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OceanBioME

Ocean Biogeochemical Modelling Environment

OceanBioME.jl is a **Julia** package providing tools for **easy** and **flexible modelling** of the coupled interactions between ocean **biogeochemistry**, carbonate chemistry, and **physics required for ocean CDR applications**

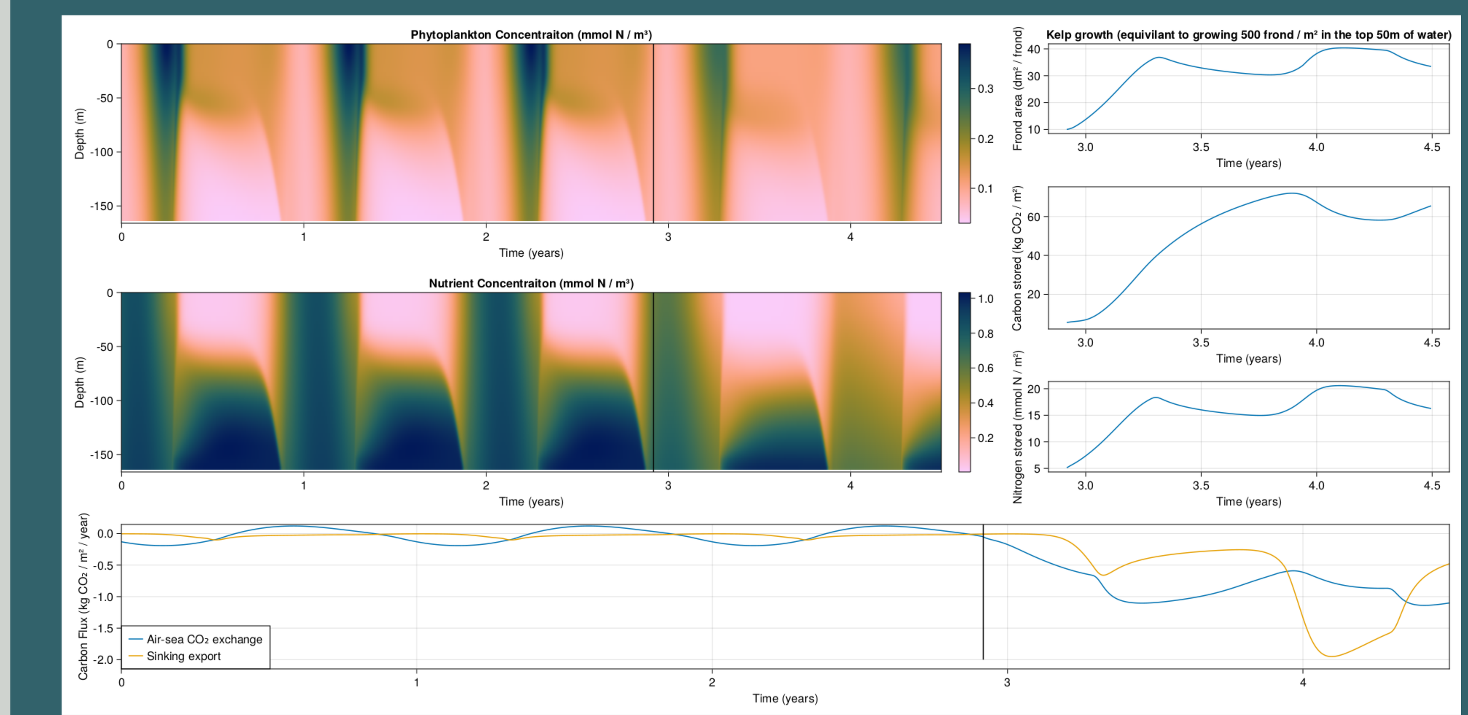
Motivation

Quantifying the effects of ocean carbon dioxide removal (OCDR) strategies is challenging due to the complex nature of the interactions between biological, chemical, and physical processes. We have built OceanBioME.jl in an attempt to ease the difficulty of modelling these systems by creating tools that provide a modular interface to the different model components, making it easy to plug in different components depending on the specific problem.

