Deliverable D6.2

Report on the Development of the Model Platform

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About this document

Title	D6.2 Report on the development of the model platform
Work Package	6 **Determine significance of key processes in the evolving Ocean C Cycle**
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1. Key messages for the Ocean ICU stakeholders

OceanICU has developed a unified model platform that makes the project's full suite of models publicly available. The platform encompasses biogeochemical models, established 3D circulation models and novel light-weight testbeds. The WP6 model platform facilitates collaboration within the project, with WP3-5 now able to evaluate the behaviour of existing models and new process parametrisations in realistic settings. The platform also supports future external uptake of OceanICU developments through compatibility with model suites from the EU Copernicus Marine Service (CMEMS) and the EU Joint Research Centre (JRC) MSFD Modelling Framework. The OceanICU model platform already underpins the first Decision Support Tools developed within WP7 for the European Digital Twin of the Ocean (https://ocean-icu.lab.dive.edito.eu/).

2. Abstract

D6.2 reports on the development of the model platform (relating to milestone 6.1 and task 6.1). The purpose of this underpinning work is to enable the linking together of the various models used in OceanICU, such that we create a multi-model platform with which to test marine carbon flux processes, in silico. The primary outputs of this work are several public, open-source codebases (in GitHub repositories) and installable software packages (on Anaconda), accompanied by online installation instructions and user documentation. This information is not repeated here; instead, we summarize the newly developed functionality and point to online resources where appropriate. We also reflect on the transfer of data into WP6 from other work packages – which remains on going, and detail the interactions with scientists in WPs 3, 4 and 5 concerning how to optimally introduce new biological processes into the model suite.

3. Work carried out

A key focus of WP6 is to incorporate knowledge emerging from WP3 to WP5, (and of course relevant external contemporary advances) into OceanICU modelling tools (regional, basin scale and global earth system models), enabling us to resolve and to quantify the importance of key biological processes on regional and global C cycles under a range of climate pathways. The range of oceanic processes that contribute to and control the carbon cycle is large and complex. Hence OceanICU is considering processes that describe dissolved components of sea water, particles, bacterial activity, phytoplankton production, zooplankton grazing and behaviour, and cetacean activity as well as human mediated process such as trawling and deep-sea mining (table 6.2.1), all in the context of governing hydrodynamic and physical processes.

Marine and ocean models generally comprise of two components:

- a hydrodynamic scheme which deals with mixing and diffusive processes, defining the model domain and resolution
- a biogeochemical component which describes the key chemical, biological and sometimes ecological processes

Earth System Models (ESMs) have atmospheric and terrestrial processes models explicitly coupled, whilst ocean only models are forced by atmospheric and terrestrial time series. The OceanICU consortium possesses expertise in a wide range of models, e.g. simple (MOPS) or complex (ERSEM) biogeochemistry, regional, oceanic and earth system set-ups generally with high computational needs, and less computationally intensive testbeds which enable rapid progress in testing process contributions and sensitivities (GOTM, GETM, TMM), (figure 6.2.1).

Given the range of processes and domains that need to be considered, no single model system provides sufficient capability. OceanICU has taken the approach of building a suite of model systems with a high degree of inter-operability, enabling transfer of process updates between models, as and when appropriate. Further by enabling the combination of most hydrodynamic schemes with most biogeochemical schemes, OceanICU has developed an internationally unique model platform that will accelerate model-based discovery across a broad range of topics into the future.

Whilst not all processes are treatable in all model systems, to optimise the outcomes of OceanICU we need to maximise the ability of our model systems to incorporate and test new process descriptions and to simplify the process of combining new combinations of process description, biogeochemistry and hydrodynamics.

The approach adopted has been to develop FABM (Framework for Aquatic Biogeochemical Models), a computational framework that allows for the easy coupling of biogeochemical and physical models, and the development of ocean simulators which provide user friendly access to a model comparison and performance tool.

We have also developed a series of informal model introduction and model use training online meetings, coupled with process specific discussions and interactions on an ad hoc basis.

