Brief communication: Intercomparison study reveals pathways for improving the representation of sea-ice biogeochemistry in models

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Abstract. Sea-ice biogeochemical models are key to understanding polar marine ecosystems. We present an intercomparison of six one-dimensional sea-ice biogeochemical models, assessing their ability to simulate algal phenology and nutrient dynamics by comparing them with sea-ice physical-biogeochemical data collected during the N-ICE2015 expedition. While no model fully captured observed bloom dynamics without tuning, adjustments improved biomass simulations but had a limited impact on nutrient representation. Variability in tuning strategies underscores key knowledge gaps and the need for further model development in more harmonised ways. Our findings can inform future efforts to enhance the reliability and predictive capacity of sea-ice biogeochemical models.

1 Introduction

Sea ice is home to an active microbial community, with ice algae displaying some of the highest Chlorophyll-a (Chl-a) concentrations of any aquatic environment (Arrigo, 2017). Ice algae play multiple pivotal roles in polar oceans, representing the largest biomass fraction in sea ice (Poulin et al., 2011), contributing to overall marine primary production (Dalman et al, 2025), acting as a critical food source for the marine food web, especially during winter (Schaafsma et al., 2017), and efficiently contributing to the ocean carbon sink (Boetius et al., 2013). Together with phytoplankton, ice algae form the foundation of the polar marine food web, supporting key under-ice foraging species such as Arctic cod (*Boreogadus saida*) in the Arctic Ocean (Geoffroy et al., 2023) and Antarctic krill (*Euphausia superba*) in the Southern Ocean (Kohlbach et al., 2017). These species depend on the presence of sea ice and play a crucial role in transferring carbon to higher trophic levels, including humans (Steiner et al., 2021).

Current environmental changes are placing considerable pressure at the base of the food web, triggering significant effects throughout trophic levels. Despite the recognised importance of the sea-ice ecosystem (Lannuzel et al., 2020), our knowledge remains limited due to its remote location and extreme weather conditions, which restrict observational data - particularly biological observations - to sparse spatial and temporal distributions. As a result, the representation of sea-ice biological and ecological processes in numerical models has historically been limited. However, in recent decades, significant advances have been made in modelling sea-ice habitats and the evolution of sea-ice biological communities (Castellani et al., In press). Progress includes improved representation of physical processes, greater biodiversity, and enhanced ecosystem complexity.

An intercomparison of three-dimensional models has already been conducted to understand similarities and differences in simulated ice algae abundance and distribution (IAMIP1, Watanabe et al., 2019). This study investigated the seasonal-to-decadal variability in ice-algal primary productivity across four Arctic regions during 1980–2009, as simulated by five participating models. Its conclusions indicated that, despite the ongoing reduction in Arctic sea ice, the decadal trend in ice-algal productivity remained unclear. The vernal bloom shifted towards an earlier onset and shorter duration over the simulated period, and the choice of maximum growth rate was identified as a key driver of inter-model differences in simulated ice-algal primary productivity. A second phase, expanding the study's scope to global coverage and centennial timescales following CMIP6 protocols, is currently underway (IAMIP2, Hayashida et al., 2021). However, given the numerous limitations and uncertainties associated with these large-scale models, they are more useful for deriving bulk properties than for investigating detailed ecological processes.

To this end, one-dimensional (1D) process models become essential for addressing knowledge gaps in sea-ice biogeochemistry and ecological dynamics, as they provide a level of detail that large-scale models lack. They also allow for direct comparisons with in-situ observations, improving the ability to validate results. However, existing process models have been developed independently during periods of limited observations and incomplete process understanding, validated by observations at different locations, leading to substantial differences across models. These differences make an intercomparison of models performances challenging. To address this, the BEPSII (Biogeochemical Exchange Processes at Sea-Ice Interfaces, https://www.bepsii.org) expert group initiated an intercomparison of 1D sea-ice biogeochemical models, presented here, aiming at understanding variability among models' results and drivers of model sensitivity, testing transferability, and with the final goal to promote harmonisation for future model developments. The focus has been on understanding the similarities and differences in simulated ice algae dynamics and investigating the controlling factors responsible for the temporal variability of ice-algal productivity among existing 1D models.