We built OceanBioME.jl to work within the tracer and particle advection of the fluids solver Oceananigans.jl (Ramadhan, et al. 2018). This means that the biogeochemical systems can be used in models of any scale, from non-hydrostatic sub-mesoscale flows, to global-scale problems. Additionally, written in Julia it is as fast as C or FORTRAN models and can easily be run on CPUs or GPUs.

Example 1: Coupled kelp growth model and biogeochemistry

Here we show the results of a 1D column model, forced by idealised light and mixing, forced with a seasonal cycle of temperature and light, which qualitatively reproduces the biogeochemical cycles in the north Atlantic. We then add kelp in December of the 3rd year which causes an increase in air-sea carbon dioxide exchange and sinking export, as well as a change in the phytoplankton growth cycle.



We are using this to investigating the effects of location and planting density on the carbon drawdown of kelp in grown in the open ocean (Chen et al., in prep).

Acknowledgements: a special thanks to Gregory Wanger and the other developers of Oceananigans.jl, without whom this work would have been significantly more difficult, to the CCRC for their continued support, and to the developers of Makie.jl (Danisch and Krumbiegel, 2021) for making the figures possible.

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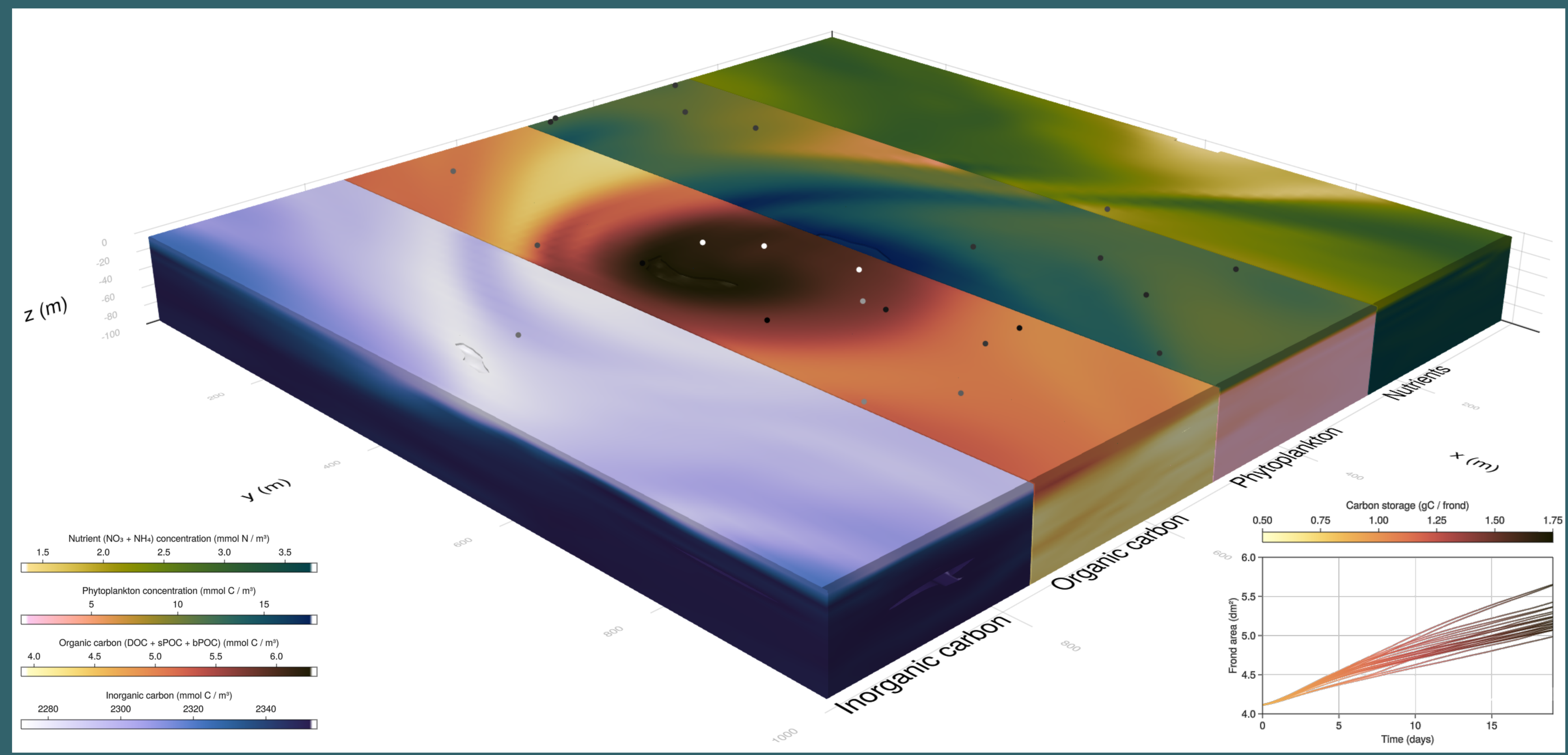
Example 2: Kelp-seeded buoys and biogeochemistry in submesoscale eddy