Category	Partners / WPs	Key scientists	Biogeochemical model	Physical model	Domain	Description
Benthos and disturbance	PML, GEOMAR, NIOZ WPs 5+6	Gennadi	ERSEM	GETM / NEMO	NWES	Inpacts of trawling on carbon storage and cycling in the benthos
		Gennadi, Rebecca, Karline	ERSEM	GOTM / NEMO	NWES	Representation of benthic fauna and predators, impact on C cycle
		Iris, Volkmar, Matthias, Lukas	MOPS possibly ERSEM	GOTM	Deep Ocean	Effects of deep sea mining / sediment addition on C cycle
Calcification	PML, Heriot Watt WP 6 + 3	Helen, Jerry B, Momme, Alex Poulton	ERSEM	GOTM / NEMO	NWES	Parameterisation and or evaluation of pelagic calcification and the fate of calcium carbonate
	LSCE (CEA), Heriot Watt WP 6 + 3	Marion G, Alex Poulton	PISCES	NEMO	Global	
	Geomar WP 6 + 3	Jan Taucher	tbc	tbc	Global	flux elemental composition (CaCO3:Si:C:N:P)
DOC and microbial pump	PML, CMCC WP 6 + 4	Helen, Momme	ERSEM, BFM	GOTM / NEMO/TMM?	NWES / Global TMM	Development of parameterisation of refractory DOC
	NORCE WP 6 + 4	Jerry T	iHAMOCC	BLOM	Global	Defining DOM into four pools, labile to refractory
Zooplankton	PML, Exeter WP 6 + 4	Rebecca, Dan Mayor, Marja Koski	ERSEM	GOTM / NEMO	NWES	Zooplankton migration (DVM) group with 6
			ERSEM	GOTM / NEMO	NWES	Stoichiometric modulation of predation
HTLs	DTU WP 6 + 5	Ken Andersen	Feisty-UVic	UVic	Global	Fish carbon flux
	IMR WP 6 + 4	Morten Skogen, Carla Freitas	IMR	NEMO	Norwegian Sea	Whale carbon pump through nutrients and migration
Respiration	CMCC WP 6	Momme, Marie-Lou	BFM	NEMO	Global	Vertical production-respiration balance evaluation
	ULPGC/CSIC WP 6 + 4	Javier, Anton (Sigrún??), Iris			Global	Dark ocean respiration (ETS vs. OUR)
	GEOMAR, CMCC WP 6 + 4	Iris, Volkmar, Momme, Marie-Lou, Giorgio Dall'Olmo	MOPS, BFM	TMM, NEMO	Global	Ecosystem respiration (BGC-Argo), evaluation
Flux attenuation	GEOMAR / CMCC / NOC WP 6 + 4	Iris, Momme, Marie-Lou, Steph, Sophie, Dan Mayor	MOPS, BFM	NEMO/TMM, NEMO	tbc	Phytoplankton/particle size links to flux attenuation
	GEOMAR? WP 6 + 4/3	Iris, Momme, Marie-Lou, Jan Taucher, Dan Mayor	MOPS (with aggregates) BFM	TMM? NEMO?	Global	flux attenuation (Martin's b) & size-dependent aggregate dynamics
	UiB, NORCE, NOC WP 6 + 4	Filippa, Jerry T, Steph	iHAMOCC	BLOM	Global	Expanding to two phytoplankton groups divided into one small and one large - > effect on export production
Misc	WP 4	Christian Tamburini	Microbial Transition State (MTS) theory of growth			Dark carbon fixation (chemoautotrophy)
	ULPGC WP3	Javier, Aja	potentially BFM			Impact of aerosols on primary production and plankton community structure
	LSCE (CEA) WP 6	Marion G, Marion B	PISCES	NEMO AGRIF		residence time, cross-shelf exchange, seasonal variability

Table 6.2.1. *The process to model table. This succinct version of the process to model table represents the working document within OceanICU where processes, models and domains are listed.*

List of Acronyms
BFM: Biogeochemical Flux Model
CMEMS: EU Copernicus Marine Service, https://marine.copernicus.eu/
ERSEM: European Regional Seas Ecosystem Model – a relatively complex biogeochemical and ecosystem model with multiple compartments, variable stoichiometry, pelagic and benthic components, commonly used for regional shelf sea applications
ESM: Earth System Model
FABM: Framework for Aquatic Biogeochemical Models
FEISTY: FishErIes Size and functional TYpe model
GETM: General Estuarine Transport Model
GOTM: General Ocean Turbulence Model
iHAMOCC: isopycnic coordinate HAMburg Ocean Carbon Cycle model
JRC: EU Joint Research Centre
MOPS: Model of Oceanic Pelagic Stoichiometry
MSFD: EU Marine Strategy Framework Directive
NORWECOM: NORWegian ECOlogical Model
PISCES: Pelagic Interactions Scheme for Carbon and Ecosystem Studies
TMM: Transport Matrix Method
UVic: University of Victoria (Earth System Climate Model)
model

4. Main results achieved

4.1. Development of the model platform – FABM

OceanICU has delivered the capability to mix-and-match physical environments and biogeochemical-ecosystem modules that represent a continuum of simple to complex, computationally efficient models. The OceanICU model platform was built on top of the Framework for Aquatic Biogeochemical Models (FABM; Bruggeman & Bolding, 2014). This ensures compatibility with a wide range of existing models, as well as with the EU Copernicus Marine Service (CMEMS; https://marine.copernicus.eu/) and the EU Joint Research Centre MSFD modelling framework (Garcia-Gorriz et al., 2018). OceanICU has constructed its model platform by:

1. Porting key biogeochemical modules that were not previously available in FABM (MOPS, iHAMOCC, UVic BGC) to the framework.
2. Providing new computationally efficient FABM-based model testbeds: the Transport Matrix Method (TMM) and UVic Earth System Model of Intermediate Complexity

These components add to the suite of physical and biogeochemical models already coupled with FABM (ERSEM, NEMO, NORWECOM, PISCES, BFM).

An overview of the model platform is shown in Fig 6.2.1.

