Preface

Back in 1905 S.S. Chetverikov (1905) in the *Diary of the Zoological Department of the Imperial Society of Lovers of Natural Science, Anthropology and Ethnography* noted that locust invasions into Russia are waves of life, thus emphasizing the important property of living matter - the ability to spread in waves. The mathematical study of the question of the propagation of the waves of biological populations originates from the work of A.N. Kolmogorov, I.G. Petrovsky, & N.S. Piskunova (Kolmogorov, Petrovsky, & Piskunov, 1937). In this work, the nonstationary diffusion equation with the source term modeling the reproduction process of a biological population was studied, and the diffusion corresponded to the chaotic mobility of individuals. The possibility of applying this work it is limited by the framework of a very simple model of the biological population: the process of feeding of organisms was not taken into account, the possibility of their directional movement (taxis), the patterns of reproduction and dying were taken in the simplest form. The formation of the waves of biological populations is the result of the manifestation of the important quality of living nature - its self - organization. Waves of biological populations can be of two types: a wave of territory conquest and a solitary wave (soliton). The wave of conquest is necessary for the resettlement of organisms over a large area. A solitary wave is the search for food for a multitude of individuals forming a population of finite size when it moves across the territory.

A vivid example of a wave of conquest in nature can be the spread of blue - green algae over the surface of the Earth several billion years ago when they emerge from the ocean (Elenkin, 1936; Zavarzin, 2002). This ensured the development of life on Earth. The flight of the gregarious locust is a vivid example of a solitary wave of a population.

Mathematical models of wave propagation of the various biological populations (communities of biological organisms) were built and studied in the number works (Zhizhin & Bolshakova, 2000 a, b, c; Zhizhin, 2004, 2005, 2012, 2014; Zhizhin, & Selikhovkin, 2012). This monograph presents studies of stationary waves of conquest and solitary waves in logistic populations and populations of Ollie, as well as a study of the flight model of the herd locust.

Nonlinear waves, which include waves of biological populations, are mobile dissipative structures (Svirezhev, 1987). The dissipative structures support themselves at the expense of energy consumption from the environment. Dissipative structures can also be fixed. They can have a different form and are called generally attractors. These are the formations that systems seeking over time (including stationary standing and traveling waves). The desire for living matter to equilibrium is also an important feature of them. An attractor can be a special point in the phase space of the system - the equilibrium position. It can be a limit cycle on which the trajectories of the phase space are wound, and it can be a torus. Attractors can form continuous manifolds of dimension n. In 1971 the term strange attractor appeared. They denote the attractor, to which the trajectories of the phase space tend in a chaotic way, approaching and moving away from it. This is accompanied by bifurcation of the special points of the phase space. The system of equations studied in 1971 was a model of turbulence (the Lorentz equations). With some form of functions included in the Lorentz equations, the system describes the dynamics of the biological population consisting of predators and preys (Volterra, 1931). Currently, a large scientific literature is devoted to the mathematical study of the strange attractors (see, for example, Marsden, & McCracken, 1976; Kolmogorov, & Novikov, 1981). Affinity by its nature is affirmed of the strange attractors and fractal attractors (Mandelbrot, 2004).

Thus, in the populations of living organisms in which they are born and die due to death from other organisms or adverse climatic conditions, an equilibrium occurs sooner or later, i.e. the system tends to attractor. In some cases, this attractor may be strange. However, what happens in populations if conditions are created that significantly reduce the likelihood of death of organisms? G. Mendel created such conditions, when in 1865 he conducted his experiments on the crossing of plants with different (constant - different) characters (Mendel, 1965). Naturally, under these conditions, the number of hybrids increases from generation to generation. This was the reason for Hardy to believe that there is no equilibrium position in this system. To get it, Hardy introduced a number of strong, unsupported assumptions (Hardy, 1908). It is known that the experiments of G. Mendel became the basis for the creation of genetics as a science. In this paper, for the first time, a mathematical model of G. Mendel's experiments on hybridization of plants with an arbitrary number of constant - distinct characters for any number of generations was constructed. This greatly expands the ability to determine the asymptotic nature of the sequence of experiments that G. Mendel could not afford. It has been shown that with an increase in the number of generations in a plant population, the number of phenotypes of organisms with different sets of genes quickly level up. With the increase in the number of generations and the absence of the death of organisms, these quantities increase synchronously, remaining almost equal to each other. This can be considered as establishing an equilibrium between plant phenotypes. In this case, the trajectories of the process in a multidimensional phase space with coordinates in the form of inverse quantities of phenotypes tend to an isolated stable equilibrium position of the node type at the origin.