We have made it straightforward to add biogeochemistry to non-trivial physical situations with possibly complex forcing. For example, here we replicate the Eady problem where a background buoyancy gradient and corresponding thermal wind generate submesoscale eddies, roughly following the setup of Taylor (2016).

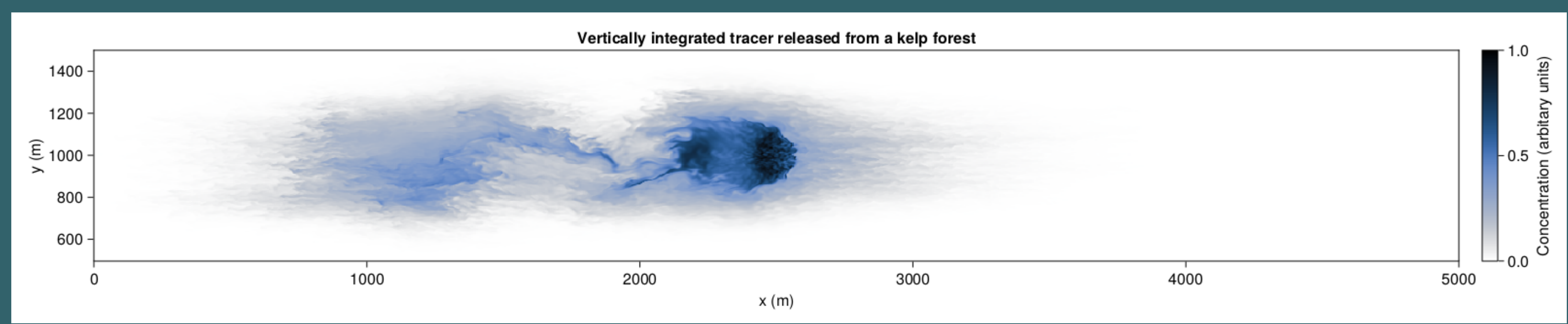


To this physical setup we added a medium complexity (9 tracers) biogeochemical model, some of which are shown above. On top of this we added particles modelling the growth of sugar kelp which are free-floating and advected by the flow, and carbon dioxide exchange from the air.

