Non-Markov stochastic dynamics of real epidemic process of respiratory infections

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1. Introduction

The functioning of network-organized statistical systems essentially depends on the nature of interaction between their elements. It is especially due to the effect of disease-causing contacts and topology of networks. This reason as well as the variety of the displayed nonlinear behavior have made this problem the subject of several studies by means of fundamental methods of statistical physics. To analyze the epidemic and disease dynamics complexity, it is necessary to understand the basic principles and notions of its distribution in long-time memory social media. Here we consider theoretical and practical aspects of the problem and present the quantitative evidence confirming the existence of stochastic long-range memory and robust chaos in a real time series of respiratory infections of human upper respiratory track. We also discuss the implications of discrete non-Markov stochastic processes in real social complex systems from the point of view of the recent theory.

In the last few years it has been well recognized that the study of epidemic and disease dynamics in social networks is a relevant theoretical issue dealing with the spread of viruses and diseases of various nature [1–8]. It is connected with the phase transitions in models of agent spreading in nonsteady systems. In particular, it concerns the development of the models describing the epidemic spread, the forest fires, the growth of populations, the activity of catalyzers, the formation of stars and galaxies. The given problem might be of interest for all those interested in physical problems, related to the critical phenomenon in the universality class of Reggeon field theory, contact processes, ordinary and directed percolation and scale-free properties in many real systems such as internet, World Wide Web, food webs, protein and neural networks.

This study is of significant interest for modern biomedicine, ecology and economy [9–26]. The epidemic means that a large number of people in a certain country simultaneously develop a disease at a certain period of time. In case of “pandemic” people in several countries develop the same disease at the same period of time. The first cases of respiratory infections with fatal outcome in the USA and Europe were described at the beginning of the 20th century when about 20 million people died of “Spanish fever” within the period of 10 months. The pandemic of “Asian” and “Hongkong” grippe with smaller quantity of fatal outcomes [9–12] were observed in the middle of the 20th century. The period of pandemic processes is about 30–40 years. As a rule, epidemics break out in the autumn or in the winter in Northern hemisphere and in the spring or in the summer in Southern hemisphere. The duration of epidemics is about 1–3 months. Seasonality is one of the typical demonstrations of the phase development of epidemic processes. Respiratory infections affect people of any age. However children aged 1–14 develop the disease four times more often than adults. Each epidemic process of respiratory infections is accompanied by increasing death rate. The

parameters of grippe death rate in the world is 0.01–0.2%. The greatest number of deaths caused by grippe is connected with serious complications after the infection. Children (up to 2 years old) and elderly people (over 65 years old) are more liable to this infection and die more often.

Various authors have discovered that the number of people developing the disease depends to a great extent on ecological and economic conditions. The most common diseases the population of the earth suffers from are infections of respiratory organs among which grippe and acute infections of the upper respiratory track are the main components. The low standard of living as well as the pollution of the environment have had their negative influence on people's health. This is the main reason for the worsening epidemic situation in the world. Respiratory infections cause significant economic damage. Expenses caused by epidemics affect successful development of economy due to the expenses needed for financing scientific actions to prevent epidemics. These expenses are commensurable only with the sums earmarked to prevent heart diseases [13–20]. In many countries of the world great money is spent on the development of vaccines and serums, as well as prevention of epidemic outbreaks. However the viruses of grippe and some other respiratory infections have great variability. There is a great variety of grippe virus cultures. Therefore any coming grippe variant is difficult to predict. The identification of the virus presents a great problem, consequently the prevention of epidemic outbreaks is complicated. Thus new preventive measures and methods of predicting possible epidemic outbreaks [21–26] are of great interest. The unexpected outbreak of grippe in March 2003 is a good example of the case.

Now various methods of description and prediction of epidemic and pandemic processes are developed in medicine [21–26]. Hypotheses about risk factors have been formulated as a result of these studies. The standard statistics indices [26] are used in traditional epidemic studies. The basic data yield the number of diseases, their intensive parameters and average sizes. Extensive parameters, cumulative data, relative number of presentation, ratio parameters and standardized parameters are used depending on the specific features of the epidemic process. However existing methods are not efficient enough. The model for the spread of an infection is analyzed [27] for different population structures. For more ordered systems, there exists a fluctuating endemic state of low infection. At a finite value of the disorder of the network, a transition to self-sustained oscillations in the size of the infected subpopulation has been recorded. A spatial model related to bond percolation for the spread of a disease that includes variation in susceptibility to infection has was in Ref. [28].

Methods of networks are all important for the solution of the problems related to the spread of epidemics of grippe and ARTI. Traditionally these systems have been modelled as random graphs, though topology and evolution of real networks are governed by robust organization principles. In this connection it should be mentioned that an excellent review of complex networks in a wide range of systems in wild nature and human society was made in Ref. [29]. A method for embedding scale-free networks in Euclidean lattices was proposed in Ref. [30]. The critical dynamics, Glauber-type and Kawasaki-type, on two typical small-world networks, adding type and rewriting type, was studied in Ref. [31]. Newman [32,33] considered assortative mixing of

various types using empirical network data analytic models, and numerical simulation. He showed that assortative (or disassortative) mixing is indeed present in many networks, it can be measured and its effect on network structure and behavior can be examined. Generalized Bethe–Peierls approach to random networks with degree correlations and the analysis of the vertex cover (VC) problem as a prototype optimization problems defined over graphs [34] has shown that uncorrelated power-law networks are simple from the point of view of combinatorial optimization, and in this case inhomogeneities of neighboring vertices can be exploited.

In hierarchical networks, the degree of clustering, characterizing different groups, follows a strict scaling law, which can be used to identify the presence of hierarchical organization in real networks [35]. The consideration of structured scale free-networks restores the order–disorder transitions in spite of the hubs, but the value of the order parameter for the disordered state reveals the existence of ordered clusters [36]. The nonstandard, susceptible-exposed-infected (SEI), compartmental model for disease epidemics comprising latency and temporal decay in the rates of infection, also known as quenching, was examined in Ref. [37]. Consequently, the study of epidemic models has been of long-standing interest for physicists. It has been stimulated by the similarity in spreading phenomena in epidemic and physical systems which means application of analytical techniques in both cases.

