A new marine ecosystem 3D CEMBS model (version 2) for the Baltic Sea

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***Abstract*—The paper presents a new marine ecosystem model designed for the Baltic Sea. The ecosystem 3D CEMBS model has been developed for incorporation into the 3D POPCICE ocean-ice model.**

The Current Baltic Sea model is based on the Community Earth System Model (CESM from NCAR – the National Center for Atmospheric Research). CESM was adapted for the Baltic Sea as a coupled sea-ice model. It consists of the Community Ice Code (CICE model, version 4.0) and the Parallel Ocean Program (version 2.1). The ecosystem model – the biological submodel consists of eleven mass conservation equations. There are eleven partial second-order differential equations of the diffusion type with the advective term for phytoplankton (three classes: small and large phytoplankton and cyanobacteria), zooplankton, nutrients (four components: NO3, NH4, PO4 and SiO3), dissolved oxygen, and dissolved and particulate organic matter (DOM and POM). This model is an effective tool for solving the problem of ecosystem bioproductivity and was tested for five selected localities

Keywords-component; 3D ecosystem model, phytoplankton, nutrient, zooplankton, oxygen, Baltic Sea

I. INTRODUCTION

The Baltic Sea is a very difficult basin in terms of numerical modelling. The water balance in the Baltic Sea consists of: precipitation, evaporation, river inflow and water exchange (inflows of saline waters and outflow of Baltic waters) through the Straits of Sound and the Great and Little Belt. Hydrology of the Baltic Sea is determined mainly by four factors: atmosphere-water-ice interactions, exchange of waters through the Danish Straits, inflows of river waters and seabed topography. The Baltic Sea − one of the largest reservoirs of brackish water – is a shallow, semi-enclosed shelf sea (the average depth of 52 m, only 10% of the sea surface area is deeper than 100 m) with a limited contact with the ocean. Due to a complex shoreline and relatively diverse seabed topography, one can distinguish different hydrological regions. The division into 7 regions is generally accepted: the Bothnian Bay (the Gulf of Bothnia), the Bothnian Sea, the Gulf of Finland, the Gulf of Riga, the Baltic Proper (the Southern Baltic) − the largest and the deepest region, the Danish and Kattegat Straits. The regions such as the Gulf of Finland and the Gulf of Ryga do not have any distinct topographic steps separating them from the remaining part of the sea area, but the existing, very strong hydrological fronts account for the division into these basins. The Baltic Proper is the largest one in terms of surface area and volume (more than 50 % of the volume and the water surface). Each region can be considered as a separate object, which includes subobjects, e.g. the Baltic Proper consists of inter alia: the Bornholm Basin, the Gdańsk Deep (Gdańsk Basin), the Słupsk Furrow and the Gotland Basin. A number of small topographic elements occur in the Baltic Sea, which despite their small dimensions are of major importance for the hydrology of the sea. The climate of the Baltic Sea is affected both by the Atlantic Ocean and the East European continent, and thus it is an area where oceanic and continental climates interact with each other. The Sea is situated within the temperate climatic zone, characterized by high weather changeability, both within a daily, annual or long-term time-scale [1].

Mathematical models are a practical and useful tool for studying the complex systems such as marine ecosystems. Coupled physical-biological models are still a developing tool in biological oceanography. Dzierzbicka-Glowacka and her co-workers published several papers on modelling the hydrodynamic and biological processes, for instance: [2], [3], [4], [5], [6]. In 2011, the operational ecohydrodynamic model of the Baltic Sea (3D CEMBS - a new version) was launched at the Institute of Oceanology of the Polish Academy of Sciences in the parallel version on the 2 km grid with rivers and the open boundary [7] http://deep.iopan.gda.pl/CEMBaltic/new_lay/index.php. This paper presents an integrated, operational mode of the Baltic ecosystem – the biological part and initial numerical results for different locations.

II. THE 3D CEMBS MODEL STRUCTURE

The integrated ocean-ice-ecosystem 3D CEMBS model consists of four parts: atmosphere, ocean (including ecosystem), ice and coupler (see Fig. 1).