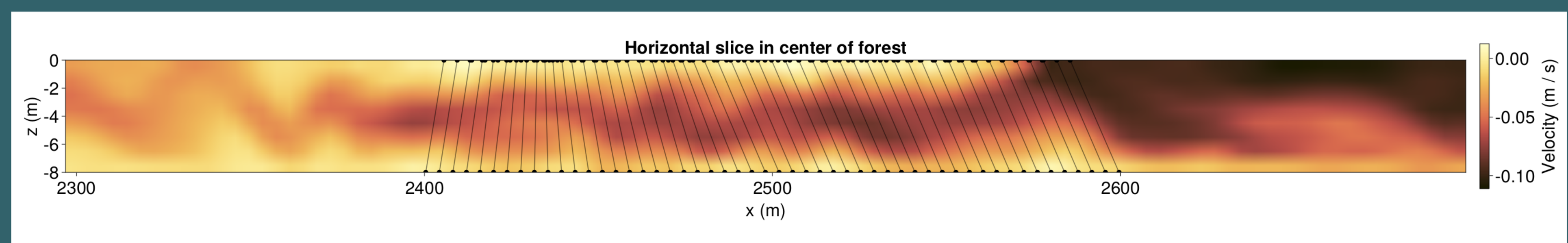
A key advantage of writing this package in Julia is it offers accessibility similar to highl-level languages such as Python, with the speed of languages like C and Fortran and built-in parallelism. This means that models can be run significantly faster than the equivalent in other high-level languages. Additionally OceanBioME can run on GPUs, allowing the above model (1km x 1km x 100m with 64 x 64 x 16 grid points) to simulate 10 days of evolution in about 30 minutes of computing time.

Example 3: flow interactions and effects on nutrients transport in a giant kelp forest

The flexibility provided by being built within a modern fluids solver makes it easy to add more complex coupled biogeochemical and physics interactions. Shown here are the flow interactions with a dynamic kelp forest, including the effects on nutrient transport and distribution (Strong-Wright and Taylor, in prep). Individual Macrocystis pyrifera (giant kelp) are modelled using floats connected with elastic lines. To visualise the flow, a tracer is released from each kelp plant.



In this model ~2000 giant kelp plants are resolved, generating complex flow interactions which affect the tracer transport. Since large parts of giant kelp float on the surface, forming a canopy, the drag force tends to be focused near the surface. Eddies and subsequent vertical mixing can be seen forming as the flow enters the forest, and the kelp are tilted more on the upstream (right) side of the forest.