Numerous methods are successfully used in statistical physics to describe distinctive characteristics of chaotic dynamics of various networks. However, three vexing features that are difficult for the detailed analysis can be observed in real networks. Among them: nonstationarity, nonlinearity, and nonequilibrium phenomena. Furthermore, the significant peculiarities of networks are directly related to the discreteness in time of object–subject registration response. Non-Markov and long-range statistical memory effects play an important role in epidemic dynamics in social networks. For this reason we offer a new statistical approach in the research of epidemic processes with the help of our statistical theory of non-Markov stochastic discrete processes [38–40]. This method has already been used by the authors to study various real problems in cardiology [38,40], seismology [39], neuropsychology [41,42] and neurophysiology [43]. With the help of this method we intend to find the full spectrum of dynamic, kinetic and spectral characteristics of the studied complex system. We shall receive a more detailed representation of the stochastic dynamics of epidemic processes taking into account the discrete behavior and nonstationarity of the dynamic and kinetic epidemic parameters.

This work deals with the study of statistical properties of epidemic dynamics. The key distinctions of grippe and respiratory infections epidemic processes are defined with the help of long-range memory effects and statistical effects of non-Markovity in these processes. In particular, one of the key problems consists in revealing the role of randomness, regularity and predictability of epidemic processes.

The paper has the following structure. In Section 2 we show the basic points of our statistical theory of nonstationary discrete non-Markov processes in complex systems [38–40]. The description of the experimental data and the technique of their processing are given in Section 3. The received results and their analysis are submitted in Section 4. The conclusions are submitted in Section 5.

2. Statistical theory of non-stationary discrete non-Markov processes in complex systems. Basic concepts and definition

A brief description of the theory is presented here. We will consider a spread of epidemic as a time evolution of the number of patient's (discrete random variable $x(T)$). Therefore, we can use the results of the statistical theory of discrete non-Markov nonstationary processes for complex systems. The comprehensive description of the theory and the representation of the quantities used here can be found in the works published earlier [38–43].

While analyzing complex systems we obtain discrete equidistant series of experimental data, the so-called random variable

$$X = \{x(T), x(T+\tau), x(T+2\tau), \ldots, x(T+k\tau), \ldots, x(T+\tau N-\tau)\} \, . \tag{1}$$

It corresponds to a time series of measured signal during the time $(N-1)\tau$, where τ is discretization time of the signal. In this work we take the number of patients/day $x(T)$ as a measurable parameter, $(N-1)\tau$ is a time interval of data recording (6 years), τ is 1 day.

For the dynamical analysis, it is more convenient to use a normalized time correlation function (TCF). For nonstationary discrete processes TCF has the following form ($t = m\tau, N-1 > m > 1$):

$$a(t) = \frac{1}{(N-m)\sigma(0)\sigma(t)} \sum_{j=0}^{N-1-m} \delta x(T+j\tau)\delta x(T+(j+m)\tau) \, , \tag{2}$$

where $\sigma(0)$ and $\sigma(t)$ is the variances of the initial ($t=0$) and final (at moment t) dynamic states of the systems, correspondingly. The properties of TCF $a(t)$ are determined by the conditions of normalization (at $t=0$) and attenuation of correlations (at $t \to \infty$)

$$\lim_{t\to 0} a(t) = 1, \quad \lim_{t\to\infty} a(t) = 0 \, . \tag{3}$$

If we take into account the nonstationarity and discreteness of complex systems for real processes, the kinetic equation for TCF $a(t)$ has the form of a closed set of the finite-difference kinetic equations of the non-Markov type [38–41]

$$\frac{\Delta a(t)}{\Delta t} = \lambda_1 a(t) - \tau \Lambda_1 \sum_{j=0}^{m-1} M_1(j\tau) a(t-j\tau) \, . \tag{4}$$

Here Λ_1 is a relaxation parameter with the dimension of square of frequency, and parameter λ_1 describes the eigenspectrum of Liouville's quasioperator $\hat{L}$

$$\lambda_1 = \mathrm{i}\frac{\langle \mathbf{A}_k^0(0)\hat{L}\mathbf{A}_k^0(0)\rangle}{\langle |\mathbf{A}_k^0(0)|^2\rangle}, \quad \Lambda_1 = \frac{\langle \mathbf{A}_k^0(0)\hat{L}_{12}\hat{L}_{21}\mathbf{A}_k^0(0)\rangle}{\langle |\mathbf{A}_k^0(0)|^2\rangle} \, , \tag{5}$$

where angular brackets mean a scalar product of state vectors.

The function $M_1(j\tau)$ in the r.h.s. of Eq. (4) represents the first-order memory function

$$M_1(j\tau) = \frac{\langle \mathbf{A}_k^0(0)\hat{L}_{12}\{1 + \mathrm{i}\tau\hat{L}_{22}\}^j\hat{L}_{21}\mathbf{A}_k^0(0)\rangle}{\langle \mathbf{A}_k^0(0)\hat{L}_{12}\hat{L}_{21}\mathbf{A}_k^0(0)\rangle}, \quad M_1(0) = 1\ . \tag{6}$$

In Eqs. (5) and (6) operator $\hat{L}$ is a finite-difference operator

$$\mathrm{i}\hat{L} = \frac{\Delta}{\Delta t}, \quad \Delta t = \tau,$$

where τ is a discretization time step, $\hat{L}_{ij} = \Pi_i\hat{L}\Pi_j$ $(i,j = 1,2)$ are matrix elements of splittable Liouville's quasioperator, $\Pi_1 = \Pi, \Pi_2 = P = 1 - \Pi$ and Π are projection operators (for more details, see, Refs. [38–42]). It is easy to see, that in Eq. (6) we deal with the time correlation of new orthogonal dynamic variable $\hat{L}_{21}\mathbf{A}_k^0(0)$.

Eq. (4) represents the first equation in the chain of finite-difference kinetic equations with memory for the discrete TCF $a(t)$. One can recognize that the memory function $M_1(t)$ takes the statistical memory about previous states of the system into account. By using Gram–Schmidt orthogonalization procedure [38] we receive the recurrent formula, in which the senior dynamic variable $\mathbf{W}_n = \mathbf{W}_n(t)$ is connected to the junior one in the following way:

$$\begin{aligned} &\mathbf{W}_0 = \mathbf{A}_k^0(0), \quad \mathbf{W}_1 = \{\mathrm{i}\hat{L} - \lambda_1\}\mathbf{W}_0, \ldots, \\ &\mathbf{W}_n = \{\mathrm{i}\hat{L} - \lambda_{n-1}\}\mathbf{W}_{n-1} + \Lambda_{n-1}\mathbf{W}_{n-2} + \ldots, \qquad n > 1\ . \end{aligned} \tag{7}$$

Introducing the corresponding projection operators we come to the following chain of connected non-Markov finite-difference kinetic equations $(t = m\tau, n = 1,2,\ldots)$:

$$\frac{\Delta M_n(t)}{\Delta t} = \lambda_{n+1}M_n(t) - \tau\Lambda_{n+1}\sum_{j=0}^{m-1} M_{n+1}(j\tau)M_n(t - j\tau). \tag{8}$$

