



SPBM v2.0: Extension of a 1-D sea-ice biogeochemical model with ice–algal ecophysiology and zooplankton seasonal vertical migration for coupled ice–pelagic ecosystem simulations in Antarctic coastal seas

5 Young Shin Kwon^{1,2*} & Tae Siek Rhee¹

1Korea Polar Research Institute, 26 Songdomirae-ro, Yeonsu-gu, Incheon 21990, Republic of Korea

2University of Science and Technology, 217 Gajeong-ro, Yuseong-gu, Daejeon 34113, Republic of Korea

Correspondence to: Y. S. Kwon (kwonys@kopri.re.kr)

Abstract. We present SPBM v2.0, an extension of the one-dimensional Sympagic–Pelagic–Benthic Model for the coupling of
10 sea-ice and pelagic ecosystems in Antarctic coastal seas. The extension introduces a temperature-gated, bottom-accumulating
ice-algal ecophysiology; a water-only zooplankton formulation with continuous overwintering; and a two-species seasonal
vertical migration scheme for krill and copepods, together with corrections to the solar forcing and to the ERSEM iron cycle
required for iron-sensitive Southern Ocean applications. A single biogeochemical parameter set is applied at three sites
15 spanning 6.5° of latitude — Terra Nova Bay (TNB, Ross Sea), the western Antarctic Peninsula (WAP), and the Amundsen
Sea polynya (ASP) — so that inter-site differences emerge under site-specific physical forcing and prescribed initial iron
inventories, without site-specific biological tuning. Evaluated against the ASPeCT circumpolar ice-core database, the model
reproduces the observed spring and autumn chlorophyll magnitude at TNB and the summer magnitude at ASP, while
underestimating chlorophyll during summer and winter at TNB and across seasons at WAP. The central result is that the
20 strength of ice–pelagic coupling emerges under contrasting physical forcing and initial iron inventories rather than being
prescribed through site-specific biological tuning: thick, cold ice at TNB sustains a strong ice-algal bloom whose released
biomass contributes to the pelagic community and is associated with a krill-dominated grazer community, whereas the thin-
ice WAP site develops a water-column-dominated regime. These contrasting environmental regimes are also associated with
different zooplankton community structures, with krill dominance at TNB and ASP and copepod dominance at WAP. The
25 weak simulated bloom at WAP also highlights a limitation of the one-dimensional framework, which omits lateral nutrient
and iron exchange.



1 Introduction

Antarctic coastal polynyas and ice-covered shelves are among the most productive regions of the Southern Ocean, distinguished from typical open-ocean environments by the tight coupling between the sea-ice habitat, under-ice primary production, and the overwintering behaviour of key zooplankton species. Sea ice is not merely a physical boundary but a living habitat: brine channels within the ice support a community of ice algae, bacteria, and grazers that operates under extreme gradients of salinity and temperature and under strongly attenuated light (Arrigo, 2014). Ice-algal production is concentrated in the bottommost layers at the ice–ocean interface (Meiners et al., 2012; Arrigo, 2017), where it provides an early-season carbon source that sustains krill and copepod populations before the open-water phytoplankton bloom begins. Ice algae released during sea-ice melt can contribute inoculum to the pelagic phytoplankton community, although the importance of this seeding mechanism varies among environments (Lizotte, 2001). Released ice algae can also aggregate and sink rapidly, transferring organic carbon to depth (Riebesell et al., 1991; Boetius et al., 2013). The seasonal vertical migration of the grazers, in turn, modulates the fate of this carbon through the biological pump (Cavan et al., 2019; Steinberg and Landry, 2017). The sea-ice habitat, the production it supports, and the behaviour of the animals that depend on it are therefore inseparable components of a single coupled system.

Despite this distinctiveness and importance, these coupled ice–pelagic processes remain comparatively understudied. In-situ observations are sparse — particularly outside the short spring–summer window and within the ice interior itself — which leaves many of the governing processes weakly constrained. Numerical models are therefore an essential complement to observations, yet sea-ice biogeochemistry remains challenging to represent (Vancoppenolle and Tedesco, 2017). Despite growing effort, ice algae are still not included in most Earth system models, motivating community initiatives such as the Ice Algae Model Intercomparison Project (IAMIP2; Hayashida et al. (2021)) to quantify their impact on lower-trophic ecosystems and the biological carbon pump. Recent intercomparisons further reveal a large spread among sea-ice biogeochemical models — with the maximum ice-algal growth rate identified as a leading source of inter-model divergence — and conclude that coarse-resolution Earth system models are better suited to reproducing bulk properties than detailed ecological dynamics, so that one-dimensional (1-D) process models remain essential for resolving sea-ice biogeochemistry and ecosystem processes (Tedesco et al., 2026). Representing the ice–pelagic linkage within such a tractable 1-D framework is therefore a central challenge for polar ecosystem modelling.