https://doi.org/10.5194/egusphere-2025-1107
Preprint. Discussion started: 15 April 2025

We present in this study an intercomparison of 1D sea-ice biogeochemical models (briefly described in Sect. 2.1), focusing on their ability to simulate ice algal dynamics and nutrient cycling. Using a refrozen lead time series (described in Sect 2.2) as a test case, we assess model performance through a structured comparison of simulated and observed biogeochemical variables. Two experiments—*no tuning* and *tuning*—were conducted (Sect 2.3) to evaluate the baseline model configurations as well as the impact of targeted parameter adjustments on model accuracy. We analyse differences in model outputs, identify key sources of variability, and discuss the challenges associated with simulating ice algal growth and nutrient fluxes (Sect 3). Finally, we highlight the implications of our findings for future model development and propose directions for improving the representation of biogeochemical processes in sea-ice models (Sect. 4).

2 Methods

2.1 Sea-ice biogeochemical models

1D process models are typically designed to represent only vertical processes, assuming little horizontal advection. Since they are computationally efficient, these models can incorporate a high level of ecosystem complexity, such as representing multiple functional groups of organisms and providing high vertical resolution by discretising sea ice into several layers.

1D sea-ice biogeochemical models vary in vertical resolution, ecosystem complexity, and whether they are coupled to the ocean and/or atmosphere (Castellani et al., In press). The biogeochemically active part of sea ice, also known as the Biologically Active Layer (BAL) (Tedesco et al., 2010), is represented either as a single layer near the ice-ocean interface of prescribed or variable thicknesses depending on sea-ice permeability, or as multiple layers spanning the vertical range of the sea ice with an active brine network (e.g., Jeffery et al., 2016). Single-layer approaches are computationally more efficient, with dynamic layering providing a more realistic representation of bottom community dynamics (Tedesco et al., 2010). Multi-layer models, on the other hand, capture the vertical variability of biogeochemical variables and allow simulating surface and infiltration communities.

As in ocean models, the structure of sea-ice microbial ecosystems is represented using a set of Chemical Functional Families (CFF). These can be inorganic, such as sea-ice micro- and macronutrients, or organic, further divided into living CFF (e.g., ice algae) and non-living CFF (e.g. sea-ice detritus). The simplest models are N-P models, which include only one nutrient (N) and one algal functional type (P). The elemental composition of ice algae is typically fixed based on prescribed Redfield Carbon, Nitrogen, Silicon, Phosphorous ratios (106:16:16:1), along with fixed Chlorophyll:Carbon ratios. The more comprehensive N-P-Z-D models also include grazers (Z) (such as ice fauna) and/or sea-ice detritus (D). In the simplest version of these models, only one limiting nutrient is considered. More complex models may represent multiple nutrients and different CFFs for ice algal communities, as well as bacteria and grazers. In simpler models, the processes associated with bacterial remineralisation or grazer feeding are often implicitly parameterised using constant rates.

The intercomparison included five modelling teams and a total of six model configurations. These models varied in several aspects, encompassing differences in physical and biogeochemical process complexity, radiation schemes, vertical resolution, choice of limiting nutrient(s), and coupling to an interactive sea-ice physical model and/or ocean biogeochemical model. Table 1 summarises the main commonalities and differences among the models. For more details on a specific model, we refer to the model's original reference (Table 1).

Table 1: Sea-ice biogeochemical models participating in the 1D intercomparison project. BGC stands for biogeochemistry. Please see the main text for the remaining nomenclature used in the table.

