Numerical implementation of biological kinetics multi-species model in the Azov Sea

A I Sukhinov¹, A V Nikitina²,³,⁴, A A Filina³,⁴, A L Leontyev²,³,⁴

¹Don State Technical University, Gagarina ave 16 Rostov-on-Don, Russia, 344002
²Southern Federal University, Bolshaya Sadovaya street 105/42, Rostov-on-Don, Russia, 344006
³Science and Technology University “Sirius”, Olimpijskiy ave. 1, Sochi, Russia, 354340
⁴Supercomputers and Neurocomputers Research Center, Italyansky lane, 106, Taganrog, Russia, 347900

Abstract. Paper covers the research of biological kinetics processes based on a multi-species model of plankton and fish interaction of the Azov Sea at low and high size considering the Verhulst and Allee effects, competition for resources, taxis, catching, spatial distribution of biogenic matter and detritus. Discrete analogue of developed model problem of water ecology, included in a software complex, were calculated using schemes of increased order of accuracy considering the partial filling of computational cells. The system of grid equations of large dimension, arising at discretization, has been solved on the basis of a two-layer variational type method – the minimum corrections method having the maximum convergence rate. Effective parallel algorithms were developed for numerical implementation of biological kinetics problem and oriented on multiprocessor computer system and NVIDIA Tesla K80 graphics accelerator with the data storage format modification of. Due to it, the reproduction processes of biogeocenose populations have been analysed in real and accelerated time.

1. Introduction
Shallow waters, such as the Azov Sea, are particularly strongly affected by anthropogenic pressure, associated with the construction of hydrotechnical facilities, various types of pollution. It led to the emergence of environmental processes that violate the conditions of sustainable development of water. The experimental research of biological kinetics processes is based on large scale experiments with the marine ecosystem and is not only extremely expensive, but also dangerous in terms of consequences. Therefore, the creation of mathematical and software-algorithmic tools for predictive modeling of significant spatial hydrobiological processes and use the data from relatively inexpensive experiments that do not have a negative impact on the ecosystem is relevant for today.

The development of concepts for research aquatic ecosystems involved many scientists such as Lotka A.J., Volterra V., Svirezhev Yu.M., Logofet D.O., Abakumov V.A. [1], Konstantinov A.S., Vinberg G.G. [2], Odum H.T. [3], Rosenberg G.S [4]. Methods for assessing the results of hydrobiological monitoring were developed by Makrushin A.V., Bakanov A.I., Mordukhay-Boltovskoi D.D., Tansley A.G., Rozenzweig M.L., MacArthur R.H., Luck R.F. [5], Berryman A.A. Nonlinear effects of biological populations’ interaction in water were researched...
Ichthyological researches of fish population dynamics are practically important and theoretically complex areas of mathematical modeling. According to the Azov Research Institute of fisheries (AzNIIRKH), commercial fishing of pelengas, bream and walleye was prohibited in the Azov Sea waters in August 2018. There are only three species of commercial fish out of 40 commercial fish: the sardelle, the goby and the hamsa. Extinction is due to sea pollution and uncontrolled fishing.

Several researches at mathematical modelling of hydrophysical and biological kinetics processes are devoted to the parallel implementation of problems in this class. Many packages use simplified models of hydrobiological processes for water objects with the slightly varying salinity, and, in most cases, with the varying depth; do not provide the operational forecasts of the environmental situation of shallow waters after the disaster; can not be replicated to other aquatic ecosystems, as focused on the description of biogeochemical cycles and species composition of biological plankton populations and their interactions in single water objects. Although the conditions for the development of catastrophic and unfavorable phenomena in shallow waters, it is necessary to predict the development of such phenomena and make decisions within tens of minutes – units of hours. In turn, it requires the simulation of hydrobiological processes on multiprocessor computer systems in the accelerated time mode.