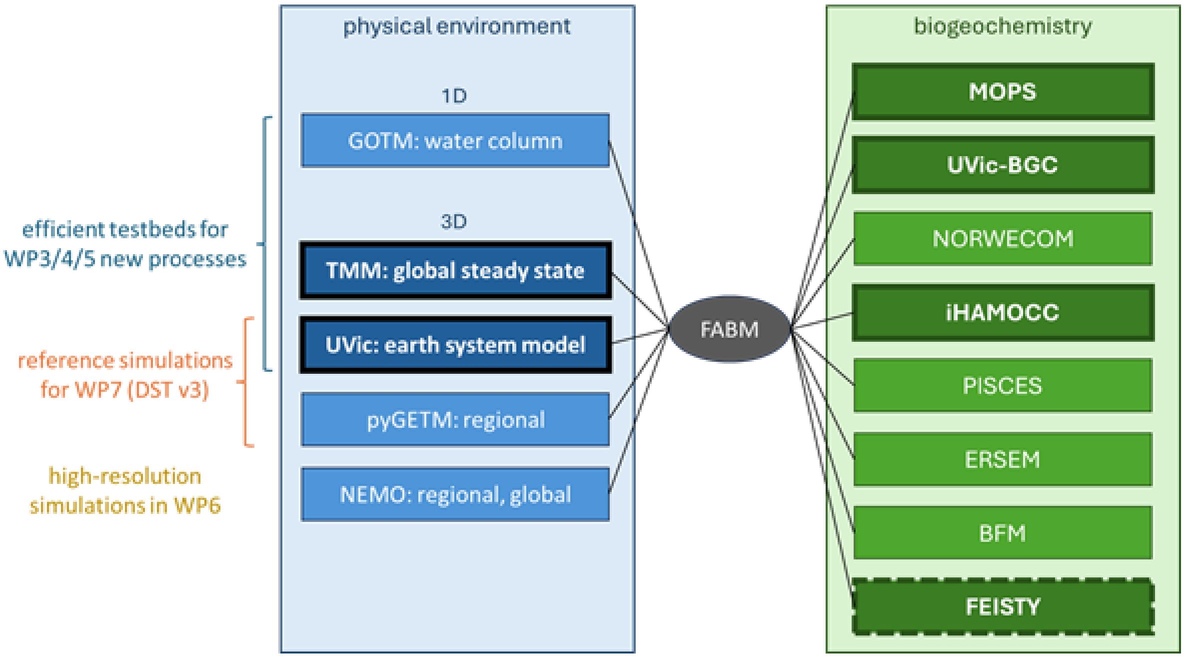

Figure 6.2.1. *The OceanICU model platform with interchangeable physical and biogeochemical components, built on the Framework for Aquatic Biogeochemical Models (FABM). Model components newly implemented within OceanICU (T6.1) are indicated with dark fills, thick borders, and bold font. Components with solid borders are ready for immediate use; those with a dashed border will be integrated in the platform in the next phase of the project. Planned applications of the different physical components within OceanICU are enumerated on the left.*

4.1.1. FABM and MOPS biogeochemistry

A FABM implementation of the MOPS (Model of Oceanic Pelagic Stoichiometry) biogeochemical model (Kriest & Oschlies, 2015) has been developed. The new implementation of MOPS, “FABM-MOPS”, was modularized to facilitate the modification or addition of new process descriptions within OceanICU. An overview of components is given in Fig 6.2.2.

	code files / Fortran types	runtime instances	explanation
core modules	carbon.F90	carbon	carbonate chemistry; surface flux of CO_2
	detritus.F90	det	detritus and sedimentation
	nitrogen_fixation.F90	nitrogen_fixation	nitrogen fixation (implicit; DIN/DIP dependent)
	oxygen.F90	oxy	oxygen solubility and surface flux
	phytoplankton.F90	phy	phytoplankton and primary production
	radiation.F90	radiation	irradiance within the water column
	remineralization.F90	remineralization	aerobic and anaerobic remineralization
	runoff.F90	runoff	surface fluxes of DIN/DIP/DIC
	tracer.F90	dop	registration of dissolved organic phosphorus
		pho	registration of phosphate tracer
	<FABM:bb/passive>	din	registration of DIN tracer
	zooplankton.F90	zoo	zooplankton and secondary production
	<FABM:interior_constant>	sil	constant silicate concentration
diagnostics / support	insolation.F90	insolation	surface irradiance
	shared.F90		fixed parameters & common functions

Figure 6.2.2*. Overview of the modules of the FABM port of the MOPS biogeochemical model. Square rectangles correspond to code files/FABM types, while the rounded rectangles correspond to the instances of those modules invoked in a full model run. The modules are separated into core modules which are required to run the model and support (or diagnostic) modules.*

FABM-MOPS is available from a public repository: https://github.com/BoldingBruggeman/fabm-mops. FABM-MOPS is further included in the FABM-plus distribution, through which it integrates with a number of publicly distributed modelling applications including GOTM, pygetm, EAT, pyfabm and the FABM offline simulator. The new MOPS implementation is also part of the biogeochemical model ensemble used in the GOTM-FABM DST demo developed within WP7. The biogeochemical structure of FABM-MOPS will be continuously updated by GEOMAR.

4.1.2. FABM and iHAMOCC biogeochemistry

The iHAMOCC biogeochemical model (Tjiputra et al., 2020) that forms part of the Norwegian Earth System Model (NorESM) has been implemented as a FABM-compatible model. As part of the new implementation, iHAMOCC was modularized. An overview of the resulting modules and their underlying code is given in Fig. 6.2.3. The FABM-iHAMOCC code has been made available in a public repository: https://github.com/BoldingBruggeman/fabm-ihamocc. In addition, it has been included in the FABM-plus distribution. The new iHAMOCC implementation is also included in the biogeochemical model ensemble used in the GOTM-FABM DST demo developed within WP7.

