

Multi-species model of interacting biological populations of shallow water

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Abstract. Paper covers research of biological processes kinetics 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 using 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 by Berdnikov S.V., Tyutyunov Yu.V., Perevarukha A.Yu [6], Stephens P.A., Sutherland W.J., Arditi R., Zhou S.-R., Liu Y.-F., Wang G.

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 of 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; cannot be replicated to other aquatic ecosystems, as focused on the description of the 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 forecast 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 its versatility is to use the limited number of models, algorithms and methods to variety of different cases. Only separate modules of specialized software (ECOSIM и 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 biogeoecology of a shallow water (Azov Sea). It considers the spatially inhomogeneous distribution of *Coscinodiscus* diatoms, Copepod zooplankton, and based on the models of 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.:

$$\begin{aligned} \frac{\partial S_i}{\partial t} + \operatorname{div}(\mathbf{U}S_i) &= \mu_i \Delta S_i + \frac{\partial}{\partial z} \left(v_i \frac{\partial S_i}{\partial z} \right) + \psi_i, \psi_1 = g_1(S_1, S_3) - \delta_1 S_1 S_2 - \lambda_1 S_1 - \sigma_1 S_1 S_5, \\ \psi_2 &= g_2(S_1, S_2) - \lambda_2 S_2 - \delta_2 S_2, \psi_3 = \gamma_3 \lambda_4 S_4 - g_3(S_1, S_3) + B(\tilde{S}_3 - S_3) + f, \\ \psi_4 &= \lambda_1 S_1 - g_4(S_4, S_5) + \lambda_2 S_2 - \lambda_4 S_4, \psi_5 = g_5(S_4, S_5) - \lambda_5 S_5 - \delta_5 S_5, \end{aligned} \quad (1)$$

where S_i is the concentration of i -th component, $i = \overline{1,5}$; ψ_i is a chemical-biological source (runoff) or a term describing aggregation (conglutination-unconglutination) if the corresponding component is a suspension, i is a type of substance, $i = \overline{1,5}$: 1 is the phytoplankton concentration (*Coscinodiscus*) (X), 2 is the zooplankton (*Copepod*) (Z), 3 is the nutrient (S), 4 is the detritus (D), 5 is the pelengas (*Mugil soiuy Basilewsky*) (P); \mathbf{u} is the velocity field of water flow; $\mathbf{U} = \mathbf{u} + \mathbf{u}_{0i}$ is the rate of convective mass transfer; \mathbf{u}_{0i} is the deposition rate of i -th substance under the gravity, $i \in \overline{1,4}$; g_i are trophic functions for substances $i \in \overline{1,5}$. Let assume that $g_1(S_1, S_3) = \gamma_1 \alpha_3 S_1 S_3$, $g_2(S_1, S_2) = \gamma_2 \delta_1 S_1 S_2$, $g_3(S_1, S_3) = \alpha_3 S_1 S_3$, $g_4(S_4, S_5) = \beta_4 S_4 S_5$, $g_5(S_1, S_4, S_5) = (\gamma_5 \beta_4 S_4 + \xi_5 \sigma_1 S_1) S_5$, where α_3 is the consumption ratio of S by phytoplankton; $\gamma_1, \gamma_2, \gamma_5$ are transfer coefficients of trophic functions; γ_3 is a fraction of S in the biomass of X; λ_1 is the coefficient taking into account the mortality and metabolism of X; δ_1 is the loss of X by eating out of Z; λ_2, λ_5 are elimination (mortality) rates of Z, P respectively; δ_2 is the loss of Z by eating out of fish; δ_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; λ_4 is the decomposition ratio of detritus; β_4 is the consumption rate of organic residues of P; σ_1 is the loss ratio of X as a result of consuming it by P; ξ_5 is the transfer coefficient of concentration growth of P due to X; μ_i, v_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 Σ_0 , the bottom $\Sigma_H = \Sigma_H(x, y)$ and the cylindrical surface σ for $0 < t \leq T_0$. $\Sigma = \Sigma_0 \cup \Sigma_H \cup \sigma$ is a piecewise smooth border of G , \mathbf{n} is the surface normal vector; \mathbf{U}_n is a normal component of the water velocity vector to the Σ .