Universal packages for modeling hydrobiological processes (FlowVision, FLUENT, GAS DYNAMICS TOOL, PHOENICS, Star-CD, etc.) are focused on multiprocessor systems, but it versatility is to use the limited number of models, algorithms and methods to variety of different cases. Only separate modules of specialized software (ECOSIM and MAQSIP), oriented on multiprocessor systems, are parallelized.

For complex geoinformation analysis of spatial-temporal processes and phenomena the expedition data [7], the data of the Unified State System of Information on the Situation in the World Ocean ("ESIMO") portal were used for modeling hydrobiological processes in the Azov Sea.

2. Problem statement
According to the literature [8, 9], biological purification of water can be performed by valuable pelengas commercial fish stocking. A multi-species model of interaction between plankton and pelengas commercial fish was developed to research nonlinear effects in the dynamics of biogydrocenosis of a shallow water (Azov Sea). It considers the spatially inhomogeneous distribution of Coscinodiscus diatoms, Copepod zooplankton, and based on the models by Rosenzweig M.L., MacArthur R.H., Ginzburg V.L., Ricker W.E. [10], Holling K.S., Arditi R., Tyutyunov Yu.V. [11], Kosyan R.D., Pryakhin Yu.V.:
substance under the gravity, $i \in \overline{1,4}$; $g_i$ are trophic functions for substances $i \in \overline{1,5}$. Let assume that $g_1(S_1,S_3) = \gamma_1 \alpha_3 S_1 S_3$, $g_2(S_1,S_2) = \gamma_2 \delta_1 S_1 S_2$, $g_3(S_1,S_3) = \alpha_3 S_1 S_3$, $g_4(S_4,S_5) = \beta_4 S_4 S_5$, $g_5(S_1,S_4,S_5) = (\gamma_5 \beta_4 S_1 + \xi_5 \sigma_1 S_1) S_5$, where $\alpha_3$ is the consumption ratio of $S$ by phytoplankton; $\gamma_1, \gamma_2, \gamma_5$ are transfer coefficients of trophic functions; $\gamma_3$ is a fraction of $S$ in the biomass of $X$; $\lambda_1$ is the coefficient taking into account the mortality and metabolism of $X$; $\delta_1$ is the loss of $X$ by eating out of $Z$; $\lambda_2, \lambda_5$ are elimination (mortality) rates of $Z, P$ respectively; $\delta_2$ is the loss of $Z$ by eating out of fish; $\delta_5$ is the loss of $P$ by eating out of fish and catching; $\tilde{S}_3$ is the maximum possible concentration of $S$; $f = f(t,x,y,z)$ is the function of pollution source; $B$ is the specific rate of $S$ receipt; $\lambda_4$ is the decomposition ratio of detritus; $\beta_4$ is the consumption rate of organic residues of $P$; $\sigma_1$ is the loss ratio of $X$ as a result of consuming it by $P$; $\xi_5$ is the transfer coefficient of concentration growth of $P$ due to $X$; $\mu_i, \nu_i$ are diffusion coefficients in horizontal and vertical directions of substances, $i \in \overline{1,5}$.

The computational domain $\bar{G}$ (Azov Sea) is a closed area bounded by the undisturbed water surface $\Sigma_0$, the bottom $\Sigma_H = \Sigma_H(x,y)$ and the cylindrical surface $\sigma$ for $0 < t \leq T_0$. $\Sigma = \Sigma_0 \cup \Sigma_H \cup \sigma$ is a piecewise smooth border of $G$; $n$ is the surface normal vector; $U_n$ is a normal component of the water velocity vector with respect to the $\Sigma$.

Let’s define the initial conditions

\[ S_i|_{t=0} = S_{i0}(x,y,z), \quad i = \overline{1,5} \]  

and boundary conditions:

\[ S_i = 0 \text{ if } U_n < 0, \quad \frac{\partial S_i}{\partial n} = 0 \text{ if } U_n \geq 0 \text{ on } \sigma; \quad \frac{\partial S_i}{\partial z} = \phi(S_i) \text{ on } \Sigma_0; \quad \frac{\partial S_i}{\partial z} = -\varepsilon_i S_i \text{ on } \Sigma_H, \]  

where $\varepsilon_1, \varepsilon_2, \varepsilon_3, \varepsilon_4, \varepsilon_5$ are non-negative constants; $\varepsilon_1, \varepsilon_3, \varepsilon_5$ take into account the lowering of plankton and fish to the bottom and their flooding; $\varepsilon_2, \varepsilon_4$ take into account the absorption of nutrients and detritus by bottom sediments; $\phi$ is a given function.

