

High-Resolution Modelling of Phytoplankton Distribution and Adaptation

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A state-of-the-art eddy-resolving ocean general circulation model has been coupled to a newly developed ecosystem and biogeochemical model that attempts to describe the physiology of phytoplankton cells, their adaptation to changing external conditions and the separate cycling of several phytoplankton nutrients (C, N, Si, Fe). In its initial state the advection of a large number of tracers in the model caused an increase in MPI-exchange costs that inhibited a good scaling behaviour with increasing number of processors used. This has been overcome by bundling the MPI exchange for all tracers. First results from the model show a much improved representation of small-scale biological features, e.g. along the axis of the Antarctic Circumpolar Current, a decoupling of the C and N cycles in nitrogen-limited subpolar gyres, and an increased Si:N ratio in iron-limited regions.

1 Introduction

The marine biology, especially the phytoplankton (suspended microscopic algae and photosynthesizing bacteria), is tightly involved in the geochemical cycling of many elements, especially of carbon, but also compound substances that may have climatic impacts, such as dimethylsulfide or organohalogens. The ocean contains approximately 50 times as much carbon as the atmosphere, and over time-scales longer than a few decades the CO₂ partial pressure of the atmosphere is tightly coupled to the distribution of carbon within the oceans. An important process in regulating this distribution is the so-called 'biological pump', the fixation of carbon through photo-synthesis close to the ocean surface, and the subsequent sinking and decomposition of parts of the produced biological material in the deep ocean. Changes in the growth, mortality and sinking of phytoplankton therefore have the potential to act as a strong feedback on the change in climate that is induced by the anthropogenic accumulation of greenhouse gases in the atmosphere¹⁻³.

The Southern Ocean is a place of extremely strong exchange fluxes between ocean and atmosphere and plays an important role also for the global carbon cycle⁴. At the same time, it is also a place where strong changes in the ocean circulation are expected under global warming, e.g. a southward shift and strengthening of the Antarctic Circumpolar Current (ACC)⁵, a reduction in sea ice cover⁶ and a warming of the water column⁷.

A good understanding of the feedbacks in this system can only be gained by the use of computer models that allow to predict the physical background that the biology operates in, i.e. the ocean circulation and other external factors that influence phytoplankton growth (nutrients, light), but also the internal regulations within the planktonic ecosystem. Owing to their often large number of advected tracers (and therefore memory requirements) and the longer integration times required, coupled physical-biogeochemical models of the ocean are still often relatively coarsely resolved (on the order of 100-200 km spatial resolution in the horizontal), i.e. they are unable to represent the action of the energetic mesoscale

eddy field that has lengths scales on the order of the Rossby radius of deformation (10-40 km). The mesoscale eddies have been shown to exert a strong influence of the mean circulation, especially in the Southern Ocean⁸. Model predictions of atmosphere-ocean carbon fluxes differ most between different models in the Southern Ocean, owing to a poor representation of the physics there in coarse-resolution models⁴. It is therefore desirable to run coupled physical-biogeochemical ocean models at the state-of-the-art spatial resolution that is used in purely physical modelling.

There are also new challenges for the biogeochemical and ecosystem part of the coupled models. Marine ecosystem models have traditionally worked on the assumptions of a single limiting nutrient, usually nitrogen, for phytoplankton growth, and a constant carbon:nitrogen ratio in biomass^{9,10}. However, over the last decade it has become clearer that (i) different phytoplankton functional groups (diatoms, coccolithophorids) have different effects on the carbon flux through the system, (ii) that other nutrients, such as iron and silicate are important regulators of ecosystem structure and functioning, and (iii) that there is some plasticity in phytoplankton physiology, allowing the cells to adapt to different light/nutrient conditions and resulting in variable elemental stoichiometry. We have developed an ecosystem model that focuses mainly on the two last challenges, by implementing a model for diatoms with variable C:N:Si:chlorophyll ratio that depends on the availability of the nutrients N, Si, and Fe. Here we show some results from implementing this model into both a coarser-resolution and a high-resolution global circulation model that have been run on the IBM system *JUMP* at NIC.