Model	Ice Physics	Transport	Radiation	Grid for sea ice BGC	Sea-ice functional groups	Cell quotas/Chl:C	Limiting elements	Ocean BGC	Reference
BFM-SI	SM 0L	Growth/melt	1 band; BL	1L bottom dynamic	3N-2P-2D-1B-1Z	Quota/prognostic	Nitrogen, Phosporous, Silicon	1D slab	Tedesco et al (2010)
BFM-SI-Clim	SM 0L	Growth/melt	1 band; BL	1L bottom dynamic	3N-1P-2D	Quota/ prognostic	Silicon	1D	Tedesco and Vichi (2014)
CICE 5.1	EC ML	Melt, Brine drainage	1 band; DE	Multi-layer	2N-1P-1D	RFD/constant	Nitrogen, Silicon	n.a.	Duarte et al (2017)
CSIB-1D	SM 0L	Melt	1 band; BL	1L bottom static	2N-3P-2Z-2D	RFD/constant	Nitrogen, Silicon	1D	Mortenson et al (2017)
SIESTA	EC ML	Desalination	32 bands; DE	Multi-layer	3N-1P-1D	RFD/constant	Nitrogen, Phosporous, Silicon	n.a.	Saenz and Arrigo (2014)
SIMBA	Prescribed	Melt	1 band; BL	1L bottom static	1N-1P-1D	RFD/constant	Nitrogen	n.a.	Castellani et al (2017)

Most of the models had interactive physical components, while only one required prescribed ice physics. Additionally, only half of the models were coupled to an interactive ocean biogeochemical model. Among the sea-ice physical models, complexities ranged from a Semtner 0-layer scheme (SM 0L) to multi-layer energy-conserving models (EC ML). All models, except one, used a single-band radiation transfer scheme, with many assuming Beer-Lambert (BL) light attenuation, while only two employed a Delta-Eddington (DE) scheme. The majority of the models simulated ice algae only in the bottom sea-ice layer, either as a static or dynamic system, while two models were multi-layer models, simulating ice algae along the entire ice column. In terms of ecosystem complexity, models varied from simple Redfield-based models (RFD)

https://doi.org/10.5194/egusphere-2025-1107
Preprint. Discussion started: 15 April 2025

with a single limiting nutrient, one algal group, and a detritus compartment to more comprehensive quota models with several functional groups, including ice bacteria, ice fauna, and multi-nutrient limitations.

2.2 The N-ICE2015 Dataset

The refrozen lead time series monitored during the N-ICE2015 expedition (Granskog et al., 2018) was selected as a test case for the model intercomparison due to the high frequency of available physical and biogeochemical measurements. The N-ICE expedition was a field campaign conducted aboard the RV *Lance,* which was frozen into pack ice north of Svalbard, drifting from 83° to 83°N to follow the direction of the drift, in the southern Nansen Basin of the Arctic Ocean from January to June 2015. Among the four ice floes monitored during the study period, the refrozen lead data were derived from Floe 3, which was studied from mid-April to early June 2015 between 81.8 and 80.5°N.

The lead, approximately 400 m wide, opened on 23 April, began refreezing on 26 April, and was fully refrozen by 1 May. The newly formed young ice in the lead was sampled from 6 May along a 100 m-long transect extending from the edge of the lead toward its centre every 2–3 days until it broke up on 4 June (Kauko et al., 2017). The algal growth period occurred in April and May. While the ice algal community was initially highly mixed, pennate diatoms of the genus *Nitzschia* became dominant later in the season.

The N-ICE2015 refrozen lead time series was chosen for this intercomparison based on two key factors:

- Observational data availability: It provides sufficient observations (Kauko et al., 2017) for comparison with model simulations of physico-biogeochemical variables.
- Ancillary data availability: It includes detailed time series of atmosphere and ocean data, necessary to force model runs, and has been successfully used in a previous 1D modelling study (Duarte et al., 2017).

2.3 Experimental setup

A strict protocol was developed and followed by all modelling groups. To accommodate the diversity of models, a minimum set of variables was selected for comparison with observations. These included sea-ice season timing, ice thickness, and snow thickness for coupled physical-biogeochemical models, as well as sea-ice nutrient concentrations and algal biomass (represented by Chl-a) for all models.

Two distinct experiments were conducted to assess model performance. The first experiment, labelled *no tuning*, aimed to run each model in its default configuration. The primary objective was to analyze the differences between model outputs and observational data and quantify the extent of biases. The intercomparison within this experiment sought to identify potential reasons for deviations from observations, such as the omission of key processes or inadequate parameterisations. The second experiment, labelled *tuning*, involved adjusting the models to better align with observed physical and biogeochemical properties. This experiment aimed to identify which processes needed to be modified or added, as well as the specific parameterisations or parameters that were adjusted and fine-tuned to improve agreement with observations.