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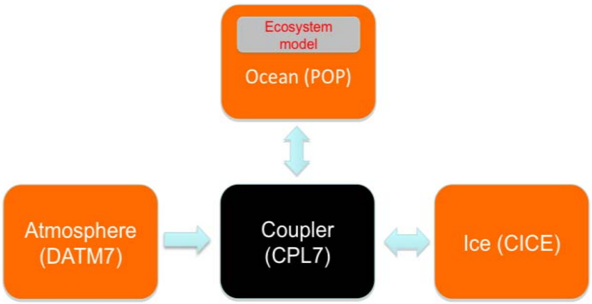


Figure 1: Schematic presentation of the Baltic model.

The Current Baltic Sea model is based on the Community Earth System Model (CESM from NCAR the National Center for Atmospheric Research). CESM was adopted for the Baltic Sea as a coupled sea-ice model. It consists of the Community Ice Code (CICE model, version 4.0) and the Parallel Ocean Program (version 2.1). The models are coupled through CPL7, which is based on MCT (The Model Coupling Toolkit) routines.

3D CEMBS model is currently configured at two horizontal resolutions of 9 km and approximately 2km (1/12° and 1/48°, respectively). The model bathymetry is represented by 21 vertical levels and the thickness of the first four surface layers was five meters. The driver time step is 1440 s and is also coupling the time step. The ocean model time step is about 480 seconds (8 minutes). The bottom topography is based on ETOPO1 1 arc-minute global relief model (http://www.ngdc.noaa.gov/mgg/global/global.html, National Geophysical Data Center). The bathymetric data were interpolated into the model grid using the kriging method. The initial state of the ocean model was prepared using the temperature and salinity climatic data. The ocean surface level (5m deep) was restored based on the monthly timescale to the monthly average T and S climatology, as a correction term to the explicitly calculated fluxes and overlying atmosphere or sea ice. The restoring time was set to 30 days at the surface and 10 days at the domain boundary. 3D CEMBS model domain is based on stereographic coordinates, but the equator of these coordinates is in the center of the Baltic Sea (so we actually use the rotated stereographic coordinates) and we can assume that the shape of the cells is square and they are identical. 3D-CEMBS model is also equipped with the ecosystem module, on which works are being currently carried out in order to incorporate it into the operational mode.

III. POP

The ocean model is based on the Parallel Ocean Program (POP, [8]) from the National Laboratory in Los Alamos (LANL), which is derived from the global ocean model [9] with additional conditions for free surface [10]. This is a model of 'z' type (identical thickness of layers for every cell); the three-dimensional equations describing the behavior of the stratified ocean are solved by parametrization. Numerically the model defines spatial derivatives in the spherical coordinates using the method of finite elements. Physical quantities of the model are embedded in the spherical grid of Arakawa B [11]. The barotropic equation is solved by "preconditioned conjugate gradient solver" (PCG), and advection is determined by a centered differential. Parametrization of a horizontal mixing is accomplished by a biharmonic operator, and vertical turbulence is determined by KPP parametrization. The equation of state, introduced by [12] is also used.

IV. CICE

CICE (Community Ice CodE) is based on elastic-visco-plastic (EVP) rheology [13], [14]. It is designed to work in accordance with the POP ocean model using the parallel computing machines. It consists of several interactive elements: the thermodynamic model, which computes local growth rates of snow and ice owing to vertical conduction of energy and momentum fluxes. It also defines velocity of each ice cell based on wind and ocean velocity. It has a few vertical categories, so that the stress distribution is much closer to the real one.

V. ECOSYSTEM

A. *Conceptual*

The biological part of 3D CEMBS consists of 11 coupled equations [15]: three for phytoplankton, two for pelagic detritus, four for nutrients and one for zooplankton and oxygen. Phytoplankton is modeled with the aid of three state variables: small phytoplankton (p1), larger phytoplankton (p2) and cyanobacteria (p3). The small phytoplankton size class is meant to represent nano- and pico-sized phytoplankton, and may be limited by available nitrogen (NO2, NH4), phosphorus (PO4) and light levels. The larger phytoplankton class is explicitly modelled as diatoms and may be limited by the above factors, as well as silicon. Growth rates of cyanobacteria may be limited by phosphorus and light. Cyanobacteria are capable of nitrogen fixation from N2 gas and cannot be nitrogen-limited. The phytoplankton concentration is taken as a dynamically passive physical quantity, i.e. it is incapable of making autonomous movements. Phytoplankton growth rates are determined by available light and nutrients using a modified form of the growth model of [16]. There are two detrital pools in the model (the labile/semi-labile fractions): a non-sinking pool, which largely represents dissolved organic matter (DOM) but would also include small non-sinking particulate organic matter, and a large particulate detrital pool, which represents particulate organic matter (POM) and sinks out of the mixed layer. Both detrital pools are remineralized at a temperature dependent rate. One state variable for zooplankton is considered. It ingests three phytoplankton groups and a large detrital pool.