If the death of organisms is possible, then equilibrium in general is achieved with final concentrations of the organisms. The book considers temporal and spatial dissipative structures in the systems of marine and oceanic phytoplankton and zooplankton, since plankton has a significant impact on the formation of climate on Earth. It is proved that the widespread mechanistic models of plankton, equating the mobility of individuals of the plankton population with the turbulent diffusion coefficient of seas and oceans, do not correspond to reality. It is shown that in violation of the processes of self - regulation between plankton populations, caused, for example, by eutrophication, the extinction regime of a population begins. Bifurcation analysis of the equations describing the spatial distribution of the concentrations of plankton components found that the most interesting area of the system parameters is a cloud in which the equilibrium position of plankton has two pairs of conjugate purely imaginary eigenvalues. See, the system of equations even after linearization in the neighborhood of the equilibrium position, in contrast to the problem considered by V. I. Arnold (Arnold, 1976) does not break up into two systems. There are no methods for analyzing such points in the modern theory of dynamical systems (Katok, & Hasselblat, 1999). These points were initially excluded from the analysis in the works of A. M. Lyapunov (Lyapunov, 1935), A. A. Andronov (Andronov and others, 1966, 1967), N. N. Bautin (Bautin, 1984).

A numerical study of trajectories in the four - dimensional phase space in a sufficiently large neighborhood of such equilibrium states revealed the existence of a strange attractor of previously unknown form (Zhizhin, 2005). It is a multilayer attractor, each layer of which is also a strange attractor with two characteristic points for a given layer, common to all trajectories of this layer. Each layer of the multilayer strange attractor corresponds to the dissipative structure of plankton, covering the surface of the aquatic environment.

It can be said that another important property of living systems, as it was established in the last monographs of author (Zhizhin, 2017, 2008), is the creation of a space of higher dimensionality due to the higher dimension of their constituent molecules. It should be emphasized that here we are not talking about Euclidean space, which by definition is infinite and three - dimensional. Based on the definition of the dimension of convex polytopes using the Euler – Poincaré formula (Poincaré, 1895), one can calculate the dimension of a convex body (in this case, a molecule), counting each atom (or functional group) as the vertices of the polytope. Then almost all compounds formed by chemical elements have the highest dimension (Zhizhin, 2017). This is especially important for biomolecules that have a complex structure. The geometry of B. Riemann is applicable here. In his famous lecture "On the Hypotheses that Lie at The Foundations of Geometry" (Riemann, 1854) he introduces the concept of n – extended manifold. It is essential, that n – dimensional extension it is determined by Riemann without introduction of infinite spaces.

Thus, the existence of closed objects of higher dimension (molecules) in a space of lower dimension does not contradict Riemann`s geometry, which assumes the boundedness of a space with a given dimension. Therefore, all studies in molecular biology in this work take into account this fact. The dimensions of the compounds of biogenic elements have been calculated, i.e. chemical elements present in living organisms and necessary for them to live. The dimensions of various types of biomolecules, including nucleic acid molecules, are calculated. A simplified three - dimensional model of this molecule and a simplified three - dimensional model of nucleic acids were built for the first time on the basis of a five - carbon sugar molecule model having dimension 12. This is important for visualizing the structure of nucleic acids. The calculations of the basic geometric characteristics of nucleic acid molecules according to this model are in good agreement with the experimental data obtained by Watson and Crick (1953). It has been proven that five - carbon sugar molecules bound by nitrogenous bases and located in two helices of one nucleic acid molecule (DNA or RNA) form a 13 - dimension polytope with anti - parallel edges. Moreover, this polytope has exactly 12 free coordinate planes in which exactly 12 possible compounds of nitrogenous bases can be located. Thus, the arrangement of nitrogenous bases in nucleic acids obtained a geometrical basis and specification. This circumstance translates the question of the genetic code into a space of higher dimension, which is considered in the last chapter of the monograph.

The concept of Big Data has become widespread in computer science in recent times (Kosrapohr, 2003; Hughes, 2011; Rodger, 2015). The higher dimensionality of molecules can be considered as an example of Big Data. Apparently, a description using spaces of higher dimensionality can be considered as an alternative to existing mathematical methods for solving problems in a domain Big Data.

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