Let's define initial conditions

$$S_i|_{t=0} = S_{i0}(x, y, z), \quad i = \overline{1,5} \quad (2)$$

and boundary conditions:

$$S_i = 0 \text{ on } \sigma \text{ if } \mathbf{U}_n < 0; \frac{\partial S_i}{\partial \mathbf{n}} = 0 \text{ on } \sigma \text{ if } \mathbf{U}_n \geq 0; \frac{\partial S_i}{\partial z} = \varphi(S_i) \text{ on } \Sigma_0; \frac{\partial S_i}{\partial z} = -\varepsilon_i S_i \text{ on } \Sigma_H, \quad (3)$$

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; φ is the 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):

$$\frac{\partial \mathbf{u}_5}{\partial t} + \text{div}(\mathbf{U}_5 \mathbf{u}_5) = \mu_u \Delta \mathbf{u}_5 + \frac{\partial}{\partial z} \left(\nu_u \frac{\partial \mathbf{u}_5}{\partial z} \right) - \alpha_u \mathbf{u}_5 + k_1 \text{grad} S_1 + k_4 \text{grad} S_4, \quad (4)$$

where $\mathbf{U}_5 = \mathbf{u} + \mathbf{u}_5$ is the rate of convective pelengas transfer; \mathbf{u}_5 is the velocity of fish movement relative to the water; k_1, k_4 are taxis coefficients; μ_u, ν_u are coefficients of horizontal and vertical diffusion component of taxis velocity; α_u is coefficient of inertial motion of fish.

For rational use, population prediction, identification of limiting factors, protection and restoration of populations of shallow water biohydrocenosis, it is necessary to consider such important factor as the Allee effect. It based on two fundamental laws of ecology about limiting factors: by Liebig and Shelford. 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 ferhulst (logistic population) and the “Allee” population. Table 1 shows the main functional forms used at mathematical modeling of the biogeocenose evolution of water considering limiting different factors (C is the salinity, T is the temperature, I is the illumination).

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 itself when 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 salinity, temperature and illumination. On the basis of the developed ichthyological model (1) – (3), Verhulst kinetics was researched under different initial conditions (2) (see Figure 2).

Table 1. Functional forms of the productivity of ecosystems (Stock-Recruitment (SR) models).

Name	Expression	Source
Ricker SR model	$\mu(P) = a \cdot \bar{P} \cdot e^{-b\bar{P}}$, \bar{P} – spawning stock; a is related to productivity (recruits per stock unit at small stock size) and b to density dependence. ($a, b > 0$)	Ricker W.E., 1954
Beverton-Holt and Myers SR model	$\mu(P) = \frac{a \cdot \bar{P}}{(1+b \cdot \bar{P})}$, a is the maximum recruitment (asymptotically) and b is the stock level needed to produce the half of maximum recruitment ($a, b > 0$)	Beverton R.J.H. and Holt S.J., 1957; Myers R.A., 1995
Saila-Lorda, Cabral SR model	$\mu(P) = a \cdot \bar{P}^c \cdot e^{-b\bar{P}}$, a, b, c are given parameters	Saila S., 1988; Cabral R.B., 2010
Eppley, Gin SR models	$\mu(T) = \mu_0 \exp(r_\mu T)$, μ_0 is the specific rate of phytoplankton growth at 0°C, r_μ is a constant	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 SR model	$\varphi(I) = \varphi_0(1 - \exp(-I/b))/(1 - aI)$, φ_0, a, b are given parameters	Belyanin V.N. et al., 1980
Dombrovskiy SR model	$\mu(\varphi) = \mu_0 \exp\left[-\left\{\frac{(\varphi - \varphi_{opt})}{\sigma_\varphi}\right\}^2 - \mu_1\varphi + \mu_2\right]$, $\varphi \in \{C, T\}$, $\mu_0, \sigma_\varphi, \mu_1, \mu_2$ are given parameters	Dombrovskiy Yu.A., 1990
Fennel SR Model	$\mu(T, I) = \alpha_0 \exp(aT)(I/I_0) \exp(1 - I/I_{opt})$, α_0 is the growth rate of phytoplankton at 0°C (0,8), a is an empirical coefficient	Fennel D.A., 1999
Logistic dependence considering the Allee effect	$R(SSB) = L/\{1 + \exp(-k(SSB - SSB_0))\}$ is the mass of fish capable for producing the offspring in an environment with a limited capacity L ; k ; SSB_0 are parameters of the degree of the Allee effect (at low population densities).	Vasilyeva N.A., Vladimirov A.A., Winter A.M., 2017