B. *Equations*

In the fluid flow environment the time derivatives in the biological model are decomposed into local and advective terms ${}^{d}\!/_{dt} = {}^{\partial}\!/_{\partial t} + V \cdot \nabla$, and a diffusion term is added to the right side of the equation. Thus, in the coupled model, there is an advection-diffusion equation, second-order partial differential equation, similar to the conservation equations for temperature and salinity in the ocean model for each compartment in the biological model:

$$\frac{\partial S}{\partial t}+(V+w_s)\cdot\nabla S=\frac{\partial}{\partial z}\left(K_z\frac{\partial S}{\partial z}\right)+\sum_{i-1}^{2}\frac{\partial}{\partial x_i}\left(K_{x_i}\frac{\partial S}{\partial x_i}\right)+F_S$$

where: S represents each model variable, V is the velocity vector, w_S (for S = Phyt or DetrP) is the sinking velocity of phytoplankton or pelagic detritus, K_z and K_x are the vertical and horizontal turbulent diffusion coefficients, and F_S is a biogeochemical source-sink term representing the equation for the variable S in the biological module.

The model is based on comparatively simple trophic interactions among a few basic variables, nutrients, phytoplankton, zooplankton and detritus. The structural relationships among the different variables in the model formulation are presented in Fig. 2. The general forms of the time rate of change equations are:

F_{NO3} = NITRIF – NO3_V_p2 – NO3_V_p1 – DENITRIF – prod_NO3_p3

F_{NH4} = – NH4_V_p2 – NH4_V_p1 – NITRIF + Q * (zoo_loss_dic + p1_loss_dic + graz_p1_dic + p2_loss_dic + graz_p2_dic + rem_POC + p3_loss_dic + graz_p3_dic) + rem_DON + p3_Nexcrete – prod_NH4_p3

F_{SiO2} = P_SiO2_rem + Qsi * (f_graz_si_rem * graz_p2 + f_p2_loss_dc * p2_loss) –prod_Si_p2

F_P = (Qp * (rem_POC + zoo_loss_dic + p1_loss_dic + graz_p1_dic + p2_loss_dic + graz_p2_dic - prod_C_p2)) + rem_DOP + p3_loss_dip –po4_V_p1 – po4_V_p3

F_{p1C} = prod_C_p1 – (graz_p1 + p1_loss + p1_agg)

F_{p1chl} = prod_ch_p1 – chC_p1 * (graz_p1 + p1_loss + p1_agg)

F_{p2C} = prod_C_p2 – (graz_p2 + p2_loss + p2_agg)

F_{p2chl} = prod_ch_p2 – chC_p2 * (graz_p2 + p2_loss + p2_agg)

F_{p2Si} = prod_Si_p2 - (Qsi * (graz_p2+p2_loss+p2_agg))

F_{p3C} = prod_C_p3 – graz_p3 – p3_loss

F_{p3chl} = prod_ch_p3 – chC_p3 * (graz_p3 + p3_loss)

F_{zooC} = graz_p1_zoo + graz_p2_zoo + graz_p3_zoo + graz_detr – zoo_loss

F_{DOC} = prod_DOC – rem_DOC

F_{DON} = prod_DON - rem_DON

F_{DOP} = prod_DOP - rem_DOP

F_{DIC} = rem_DOC + rem_POC + graz_p1 + zoo_loss_dic + p1_loss_dic + graz_p1_dic + p2_loss_dic + graz_p2_dic - prod_C_p1 – prod_C_p2 + graz_p3_dic + p3_loss_dic - prod_C_p3