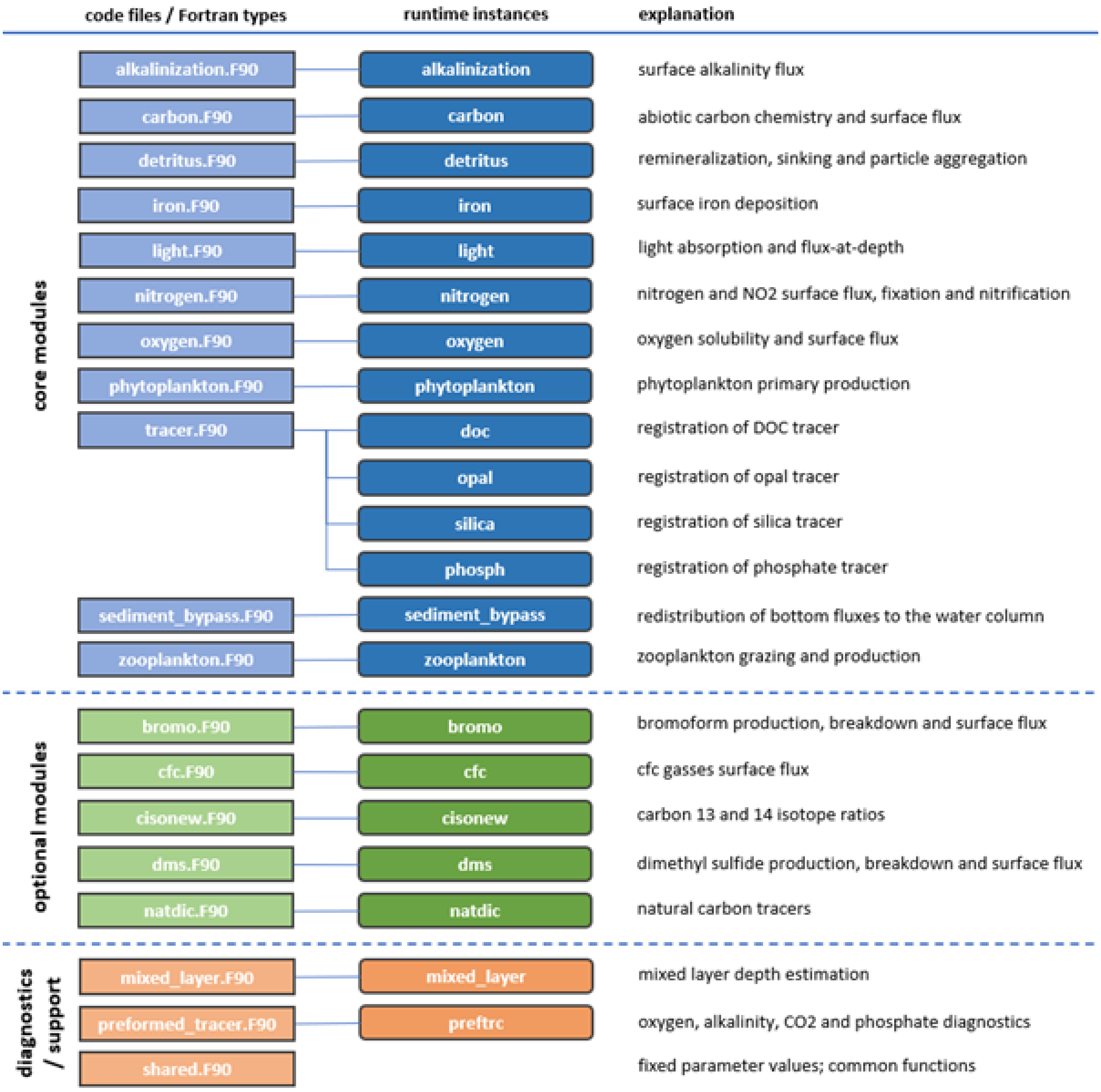

***Figure 6.2.3**. Overview of the modules of the FABM port of the iHAMOCC biogeochemical model. Square rectangles correspond to code files/FABM types, while the rounded rectangles correspond to the instances of those modules invoked in a full model run. The modules are separated into core modules which are required to run the model; optional modules; and support (or diagnostic) modules.*

4.1.3. FABM and UVic biogeochemistry

The first FABM implementation of the biogeochemical component of the University of Victoria Earth System Model (UVic ESCM) has been developed. The code is available from a public repository: https://github.com/BoldingBruggeman/fabm-uvic.

4.1.4. The Transport Matrix Method with FABM support

A FABM-compatible implementation of the Transport Matrix Method (TMM; Khatiwala, 2007), which provides a computationally efficient way to obtain equilibrium (climatological) simulations of global 3D biogeochemistry has been developed. It typically allows global simulations to be run on a single computer workstation or laptops, with runtime ranging between 25 seconds and 8 minutes per simulated year, depending on the complexity of the biogeochemical model. The code is parallelized to use multiple cores, allowing it to run on high-performance computing (HPC) systems to further speed up simulations.

The TMM implementation was written from scratch in Python as a new transport module in the FABM offline simulator: a flexible framework for simulation of marine biogeochemistry. By building on this framework, the new TMM implementation is (1) immediately available on all platforms (Windows, Mac, Linux), (2) easy to use and customize (a number of examples are provided), and (3) directly usable with any FABM-based biogeochemical model. The code is available from a public repository (https://github.com/BoldingBruggeman/fabmos) and also as ready-to-install application from Anaconda (https://anaconda.org/bolding-bruggeman/fabmos). Detailed installation instructions and a user guide are available from the wiki at https://github.com/BoldingBruggeman/fabmos/wiki.