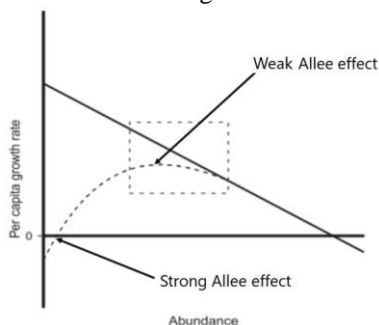


Figure 1. Allee effect in the ichthyological model.

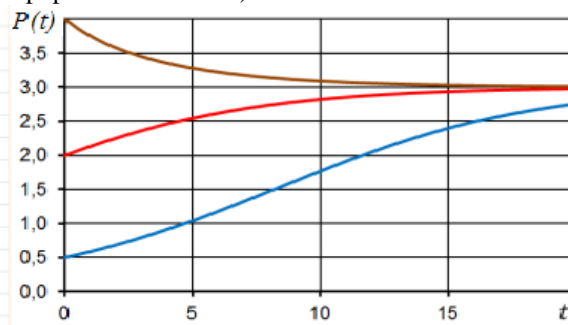


Figure 2. Verhulst kinetics in the fish model.

4. Solution method

Each equation of the system (1) – (3) after linearization was represented as the convection-diffusion equation. Schemes of high-order of accuracy considering the partial filling of computational cells were used for model discretization [15, 16]:

$$c'_t + uc'_x + vc'_y = (\mu c'_x)'_x + (\mu c'_y)'_y + f \quad (5)$$

with boundary conditions:

$$c'_n(x, y, t) = \alpha_n c + \beta_n,$$

where u, v are water velocity components; μ is the turbulent exchange coefficient; f is the function, describing the intensity and distribution of sources.

For numerical implementation of the discrete mathematical model we used a uniform grid:

$$w_h = \{t^n = n\tau, x_i = ih_x, y_j = jh_y; n = 0, N_t, i = 0, N_x, j = 0, N_y; N_t\tau = T, N_x h_x = l_x, N_y h_y = l_y\},$$

where τ is the time step; h_x, h_y are spatial steps; N_t is the upper time boundary; N_x, N_y are spatial boundaries.

Discrete analogs of convective uc'_x and diffusive $(\mu c'_x)'_x$ operators of the second order of accuracy in the case of partially filled cells can be written as:

$$(q_0)_{i,j}uc'_x \simeq (q_1)_{i,j}u_{i+1/2,j} \frac{c_{i+1,j}-c_{i,j}}{2h_x} + (q_2)_{i,j}u_{i-1/2,j} \frac{c_{i,j}-c_{i-1,j}}{2h_x},$$

$$(q_0)_{i,j}(\mu c'_x)'_x \simeq (q_1)_{i,j}\mu_{i+1/2,j} \frac{c_{i+1,j}-c_{i,j}}{h_x^2} - (q_2)_{i,j}\mu_{i-1/2,j} \frac{c_{i,j}-c_{i-1,j}}{h_x^2} - |(q_1)_{i,j} - (q_2)_{i,j}| \mu_{i,j} \frac{\alpha_x c_{i,j} + \beta_x}{h_x}, (6)$$

where $q_l, l \in \{0,1,2\}$ are coefficients, describing the “fullness” of computational domains.

The adaptive modified alternately triangular variational method (MATM) obtained on the basis of scheme (6), was used to solve the obtained grid equations [16, 17].

For numerical implementation of the developed model of biological kinetics (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 interacting populations of biogeoecenosis.

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, $i \in \{1, \dots, m\}$, m is a given number of subdomains. $Q = \sum_i \frac{1}{|X_i|} \sum_{x \in X_i} d^2(x, c_i) \rightarrow \min$, 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 the subdomain c_i in the Euclidean metric. The k-means method is convergent only when all subdomains are approximately equal.

