History of Development of Evolutionary Methods in St. Petersburg School of Computer Simulation in Biology

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Abstract—The work presents a short history of development of evolutionary methods in the St. Petersburg school of computer simulation of biological processes. Several moments confirm priority of this school in modeling of micro- and macroevolutionary processes. A peculiarity of the school is a combination of the applied and theoretical study, penetration into the biological essence of phenomenon, consideration of real interrelationships of ecological and physiological parameters. The natural tendency for transition to modeling at the level of single individuals and then—to imitation of evolutionary processes on computer is traced. Paradoxically, such detalization sometimes does not worsen, but improves prognostic properties of models of populations, communities, and ecosystems, and besides, makes unnecessary monitoring of some variable characteristics, because the individual-based approach allows to direct account for adaptive processes and hidden evolutionary relationships between the life history parameters. Problems and perspectives of development of evolutionary methods of modeling are analyzed.

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INTRODUCTION

The goal of this work is to show development of computer simulation in the field of ecology and the inevitability and logicality of transition to evolutionary modeling. The authors restricted this consideration quite deliberately with analysis predominantly of St. Petersburg and to a lesser degree the Russian scientists as a whole by using foreign studies only to demonstrate general tendencies in development of cybernetic modeling in ecology and evolution. This does not mean at all that the considered examples in all cases were the key stages in development of the ecological modeling in general. In the complete volume, even the most superficial exposure of history of ecological modeling would have required a voluminous monograph. In international publications (see, for instance, [1]) references to works of the Russian authors are absent almost completely, so this essay is to fill this gap at least to some degree.

The phenomenon of the organic use of evolutionary methods in ecological modeling in frameworks of the St. Petersburg school is explained by the perspective basal structure of the models, which initially took into account life history parameters of biological populations, the ecological-physiological characteristics of organisms. In the beginning of this work, we present a popular, at the verbal level, description of this basic structure of models with element in the form of age group and trophic-ecological group. The second part
provides information about models with a single individual as the basic element whose development prepared basis for transition to evolutionary stochastic models. In the next part, information about models of evolutionary processes is completed by a brief description of a particular model of the macroevolutionary process Macrophylon. In Conclusion, the general pragmatic assessment of the role of ecological and evolutionary models in science and practice is presented.

MATHEMATICAL MODELS
OF POPULATIONS AND COMMUNITIES

Analytical models of populations and communities exhausted their prognostic possibilities very soon, and turned out to be poorly applicable for solution of practical problems. The use of computers has become the real breakthrough in ecological modeling. The first work of such type—the model of perch population in the Kherya-yarvi Lake (the Karelian Isthmus)—was carried out by Zhakov and Menshutkin [3]. This model had had attributes that subsequently became necessary for long years for each similar model: the block-scheme of the model and of the modeling algorithm (or a computer program), formulation of task in the form of a system of differential or finite-difference equations, identification of the model by data of independent natural observations. In such models the element usually is the age group, size group or sexual group of individuals. The processes described in the model represent reproduction, mortality, feeding, and sometimes foraging and spawning migrations. It is characteristic that the Canadian work of similar content and performed quite independently was published in 1964 [4].

The next stage in development of ecological modeling was the work of Krogius and coauthors [5]. The peculiarity of this work was that it was based on uninterrupted observations for 40 years in the Dalnee Lake (Kamchatka) on the state of population of the sockeye salmon that is of important marketable significance. The work was ordered by the USSR Ministry of Fishery, and its results were used in the course of work of the Soviet—Japanese Fishing Commission at setting of the fishing out quotas.

The approach designed by V.V. Menshutkin for modeling of dynamics of the fish populations and communities was developed by A.B. Kazanskii [6], the modeling algorithm being unified and presented in the form of standard operations with matrices. The algorithm was successfully used at creation of the fishery-ecological model of the fish community of the Tsymlyansk water reservoir and at creation of models of the fish populations in the water reservoirs of the Volga and Don Rivers [7, 8]. A peculiarity of these models is a possibility of taking into account the wide fluctuations of fish reproduction and feeding conditions, change of selectivity and rate of fishing, trophic interrelations in the community. These models were used for elaboration of rational fishery strategy of abundant fish species in water reservoirs, optimal fishery parameters were found as well.

In ecological models of the type considered above, both populations and communities and in principle the entire ecosystems are represented by superimposed connected structures with their basic elements. The age-related or stage structure of population with basic element—the age group or the stage of development of the individual allows to model dynamics of the superimposed generations. Structure of biomasses of the trophic-ecological groups, into which the individuals with similar trophic status are combined, is the more “large-block” one. With the aid of this structure, trophic relations are modeled, the energy and substance flows are calculated per one instrumental time step. Such method unites the energetic balance approach as, for instance, in phytocenology of productive hydrobiology [9], with the approach describing dynamics of the amount of generations of animal populations. The algorithm of calculation of flows of substance and energy in the models reminds the Bayes approach, when maximal requests of trophic groups are calculated with respect to different resources. All food requests are compared with real size of each resource and those who are requesting obtain the real amount of each resource with maintenance of laws of conservation of substance and energy. The real rations of individuals of the trophic-ecological group and the energy expenditures for metabolic processes determine real increments of individual mass per one time step.

The models of populations and communities of animals of considered type were used widely not