Both experiments were carried out independently by each modelling group, without prior knowledge of the work undertaken by others. This approach was adopted to eliminate potential biases, whether conscious or unconscious, during the implementation phase. To ensure a standardized comparison across models, all simulations used the same atmospheric forcing, as well as identical initial and boundary conditions. For the sea-ice biogeochemical model without a thermodynamic component, observed ice and snow thickness data were provided. This standardised approach improved the comparability of the models, allowing for a robust evaluation of model performance. In the final phase, results were presented by each modelling group, and teams collaboratively discussed challenges, adjustments, and tuning choices.

3. Results and discussion

Although the N-ICE refrozen lead resembles a typical ice season, in the *no tuning* experiment, none of the models accurately captured the observed algal phenology and bloom magnitude (Fig. 1, top left). Most models exhibited deviations in either phenology or bloom magnitude, underestimating or overestimating Chl-a and producing either an earlier or delayed bloom onset. Notably, most models underestimated algal biomass, except SIMBA, though performance varied across diagnostic measures.

Due to limited nutrient data, few considerations can be drawn about simulated nutrient dynamics beyond an assessment of the potential model error's order of magnitude. Here, models underestimated nitrate and silicate concentrations, except BFM-SI and BFM-SI Clim, which overestimated nutrient concentrations (Fig. 1, mid and bottom left), though all remained within a reasonable range.

In the *tuning* experiment, all models were able to reasonably simulate the ice algal phenology, though performance still varied across models (Fig. 1, top right). However, little improvement was achieved in the simulation of nitrate and silicate dynamics. Interestingly, tuning focused on different processes and parameters among models (Table 2), including:

- Change in the algal growth rate,
- The possibility of downward vertical migration during melting,
- Change in the initial simulation date, and
- Magnitude of silic acid limitation by changing the half saturation constant and/or the Nitrogen: Silicon ratio of ice algae.