The developed model (1) – (3) considers the convective transport, microturbulent diffusion, deposition of substances under gravity, the influence of salinity and temperature of water environment, plankton and fish taxis, catch. As input data for model (1) – (3) we used the results of calculations on the model of the Azov Sea hydrodynamics [12, 13] considering wind impact, river flows (Don, Kuban, Mius and about 40 small watercourses), water exchange with other waters, bottom relief, complex shape of the coastline, friction on the bottom, temperature, salinity, evaporation and precipitation, Coriolis force.

3. Research the nonlinear effects of biogeocenose dynamics of shallow water

One of the most characteristic properties of biological objects is a wide range of nonlinear effects, within which the system functions normally [14]. The most important property of water ecosystems is the high velocity of biotic cycle. This is facilitated by both the mobility of water environment, mixing, conditions favourable for bacterial decomposition, dissolution and distribution of mineralization products, and intensive exchange due to the small size of producers (phytoplankton) and enzymes (zooplankton, fish).

The taxis of pelagic (living in the water column) fish was considered explicitly at modeling, since it determines the movement of fish crowding in water area at any scale. The effect of such wanderings on the collective taxis is analogous to the effect of turbulent velocity pulsations on large-scale fluid flow. It can be considered as a kind of diffusion in the equation for the pelengas feed taxis. We added the following equation to the system (1) – (3):

\[ \frac{\partial u_5}{\partial t} + div (U_5 u_5) = \mu_5 \Delta u_5 + \frac{\partial}{\partial z} \left( \nu_5 \frac{\partial u_5}{\partial z} \right) - \alpha_5 u_5 + k_1 grad S_1 + k_4 grad S_4, \]  

(4)
where $U_5 = u + u_5$ is the rate of convective pelengas transfer; $u_5$ is the velocity of fish movement relative to the water; $k_1, k_4$ are taxis coefficients; $\mu_a, \nu_a$ are coefficients of horizontal and vertical diffusion component of taxis velocity; $\alpha_a$ is coefficient of inertial motion of fish.

For rational use, population prediction, identification of limiting factors, protection and restoration of shallow water biogeoecenoses populations, it is necessary to consider such important factors as the Allee effect. It based on two fundamental Liebig and Shelford laws of ecology about limiting factors. According to the Liebig law, the limiter is the limiting factor, which is in the minimum; the Shelford law – in a maximum. Various types of demographic processes were researched, including the Verhulst (the logistic curve) and the “Allee” population. Table 1 shows the main functional forms used at mathematical modeling of the water biogeoecenose evolution considering the limiting different factors ($C$ is the salinity; $T$ is the temperature; $I$ is the illumination; $P$ is a spawning stock; $r_\mu$ is a constant; $\alpha_0$ is a phytoplankton growth rate at 0°C (0,8); $L, k, SSBO$ are parameters of the Allee effect degree (at low population densities)).