Here λ_{n+1} is an eigenvalue of the Liouville's quasioperator, and relaxation parameters Λ_{n+1} are determined as follows:

$$\lambda_n = \mathrm{i}\frac{\langle \mathbf{W}_n\hat{L}\mathbf{W}_n\rangle}{\langle|\mathbf{W}_n|^2\rangle}, \quad \Lambda_n = -\frac{\langle \mathbf{W}_{n-1}(\mathrm{i}\hat{L} - \lambda_n)\mathbf{W}_n\rangle}{\langle|\mathbf{W}_{n-1}|^2\rangle}, \ldots\ .$$

In this work we analyze the short time series with the help of Eqs. (4)–(8) where nonstationary functions may not be taken into account [40]. So, we shall use full set of the dynamic, kinetic and spectral parameters, functions and characteristics as a quantitative information measure to describe of spread of epidemic in human population. Among them, here are temporal dynamics of the first four orthogonal dynamic variables, phase portraits in some planes of dynamic variables, TCF, junior memory functions and their power spectra, frequency dependence of first three points of non-Markovity parameter, and local time behavior of the locally average relaxation parameters.

3. Experimental data and data processing

The registration and accounting materials, as well as the results of certain studies are the initial data for epidemic research in medicine. We have made use of the accounting materials of Kazan sanitary–epidemiological stations located in industrial districts. The concrete data were given by the sanitary–epidemiological station of the Privolzhskii district of Kazan covering the period from 10.27.1995 to 03.05.2002. Fig. 1A presents the experimental raw data of the epidemic spread, involving the total population of the Privolzhskii district (about 300 thousand people). The first group of the data represents a 6-year dynamics of grippe, the second group describes a 6-year dynamics of acute respiratory track infections in this district. The obtained data were processed with the help of the above introduced technique. The set of three memory functions was calculated for each sequence of the data. The power spectra for each of these functions are obtained by the fast Fourier transform (FFT). We will also show the phase portraits in plane projections of the multidimensional space of the dynamic orthogonal variables. For a more detailed diagnosis of the system we will consider the frequency spectrum of the first three points of the statistical spectrum of the non-Markovity parameter. In this study we will use the frequency dependence of the statistical spectrum of non-Markovity parameter [38–40]

$$\varepsilon_i(\omega) = \left\{ \frac{\mu_{i-1}(\omega)}{\mu_i(\omega)} \right\}^{1/2} . \tag{9}$$

Here $i = 1, 2, \ldots$ and $\mu_i(\omega)$ is a power spectrum for ith order memory function of the ith relaxation level. The statistical spectrum of non-Markovity parameter $\varepsilon_i(\omega)$ constitutes an information measure of Markovity and non-Markovity or randomness and regularity in time evolution of the underlying systems.

4. Discussion of the results

In this section the quantitative and comparative analysis of the 6-year period of grippe chaotic dynamics (Fig. 1B(a)) and of ARTI (Fig. 1B(e)) will be carried out on the basis of the theory submitted in Section 3. The time series of the initial signals, the phase portraits of the dynamic variables, the power spectra of TCF and the junior functions of memory as well as frequency dependence of the first three points of the statistical non-Markov parameter are submitted in Figs. 1–4. We develop a new approach in the study of epidemic processes on the basis the local time behavior of the relaxation and kinetic parameters λ_1–λ_3, Λ_1 and Λ_2 (Figs. 5 and 6).

The 6-year sampling of grippe and ARTI dynamics are submitted in Fig. 1B (Figs. 1B(a)–(d) for grippe, Figs. 1B(e)–(h) for ARTI). The time series of the orthogonal variable W_0 (Fig. 1B(a)), W_1 (Fig. 1B(b)), W_2 (Fig. 1B(c)), W_3 (Fig. 1B(d)) for the chaotic dynamics of grippe and ARTI have appreciable symmetry relative to straight line $W_i = 0$, where $i = 1$–3. The analysis of the time series of variable W_0 (Fig. 1B(a)) for a grippe epidemic shows that the moment of the grippe outburst or the beginning of an epidemic corresponds to the most significant fluctuations of this dynamic variable.