Examples of TMM results are shown in figs 6.2.4 and 6.2.5. It should be noted that these show a proof of concept only, as the underlying simulation was initialized with constant concentrations of all biogeochemical variables throughout the domain and run for only 10 years. In practice, simulations would be initialized from spatially varying climatologies such as the World Ocean Atlas (Reagan et al., 2024) or GLODAP (Lauvset et al., 2016), run for much longer (e.g., 3000 years), or both.

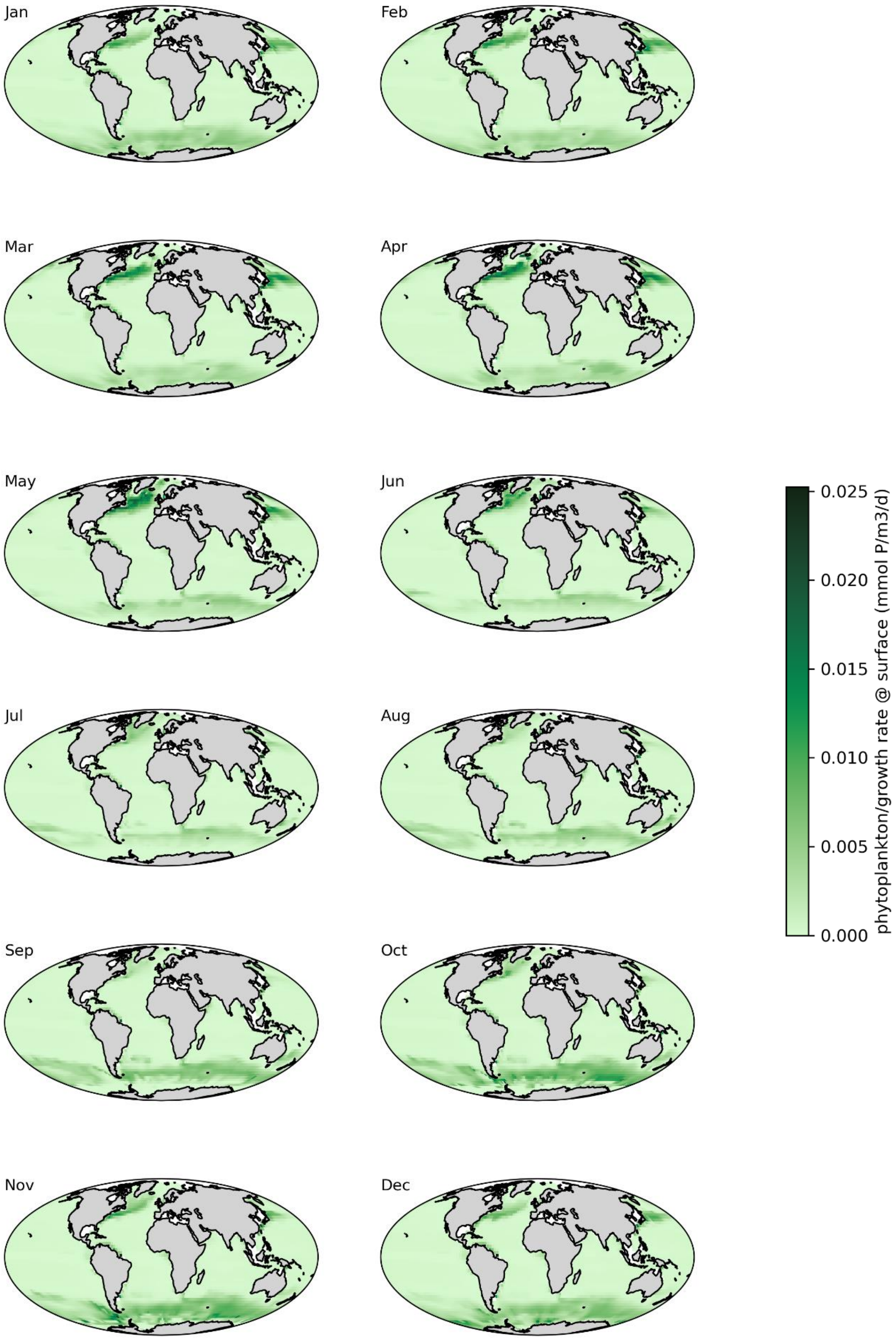

***Figure 6.2.4**. Monthly mean phytoplankton growth rate at the surface, produced with the MOPS biogeochemical model* (Kriest & Oschlies, 2015) *and the MITgcm 2.8˚ transport matrix after 10 years of simulation.*