F_{POC} = prod_POC – rem_POC

F_{O2} = O2_PRODUCTION - O2_CONSUMPTION

where F_S for nutrients: F_{NO3}, F_{NH4}, F_{PO4}, F_{SiO2}; for small phytoplankton: F_{p1C}, F_{p1ch}; for larger phytoplankton: F_{p2C}, F_{p2ch}; for cyanobacteria: F_{p3C}, F_{p3chl}, in carbon and chlorophyll-*a*, respectively; for zooplankton: F_{zooC},; for DOM: F_{DOC}, F_{DON}, F_{DOP}; for DIC: F_{DIC}; for POC: F_{POC}; for dissolved oxygen: F_{O2}. The biogeochemical processes are given in Fig. 2.

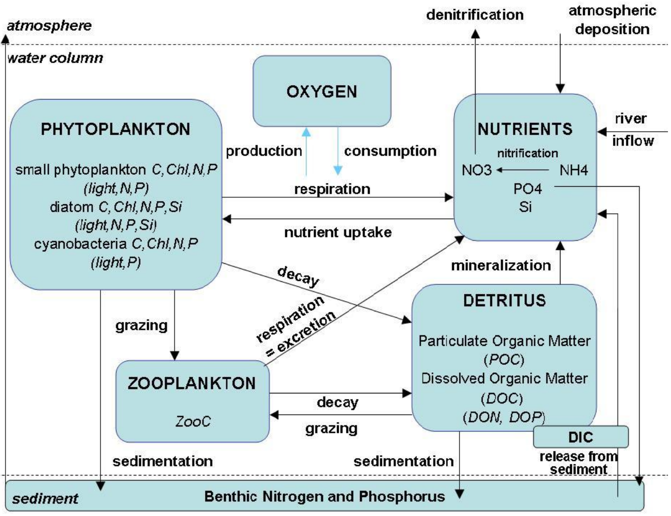


Figure 2: Structure of the biological module.

C. *Comparsion of model results with measurements.*

The modeled values were compared with the experimental data in 1979-2000 on five measuring buoys located at the Baltic Sea (Fig. 3) from HELCOM:

http://ocean.ices.dk/helcom/Helcom.aspx?Mode=1

The relationship between the measured and calculated results was obtained. The Pearson product-moment correlation coefficient was used to compare the model results with the measurements; the correlation coefficients for five selected points are presented in Table 1. The modelled values resembled the observations, with mean (for five points) correlation coefficients of 0.9634 for temperature, 0.9083 for nutrients, 0.6067 for chlorophyll-*a*, 0.6189 for phytoplankton and 0.6404 for oxygen. Correlation for chlorophyll includes only first half of the year. Modelled values are only diatoms while experimental data gives summary value of all phytoplankton types. Additionally modeled parameters are mean values from 5m layer while experimental data stands for surface only measurements. The consistency of the calculated values with the measured distribution was particularly good for the temperature and nutrients. The spatial and temporal variability of plankton is usually so great that any model with right orders of magnitude in its outputs will fit the data. So even if the correlation coefficient is c. 0.6, it is still a good value.

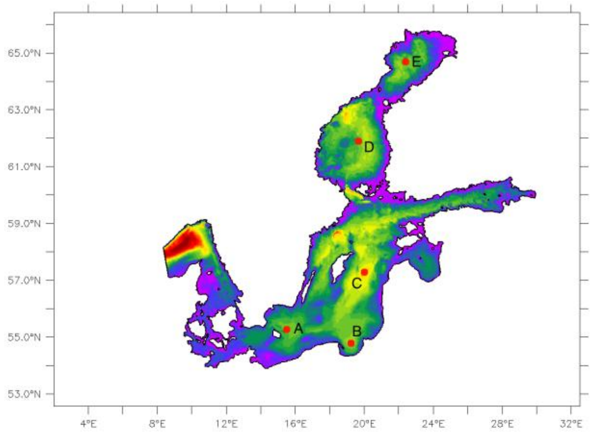


Figure 3: Distribution of measuring buoys for which the comparison was performed (A – Bornholm Deep, B – Gdansk Deep, C – Gotland Basin, D – Bothnian Sea, E – Gulf of Bothnia).