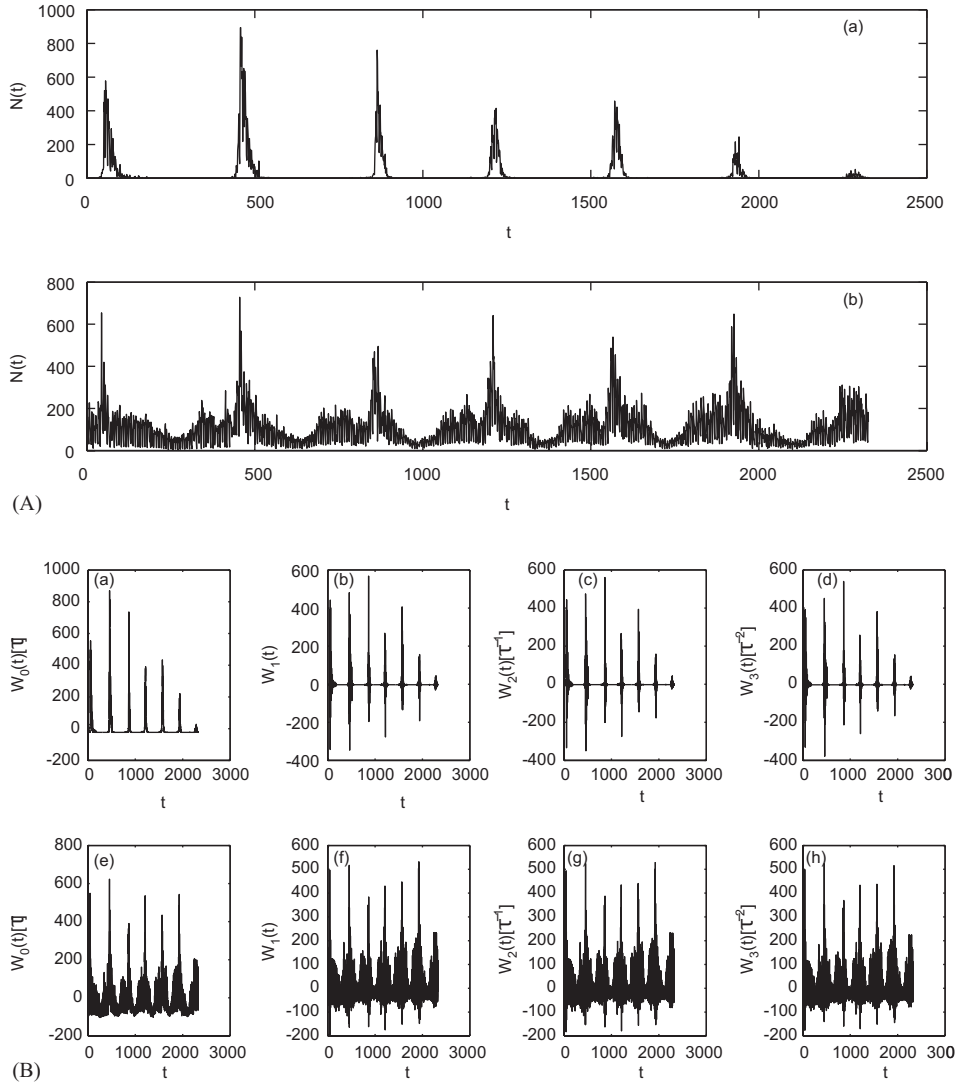

Fig. 1. (A) 6-year temporal dynamics of the experimental raw data of grippe (1A(a)) and acute respiratory track infections (1A(b)) in Privolzhskii district of Kazan, Russia, from 10.27.95 to 03.05.02. The dynamics of ARTI is initially characterized by a slow increase and then by a slow decrease in the number of patients. With grippe we have a more sharp picture, characterized by a low level of the background noise, then by a sudden increase and decrease of the disease. (B) Time series of orthogonal variables W_0 (a, e), W_1 (b, f), W_2 (c, g), W_3 (d, h) of chaotic dynamics of grippe (a–d) and acute respiratory track infections (ARTI)(e–h). The spectral peaks in time series display the seasonal periodic occurrence of grippe and ARTI epidemics. The time series of orthogonal variables for the epidemic process of ARTI differ due to the occurrence of an appreciable noise.

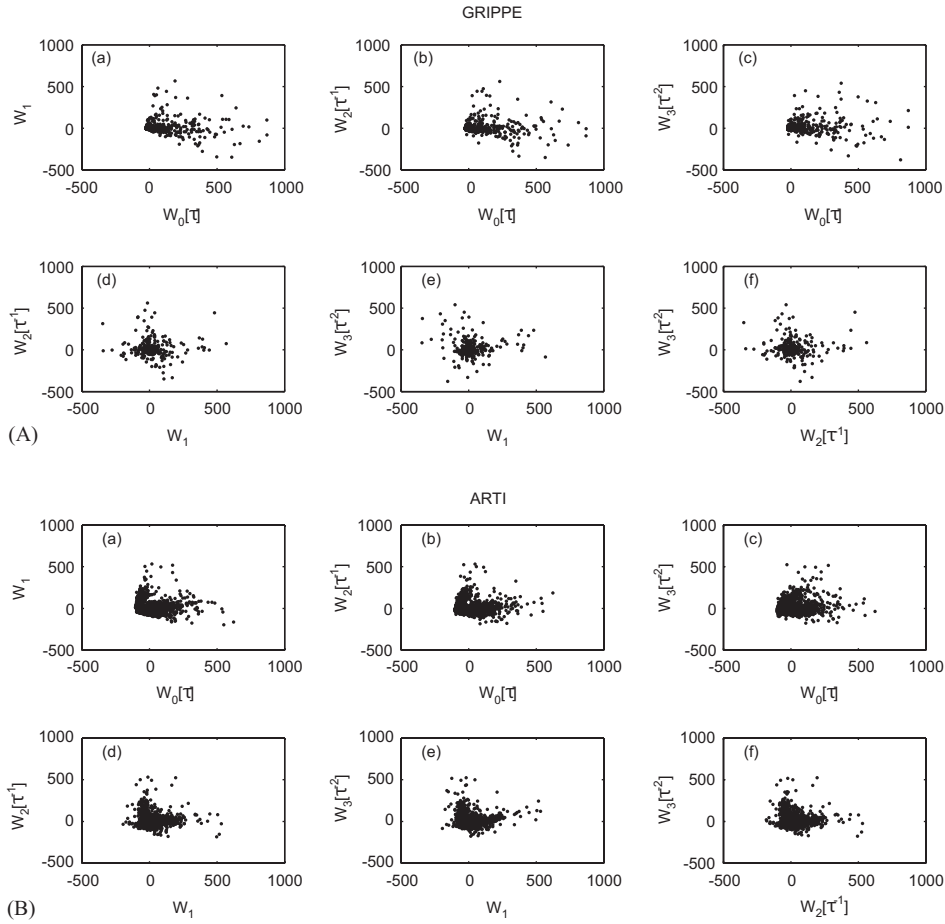

Fig. 2. The phase clouds for epidemic processes of (A) grippe and (B) acute respiratory track infections (ARTI) in plane projections for the various combinations of orthogonal variables W_i, W_j where $i, j = 0$–3. During the epidemic of grippe the phase points disperse about the nucleus. The phase clouds for the epidemic process of ARTI acquires the shape of a "boot" and they clustered around nucleus.

Epidemic outbursts of the disease are located at equal distances from each other. This is the evidence of periodicity and interval constancy between grippe epidemics within the whole period of observation. The time series for three orthogonal variables W_1 (Fig. 1B(b)), W_2 (Fig. 1B(c)), W_3 (Fig. 1B(d)) of grippe epidemics are almost perfectly symmetrical. The time series of dynamic variables W_0 (Fig. 1B(e)), W_1 (Fig. 1B(f)), W_2 (Fig. 1B(g)), W_3 (Fig. 1B(h)) of ARTI epidemiological processes present a different picture. The visible fluctuations of the dynamic variables for ARTI are observed in the autumn–winter period same as in case of grippe epidemics. However, dynamic noises can be observed between the outbursts of ARTI epidemics. They