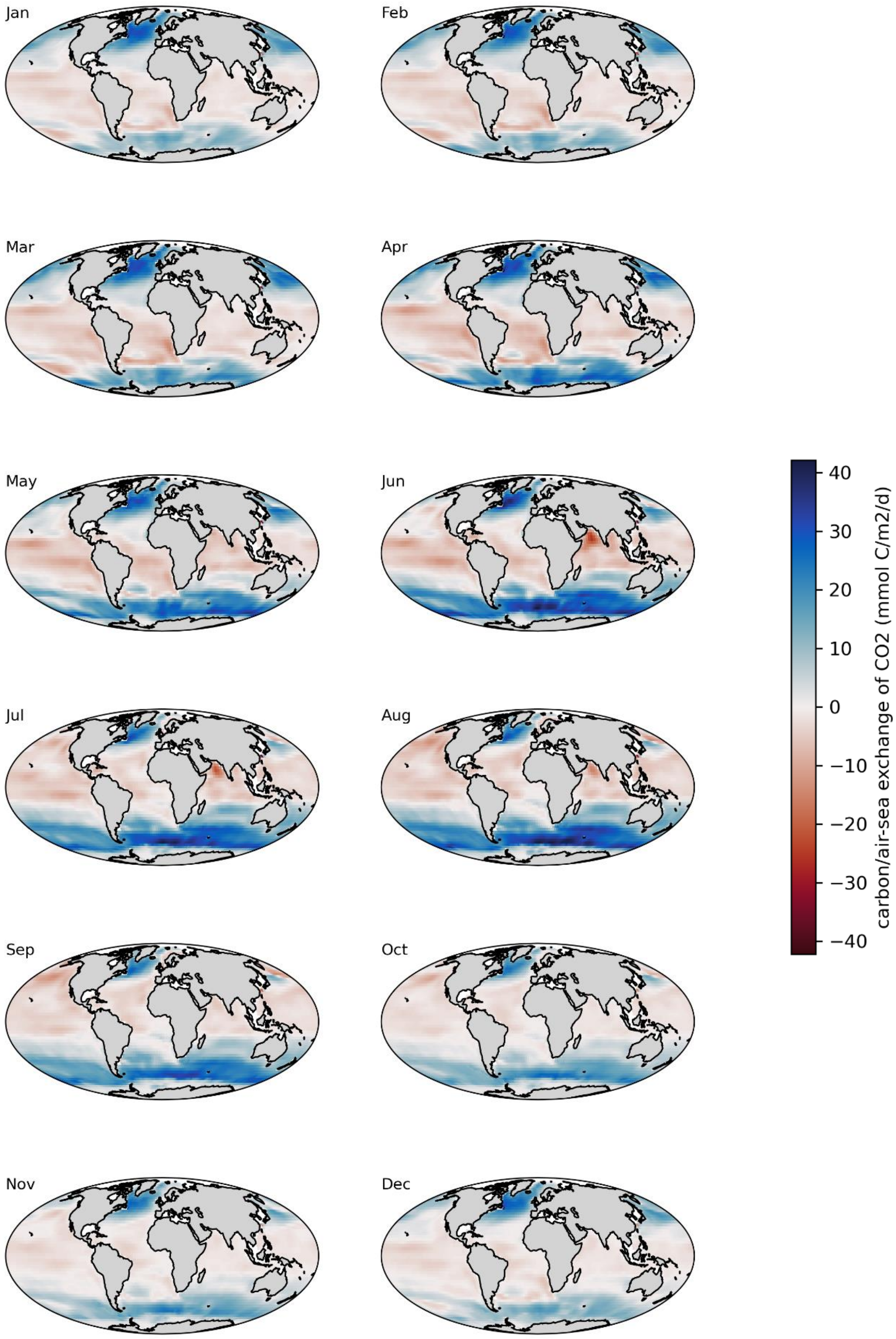

Figure 6.2.5*. Monthly mean CO_2 gas exchange, produced with the MOPS biogeochemical model* (Kriest & Oschlies, 2015)*and the MITgcm 2.8° transport matrix after 10 years of simulation. Positive values indicate a flux from atmosphere into the ocean.*

A comparison between results from the new TMM implementation described here, and the original from https://github.com/samarkhatiwala/tmm, indicate that the new implementation produces results are indistinguishable from the original (within numerical precision), while being about five times faster when run in serial (results obtained with MITgcm 2.8° and MOPS). A comparison of performance in parallel was not performed, but the new TMM implementation scales well to multiple cores, in particular when the biogeochemical time step is smaller than the transport times step (Table 6.2.2).

Table 6.2.2. Performance of the TMM implementation with various biogeochemical models. All simulations use the MITgcm 2.8° transport matrix (https://doi.org/10.5281/zenodo.5517237) with a time step of 12 h for transport. They were run on a workstation with an Intel Core i7-10700 CPU (8 physical cores) and 32 GB of memory.

Biogeochemical model	**Time step for biogeochemistry**	**Number of CPU cores**	**Runtime per year (s)**
MOPS (Kriest & Oschlies, 2015)	12 h	1	47
MOPS (Kriest & Oschlies, 2015)	12 h	5	25
ERSEM (Butenschön et al., 2016)	1 h	1	1571
ERSEM (Butenschön et al., 2016)	1 h	5	499
PISCES (Aumont et al., 2015)	1 h	1	506
PISCES (Aumont et al., 2015)	1 h	5	157

4.1.5. The UVic Earth System Model with FABM support

UVic ESCM (Weaver et al., 2001) is a widely used earth system model developed in the 1990s at the University of Victoria, Canada. The model consists of atmosphere, ice, and ocean components. One reason for its widespread adoption is the model's running speed. There are two reasons for this: first, the atmospheric component is very simple; second, the model is typically run at a relatively coarse horizontal resolution and modest vertical resolution. The implication is that the model can be run on a normal desktop/laptop.

For production runs the model is typically run on dedicated hardware as it is often the wish to make very long simulations – thousands of years – to e.g. spin up a biogeochemical model to equilibrium.

In this project the aim is to be able to use FABM as a drop-in replacement for the hardcoded biogeochemical model – but still maintain the option to run the original code.