| Table 1. Functional forms of ecosystem productivity (Stock-Recruitment (SR) models) |
|-----------------------------------------------|---------------|---------------------------------|
| **Name** | **Expression** | **Source** |
| **Ricker model** | $\mu(P) = a \cdot P \cdot \exp(-bP)$, $a$ is related to productivity (recruits per stock unit at small stock size), $b$ – to density dependence ($a, b > 0$) | Ricker W.E., 1954 |
| **Bevorton-Holt and Myers SR model** | $\mu(P) = \frac{aP}{(1+bP)}$, $a$ is the maximum recruitment (asymptotically), $b$ is the stock level to produce half of maximum recruitment ($a, b > 0$) | Beverton R.J.H., 1957; Holt S.J., 1988; Myers R.A., 1995 |
| **Saila-Lorda, Cabral SR model** | $\mu(P) = a \cdot P^c \cdot e^{-bP}$, $a, b, c$ are given parameters | Saila S., 1988; Cabral R.B., 2010 |
| **Eppley, Gin SR models** | $\mu(T) = \mu_0 \cdot \exp(r_\mu T)$, $\mu_0$ is a specific rate of phytoplankton growth at 0°C | Eppley R.W., 1972; Gin K.Y.H et.al., 1998 |
| **Sidko SR model** | $\varphi(I) = (bI + c^2)^{1/2} - aI - c$, $a, b, c$ are given parameters | Sidko F.Y. et.al., 1975 |
| **Belyanin model** | $\varphi(I) = \varphi_0 (1 - e^{\exp(-I/b)} / (1-aI))$, $\varphi_0, a, b$ are given parameters | Belyanin V.N. et.al., 1980 |
| **Dombrovsky SR model** | $\mu(\varphi) = \mu_0 \cdot \exp \left[ \frac{-((\varphi - \varphi_{opt})/\sigma_{\varphi})^2 - \mu_1 \varphi + \mu_2}{\sigma_{\varphi}} \right]$, $\varphi \in \{C, T\}$, $\mu_0, \sigma_{\varphi}, \mu_1, \mu_2$ are given parameters | Dombrovsky Yu.A., 1990 |
| **Fennell Model** | $\mu(T, I) = a_0 \cdot \exp(aT)(I/I_0) \exp(1-I/I_{opt})$, $a$ is an empirical coefficient | Fennell D.A., 1999 |
| **Logistic dependence considering the Allee effect** | $R(SSB) = \frac{L}{\{1 + \exp(-k(SSB - SSBO))\}}$ is the mass of fish capable for producing the offspring in the environment with a limited capacity | Vaskilyeva N.A., Vladimirov A.A., Winter A.M., 2017 |

In [14], nonlinear effects arising in the model of the age structure of commercial fish populations were analysed. To research the weak or strong Allee effect, it is necessary to analyse the intensity of commercial fish catch and select its threshold value, at which collapse is impossible (see Figure 1). Intensive commercial fishing near the coast of Canada led to the
collapse of the cod population in 1992 [6].

The increased fishing load on this facility since 2000, especially in winter, has also had a significant impact. The demographic Allee effect is due to the properties of the population itself and always manifests if its population is low. This effect can occur due to the characteristics of the food chain, as well as under the influence of external factors, including the salinity, temperature and illumination. On the basis of the developed ichthyological model (1) – (3), the Verhulst kinetics was researched under different initial conditions (2) (see Figure 2).

4. Solution method
Each equation of the system (1) – (3) after linearization was represented as the convection-diffusion equation. For numerical implementation of the discrete mathematical model we used a uniform grid. Schemes considering the partial filling of computational cells were used for model discretization with boundary conditions [15, 16]. The adaptive modified alternately triangular variational method (MATM) obtained on the basis of scheme, was used to solve the obtained grid equations [16, 17].

For numerical implementation of the developed biological kinetics model (1) – (3), a parallel algorithm oriented on a multiprocessor computer system (MCS) was developed. NVIDIA Tesla K80 graphics accelerator was used to improve the efficiency of the algorithm of numerical implementation of the set multi-species model of biogydrocenosis interacting populations.

We describe parallel algorithms with various types of domain decomposition for solving problems (1) – (3) on MCS. Parallel algorithms for the MATM were implemented on MCS of the Southern Federal University (SFU). MCS technical parameters: the peak performance is 18.8 TFlops; 8 computational racks; the computational field of MCS is based on the HP BladeSystem c-class infrastructure with integrated communication modules, power supply and cooling systems; 512 single-type 16-core HP ProLiant BL685c Blade servers are used as computational nodes, each of which is equipped with four 4-core AMD Opteron 8356 2.3 GHz processors and 32 GB RAM; the total number of computational nodes is 2048; the total amount of RAM is 4 TB.