Existing one-dimensional sea-ice biogeochemical models differ mainly in how they resolve the ice-algal habitat itself. Some confine ice algae to a thin basal layer of fixed thickness, while others resolve the ice column vertically, an approach that avoids the biases arising from assuming either a purely basal or a homogeneous vertical distribution (Vancoppenolle and Tedesco, 2017; Yakubov et al., 2019). What these models share is a focus on the sympagic compartment itself: the ice-algal community, its nutrient supply and its exchange with the surface ocean. The grazers that consume ice-derived production are typically absent or represented as passive tracers (Vancoppenolle and Tedesco, 2017; Tedesco et al., 2026), so that the behavioural link between the ice-algal bloom and the depth at which the resulting carbon is respired remains unresolved. Most of these models



have also been developed and evaluated for the Arctic, where iron limitation has generally not been a central constraint in model development and where the dominant grazers do not include a swarm-forming euphausiid with a strong sea-ice association. Both gaps are directly relevant to the Antarctic coastal setting addressed here.

The original Sympagic–Pelagic–Benthic Model (SPBM; Yakubov et al. (2019)) provides a natural starting point for this task. It introduced a coupled ice–water–sediment column built on the Framework for Aquatic Biogeochemical Models (FABM; (Bruggeman and Bolding, 2014)), combining the European Regional Seas Ecosystem Model (ERSEM; Butenschön et al. (2016)) for the plankton ecosystem with the Bottom Redox Model (BROM; Yakushev et al. (2017)) for redox and carbonate biogeochemistry, and it represented sea-ice algae as a distinct diatom group. Building on this framework, Kwon et al. (2023) applied SPBM to the Amundsen Sea and showed that the release of ice algae can contribute to particulate organic carbon export before the onset of the pelagic bloom.

Several limitations relevant to Antarctic applications nonetheless remained. First, ice–algal ecophysiology was only partially adapted from temperate values: earlier configurations adjusted the light-harvesting parameters but retained the standard temperature response, so that ice–diatom tracers could grow spuriously when mixed into the warmer water column. Second, and most consequential for the ice–pelagic linkage, zooplankton were treated as passive tracers with no capacity for vertical migration or structured overwintering, even though the seasonal descent and contrasting overwintering strategies of Antarctic krill and copepods are precisely the behaviours that connect ice-derived production to the biological pump. Third, silicate cycling underestimated the rapid within-water-column dissolution of biogenic silica, leading to a progressive depletion of dissolved silicate in deep columns. Finally, iron was not conserved in the standard configuration — a deficiency that was less apparent in the original Arctic application but becomes critical in the iron-limited Southern Ocean.

Here we describe SPBM v2.0, which addresses these gaps through a set of targeted developments while preserving the original model architecture and FABM/ERSEM/BROM coupling. The developments are: (1) improved ice–algal ecophysiology — a logistic temperature gate that suppresses ice–diatom production under comparatively warm conditions, revised photosynthesis–irradiance parameters for the under-ice light regime, and enhanced downward transport within the ice that promotes basal accumulation, together with nutrient-dependent sinking in the water column; (2) accelerated silicate recycling that regenerates most diatom-derived silica within the water column during sinking; (3) a water-only zooplankton category, including an explicitly resolved krill group, that restricts the large-bodied grazers to the liquid water column throughout the annual cycle; (4) a continuous overwintering scheme that replaces binary prey-threshold switching with a smooth food-availability index; and (5) a two-species seasonal vertical migration (SVM) scheme in which krill and copepods migrate between shallow high-light and deep overwintering target depths, with food-dependent behavioural suppression. These are supported by corrections to the yearday computation that ensures accurate solar forcing, to the seawater density passed to the carbonate-chemistry module, and by a closure of the ERSEM iron budget required for iron-sensitive applications.

We apply the extended model, under a common biogeochemical parameter set, to three contrasting Antarctic sites spanning 6.5° of latitude — Terra Nova Bay (TNB, Ross Sea, 75° S), the western Antarctic Peninsula (WAP, 68.5° S), and the Amundsen Sea polynya (ASP, 72.5° S) — whose sea-ice regimes differ markedly. Because the biological parameterisation is identical at



the three sites, this design examines the response of the coupled ecosystem to contrasting site-specific physical environments and prescribed initial iron inventories without site-specific biological tuning. The remainder of the paper is organized as follows. Section 2 describes the model developments and the site configurations; Section 3 evaluates the model against ASPECT circumpolar ice-core observations and describes the simulated water-column and zooplankton dynamics; Section 4 discusses the emergent ice–pelagic coupling, the origins of the underestimated bloom at WAP, the simulated zooplankton community structure, and the structural limitations of the one-dimensional framework; and Sect. 5 concludes.