To achieve this two GitHub repositories have been created. The first one - UVic_2.10_updates_fabm - with the source code necessary to use FABM with UVic ESCm. The naming of the repository is in accordance with the naming scheme used at GEOMAR, Kiel, Germany for updates to the original UVic ESCM v2.10 (Mengis et al., 2020) which we have used as our basis. The second one - uvic_fabm_setups - different configurations for applying different biogeochemical models when running UVic ECSM.

Being more than 30 years old, and considering the developments in computer science, the model structure and build/compilation system is quite far from how things would be done today, but due to the reputation and robustness no significant changes have been made to the code over the years – except for improvements/changes in the scientific algorithms.

The ocean component of UVic – which is of main interest in this project – is an early version of the Modular Ocean Model (MOM) (https://www.gfdl.noaa.gov/ocean-model/) from Princeton University. A biogeochemical model has been hardcoded in MOM.

Further information on the code structure, implementation detail and how to compile UVic ESCM with FABM support can be found in the repositories README.

With a compiled version of UVic ESCM a fully functional experiment must be created. In addition to the executable this includes creation of the *control.in* configuration file with all runtime configuration and the creation of optional input files. A full description of the necessary steps are provided in the README.

As a simple example a passive tracer experiment has been done. It is used to investigate and prove the technical implementation of FABM in UVic. It may be used for the evaluation of:

- The configuration and initialization of the coupling when reading *fabm.yaml*
- Allocation of memory, i.e. proper specification of *nt*, *nsrc* and *numsbc*

- The proper injection of FABM specific subroutines in the UVic code base
- The conservation of mass when only UVic's advection/diffusion operator + a provided sinking speed is considered – i.e. no biogeochemical processes
- The FABM link to the UVic output system including calculation of temporal and space averages, adding variables to files.
- Link to externally specified files
- And finally, the proper integration to the UVic time integration

Below are the results for 2 passive tracers after integrating one year and taking an annual average. In both cases the plot shows the surface concentrations – the top layer being 17m. The only difference is the initial conditions and the sign of the sinking velocity.

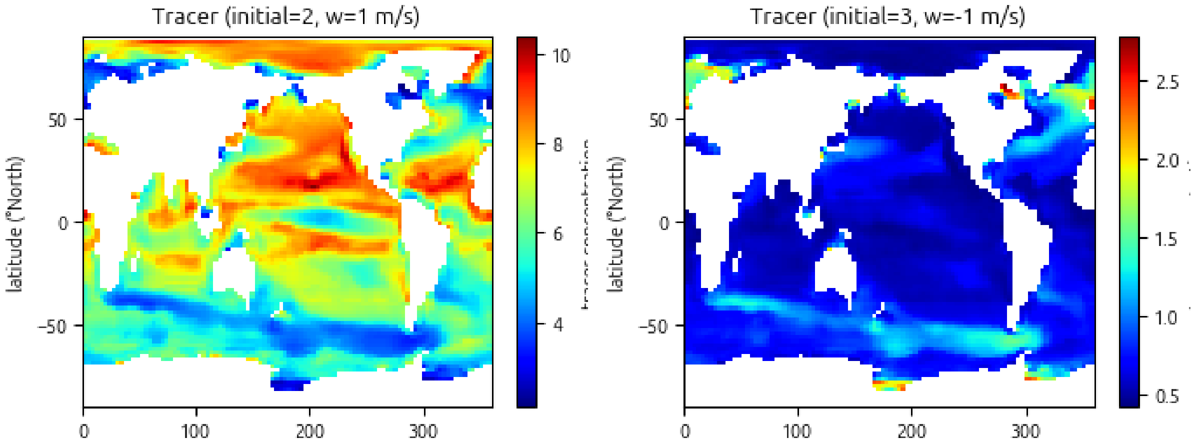

Figure 6.2.6: Passive tracer experiment with mean annual concentration after one year simulation. The difference between the two is the value of the initial condition and the sinking speed. To the left the initial condition is 2 and the sinking speed is 1 m/s. To the right initial condition is 3 and the sinking speed is -1 m/s.

The implementation has not been extensively tested yet and issues are likely to show up when used in complicated configurations.

4.1.6. FEISTY

The FEISTY framework has been re-implemented in Fortran and as an R package. FEISTY will be used in other tasks to model fish carbon sequestration. This makes the model framework ready for inclusion with FABM. The implementation is described in Zhao et al. (2025).

4.1.7. BFM

Model code and documentation, including its FABM flavour, has been provided to project partners, and the modelling framework has been presented at the model introduction workshop. The “mix-and-match” flexibility that BFM acquired through FABM framework has recently been demonstrated by new work outside OceanICU (Álvarez et al., 2025).

