

Nikitina A. V. (Don State Technical University, Rostov-on-Don), **Dolgov V. V.** (Don State Technical University, Rostov-on-Don) **Research of the allelopathic interaction of hydrobionts based on a stochastic approach**

Currently, we can distinguish two main directions in the development of mathematical modeling, where quite constructive methods are proposed to compensate for a priori uncertainty arising from the non-stationary and stochastic nature of ecological systems. The first direction is a methodology for solving identification and verification problems as a sequential process of determining and refining numerical values of model coefficients. The second direction is related to the development of a strategy for finding the hidden patterns of the system under study and integrating them into the model. The aim of the study was to develop and numerically implement a mathematical model of biological kinetics that takes into account the movement of water flow, microturbulent diffusion, spatial distribution of nutrients, salinity, temperature, oxygen regime, complex bottom and coastline geometry. The model is designed to study the mechanism of external hormonal regulation of phytoplankton as well as allelopathic interaction of the Azov Sea hydrobionts, including the most common summer plankton species. Let us consider phytogetic factors: algae, being a part of various communities, experience a diverse influence of neighboring species and themselves have an impact on them. Relationships can be both direct (competition, symbiosis, epiphytism), and indirect - through microorganisms and animals, as well as through allelopathy. Allelopathy is understood as the effect of some autotrophic organisms on others through alteration of the environment by the release of their metabolites into it [1]. Algal metabolites include products of nitrogen and carbohydrate metabolism, highly specialized substances such as vitamins, growth agents, antibiotics, etc., which sometimes have high biological activity [2]. Such substances can act both as inhibitors and as stimulants. According to studies, the change of species in the community occurs as follows: when some species proliferate in the pond, they release enough inhibitors to suppress the development of other species of algae, which gradually die except for the individual more resistant representatives of each species. When the dominant algae disappears, probably as a result of autotoxins, its antibiotic effect ceases, and resistant representatives of other species begin to multiply rapidly [3]. Any hydrobiological environment is a large, complex, weakly deterministic and evolving object of study [4-6]. The theory of self-organization of models shows that the vast majority of processes in nature can be described, in particular, in the form of high-degree polynomials, which are a special case of the generalized Kolmogorov-Gabor polynomial:

$$y = a_0 + \sum_{i=1}^n a_i x_i + \sum_{i=1}^n \sum_{j=1}^n a_i a_j x_i x_j + \sum_{i=1}^n \sum_{j=1}^n \sum_{k=1}^n a_i a_j a_k x_i x_j x_k.$$

The number of terms of the complete polynomial is C_{m+q}^q where m is the number of variables and q is the degree of the polynomial. Therefore, the main task of modeling complex systems using regression equations is to exclude a subset of "superfluous" uninformative coefficients in the polynomial and to preserve the combination of "explanatory terms" [7]. The difference scheme for the homogeneous equations presented in the mathematical model of biological kinetics of a shallow water body (using the example of the Azov Sea) will be written in the form:

$$\frac{C^{n+1} - C^n}{\tau} + A_x C^n + A_y C^n + A_z C^{n+\sigma} = 0, \quad (1)$$

where C - impurity concentration; τ - time increment; n - time layer number; σ - layout weight, $\sigma \in [0, 1]$; A_x, A_y, A_z - discrete analogs of transfer operators along coordinate directions Ox, Oy, Oz :

$$(A_x C)_i = u_{i+\frac{1}{2}} \frac{C_{i+1} - C_i}{2h_x} + u_{i-\frac{1}{2}} \frac{C_i - C_{i-1}}{2h_x} - \mu_{i+\frac{1}{2}} \frac{C_{i+1} - C_i}{h_x^2} + \mu_{i-\frac{1}{2}} \frac{C_i - C_{i-1}}{h_x^2}, 0 \leq i \leq N,$$

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where i – discretization index, h_x – step of spatial variable; N – number of steps, μ – diffusion coefficient; u – water flow velocity. Discrete operators A_y, A_z are written in the same way.

When using a difference scheme of the form (1), the problem of biological kinetics is solved by direct methods, and in the case of regions for which the linear size in one direction is significantly smaller than in the remaining ones, the time step can be taken much larger, which makes it possible to speed up the prediction of changes in impurity concentrations.

Theorem. When the condition $\tau \leq \left(\max \left(\frac{2\mu}{h_x^2} + \frac{2\mu}{h_y^2} \right) \right)^{-1}$ is met, then the difference scheme is conditionally stable, and we have the estimate $\|C^{n+1}\| \leq \|C^0\|$.

During statistical processing of field data for the numerical implementation of the mathematical model of biological kinetics, coefficients of asymmetry, kurtosis, variance, standard deviation, and coefficient of variation were calculated.

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