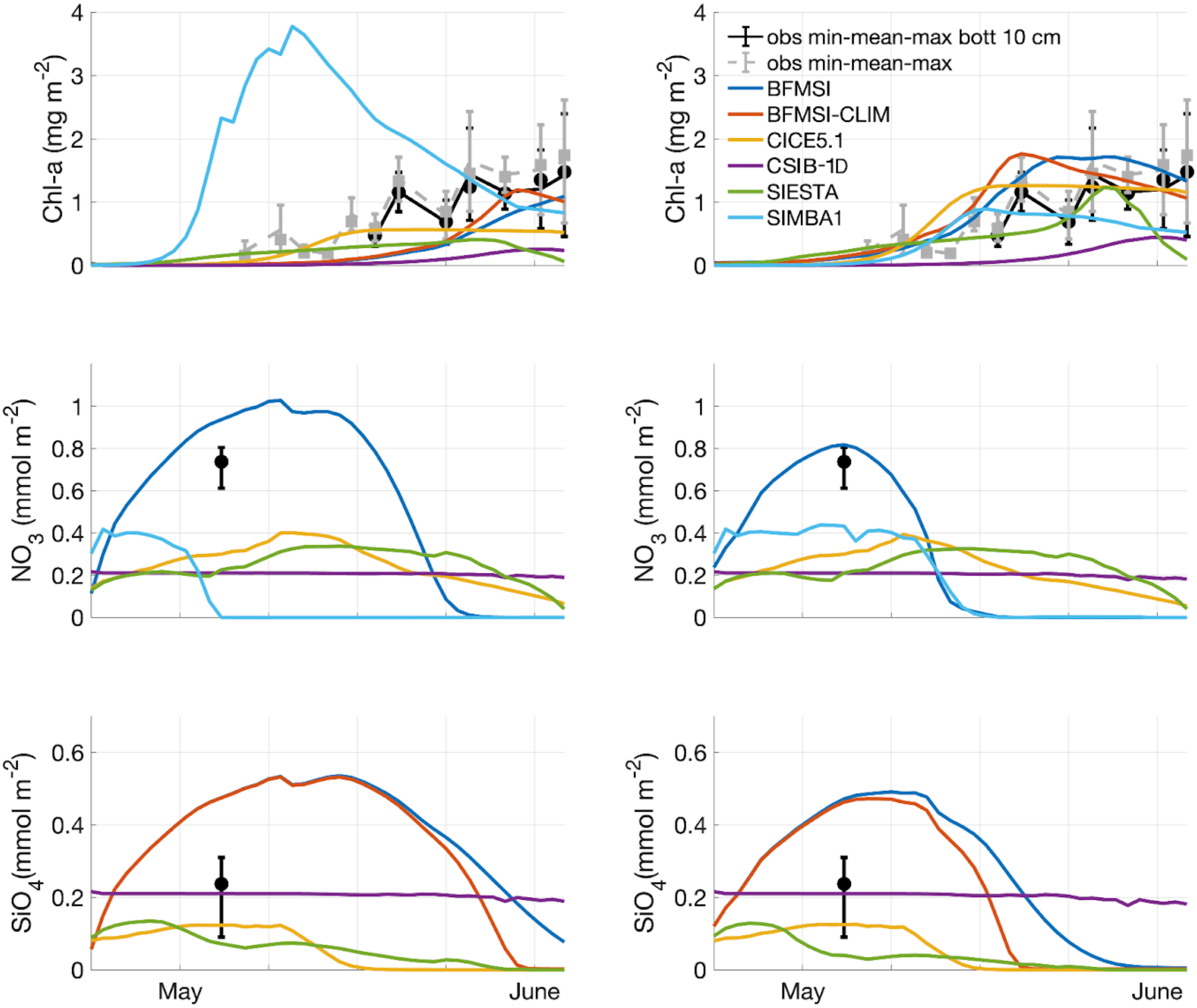

Figure 1: Experiment with *no tuning* (left) and *tuning* (right). Model results for ice algae Chl-a (top), nitrate (middle), and silicate (bottom). Observations are shown as dots for the mean of the entire ice core or the bottom 10 cm, while associated bars indicate the variability of the measurements between their maximum and minimum measures.

Despite tuning efforts, none of the models significantly improved the simulation of nitrate magnitude, except for BFM-SI (Fig. 1, mid right), which was also the only model that did not underestimate nitrate and silicate before tuning (Fig. 1, mid and bottom left). After tuning, BFM-SI's simulated nitrate concentrations quite closely matched the observed values (Fig. 1, mid right), attributed to increased nutrient uptake via enhanced algal growth. When comparing nutrient parameterisations across models (Table 1), BFM-SI stands out as the only model in which the variability of the dynamic sea-ice BAL modulates the upward fluxes of dissolved inorganic matter. Instead, CSIB-1D was the best model to simulate the silicate magnitude, matching observations before and after tuning. Overall, it remains unclear what element limited mostly algal growth since models show to disagree, either structurally, by not including the limiting element of interest, or by using different parameterisations. While all models may reasonably fit the chlorophyll observations, some models might achieve good results for the wrong reasons. In general, models performed more poorly when simulating sea-ice nutrient dynamics. Despite the scarcity of available data, the simulation of nutrient processes appears poorly constrained, pointing to the need for more in-depth observational and experimental work.

The *tuning* experiment highlights the diversity of tuning parameters across models (Table 2), prompting critical questions about model functionality and calibration. While models can be adjusted to align with observations, there is a risk of achieving accurate results for the wrong reasons. This risk arises when tuning compensates for a missing process in the model, leading to incorrect adjustments of parameters or processes. As a result, intercomparison modelling projects like this play a crucial role in identifying and addressing missing or misrepresented processes, ultimately contributing to the improvement of model performance and reliability.

Table 2. Comparison among models' performances before and after tuning.