These errors result from the following facts: (i) the CEMBS model calculates the surface values of variables of the whole pixel (an area of 2×2 km^2) from the first layer - 5 m, and not of a particular point at the sea surface where in situ measurement was taken, (ii) phytoplankton is represented in this 3D model only by three state variables (iii) the Baltic Sea is very difficult water region in terms of modeling and (iv) the influence of meteorological and hydrodynamic data as input data of the model, as they are also burdened with a certain error. The spatial differences between the simulated and observed results and their temporal variability in the seasonal cycle were quite similar in each considered grid box.

TABLE I. CORELATION COEFFICIENTS FOR THE ESTIMATED PELAGIC VARIABLES FROM 3D CEMBS MODEL

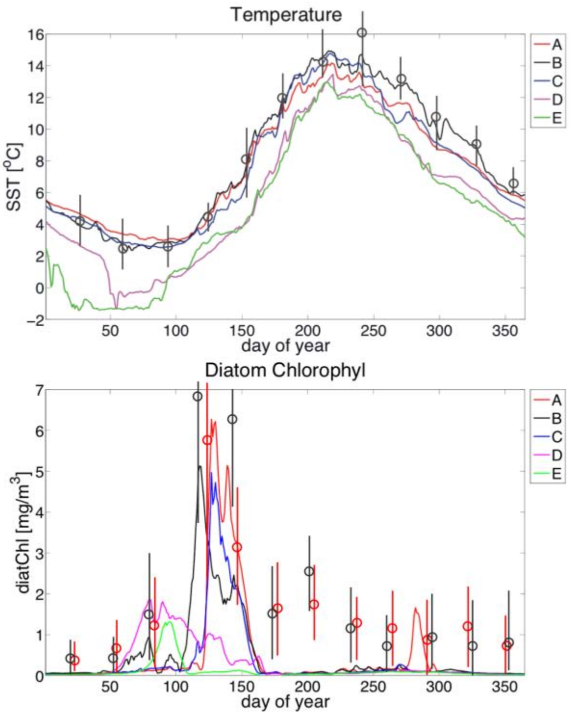
Variables	**A**	**B**	**C**	**D**	**E**
Temp	0.9711	0.9801	0.9725	0.9598	0.9459
NO_3	0.9206	0.9318	0.9215	0.9168	0.9071
NH_4	0.9193	0.9021	0.8769	0.7703	0.6107
PO_4	0.9584	0.9611	0.9341	0.9282	0.9002
$Si0_2$	0.9383	0.9297	0.9179	0.9098	0.8908
Chl-a	0.6418	0.6109	0.5993	0.5748	0.5407
Phyt	0.6605	0.6241	0.6005	0.5904	0.5571
O2	0.6712	0.6640	0.6262	0.6004	0.5913