The result of the k-means method for model two-dimensional and three-dimensional regions is shown in Figure 3.

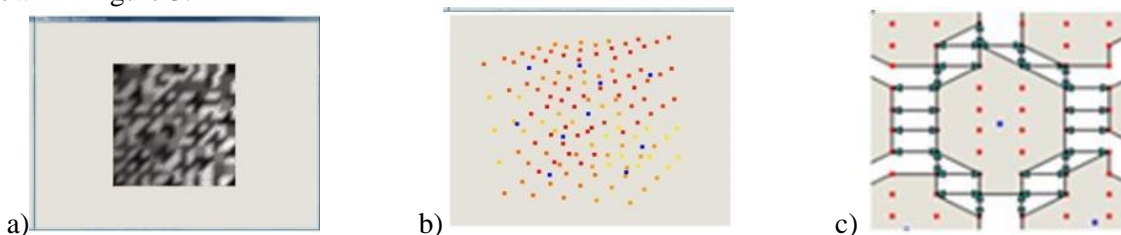


Figure 3. Domain decomposition for the k-means method into 150 (two-dimensional domain) (a), 10 subdomains (three- dimensional domain) (b); data transfer between neighbouring subdomains (c).

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

$$E^t = S^t/p = \chi / \left\{ 1 + (\sqrt{p} - 1) \left(\frac{36}{50N_z} + \frac{4p}{50t_0} \left(t_n \left(\frac{1}{N_x} + \frac{1}{N_y} \right) + \frac{t_x \sqrt{p}}{N_x N_y} \right) \right) \right\},$$

where χ 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 the 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.

Table 2. Comparison of acceleration and efficiency of algorithms.

p	t, s	S^t	S	E^t	E
1	6.073	1.0	1.0	1	1
2	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 efficiency of the standard algorithm; $E_{(2)}$ is efficiency of the algorithm on the basis of the k-means) has the form:

$$\delta = \sqrt{\sum_{k=1}^n (E_{(2)k} - E_{(1)k})^2} / \sqrt{\sum_{k=1}^n E_{(2)k}^2}. \quad (7)$$

We obtained that the efficiency is increased on 10 – 20% using of algorithm on the basis of k-means method for solving problem in the form (1) – (3) compared to the standard algorithm.

For numerical implementation of 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 both the 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 for implementation the corresponding algorithm (see Figure 4).

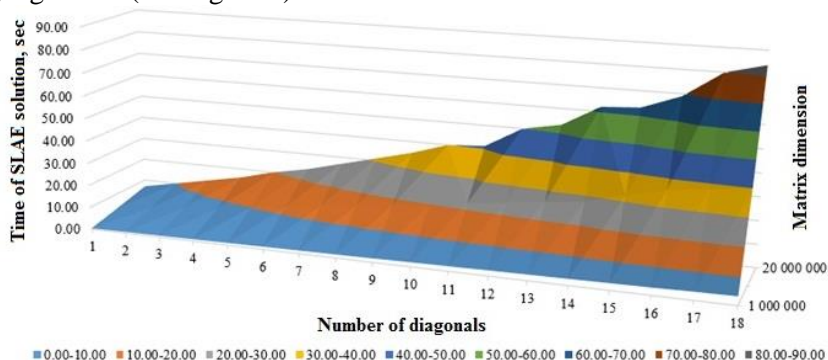


Figure 4. Dependence of SLAE solution time on matrix dimension and the number of nonzero diagonals.