2 The Model

2.1 Biogeochemical Model

The ecosystem model is based on the physiological model for the adaptation of algal cells to light, nutrient and temperature by Geider et al.¹¹ that describes the variation of the cells C:N:chlorophyll ratios with varying conditions assuming balanced growth. This model has been somewhat extended and implemented into a full marine ecosystem model, which describes also the mortality of phytoplankton from zooplankton grazing, the formation of detritus (also through the excretion and aggregation of transparent exopolymeric particles), and other processes by Schartau et al¹².

We have extended this Regulated Ecosystem Model (REcoM)¹² to a model for diatom growth that also includes limitations by silica and iron availability. The parameterization for the uptake of silica and the dependence of growth on the silica quota is based on physiological observations. It results in increased Si:N ratios in the cells under iron-limiting conditions without prescribing this effect explicitly (Hohn et al., in preparation).

2.2 Physical Model and CS510 Configuration

The simulation of the ocean circulation is done using the Massachusetts Institute of Technology general circulation model (MITgcm)^{13,14} which solves the time-dependent, Boussinesq-approximated Navier-Stokes equations with or without hydrostatic approximation, and conservation equations for salinity and energy (in the form of an equation for potential temperature). Turbulent diffusion and viscosity are parameterized following the

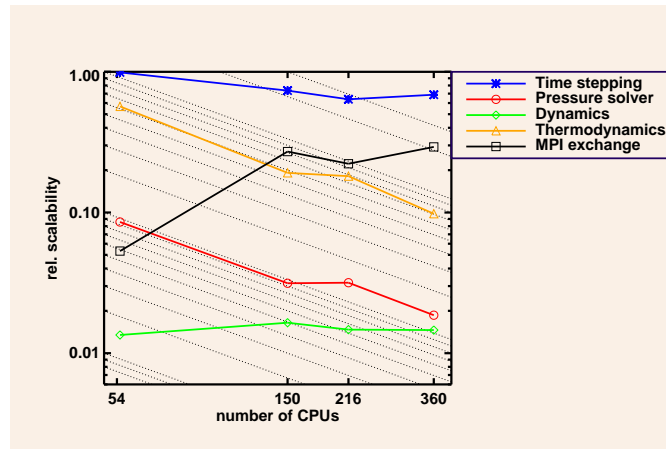


Figure 1. Relative execution times for certain/different parts of the MITgcm model. Here the biogeochemistry module (including 16 tracers) has been switched on. The diagonal lines show an ideal scaling behaviour (computing time inversely proportional to the number of CPUs).

scale-dependent Smagorinsky approach. For the vertical mixing in the surface layer, the KPP model by Large et al.¹⁵ is used.

The equations are discretized using a finite-volume method on an orthogonal grid. To avoid the singularity of a latitude-longitude grid at the poles and to ensure an approximately homogeneous spatial resolution, we have used the 'cubed sphere' grid configuration provided by the MITgcm, which is obtained by mapping a regular grid on the surface of a cube onto a sphere. The high-resolution runs were performed with a horizontal resolution of 510×510 grid points on each of the 6 sides of the cube.

3 Scalability

The MITgcm model has been chosen among other reasons, because of its known good multi-processor scalability over a large range of processor numbers and computer architectures. However, contrary to our previous experiences, the coupled system MITgcm + REcoM shows a bad scaling behaviour on the IBM system *JUMP* with increasing number of processors used. The wall-clock time only weakly decreases with increasing processor number, and even slightly increases in the simulation with 360 processors, compared to a 216-processor configuration. An analysis of the execution times for individual parts of the program (Figure 1) shows the reason for this scaling behaviour. While the main parts of the model (dynamical, thermodynamical and biogeochemical) scale approximately linearly, the required computing time for MPI interprocessor exchange increases with increasing number of processors used. The fact that the execution time for the pressure solver also does not decrease linearly with processor number does not influence the overall execution time significantly, as it is only a small fraction of the total.

A comparison to test without the biogeochemical module (Figure 2) shows that it is the MPI-communication for the 16 passive tracers that is responsible for the bad scaling

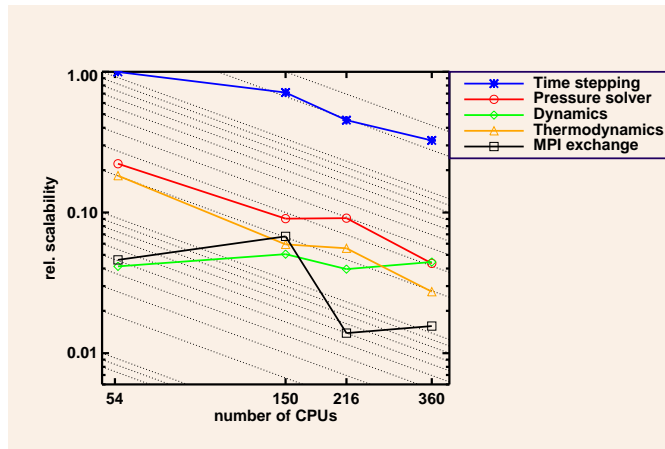


Figure 2. Same as Figure 1, but the biogeochemistry module has been switched off (no passive tracers).