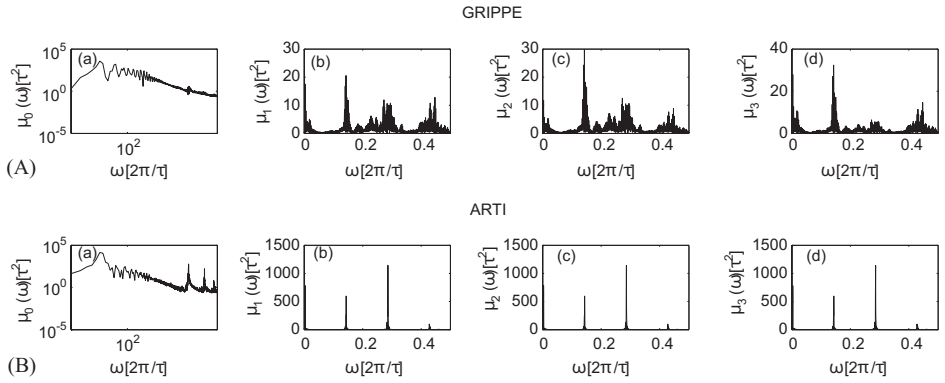

Fig. 3. The power spectra of time correlation function (TCF) $\mu_0(\omega)$ (a) and of the three junior memory functions $\mu_i(\omega), i = 1$(b), 2(c), 3(d) for the epidemic processes of (A) grippe and (B) acute respiratory track infections (ARTI). For a more detailed analysis the power spectrum of TCF $\mu_0(\omega)$ (a) is submitted in double logarithmic scale. In the area of high frequencies three additional spectral splashes are observed. The spectral peaks in the registered spectra are the evidence of long-range memory in the system.

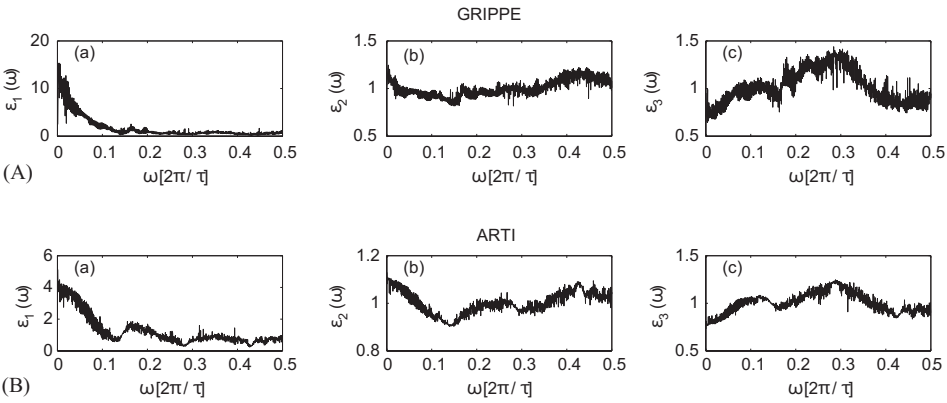

Fig. 4. The frequency dependence of the first three points of statistical non-Markov parameter $\varepsilon_i(\omega)$ for epidemic processes of (A) grippe and (B) acute respiratory track infections (ARTI). For the first point of $\varepsilon_1(\omega)$ the splash of Markovization process is observed in the vicinity of $\omega=0$. The values of other parameters $\varepsilon_2(\omega)$ and $\varepsilon_3(\omega)$ change in a narrow interval about a unit. This reflects the existence of long-range memory order in the system.

are represented by monotonously inequable parabolas. One of the half-parabolas corresponds to one of the epidemics and another corresponds to the next one. The time development of orthogonal variables W_1 (Fig. 1B(f)), W_2 (Fig. 1B(g)), W_3 (Fig. 1B(h)) of the ARTI epidemiological process presents a symmetric series about straight line $W_i = 0$. There are seven outbursts in the time behavior of the dynamic variables in the seven autumn–winter periods (from 10.27.1995 to 03.05.02). They corresponds to the seven cycles of grippe and ARTI epidemics. However the time series of orthogonal

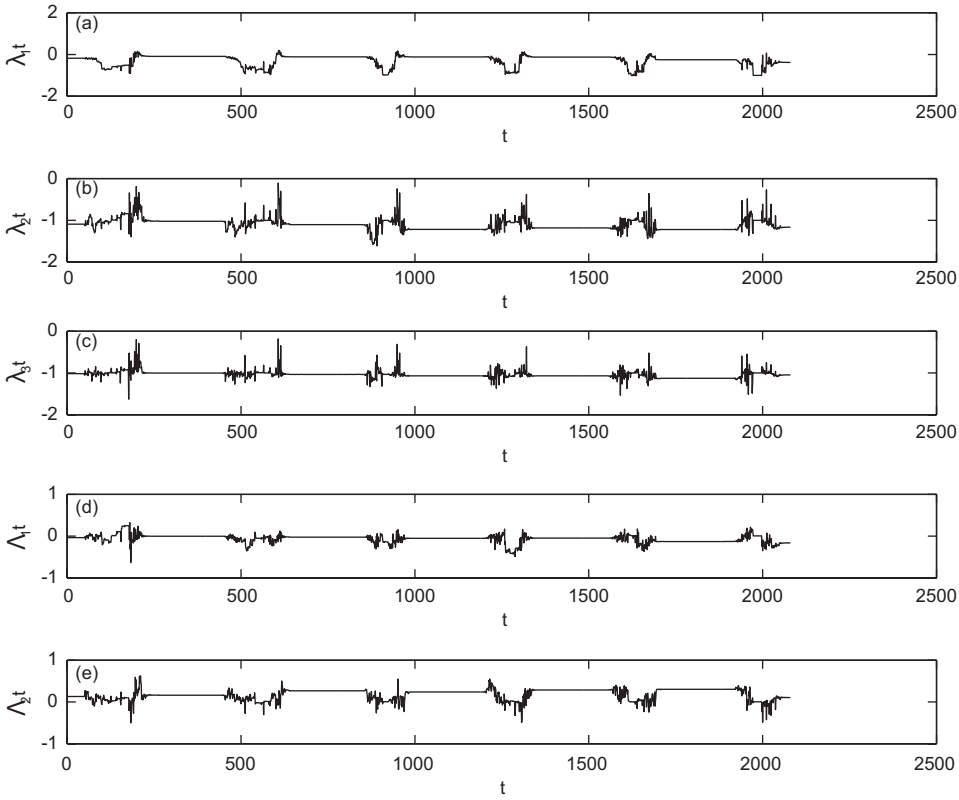

Fig. 5. (a–e) The time dependence of local kinetic and relaxation parameters λ_1–λ_3, Λ_1 and Λ_2 for the epidemic process of grippe in units of τ. The sampling of local averaging is equal to 200 points. The sudden dropout of the system from a balanced condition is determined by the epidemic of grippe. The reversion of the system into a former steady state defines the intervals between the epidemics of grippe.

variables W_i $(i = 1\text{–}3)$ for ARTI differ from grippe's case in the strongly expressed asymmetry and the existence of a clearly expressed noise.

