m < 0$ corresponds to the odd numbers $m=3, 7, 9, 11, 13$ for a healthy men and odd $m=3, 7, 9, ..., 43$ for oncology, which reflected in Figs. 4c, d by means round and triangle points for positive values of $\ln | -M_m |$. All others moments $M_m$ with numbers $m=1$ and $m>13$ in Fig. 4c and $m=1, m>43$ in Fig. 4d have only positive values $M_m > 0$. This asymmetric situation also is reflected in distributions and switching different ragged branches of Hölder’s averages $H_m$ in Fig 4a.

Thus, non-Gaussian statistics for information activity DNA lead to the exponential increase of high order’s central moments $M_m(j(r))$ for fluctuations of information $j(r)$ instead of the exponential decrease of high order’s central moments, as usual. This behavior reflects the rare irregular bright flashes in time [3, 13]. Thus, irregularity and intermittency characterize and reflect real information activity of DNA in all living cells.

Fast growth of high order’s moments $M_m(j)$ means that multiple correlations ($m>2$) are dominant compared with single averages and pair ($m=1,2$) correlations DNA. Multiple correlations belong to the full set of all chromosomes [2, 5, 7].

Fast exponential growth of higher statistical moments $M(j(r),m)$ means that even a low level small noise for fluctuations information ensures intermittency in DNA activity and chaotic mixes corresponding fluctuations of information activity DNA inside cell. All perturbations of information activity DNA are interconnected and ensure very quick and effective DNA reaction on any local perturbation in oxidative activity DNA, such as illness, stress oxidation, virus, traumas, medication, etc. This determines the defensive response and immunity during reconstruction of complex networks DNA in all cells living inside us [7].

More strong intermittency in Figs. 4 corresponds to inflammations at asthma. The exponential dependencies of $M_m(j(r))$ on $m$ ensure high sensitivity of intermittency for registration and diagnostics of health status.

Fast exponential growth $M_m(j(r))$ (see Figs.4), i.e. intermittency of information, ensures very effective self-regulation of informational homeostasis $E(r) = \ln r$, i.e. very effective connections between perturbations any scale for oxidation and information DNA inside cells for local distributions (and redistributions) Shannon entropy $E_k(r) = \ln p_k(r) \times \ln p_k(r) \approx j_k(r) \times \ln j_k(r)$ near homeostatic level of total entropy [7]. Thus, intermittency in DNA information ensures the stable cell life.

Let us consider a question about physical nature of support of informational homeostasis inside cells. We have informational homeostasis and overall relation $E(r) = \ln r$ regardless of cell type, conditions of initiation and recording of fluorescence and individual features of DNA [2]. This means existence of one, overall unified nature of physical processes to maintain informational homeostasis and very high efficiency of universal change for all electronic excitations of DNA for quick stabilization of homeostasis in any cell, in any being. Currently known one overall universal type of very effective, large-scale transformations for all collective electronic excitations of DNA, i.e. resonance of Förster (dipole resonance), which can to ensure effective support of homeostasis, regardless of the individual features of DNA [2]. In this case large-scale heterogeneities in fluorescence of DNA are connected with Förster’s radius or with corresponding
length of correlations in clusters of fluorescing DNA. Here are possible various correlations for different sections and parts of one given DNA and different correlations inter various chromosomes, inside cells, for various localizations and changes of chromosomal coils. It is possible to propose that here exist varied dipole, quadruple, etc resonances for varied fractal clusters in coil of chromosomes, but currently we don't know anything concrete about these possibilities.

Any regulation of informational homeostasis must be very quick, effective and must have general universal physical nature, as multiple resonances in large fractal multi-clusters, etc, without dependence on type and origin of excitations. In this case we, possible, shall to come to different scenarios of deterministic chaos for nonlinear interactions and fast (resonance) synchronizations various clusters in large-scale activity DNA, as for universal mechanisms for support self-regulation informational homeostasis. Fast turbulent diffusion for electronic excitations of DNA in super dense networks of ‘exponentially small worlds’ is more effective than any molecular diffusion of any origin. In this case will change behavior of Hölder averages $H_m$, if $|H_m| > 1$, with the absence of saturations for numbers of correlations $m>46$ [14], because arise new classes of chromosomal correlations. Absence of saturation $H_m$ at $m>46$ is observed for all Hölder averages $|H_m| > 1$ for fluctuations of information due to intermittency in Fig. 4a. Saturation of Hölder averages at $m=46$, when $|H_m| < 1$ [2,5,7], for other fluctuations of other functions DNA inside cells occurs at decreasing of high order’s central moments, in absence of intermittency, for the exponential decrease of corresponding correlations.

5. Intermittency for chromosomal associations of information complexes DNA inside living cells

Let us consider collective statistical peculiarities for DNA associations in information activity inside cells. Such coalitions of different chromosomes necessarily exist in cells. For instance, there are separate male and female illnesses, which are defined in some of these coalitions involving different pairs the sex chromosomes.