MODEL	Ice algal phenology before tuning	Tuning strategy	Sea-Ice biogeochemistry after tuning
BFM-SI	Good algal growth timing but lower algal biomass	Lower silica limitation and higher algal biomass in seawater	Algal phenology and magnitude within observed range; Nitrate within range; Higher silicate
BFM-SI Clim	Good algal growth timing but lower algal biomass	Lower silica limitation and higher algal biomass in seawater	Algal phenology and magnitude within observed range; Higher silicate
CICE5.1	Good algal growth timing but lower algal biomass	Lower silica limitation and reduced recruitment	Algal phenology and magnitude within observed range; Lower nitrate, Silicate within range
CSIB-1D	Delayed algal growth and lower algal biomass	Higher algal growth rate	Delayed phenology; Peak magnitude within observed range; Lower nitrate; Silicate within range
SIESTA	Good algal growth timing but lower algal biomass and earlier algal loss	Algal migration (possibility to keep position and lower Si half-saturation constant	Algal phenology within observed range; Earlier decay; Lower nutrients
SIMBA	Earlier algal growth and higher algal biomass	Lower algal growth rate and removal of winter drainage of nutrients	Algal phenology and magnitude mainly within observed range; Lower nitrate

4. Conclusions

This study presents an intercomparison of one-dimensional sea-ice biogeochemical models, evaluating their ability to simulate algal phenology, bloom magnitude, and nutrient dynamics in a refrozen lead environment. The results highlight significant disparities in model performance, with most models struggling to accurately reproduce the observed algal biomass and nutrient concentrations, the latter also after tuning. While adjustments improved the representation of ice algal phenology, they had a limited impact on nutrient dynamics, emphasizing the challenges of parameterizing key processes such as nutrient fluxes and reinforcing the need for continued model development and validation supported by dedicated field and experimental observations.

The intercomparison highlights the unexpected challenges encountered in simulating a refrozen lead, primarily attributed to the short ice season and the difficulty most models faced in accumulating sufficient sympagic biomass. In a future Arctic Ocean characterized by increased lead openings, refreezing events, and young ice formation, there is an urgent need for models to be able to represent such a dynamic environment. This study underscores the importance of understanding and addressing the complexities involved in simulating specific and dynamic environmental scenarios.

The diversity of adjustments across models highlights both the range of tuning options available and the persisting knowledge gaps. The insights gained contribute valuable knowledge to ongoing efforts aimed at refining and improving numerical models, ensuring their accuracy and reliability in capturing complex interactions. To further advance this field of science, collaborative and harmonized modelling developments are recommended. A *Phase 2* of the intercomparison is auspicabile, potentially extending the study to the variability of habitats that characterizes Antarctic sea ice. Collaborative sensitivity tests could be conducted, with all models evaluating biological responses to the same tuning adjustments, tuning options could be expanded, and standard parameter ranges could be revisited based on newer data collected in recent years. Increased clarity of model sensitivities will improve future model robustness and enhance confidence in simulations of biogeochemical processes in ice-covered oceans.

Code and data availability

All relevant data, model code and numerical simulations presented in this work will be publicly made available upon manuscript's acceptance.

Author contributions

LT and MV conceived the study. LT, GC, PD, EM, and BS produced the model runs. LT merged results from different models and wrote the first draft of the ms. All authors contributed to the analysis of results, discussion, and editing of the manuscript.

Competing interests

The authors declare no competing interests.

Acknowledgements

This work was written under the auspices of BEPSII (Biogeochemical Exchange Processes at the Sea-Ice Interfaces) Expert Group (www.bepsii.org).

Financial support

LT and PD received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 101003826 via project CRiceS (Climate relevant interactions and feedbacks: the key role of sea ice and snow in the polar and global climate system). GC, PD, and SM received funding from the RCN BREATHE project (Bottom sea ice Respiration and nutrient Exchanges Assessed for THE Arctic, #325405). PD and SB also received funding from the iC3 Center of Excellence (Centre for ice, Cryosphere, Carbon and Climate, #332635). EM received funding through ArcticNet and the National Science and Engineering Council in Canada. NS acknowledges Fisheries and Oceans Canada.

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Preprint. Discussion started: 15 April 2025

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