Due to it, in particular, we can choose the grid size and to determine the time for SLAE solution based on the amount 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 CSR (Compressed Sparse Rows) matrix storage format avoids the need to store their null elements. However, all nonzero elements, including many repeating, are

stored in the corresponding array. This disadvantage is not critical at using computing systems with shared memory. However, this can adversely affect performance at data transferring between nodes in heterogeneous and distributed computing systems. We performed the 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 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 memory capacity for the CSR format was estimated as:

$$P_{csr} = N_{nz}B_{nz} + (N_{nz} + R + 1)B_{idx},$$

for the CSR1S format:

$$P_{csr1s} = B_{nz}[N_{nz}(k_i + 1) - N_{seq}(k_i k_r R + k_r R + 1) - k_i(k_r R - R - 1)], \quad k_r = \frac{R_{seq}}{R}, \quad k_i = \frac{B_{idx}}{B_{nz}},$$

where R is the number of matrix rows; R_{seq} is the number of matrix rows that contain a repeating sequence of elements; N_{nz} is number of non-zero matrix elements; N_{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 format to CSR format by sequential (a) and parallel (b) algorithms from k_r and N_{seq} are shown in Figure 5.

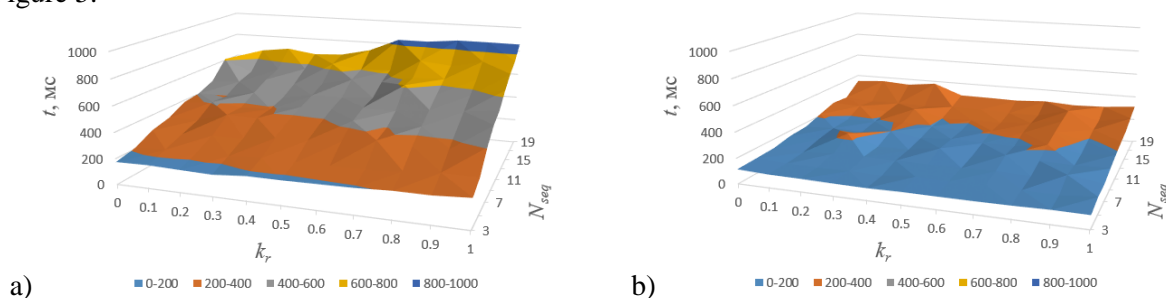


Figure 5. The runtime of matrix conversion from CSR1S to CSR format.

Analysis of the CUDA architecture characteristics showed the algorithms for numerical implementation of the developed mathematical model of hydrobiological processes could be used for creation high-performance information systems.

5. Description of software complex

The “Azov3D” software complex (SC) was developed for solving biological kinetics 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) is given in Figure 6(a), and changes in phytoplankton concentration (S_1) – in Figure 6(b) (initial distribution of water flow fields for north wind). Parameter values: $\mu_3 = 5 \cdot 10^{-10}$; $\nu_3 = 10^{-10}$; $B = 0,001$; $\tilde{S}_3 = 1$; $f = 3$; $\tau_i = 0,1$; $i \in \{1,5\}$; $\lambda_2 = 0,8$; $\mu_1 = 5 \times 10^{-11}$; $\nu_1 = 10^{-11}$.

Using the developed SC, we researched the mechanism of suffocation areas in shallow waters [20]. Simulation results of possible scenarios for the development of the Azov Sea ecosystem (changes in the concentration of pelengas commercial fish) are given in Figures 7, 8 (the initial distribution of

water flow fields for the north wind direction). In Figure 7: a) time interval $T=26$ days; b) $T=62$ days. In Figure 8: a) time interval $T=25$ days; b) $T=76$ days. The maximum values of pelengas and detritus concentrations indicate by white colour. Parameter values: $\mu_4 = 5 \cdot 10^{-11}$; $\nu_4 = 10^{-11}$; $\varepsilon_4 = 1.9 \cdot 10^{-5}$; $\beta_4 = 0.1$; $\lambda_4 = 0.4$; $\mu_5 = 1.5 \cdot 10^{-3}$; $\nu_5 = 1.6 \cdot 10^{-3}$; $\gamma_5 = 0.125$; $\lambda_5 = 1.16 \cdot 10^{-3}$; $\xi_5 = 0.8$; $\varepsilon_5 = 0.47$; $\delta_5 = 0.05$.