In Fig. 2 the phase clouds in the six plane projections of the four first dynamic variables W_i, $i = 0\text{–}3$ for epidemic processes of grippe and ARTI are submitted. In case of grippe the phase clouds have a well-defined asymmetry about the center of coordinates. All the phase clouds contain a centralized nucleus and an aggregate of points scattered on perimeter in a fan-shaped way. The interval of the dispersal makes up 900τ. Owing to such asymmetric stratification the phase clouds take an elongated shape. The phase portraits of the ARTI epidemiological process are less symmetrical about the center of coordinates. The nucleus of the portrait takes the shape of a right angle and resembles a "boot". Apical emissions of separate points are appreciable on each side of the "boot". The interval of the dispersal of the points decreases up to 700τ. The stratification of the phase clouds of a grippe epidemiological process is more prominent, than in case of an ARTI epidemic. The analysis of the data in other Kazan

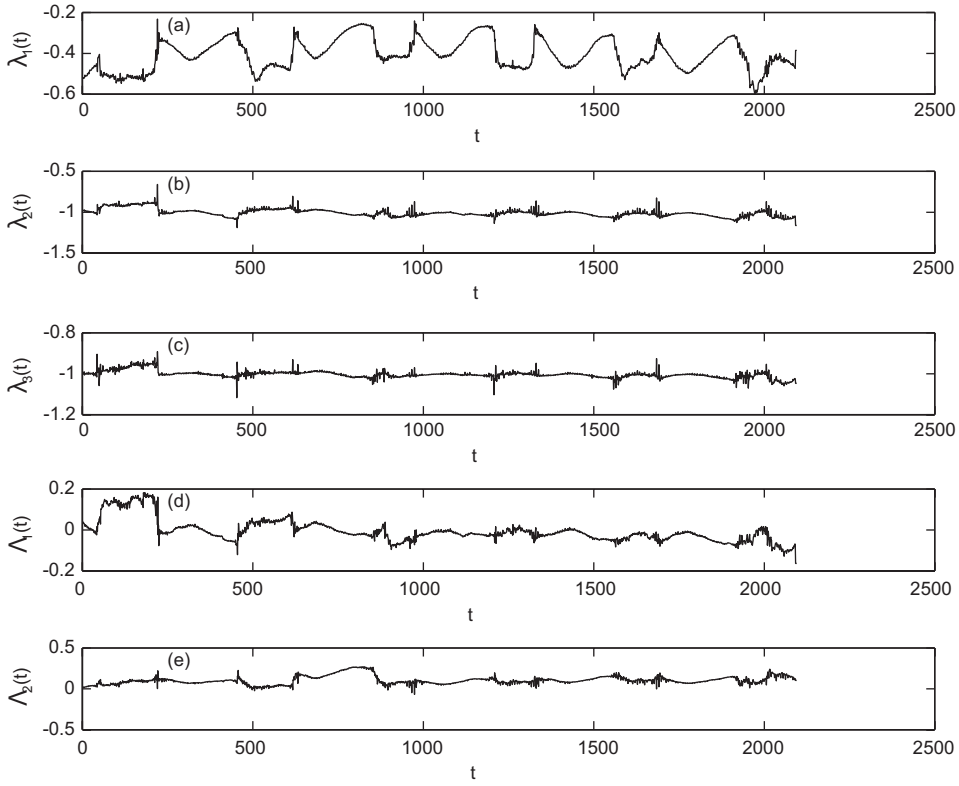

Fig. 6. (a–e) The time dependence of local kinetic and relaxation parameters λ_1–λ_3, Λ_1 and Λ_2 for epidemic process of acute respiratory track infections (ARTI) in units of τ. The length of the sampling of local averaging is equal to 200 points. The sharp splash in a time series demonstrates the beginning of an ARTI epidemic. The end of the epidemic process is defined by the following peak. At the moment of epidemic the system is in an unstable state.

districts reveals a prominent phase portrait of a grippe epidemic. It is an elongation of the phase portrait for an ARTI epidemic namely its "boot-type" shape.

In Fig. 3 the power spectra of TCF $\mu_0(\omega)$ and three junior memory functions $\mu_i(\omega)$, $i = 1$–3 for grippe and ARTI epidemiological processes are submitted. The frequency spectra of $\mu_0(\omega)$ are given in doubly-log scale for a more detailed analysis of the data. In case of grippe the fractal dependence in the region of intermediate and high frequencies is found in the power spectrum of the initial TCF $\mu_0(\omega)$. The area of these frequencies is divided by a small outburst of power on frequency $\omega = 3 \times 10^{-1}$ f.u. (1 f.u. $= 2\pi/\tau$). In the domain of the low frequencies sharp breaks of the spectrum are observed. The frequency dependency of the next three junior memory functions $\mu_i(\omega), i = 1$–3 are accompanied by spectral outbursts at equal intervals and by condensation of spectral lines near the outbursts. A spectral noise is present in all diagrams of the frequency dependencies. The spectrum of the initial TCF $\mu_0(\omega)$ for an

ARTI epidemic process differs from a grippe epidemic only in the high frequency area. Additional spectral peaks are appreciable at frequencies $\omega{=}10^{-1}$ f.u. and $\omega{=}10^{-1/2}$ f.u. The power spectra of the three junior memory functions $\mu_i(\omega), i = 1\text{–}3$ for an ARTI epidemic have bright fractal dependence with several spectral peaks at every 0.15 f.u.

In Fig. 4 the spectra of the first three points of statistical non-Markov parameter $\varepsilon_i(\omega)$, where $i = 1\text{–}3$ are presented. Fractalness is appreciable only in the behavior of $\varepsilon_1(\omega)$. With approximation to frequency $\omega = 0$ the monotonous amplification of markovization is observed. The second point $\varepsilon_2(\omega)$ in the spectra of the non-Markovity parameter for ARTI and grippe epidemics accept value $\varepsilon_2(\omega) = 1$, they are almost identical with small fluctuations. It testifies to strong non-Markovity. The sinuosity with two frequency crests in area $\omega = 0.1$ and 0.3 f.u. is appreciable in frequency spectra of the third point of statistical non-Markovity parameter $\varepsilon_3(\omega)$.

In Fig. 5 the time dependence of local (with local averaging) kinetic and relaxation parameters λ_1–λ_3, Λ_1 and Λ_2 for a grippe epidemic is submitted. The sampling for the local averaging includes 200 points. The similar size of the sampling allows to consider the physical nature of a real object (a grippe and ARTI epidemics) in a more detailed way. Breaks are observed at a great number of points in the time scanning of the parameters. In the time dependence of all the parameters within 6 years of every autumn–winter period the system drops out of the steady state and returns to it. The whole process can be described as recurrence of two various processes. At first small fluctuations of the parameter are observed. The fluctuations visibly grow in the moment of seasonal epidemics. Then the system acquires the state of quasistable balance. The time interval for each process is 125 points, that corresponds precisely to one of the autumn–winter periods.