The k-means method was used for geometric partition of computational domain for the uniform loading of MCS calculators (processors). It based on the minimization of the functional of the total variance of the element scatter (nodes of computational grid) relative to the gravity center of subdomains. Let $X_i$ is a set of computing grid nodes included in the $i$-th subdomain, $i \in \{1, ..., m\}$, $m$ is a given number of subdomains. $Q = \sum_i \frac{1}{|X_i|} \sum_{x \in X_i} d^2(x, c_i) \to min$, where $c_i = \frac{1}{|X_i|} \sum_{x \in X_i} x$ is the center of subdomain $X_i$, and $d(x, c_i)$ is distance between the computing
grid node \( x \) and the center of subdomain \( c_i \) in the Euclidean metric. The k-means method is convergent only when all subdomains are approximately equal.

Figure 3 shows the result of the k-means method application for model two- and three-dimensional domains.

![Figure 3](image)

**Figure 3.** Domain decomposition for the k-means method into 150 (two-dimensional domain) (a) and 10 subdomains (three-dimensional domain) (b); data transfer between neighbouring subdomains (c).

Theoretical estimates of the acceleration and efficiency of the developed parallel algorithm:

\[
E^t = \frac{S^t}{p} = \chi \left\{ 1 + \left( \sqrt{p} - 1 \right) \left( \frac{36}{50N_z} + \frac{4p}{50t_0} \left( t_a \left( \frac{1}{N_x} + \frac{1}{N_y} \right) + t_x \sqrt{\frac{p}{N_xN_y}} \right) \right) \right\}
\]

where \( \chi \) is the ratio of the number of computing nodes to the total number of nodes (computing and fictitious); \( p \) is the total number of processors; \( t_0 \) is the execution of an arithmetic operation; \( t_x \) is the response times (latency); \( N_x, N_y, N_z \) are the number of nodes in the spatial directions.

Results of parallel implementation the proposed algorithm for solution the problem (1) – (3) were compared and presented in Table 2, where \( t, S, E \) are operating time, acceleration and efficiency of the algorithm; \( S^t, E^t \) are theoretical estimates of the acceleration and efficiency of the algorithm.

| \( p \) | \( t, s \) | \( S^t \) | \( S \) | \( E^t \) | \( E \) | \( p \) | \( t, s \) | \( S^t \) | \( S \) | \( E^t \) | \( E \) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1  | 6.073 | 1.0 | 1.0 | 1.0 | 1.0 | 3.121 | 1.181 | 1.946 | 0.59 | 0.973 |
| 4  | 1.811 | 2.326 | 3.354 | 0.582 | 0.839 | 8  | 0.997 | 4.513 | 6.093 | 0.654 | 0.762 |
| 16 | 0.620 | 8.520 | 9.805 | 0.533 | 0.613 | 32 | 0.317 | 15.344 | 19.147 | 0.48  | 0.598 |
| 64 | 0.184 | 25.682 | 33.018 | 0.401 | 0.516 | 128 | 0.117 | 39.013 | 51.933 | 0.305 | 0.406 |

The estimation for comparing the efficiency values of algorithms (\( E_{(1)} \) is the efficiency of the standard algorithm; \( E_{(2)} \) is the efficiency of the algorithm based on the k-means) has the form:

\[
a = \sqrt{\frac{\sum_{k=1}^{n} (E_{(2)k} - E_{(1)k})^2}{\sum_{k=1}^{n} E_{(2)k}^2}}.
\]

We obtained that the efficiency was increased on 10 – 20% using the algorithm based on the k-means method for solving the problem (1) – (3), compared to the standard algorithm.