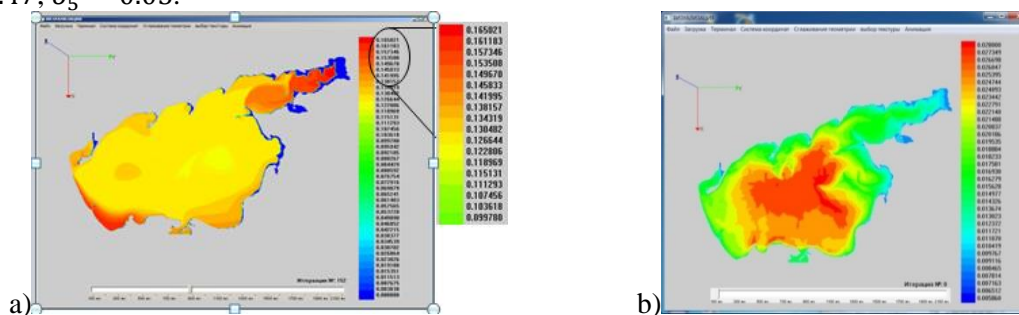


Figure 6. Distribution of nutrients (a) and phytoplankton (b) concentrations.

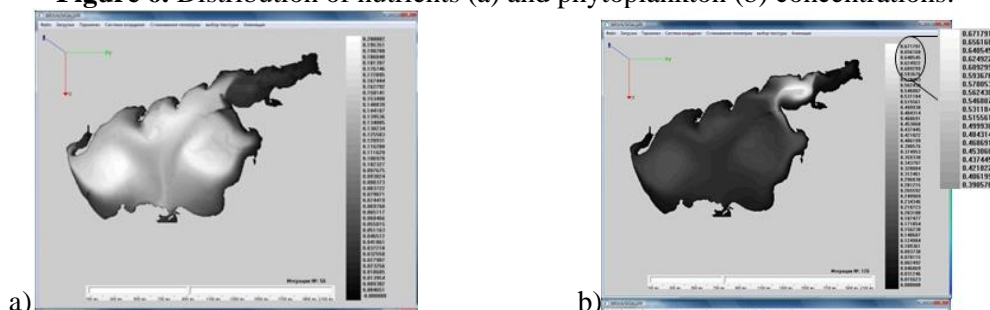


Figure 7. Distribution of detritus concentration.

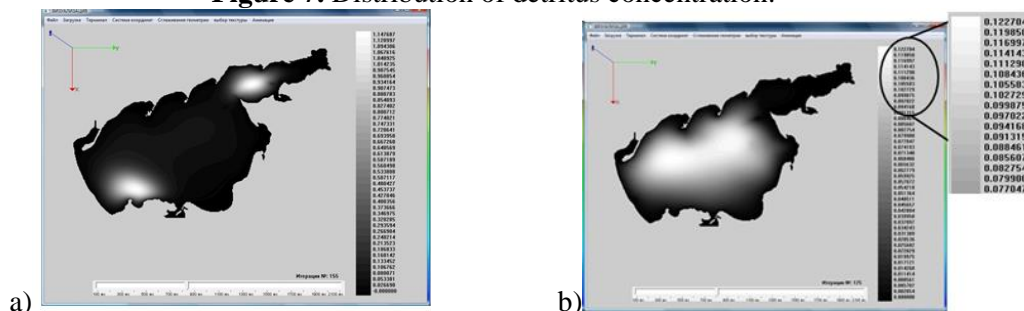


Figure 8. Distribution of pelengas concentrations.

Using the results of numerical experiment, we can analyse the possible scenario of waters stocking of the Azov Sea by 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 a decrease in the concentration of bottom sediments in the Central-Eastern part of the Azov Sea. It ultimately will lead to a decrease of suffocation areas and improve the water quality in this water basin.

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

6. Conclusion

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 it, we researched influence of competition for resources, features of the food chain, biotic and abiotic factors on the water reproduction processes. Discretization of the developed model problem of water ecology as the part of software was performed on the basis of schemes of second order of accuracy considering the partial fullness of computational cells. It allowed to significantly reducing the solution error in the computational domain of complex shape. The comparative analysis of two-layer methods of variational type was performed. MCM was used as the main method of solving the system of grid equations arising in the discretization in view of its highest convergence rate. Effective parallel algorithms were developed for numerical implementation of biological kinetics problem and oriented on multiprocessor computer system and graphics accelerator. Due to it, the hydrobiological processes have been analysed in real and accelerated time.

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8. References

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