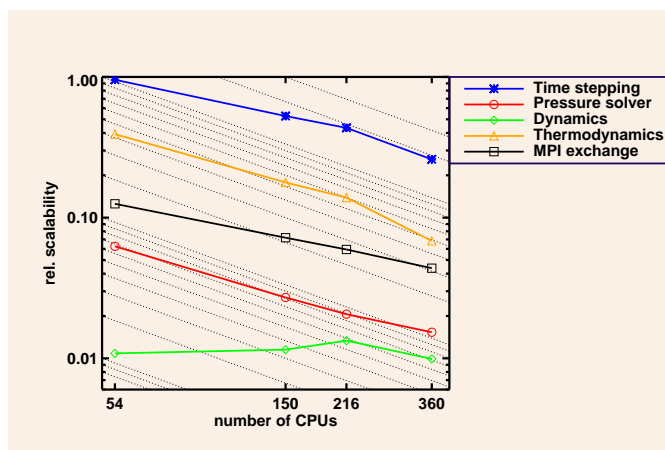


Figure 3. Same as Figure 1, but now including the biogeochemistry module and an optimized passive tracer communication.

behaviour of the model. Without the additional biogeochemical tracers the MPI exchange (and therefore the model as a whole) scales reasonably linear.

This showed that the MPI communication for the advection of the passive tracers had to be optimized. Instead of sending the data packages for the advection of each tracer over the halo boundaries of each model time individually, a new communication scheme was implemented that is adapted to the properties of the network, where the data for all passive tracers is exchanged jointly with one MPI_SEND/MPI_RECV statement. As Figure 3 shows, this decreased the time for the MPI exchange in the target model configuration with 216 processors significantly (by about 60%), which also resulted in an overall gain in efficiency.

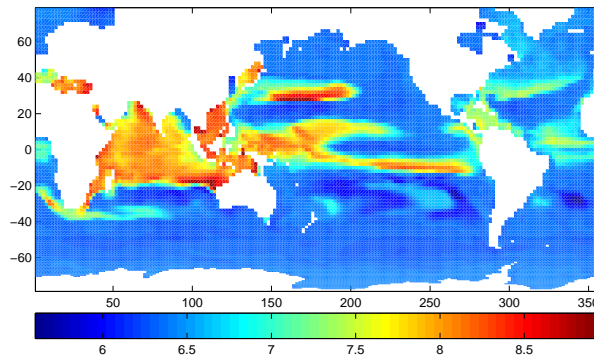


Figure 4. Modelled ratio between carbon and nitrogen (mol:mol) in the biomass within the oceanic surface mixed layer. At a sufficient supply of light and nutrients, phytoplankton cells tend toward a C:N ratio of around 6.6. The elevated values in the subtropical gyres are a consequence of strong nutrient limitation.

4 Results

Our main goal, a high-resolution run of the coupled physical-biogeochemical model over a decade, has not been reached during the first phase of the project due to the described scaling problems. We therefore just briefly demonstrate the potential of the model with some results from a coarse-resolution run and from the spinup phase of a high-resolution run.

The coarse-resolution model runs show that the representation of phytoplankton physiology in the model and the resulting decoupling of the elemental cycles of Si, C and N lead to new insights. In the subtropical gyres, which are biological 'deserts' due to the scarcity of nutrients, significantly elevated C:N ratios are modelled in the biomass (Figure 4). This would imply that these regions would contribute more than hitherto assumed to the vertical export of carbon into the deep ocean, given a fixed N and Si supply. This has consequences for the strength of the feedback between climate change and the marine carbon cycle through changes in stratification and therefore nutrient supply. The model also is able to reproduce the so-called 'opal-belt', a region of high deposition of diatom silica in the sediment around Antarctica, a feature that is usually not found in fixed-composition models (not shown).