For the numerical implementation of the proposed interrelated mathematical model of biological kinetics, we developed parallel algorithms which will be adapted for hybrid computer
systems using the NVIDIA CUDA architecture. The NVIDIA Tesla K80 computing accelerator has the high computing performance and supports all modern closed (CUDA) and open (OpenCL, DirectCompute) technologies. The NVIDIA Tesla K80 specifications: the GPU frequency of 560 MHz, the GDDR5 video memory of 24 GB, the video memory frequency of 5000 MHz, the video memory bus digit capacity is equalled to 768 bits. The NVIDIA CUDA platform characteristics: Windows 10 (x64) operating system, CUDA Toolkit v10.0.130, Intel Core i5-6600 3.3 GHz processor, DDR4 of RAM 32 GB, the NVIDIA GeForce GTX 750Ti video card of 2GB, 640 CUDA cores.

Using the GPU with the CUDA technology is required to address the effective resource distribution at solving the system of linear algebraic equations (SLAE). The dependence of the SLAE solution time on the matrix dimension and the number of nonzero diagonals was obtained to implement the corresponding algorithm (see Figure 4).

![Figure 4](image_url)

**Figure 4.** The dependence of the SLAE solution time on the matrix dimension and the number of nonzero diagonals.

Due to this, in particular, we can choose the grid size and to determine the SLAE solution time based on the number of nonzero matrix diagonals.

The solution of biological kinetics problem (1) – (3) by the finite difference method (FDM) on uniform grids leads to the necessary operate with sparse matrices, elements of which are a repeating sequence for internal nodes. In the case of high-dimensional problems, this leads to inefficient memory consumption [31]. Using the Compressed Sparse Rows (CSR) matrix storage format excludes the need to store their null elements. However, all nonzero elements, including many repeating ones, are stored in the corresponding array. This drawback is not critical when using computing systems with shared memory. In heterogeneous and distributed computing systems, it can adversely affect the performance at when data transferring between the nodes.

We performed a modification of the CSR format to improve the efficiency of data storage with a repeating sequence of CSR1S elements for modeling continuous biological kinetics processes by the finite difference method. In this case, it is enough to just change them in an array that preserves a repeating sequence to change the differential operator, instead of repeatedly finding and replacing values of non-zero elements in an array. The required memory capacity in CSR and CSR1S formats:

\[
P_{\text{csr}} = N_{\text{nz}}B_{\text{nz}} + (N_{\text{nz}} + R + 1)B_{\text{idx}},
\]

\[
P_{\text{csr1s}} = B_{\text{nz}}[N_{\text{nz}}(k_i + 1) - N_{\text{seq}}(k_{\text{r}}k_{\text{r}}R + k_{\text{r}}R + 1) - k_i(k_{\text{r}}R - R - 1)],
\]

\[
k_{\text{r}} = R_{\text{seq}}/R, k_i = B_{\text{idx}}/B_{\text{nz}},
\]

where \(R\) is the number of matrix rows; \(R_{\text{seq}}\) is the number of matrix rows that contain a repeating sequence of elements; \(N_{\text{nz}}\) is number of non-zero matrix elements; \(N_{\text{seq}}\) is the number of elements.
in a repeating sequence; $B_{nz}$ is the memory capacity to store one non-zero element; $B_{idx}$ is the memory capacity to store one index. The graphs of the dependence of the matrix conversion time from CSR1S to CSR format by the sequential (a) and parallel (b) algorithms from $k_r$ and $N_{seq}$ are shown in Figure 5.

![Figure 5. The runtime of the matrix conversion from CSR1S to CSR format.](image)

The analysis of CUDA architecture characteristics showed the algorithm applicability for the numerical implementation of the developed mathematical model of hydrobiological processes to design high-performance information systems.

5. Description of software complex

The “Azov3D” software complex (SC) was developed for solving the biological kinetic problem to research Allee and Verhulst effects [18] with implementation on MCS and graphic accelerator. The SC includes the following modules: control module, oceanological and meteorological databases, application library for solving hydrobiology grid problems, integration with various geoinformation systems (GIS), Global Resource Database (GRID) for geotagging and access to satellite data collection systems, NCEP/NCAR Reanalysis database.