Total information $J= \sum \ln P_i = \ln \Pi_i P_i$ is additive and therefore is summed up on all chromosomes. Information for one, two, three, etc. of correlated chromosomes is $J/46$, $2J/46$, $3J/46$, etc. How much chromosomes must be correlated for combined intermittent behavior? Data analysis shows that small number of chromosomes, i.e. one, two or three chromosomes never ensures intermittency of DNA information. Intermittency of DNA information inside cells exists only in the coalitions of chromosomes; this is the collective effect.

Local deviations of information $J_i(k,r) = -(k/46) \ln P_i(r)$ for ‘k’ correlated chromosomes from average value $<J(k,r)>$ for given i’ channel with the number $i=1,2,...,r$ is $j_i(k,r)$,

$$j_i(k,r) = J_i(k,r) - <J(k,r)>$$

$$<J(k,r)> = - (k/46) \times \ln P(I,r) = \sum_{i=1}^{m} J_i(k,r) \times P_i(r)$$

(11)
Central moments $< j^m(k, r) >$ the order of $m$ are defined as

$$< j^m(k, r) > = M(j(k, r), m) = M_m(j(k, r)) = \sum_{i=1}^{ir} j^m(k, r) \times P_i(r)$$  \( \quad (12) \)

Distributions $M_m(j(k,r))$ are individual for given person in given time with individual dependences on $m$, as it is shown in Figs.5

Figs. 5. Various distributions of central moments $M_m(j(k, r=256))$ for fluctuations of information $j_i(k, r)$ in the dependence on the order $m$ at changing of number $k$ of correlated chromosomes: (a),(b) asthma; (c),(d) oncology; (e)-(h) good health.

In Figs.5 are shown different rather blurred transitions and switching various distributions of central moments $M_m(j(k, r=256))$ for fluctuations information $j_i(k,m)$ at changing of number $k$ of correlated chromosomes inside cells for different states of health. Here the exponential decay of high order’s central moments $M_m(j(k, r=256))$ (Figs.5a,c,e) goes into the exponential growth of high order’s central moments $M_m(j(k, r=256))$ at increasing numbers $k$ of correlated chromosomes. These transitions depend on a human health status and are accompanied by different monotonic and non-monotonic changes, by mixed and oscillatory distributions of $M_m(j(k))$ in Figs.5. The minimal number of correlated chromosomes $7 < k_{min} < 9$ in given experiments is observed for asthma in Figs.5a,b. More high values of minimal numbers of correlated chromosomes $16 > k_{min} > 13$ and $22 > k_{min} > 19$ are observed for healthy man in Figs. 5e-5h and for oncology in Figs.5c,d. Upon further increase number $k > k_{min}$ occurs the exponentially rapid...
growth of $M_m(j(k,r=256))$ which reaches maximum value when $k = 46$ (Figs.4b). Upon further decrease number $k < k_{\text{min}}$ occurs the exponentially rapid decreasing of $M_m(j(k,r=256))$ with very strong decrease at $k = 1$, for one chromosome. Thus, the minimal boundary for number $k$ of correlated chromosomes $k_{\text{min}}$ and existence intermittency in information activity DNA complex defines everyday informational life of cells. These collective characteristics depend on health status. Growth speed and level of intermittency in Figs.4, 5 also depend on health status.

Various types of intermittency in information activity DNA are reflected in various kinds of growth central moments $M_m(j(k,r))$ in Figs.5 and in ragged distributions $M_m(j(k=46,r))$ for even and odd $m$ in Figs.4c,d. Intermittency of information activity DNA also depends on rank $r$ (i.e. scales of DNA correlations) [12] with rather asymmetric behavior for odd and even $m$ in networks of Shannon entropy [14]. For large correlation scales, if $r<4$ and correlation length DNA is the order of cell size or coincides with cell sizes, intermittency may be absent [12].

Intermittency is typical for turbulence [13] and for autocatalysis [15]. Intermittency defines the basic natural properties of DNA activity inside cells [3, 16]. Intermittency in DNA chips was observed in [17].

Intermittency is typical for a cell life in a wide range of time scales from nanoseconds [19] to many hours [19]. In our experiment average measuring time is about 1-2 minutes. In this case a time scale for intermittency in DNA fluorescence are defined by the scales from tens $\mu$s to some seconds [20].

All described features are based on non-Gaussian statistics of different events at extremely dense fractal packing networks DNA correlations for oxidative and information activity DNA. These conditions ensure high sensitivity and susceptibility of DNA complexes to changeability in life. Even very rare unexpected and accidental events are accompanied by effective self-regulation of informational homeostasis in DNA activity [7] for flexible variations of information complexes DNA in living cells, for health and illnesses, for immune response and other signs life.

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