4.1.8. ERSEM

ERSEM (Butenschön et al., 2016) has previously been fully coupled to FABM and routinely used with GOTM, NEMO and FVCOM hydrodynamic models. Within OceanICU the ERSEM code has been coupled to and tested with the GETM (Fig 6.2.7) and TMM hydrodynamics, with acceptable skill. The ERSEM code repository is hosted at: GitHub - pmlmodelling/ersem: European Regional Seas Ecosystem Model

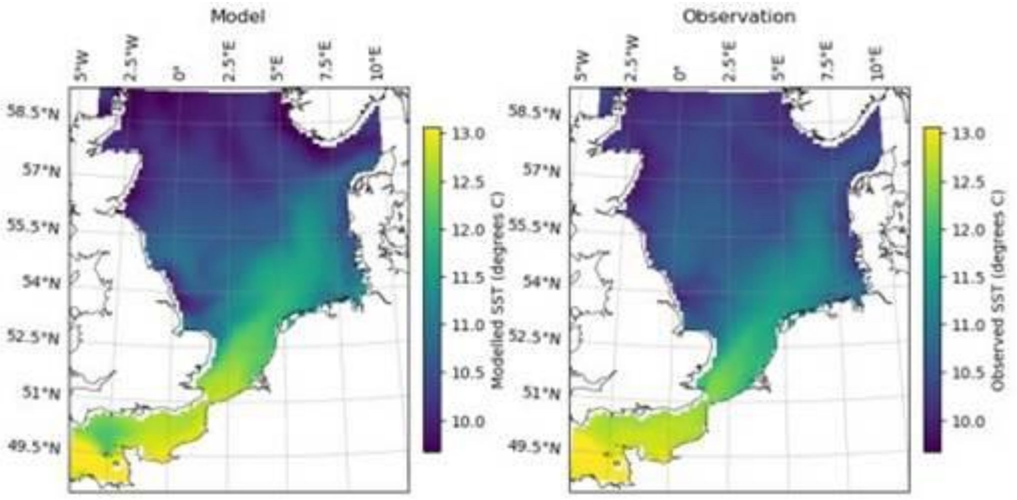

Figure *6.2.7. Comparison of GETM/ERSEM modelled temperature with observations.*

4.2. Dialogue and data exchange

Via the implementation plan and early conversations, the project participants identified a set of processes to target, based on their likely importance to the carbon cycle, the status of their representation in existing models, and the capability within the project. Process choices are subject to review; we retain a flexible approach guided by emerging knowledge. The “Process to Model table (of which a succinct version is shown in table 6.2.1) is used to manage the evolution of process development and connectivity between the model centric work package (WP6) and the empirical work packages (WPs 2-3-4-5). Small group discussions on each process development are held as required and also within OceanICU annual meetings.

Three workshops have been organised to facilitate seamless integration from WPs 3-5 through WP 6 to WP7: a model introduction workshop where model authors presented the features of their biogeochemical models (lead: GEOMAR; contributors: BB, CMCC, DTU, IMR, NORCE, PML, July 2023), a hands-on workshop where OceanICU partners could run a biogeochemical model of their choice in the GOTM water column model (lead: BB, contributors: GEOMAR, PML, CMCC, Sept 18, 2023), and a hands-on workshop where OceanICU partners could run a biogeochemical model of choice in global ocean circulation simulated with the TMM (lead: BB, contributors: GEOMAR; 8 November 2023).

5. Contribution to the overall objectives and relevant (KPIs)

This work underpins the following OceanICU objectives:

- **ST2** Use the understanding developed under ST1 to give us increased predictability of the ocean carbon cycle, particularly around the role of marine pelagic and benthic invertebrate and vertebrate C. **(WP6)**
- **ST3** Incorporate the new knowledge from ST2 into OceanICU modelling tools (regional, basin scale and global earth system models) to resolve and quantify the importance of key biological processes on regional and global C cycles under a range of climate pathway scenarios and thus support the international intergovernmental architecture relevant for climate and ocean management **(WP6)**
- **ST4** Develop a suite of tools to predict the impact of resource extraction processes on the contemporary ocean C cycle, the optimal measurement of the Ocean C cycle and build Decision Support Tools (DSTs) to predict the impacts of industrial processes in a future ocean **(WP 5-7)**

and Key Performance Indicators (KPIs):

- (1) Full description of the abundance of 10 functional groups and their biogeochemical rates across basin scales or through the mesopelagic
- (2) Numerical code describing 10 new processes available for modelling by OceanICU and other CMIP Models
- (6) Model predictions of C cycle made using 2 OceanICU models containing 5 new parameterizations.
- (8) Library of 10 OceanICU parameterizations

6. Impact and progress beyond state of the art

The OceanICU model platform underpinned a half-day, in-person workshop “Introduction to new capabilities in marine biogeochemical and ecosystem modelling", held as part of the 2024 Advances in Marine Ecosystem Modelling Research conference (AMEMR; https://www.amemr.com/). At this workshop, 36 early-career and experienced researchers from all over the world used the OceanICU models and testbeds to perform water column and global simulations of ocean biogeochemistry.

The model platform underpins the first OceanICU Decision Support Tool (DST), released on the European Digital Twin of the Ocean (https://ocean-icu.lab.dive.edito.eu/). This DST is developed in OceanICU WP7. By directly incorporating the model platform, it is able to benefit from the fast-running OceanICU model testbeds. The DST also exploits the platform's ability to mix and match models to perform simulations with ensembles of different biogeochemical models.

7. Lessons learnt and links built

The model framework provides a key conduit between empirical (WP 2-5) and modelling (WP6) work packages by making models and testbeds more easily accessible to all partners. This was facilitated by the three dedicated workshops that demonstrated the ingredients of the model platform to WPs 2-5 (see section Dialogue and data exchange). The model platform also provides a direct mechanism through which model developments can feed into the OceanICU decision support tools (DSTs), as the first iteration of the WP7 DST, now live on the EU Digital Twin of the Ocean, has been built directly on top of the WP6 platform.

8. References

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