Recently the correlation analysis has experienced a marked lack of information concerning the object of the research. The procedure of local averaging of various parameters allows to examine separate hidden properties of the studied objects. The characteristic feature of the usual correlation analysis is the fact that the greatest possible set of signals is required for the qualitative analysis of the properties of the object of the research. With a longer sample of such signals it is possible to receive more reliable information with the help of the correlation analysis. Let us take a random non-Markov process as an example. This process consists of a sequence of alternating states. Thus there is necessity for more information about the whole process as well as its separate states. In this case the use of the correlation analysis for all the time series will be inefficient. The processing of the signals is necessary for separate local sites of the whole time series. It will allow to consider the properties of separate dynamic states of the system.

Hereinafter a new method of data processing based on the local averaging of kinetic and relaxation parameters is offered. This method allows to consider the properties of separate, non-stationary states of the systems. The idea of the method is the following: there exists an initial data set. Let us take a sampling in length N of signals and calculate its kinetic and relaxation parameters. Then the operation of “step-by-step shift to the right” for one time interval is carried out. The kinetic and relaxation parameters are calculated again. The “step-by-step shift to the right” is continued to the end of a time series. Such locally averaged parameters have high sensitivity to the effects of

intermittency and non-stationarity. If the initial time series has some irregularity, it is instantly reflected in the behavior of the locally averaged parameters.

The use of this method requires the choice of the optimal length of a sampling which enables to receive the most trustworthy information. If a sampling is too short, noise effects do not allow to receive qualitative information. Besides with a short length sampling we have significant errors. On the other hand at a great length of a sampling locally averaged parameters lose "sensitivity" necessary for the study. As a result of the studies of different lengths of local samplings we have received the optimal length which makes 100–120 points. Further proofs of all aforesaid will be given below.

In Fig. 6 the time dependence of local kinetic and relaxation parameters λ_1–λ_3, Λ_1 and Λ_2 for an ARTI epidemic is submitted. Two hundred points where selected for the procedure of localization. Due to a more significant noise of the ARTI chaotic dynamics the time scanning of the parameters essentially differs from grippe. The time dependence of the first parameter λ_1 reflects the physical features of an ARTI epidemic process. Instead of small fluctuations sharp fluctuation splashes appear at the beginning of the epidemic. Between them the system acquires a rather quiet state followed by a new epidemic peak. When the epidemic is over only small fluctuations in the system can be appreciable. This process repeats periodically during the whole long-term interval. Some definite regularity can be observed in the time dependence of the next kinetic and relaxation parameters. The sharp peak at the beginning and at the end of an ARTI epidemic process is related to them. Only small fluctuations of the system are appreciable at the time of an epidemic. After each ARTI epidemic the considered system comes back to the state of relative balance.

Judging by the behavior of the parameters the distinction between the epidemic of grippe (I) and that of ARTI (II) comes to the following. The initial values of the intensity $\mu_i(\omega = 0)$ for all $i = 0$–3 for systems I and II differ by more than one order. It is the evidence of remarkable distinction in times of relaxation (correlations). For system I these times are almost 20–50 times shorter, than for system II. The intensity scales also differ almost by 50 times. Thus the initial values of $\varepsilon_1(\omega = 0)$ differ almost by 5 times for systems I and II.

On the basis of the aforesaid it is possible to come to certain conclusions about great randomness of grippe dynamics in comparison with ARTI dynamics. The last one has greater regularity and predictability. An other feature of the investigated epidemics is the existence of three additional well-defined spectral splashes besides the basic annual one. From Figs. 3(b)–(d) and (f)–(h) one can see that these groups of spectral peaks correspond to the characteristic frequencies equal to 0.14, 0.28 and 0.43 f.u. accordingly. The intensity of the high-frequency peak is almost an order lower, than the two other peaks of lower frequencies.

The clear-cut distinction in the dynamic behavior of grippe and ARTI epidemics is shown in local time dependence of relaxation constants λ_1–λ_3, Λ_1 and Λ_2. Parameters $\lambda_i, i = 1, 2, 3, \ldots$ remind Luapunov's exponents for various relaxation levels. For system II great regularity is observed. All parameters of λ_1–λ_3 are negative, which is the evidence of relative stability of the system. For system I (grippe) parameter $\lambda_1(t)$ gets small positive values on tail owing to the general instability. It corresponds to the

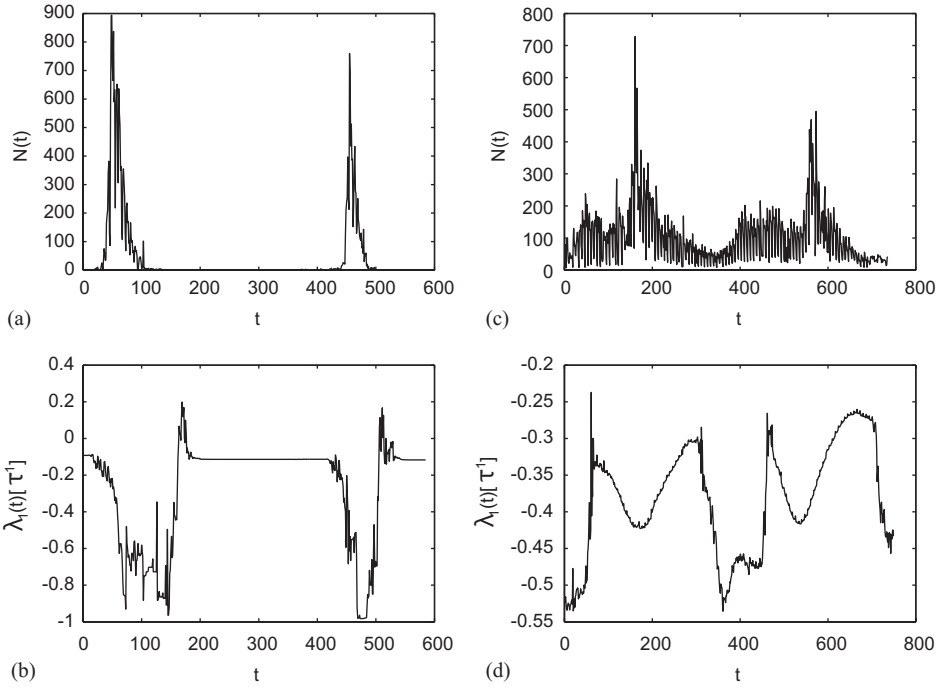

Fig. 7. Time dependence of local relaxation rate $\lambda_1(t)$ for grippe (b) and ARTI (d) with initial row data for grippe (a) and ARTI (c). We show extracted sampling for comparison. One can see the dramatic revising of $\lambda_1(t)$ during both epidemic. Time behavior $\lambda_1(t)$ at grippe contains isoline's regime whereas in case of ARTI one can notice continuous alteration of $\lambda_1(t)$.

slump of epidemic. From Eq. (8) one can see, the system becomes unstable at values $\lambda_1(t) > 0$.