At the same time, Figure 4 clearly shows deficits in the representation of the ocean circulation, such as an overestimate of nutrient upwelling along the equator. It will be very interesting to see whether the better reproduction in the high-resolution model of sharp fronts between nutrient-rich and nutrient-poor waters, e.g. in the ACC, will lead to an enhanced export of high C:N biomass into the deep ocean.

Model results from the high-resolution run (Figure 5) are not yet in equilibrium. However, they clearly show that the activity of eddies is reflected in the distribution of chlorophyll, especially along the ACC, and that the overly strong primary production around upwelling regions in the coarse-resolution run has been reduced and is much more in line

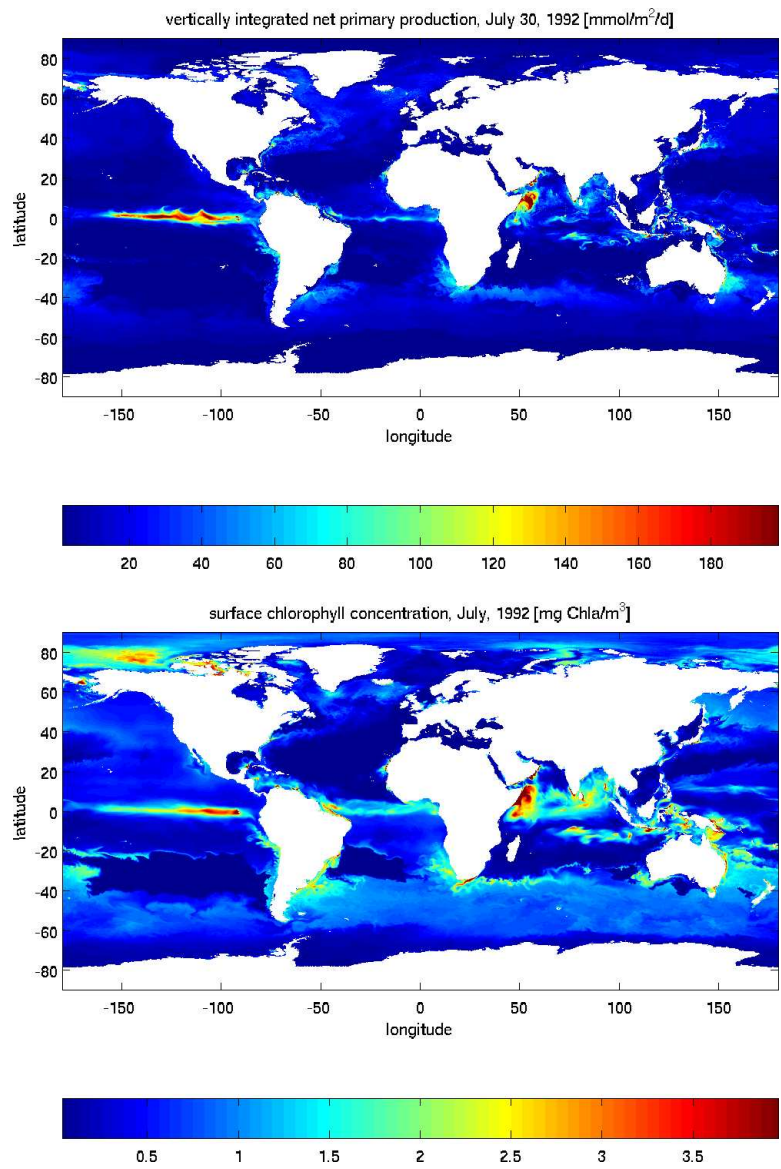


Figure 5. Results from a high-resolution run after 7 months of integration. Above: vertically integrated primary production on July 30, 1992. Below: mean concentration of chlorophyll-a at the sea surface for July, 1992.

with satellite-based estimates.

5 Concluding Remarks and Outlook

In spite of initial problems with scalability, the coupled MITgcm-REcoM model shown here shows some promise regarding the model-based description of the decoupling between the elemental cycles of carbon, nitrogen, silica and iron in a high-resolution model setup. Further model experiments will start from an optimized set of ecosystem parameter values that has been obtained by tuning the coarse-resolution model to observations of chlorophyll and export production, and will increasingly focus on the role of inter-annual variability on biogeochemical fluxes.

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