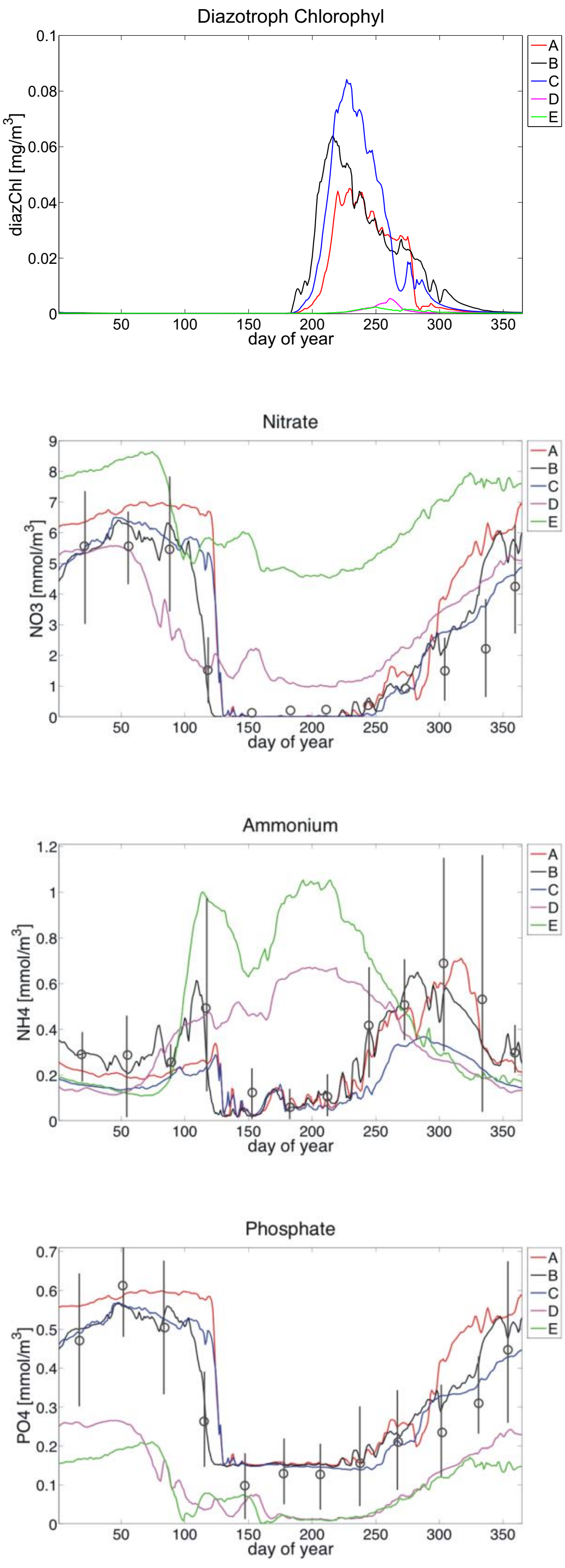
VI. RESULTS

The ecosystem model has been developed for incorporation into the 3D POPCICE ocean-ice model. Annual, seasonal, monthly and daily variation of the pelagic variables was calculated. The time needed for computing 1 model year for the ecohydrodynamic model and for the resolution of 9km is 30h on 16 processors, and for the resolution of 2km – 120h on 256 processors. The starting-point of the numerical simulations was assumed to be the end of 1959. Model is forced by fields from the European Centre for Medium Weather Forecast (ERA 40). In the operational mode, however, 48-hour atmospheric forecasts are used, which are supplied by the UM model of the Interdisciplinary Centre for Mathematical and Computational Modeling of the Warsaw University. The current calculations are performed on supercomputers of cluster type (Galera), which is located at TASK (the Academic Computer Centre in Gdańsk).

We selected five locations within the domain of the Baltic Sea (Gdansk Deep, Bornholm Deep, Gotland Deep, Bothnia Sea and the Gulf of Bothnia) to present our results.

Examples of results – daily model outputs for the first layer of five selected points for the year of 2011 are shown in Fig. 4 for different model variables: temperature, chlorophyll-*a*, nutrients (NO3, NH4, PO4 and SiO2), zooplankton and oxygen.