The time behavior of parameters $\Lambda_1(t)$ and $\Lambda_2(t)$ is more dramatic. If $\Lambda_i(t) > 0, i = 1,2$ then solution of Eq. (8) corresponds to a steady condition of social network, if $\Lambda_i(t) < 0$ instability grows. From Figs. 5(d) and (e) and 6(d) and (e) it is clear, that annual epidemics of grippe has a greater instability of the system. In case of ARTI (system II)the behavior of $\Lambda_2(t)$ has steady everywhere. However the parameter of $\Lambda_1(t)$ in the greater part of the time scale is negative, this testifies to a loss of stability in this area.

So, parameter $\lambda_1(t) = R$ means a relaxation rate of random process. In case of grippe (I) isoline exists in the behavior of $\lambda_1 = \lambda_1(t)$ with values $0.08\tau^{-1} \leqslant R \leqslant 0.24\tau^{-1}$. Simultaneously, relaxation rate on recession of grippe epidemic sharply grows up to (0.8–1.0) τ^{-1}, that it is by 4–12 times, approximately. This implies greater stabilization of the system, than during its rise or at the peak of the epidemic (see, Fig. 7(a) and (b) for more details).

In case of ARTI isoline does not exist at all in the behavior $\lambda_1(t)$. It testifies to quasistability and seasonal prevalence in the relaxation behavior, in-whole. Absolute

Table 1
Some kinetic and relaxation parameters for grippe and ARTI, calculated from our theory, in comparison

	$\lambda_1(\tau^{-1})$	$\lambda_2(\tau^{-1})$	$\lambda_3(\tau^{-1})$	$\Lambda_1(\tau^{-2})$	$\Lambda_2(\tau^{-2})$
Grippe	−0.1127	−1.1093	−1.0278	−0.0262	0.1972
ARTI	−0.3775	−1.0313	−1.0092	−0.0307	0.1149

values of the relaxation rates fluctuate within the interval of $0.24\tau^{-1} \leqslant R \leqslant 0.6\tau^{-1}$. The relaxation rate on recession of epidemic ARTI increase in 2–2.5 times. Therefore the system, as a whole, acquire greater macroscopic stability.

We can draw the following conclusion from comparison of relaxation parameter $\lambda_1(t)$ of grippe and ARTI (see, Table 1 for the whole sampling). Relaxation rates differ almost by 3.4 times. It testifies to macroscopic stability of the epidemiological process of ARTI. On the other hand, local amplification of the relaxation rate (on a recession of grippe epidemic) in case of grippe creates an additional source of stabilization for the unstable process of grippe epidemic.

The spread of atypical pneumonia (SARS) makes any research into ARTI epidemics especially timely. Cases similar to SARS may become more numerous. Thus the method introduced here might be of great scientific significance.

5. Conclusions

In this paper we have shown that the chaotic dynamics of epidemic processes of grippe and ARTI in real social network may be considered as a stochastic discrete non-Markov process. It is more convenient to use the statistical theory of discrete non-Markov processes for real objects and live systems [38–40] to study the similar processes. The used theory allows to define essential distinctions between the epidemic processes of grippe and acute respiratory track infections by degrees of randomness, regularity and predictability. By processing the experimental data about the number of patient's we received the time series of dynamic variables $W_i(t)$ and calculated the memory functions and the first three points of the statistical spectra of the non-Markovity parameter. We used the power spectra, which were received with the help of the fast Fourier transform (FFT) to analyze diverse time functions (correlation and memory functions).

The new qualitative approach in studying statistical properties of epidemic processes of grippe and ARTI originates when using locally average kinetic and relaxation parameters λ_1–λ_3, Λ_1 and Λ_2.

On the basis of the conceptions about long-range memory and localization of parameters it is possible to come to the following conclusions. The epidemic process of grippe causes a great danger to mankind because of its randomness and unpredictability. Each epidemic process of grippe is characterized by a sudden outburst and sudden attenuation. The peak of an epidemic lasts a comparatively short period of time (60 days). It takes great efforts to liquidate the consequences of a grippe epidemic. The epidemic process of ARTI is characterized by a greater regularity and predictability.

It is accompanied by a small outburst at the beginning of the epidemic, then the number of patients diminishes. After it a drastic outburst corresponding to the epidemic peak is observed. The process ends with small short-term splashes which later quickly fade. Unlike grippe, an ARTI epidemic is characterized by a less drastic outburst and attenuation. During the interval insignificant outbursts of respiratory infections are observed followed by periodic outbursts of ARTI.

We have revealed and explained essential distinctions in phase portraits, frequency spectra and quantitative estimations of memory functions and statistical non-Markov parameters between the epidemic processes of grippe and ARTI. Relative distinctions of the quantitative data on epidemics of grippe and ARTI are the evidence of the distinction in long-range memory, order and organization of each process in a certain social system. These distinctions allow to define the degree of importance of each epidemic. In particular, we have shown that the epidemic processes of grippe and respiratory infections have essentially different quantitative measure of randomness and regularity.

The local kinetic and relaxation parameters of epidemic processes of grippe and ARTI allow to study statistical features of these systems in detail. The local time dependencies allow to find the internal features of the epidemic process. It helps in the study of real objects. With abundant experimental data the method allows to define the laws of epidemic processes.

The received results can be of practical value when studying other diseases as well as in estimation how serious the threat of epidemic might be.

In this paper we have demonstrated that the set of relaxation, kinetic and spectral parameters and characteristics of discrete non-Markov stochastic processes are valuable for the description of the role of randomness, regularity and predictability of epidemic processes, the spread of grippe and ARTI in the world.

Since the similar situation is typical of the majority of epidemic diseases on networks our conclusions are of profound importance for a large number of physical, biological and technological networks. The results received here are connected with non-stationary and non-ergodic processes in stochastic systems. Therefore they are certainly of value for physics of the disorder matter in which similar processes can occur on molecular or structural levels.

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