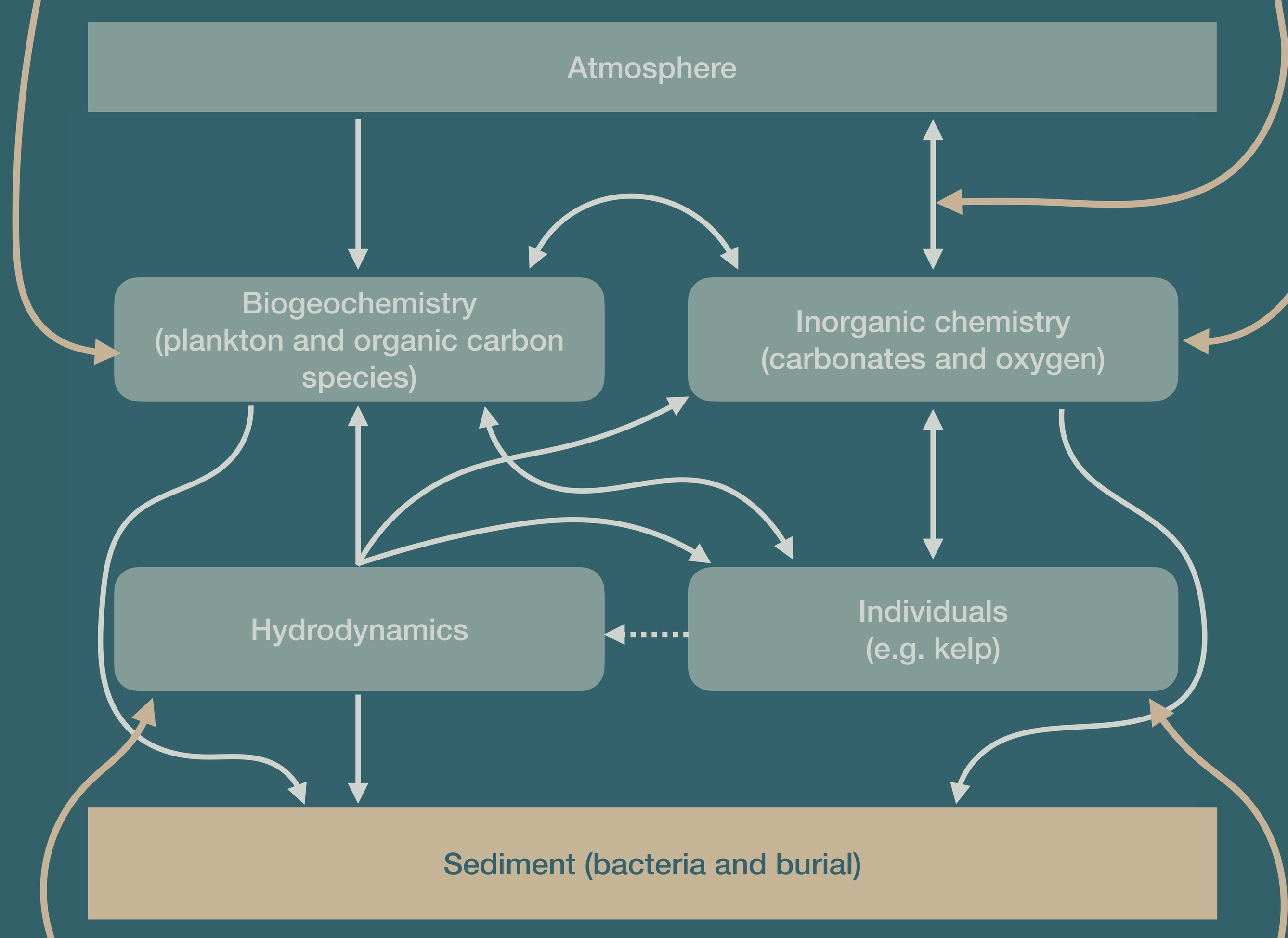
OceanBioME Features

Multiple biogeochemical models:
- Simple NPZD (Kuhn, et al. 2015)
- Medium complexity extended LOBSTER with optional variable Redfield ratio compartments (Resplandy, et al. 2012; Strong-Wright, In Prep; etc.)
- High complexity PISCES (Aumont, et al. 2015) as used in CMIP, not yet complete

Optional carbonate and oxygen chemistry models including carbon dioxide partial pressure calculation by the standard OCMIP protocol (Dutay, et al. 2002).

Air-sea gas exchange boundary condition options (e.g. Wanninkhof, 1992)

$$F = k_0 u_{10}^2 Sc^{-1/2}(C_w - \alpha C_a)$$



Tracer advection-diffusion solved by Oceananigans.jl (or optionally ignored in favour of a box model)

$$\frac{\partial c}{\partial t} = -\mathbf{u} \cdot \nabla c - \nabla \cdot \mathbf{q}_c + F_c$$

We have created a framework for easily adding biological particles which can grow and interact with tracers (e.g. up taking nutrients and excreting waste). On top of this we have also implemented a well established sugar kelp model (Broch, et al. 2019) which others can use as an example for setting up active particles and individual models.

This code snippet produces a 3D model with a biogeochemistry and kelp individuals which will grow on free-floating buoys in the open ocean*. This shows the simplicity with which users can activate different model elements and test different ideas.

* Here we are not attempting to capture the nuance of such a real life system but serve as a simple example demonstrating the ease with which different elements can be used

```julia
using OceanBioME, Oceananigans
using Oceananigans.Units

grid = RectilinearGrid(size = (32, 32, 16), extent = (1000, 1000, 100))

particles = SLatissima(; )

biogeochemistry = LOBSTER(; grid, particles, carbonates = true)

boundary_conditions = (DIC = FieldBoundaryConditions(top = GasExchange(; gas = :CO₂)), )

model = NonhydrostaticModel(; grid, biogeochemistry, particles,
                              boundary_conditions,
                              buoyancy = SeawaterBuoyancy(), tracers = (:T, :S))
```

Available at:
github.com/OceanBioME/OceanBioME.jl or scan here →

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