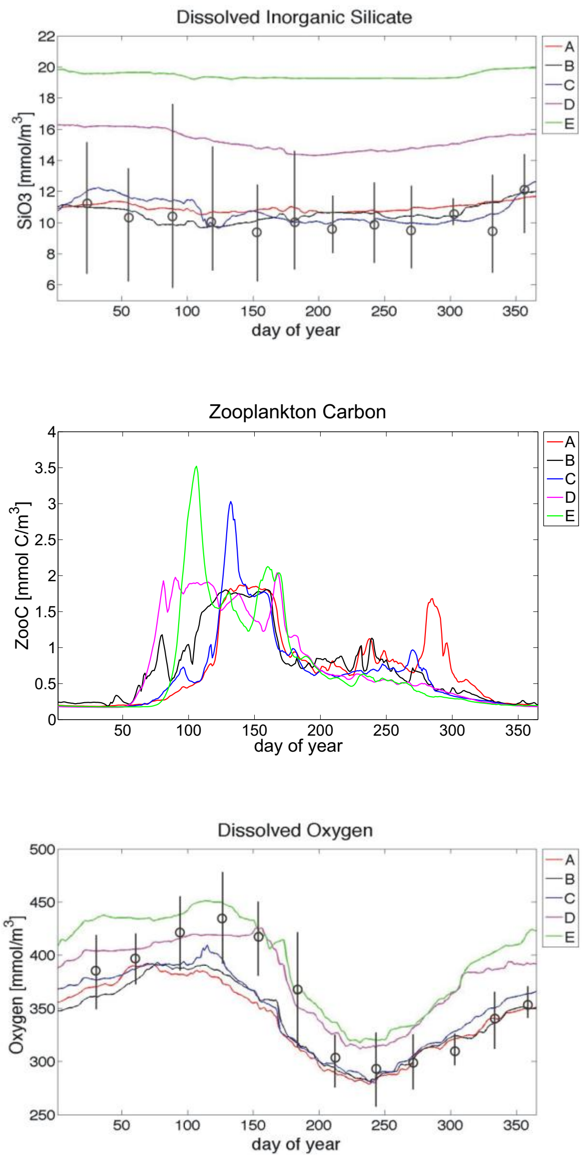


Figure 4: Annual concentrations of biological variables for measuring buoys shown on Fig. 3 (A – Bornholm Deep, B – Gdansk Deep, C – Gotland Basin, D – Bothnian Sea, E – Gulf of Bothnia). Circles – mean experimental surface values of the parameter for each month (for location A, A+B). Bars – plus/minus standard deviation for the yearly means.

The season begins with high total nutrient (NO3, NH4, PO4 and SiO2) concentrations in the whole column water. As the spring starts, the nutrient is consumed. The phytoplankton prefers ammonia to nitrate, so as long as ammonia is available, ammonia is consumed. As soon as the ammonia pool in the surface layer is emptied, the phytoplankton turns towards the nitrate for assimilation. It is also noticeable that once the spring bloom has started, and the total inorganic nitrogen concentrations turn low, the bloom is maintained by the external supply of inorganic nitrogen. At the end of June, when the system is depleted of nitrate, the nitrogen fixation starts and the phosphorus pool is recovered, and at the same time a cyanobacteria bloom is observed. However, winds are strong enough in September to replenish the full water column with abundant nutrients. In autumn, there is a slight increase in the phytoplankton biomass. It is caused by an increase in nutrient concentrations resulting from the deeper mixing of water. However, the growing season ended in December, when the phytoplankton biomass dropped to the January-February level. The phytoplankton biomass decreased together with the increasing depth. The phytoplankton biomass (as the sum *Phyt* =p1+p2+p3) is the highest in the surface layers and reached the maximum in April with the peak ranging from c.27 mmolC m^{-3} (= c. 6.7 mgChl-*a* m^{-3}) in the southern part (Gdansk Deep, Bornholm Deep, Gotland Deep) to c. 7 mmolC m^{-3} (= c. 2 mg Chl-*a* m^{-3}) in the northern Baltic Sea (Bothnia Sea and Gulf of Bothnia). The growth of zooplankton is closely correlated with the growth of phytoplankton classes, diatoms, cyanobacteria, and a small phytoplankton class. The biomass of zooplankton has the highest values in the upper layers (from 2 to 3 mmolC m^{-3}), when there is high algal biomass. A considerable increase in ZooC takes place in April-May during the spring bloom. The concentration of dissolved oxygen is determined by the interaction of two factors, production and consumption, which depend on a few biogeochemical processes $F_S = f(T)$, which in turn are a function of temperature. The distribution of O2 is inversely related to the distribution of temperature.

VII. CONCLUSION

This work presents simulated temporal changes in pelagic variables, i.e. nutrients (NO3, NH4, PO4 and SiO2), three phytoplankton classes (diatoms, cyanobacteria, and a small phytoplankton class), zooplankton, dissolved oxygen. The numerical simulations were done with 3D CEMBS, Coupled Ecosystem Model Baltic Sea, which is embedded in the existing 3D POPCICE hydrodynamic model of the Baltic Sea. The POPCICE sea-ice model, the Parallel Ocean Program (version 2.1) and CICE model (version 4.0), were used to apply biological equations to plankton systems. The calculations are presented for five selected locations within our domain in 2011. The differences between the modelled and mean observed data depend on the time (year and month) and place for which the calculations were made.

Reduction of the discrepancies may be caused by future improvements in this model, both in the hydrodynamic and biologic module.