The use of GIS provides additional possibilities for more qualitative and complex spatial analysis, and solutions based on it are more accurate. The problem was solved on a high-performance computer system [19] capable for performing a large amount of complex calculations and huge data processing in limited time.

Calculation results of pollution biogenic substance concentration ($S_3$) for the model problem of biogeocenose evolution of shallow water (1) – (3) are given in Figure 6(a), and changes of phytoplankton concentration ($S_1$) – in Figure 6(b) (the initial distribution of water flow fields for the northern wind). Parameter values: $\mu_3 = 5 \cdot 10^{-10}$; $\nu_3 = 10^{-10}$; $B = 0.001$; $\tilde{S}_3 = 1$; $f = 3$; $\tau_i = 0.1$; $i \in \{1, 5\}$; $\lambda_2 = 0.8$; $\mu_1 = 5 \times 10^{-11}$; $\nu_1 = 10^{-11}$.

![Figure 6. Distribution of the nutrients (a) and phytoplankton (b) concentrations.](image)

Using the developed SC, we researched the mechanism of suffocation areas in shallow waters [20, 21]. Simulation results of possible development scenarios of the Azov Sea ecosystem (changes...
of pelengas commercial fish concentration) are given in Figures 7, 8 (the initial distribution of water flow fields for the northern wind direction). The time intervals in Figure 7: a) T=26 days, b) T=62 days; in Figure 8: a) T=25 days, b) T=76 days. The maximum values of pelengas and detritus concentrations indicate by white colour. Parameter values: \( \mu_4 = 5 \times 10^{-11} \); \( \nu_4 = 10^{-11} \); \( \varepsilon_4 = 1.9 \times 10^{-5} \); \( \beta_4 = 0.1 \); \( \lambda_4 = 0.4 \); \( \mu_5 = 1.5 \times 10^{-3} \); \( \nu_5 = 1.6 \times 10^{-3} \); \( \gamma_5 = 0.125 \); \( \lambda_5 = 1.16 \times 10^{-3} \); \( \xi_5 = 0.8 \); \( \varepsilon_5 = 0.47 \); \( \delta_5 = 0.05 \).

![Figure 7. Distribution of the detritus concentration.](image1)

![Figure 8. Distribution of the pelengas concentrations.](image2)

Using the results of numerical experiments, we can analyse the possible scenarios of Azov Sea water stocking by the pelengas involved in a bottom-land reclamation areas of detritus accumulation. According to the presented results, there is a decrease of detritus concentration at the value of time interval, starting from 61 days. This means the decreasing of bottom sediments concentration in the Central-Eastern part of the Azov Sea. It ultimately will lead to decrease the suffocation areas and improve the water quality in this water basin.

Based on the developed special software, we can explore problems about acclimatization of pelengas on the environmental regime of shallow water, as well as to assess the specificity of water conditions. This will excludes the unforeseen negative technological impacts and plan the increasing of this fish production. Analyzing the obtained results, we can conclude the properties of the detritus-pelengas mathematical model and possibilities to water quality management of shallow waters, such as the Azov Sea, using the methods of mathematical modeling.

6. Conclusions
The analysis of nonlinear effects in biological kinetics processes, considering the Verhulst and Allee effects, competition for resources, taxis, catch, spatial distribution of nutrients and detritus, was performed on the basis of a multi-species model of interaction between plankton and pelengas commercial fish. Due to this, we researched the influence of competition for resources, features of the food chain, biotic and abiotic factors on the water reproduction processes. Discretization of the developed water ecology model problem, as the part of software, was performed on
the basis of schemes of second order of accuracy taking into account the partial filling of computational cells. It allowed to significantly reduce the solution error in the computational domain of complex shape. The comparative analysis of two-layer methods of variational type was performed. MATM was used as the main method for solution the system of grid equations arising at discretization in view of its highest convergence rate. Effective parallel algorithms were developed for the numerical implementation of biological kinetics problem and oriented on multiprocessor computer system and graphics accelerator. Due to this, the hydrobiological processes have been analyzed in real and accelerated time.

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