2 Model Description

2.1 Original SPBM structure

SPBM resolves the full vertical column from atmosphere to sediment in one dimension (Fig. 1), comprising dynamically formed sea-ice layers (~0.06 m each), a water column at site-dependent vertical resolution, a bottom boundary layer (BBL), and sediments. Physical forcing — temperature, salinity, density, eddy diffusivity, ice thickness, and shortwave radiation — is prescribed from reanalysis- or observation-based NetCDF files and read at each model timestep (300 s). Sea-ice layers are added and removed dynamically as the prescribed ice thickness changes, and tracers are exchanged with the uppermost water layer as ice forms and melts. Vertical transport within the ice is controlled by the brine-volume fraction of each layer, which sets both the diffusivity and the permeability of the ice matrix; the details of the grid and of these exchanges are given in Sect. 2.7.3. Biogeochemistry is handled through FABM-coupled ERSEM, which includes four water-column phytoplankton functional types (P1: diatoms, P2: nanophytoplankton, P3: picophytoplankton, P4: microphytoplankton), one ice-algae group (P1_i: ice diatoms), three zooplankton groups (Z4: mesozooplankton/copepods, Z5: microzooplankton, Z6: heterotrophic nanoflagellates), heterotrophic bacteria (B1), three particulate organic matter pools (R4, R6, R8), and full nutrient cycles including NO₃, NH₄, PO₄, silicate, and dissolved iron. A full description of the original model is given by Yakubov et al. (2019).

2.2 Ice-algal ecophysiology (new in v2.0)

Sea-ice diatoms (P1_i) were introduced to SPBM as a distinct ERSEM phytoplankton group by Yakubov et al. (2019), who adapted the standard pelagic-diatom parameterization by adjusting only the photosynthesis–irradiance (PI) parameters for low-light growth, leaving the temperature and nutrient responses unchanged. Kwon et al. (2023) subsequently applied this configuration to the Amundsen Sea and further modified several ice-diatom parameters, including a reduced temperature sensitivity (Q₁₀ = 1.06). SPBM v2.0 builds on this lineage but revises the temperature treatment by introducing a logistic temperature gate for P1_i gross production, as described below. The parameter changes are summarised in Table 1.



Table 1. Key ERSEM parameter changes in SPBM v2.0, relative to the configuration of Yakubov et al. (2019). Z3 is the Antarctic krill group newly introduced in this study (Sect. 2.3.1).

Parameter	Baseline	v2.0 (This study)	Applies to	Justification
P1_i temperature treatment	Standard ERSEM Q_{10} temperature response ($Q_{10} = 2.0$; Yakubov et al., 2019)	Logistic temperature gate for gross production ($T_{\text{cutoff}} = -2.5\text{ }^{\circ}\text{C}$, $T_{\text{width}} = 0.5\text{ }^{\circ}\text{C}$); standard ERSEM Q_{10} temperature response ($Q_{10} = 2.0$) retained for resting respiration	P1_i	Suppresses proliferation of ice diatoms after release into the water column while retaining a conventional temperature dependence for maintenance respiration
α (PI initial slope)	~6	12.0	P1_i	High light-use efficiency at low PAR
β (photoinhibition)	0.2	1.5	P1_i	Strong photoinhibition at high PAR
Si routing on death	100 % $\rightarrow$ POM	90 % $\rightarrow$ dissolved, 10 % $\rightarrow$ POM	P1, P1_i	In-column biogenic Si dissolution during sinking
Water-column Fe dissolution, $k_{1,f}$ (d^{-1})	not applied	0.0051 (R4); 0.020 (R6)	R4, R6	Returns particulate iron to the dissolved pool during sinking
Within-ice downward velocity	3 cm d^{-1}	30 cm d^{-1}	P1_i	Basal accumulation of ice algae
Nutrient-limited sinking, resm	5 m d^{-1}	10 m d^{-1}	P1_i	Enhanced sinking potential under nutrient limitation
Overwintering scheme	Binary (prey threshold)	Continuous (f_{active})	Z3, Z4	Smooth seasonal dormancy transition
Dormant respiration, repw (d^{-1})	0.0025	0.001 (Z3); 0.00005 (Z4)	Z3, Z4	Energy-saving dormancy; roughly 20-fold stronger in copepods
Dormant mortality, mort (d^{-1})	0.0025	0.0025 (Z3); 0 (Z4)	Z3, Z4	Near-complete overwinter survival in copepods; background mortality in krill

2.2.1 Temperature treatment of ice diatoms

In the ice-diatom configuration inherited from Yakubov et al. (2019), P1_i retained the standard pelagic-diatom Q_{10} temperature response and therefore remained capable of growth after transport from the ice into the comparatively warm surface water. Kwon et al. (2023) reduced the Q_{10} coefficient to 1.06 to suppress this tendency. This approach, however, uses a physiological temperature-sensitivity parameter to control the habitat in which P1_i can proliferate.