Mathematically simulated data presents only some approximation of environmental processes. Nonetheless, an accurately validated model provides significant information on spatial and temporal resolutions of the processes that are very difficult to obtain based on in situ measurements. The 3D CEMBS model is a proper tool for analyzing the annual, seasonal, monthly and daily variation patterns of marine plankton in the Baltic Sea, and therefore, it can be successfully applied to forecast ecological changes in the Baltic Sea.

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REFERENCES

[1] R. Osinski, “Symulacja procesów dynamicznych w Morzu Bałtyckim zintegrowanym modelem ocean-lód,” PhD Thesis, Institute of Oceanology, Polish Academy of Sciences, Sopot, Poland, 2007, pp. 113, (in Polish).

[2] L. Dzierzbicka-Glowacka, ”Mathematical modelling of the biological processes in the upper layer of the sea,” Diss. Monogr., vol. 13, Institute of Oceanology PAS, Sopot, 2000, pp. 124 (in Polish).

[3] L. Dzierzbicka-Glowacka, L. Bielecka, and S. Mudrak, ”Seasonal dynamics of *Pseudocalanus minutus elongatus* and *Acartia* spp. in the southern Baltic Sea (Gdańsk Deep) – numerical simulations,” Biogeosciences, vol. 3 (4), 2006, pp. 635–650.

[4] L. Dzierzbicka-Glowacka, I. M. Zmijewska, S. Mudrak, J. Jakacki, and A. Lemieszek, ”Population modelling of Acartia spp. in a water column ecosystem model for the South-Estern Baltic Sea,” Biogeosciences, vol. 7, 2010, pp. 2247–2259.

[5] L. Dzierzbicka-Glowacka, K. Kulinski, A. Maciejewska, J. Jakacki, and J. Pempkowiak, ”Numerical modelling of POC dynamics in the southern Baltic under possible future conditions determined by nutrients, light and temperature, ”Oceanologia, vol. 53(4), 2011a, pp. 971–992.

[6] L. Dzierzbicka-Glowacka, J. Jakacki, M. Janecki, and A. Nowicki, “Variability in the distribution of phytoplankton as affected by changes to the main physical parameters in the Baltic Sea,” Oceanologia, vol. 53(1-TI), 2011b, pp. 449–470.

[7] L. Dzierzbicka-Glowacka, J. Jakacki, M. Janecki, and A. Nowicki, “Activation of the operational ecohydrodynamic model (3D CEMBS) – a hydrodynamic part,” 2012 submitted.

[8] R. Smith, and P.Gent, “Reference manual for the Parallel Ocean Program (POP),” Los Alamos National Lab, New Mexico, 2004. pp 75

[9] A. J. Semtner, “A general circulation model for the World Ocean,” UCLA Dept. of Meteorology Tech. Rep., vol. 8, 1974, pp. 99.

[10] P. D. Killworth, D. Stainforth, D. J. Webb, and S. M. Paterson, “The development of a free-surface Bryan-Cox-Semtner ocean model,” J. Phys. Oceanogr., vol. 21(9), 1991, pp. 1333–1348

[11] A. Arakawa and, V. R. Lamb, “Computational design of the basic dynamic processes of the UCLA general circulation model,” Methods Comput. Phys., vol. 17, 1977, pp. 173–265

[12] T. J. McDougall, D. R. Jackett, D. G. Wright, and R. Feistel, “Accurate and computationally efficient algorithms for potential temperature and density of seawater,” J. Atm. Ocean. Technol., vol. 20, 2003, 730–741

[13] E. C. Hunke, and J. K. Dukowicz, “An elastic-viscous-plastic model for sea ice dynamics,” J. Phys. Oceanogr., vol. 27, 1998, pp. 1849–1867.

[14] W. H. Lipscomb, E. C. Hunke, “Modeling sea ice transport using incremental remapping,” Mon. Wea. Rev. vol. 132, 2004, pp. 1341–1354.

[15] J. K. Moore, S. C. Doney, J. A. Kleypas, D. M. Glover, and I. Y. Fung, “An intermediate complexity marine ecosystem model for the global domain,” Deep-Sea Res. II, vol. 49, 2002, 403-462.

[16] R. J. Geider, H. L. MacIntyre, and T.M. Kana, “A dynamic regulatory model of phytoplankton acclimation to light, nutrients, and temperature,” Limnology and Oceanography, vol. 43, 1998, pp. 679–694.