SPBM v2.0 instead applies a one-sided logistic temperature gate specifically to the gross production of P1_i:

$$f_T = \frac{1}{(1 + e^{\frac{(T - T_{\text{cutoff}})}{T_{\text{width}}}})} \quad (1)$$

where $T_{\text{cutoff}} = -2.5$ °C and $T_{\text{width}} = 0.5$ °C. The gate approaches 1 at temperatures well below -2.5 °C and decreases rapidly as temperature rises above the cutoff. At approximately -1.8 °C, near the seawater freezing point, the gate is about 0.20, while at temperatures above -1 °C it falls below 0.05. The formulation therefore strongly suppresses new P1_i production after cells enter the comparatively warm water column, while allowing the released biomass to remain subject to grazing, mortality, lysis, sinking and other transport and loss processes.

The logistic production gate is not applied to resting respiration. Resting respiration retains the standard ERSEM temperature response with $Q_{10} = 2.0$. Production and maintenance metabolism are therefore treated separately: the logistic function restricts the ability of P1_i to generate new biomass at warm temperatures, whereas respiration continues to respond to temperature through the conventional ERSEM formulation. This distinction prevents P1_i released from melting ice from acquiring an unrealistically low maintenance cost solely because its production is temperature-gated.

The value $T_{\text{cutoff}} = -2.5$ °C was retained because shifting the cutoff toward warmer temperatures weakened the suppression of P1_i production in the water column. The formulation should therefore be regarded as a pragmatic constraint on P1_i production rather than as a physiological cold-adaptation curve.

2.2.2 Light-use parameters

The PI curve of ice algae differs fundamentally from that of water-column phytoplankton, because the sea-ice matrix transmits only a small fraction (typically 1–5 %) of incident irradiance; cells must therefore harvest light efficiently at very low PAR while remaining prone to photoinhibition when exposed to higher irradiances during ice melt (Arrigo and Sullivan, 1994; Palmisano and Sullivan, 1983). Yakubov et al. (2019) captured this to first order by raising the ice-diatom initial PI slope (α) to about 6 and the photoinhibition parameter (β) to 0.2, under a constraint that preserved the area beneath the PI curve over 0–20 W m⁻². SPBM v2.0 relaxes that constraint to represent the more extreme under-ice regime: alpha for P1_i is increased to 12.0 (mg C mg Chl⁻¹ d⁻¹ (W m⁻²)⁻¹), roughly three times the water-column diatom value, and beta is increased to 1.5, giving both stronger low-light efficiency and stronger high-light inhibition than in previous configurations. Together these parameters define a PI curve optimized for the dim, cold environment of the basal ice.

2.2.3 Silicate recycling

In the standard ERSEM configuration, biogenic silica (BSi) produced by diatoms is remineralized to dissolved silicate only after the particulate material reaches the sea floor. In reality, however, a substantial fraction of biogenic silica dissolves within the water column as it sinks — roughly 60% of surface production in the Southern Ocean redissolves within the upper ~100



160 m, with dissolution enhanced near the receding ice edge (Nelson et al., 1995; Van Cappellen et al., 2002; Nelson and Gordon, 1982). This occurs because seawater is undersaturated with respect to amorphous silica, and dissolution accelerates once the protective organic coating of the frustules is bacterially degraded following bloom senescence. By omitting this in-column dissolution, the standard configuration fails to regenerate dissolved silicate in the water column, and in deep columns this produces a persistent, progressive depletion of silicate over multi-year simulations, as Si is continually exported to depth without being returned to the upper layers. To represent in-column regeneration, SPBM v2.0 returns 90% of the biogenic Si released on diatom mortality directly to the dissolved silicate pool in the water column, with the remaining 10% entering the detrital pool. The 90 % fraction is not directly comparable to the ~60 % dissolution reported for the upper 100 m: the latter is the proportion dissolved within a specific depth interval during sinking, whereas the model partitions silica at the moment of mortality between an immediately dissolved fraction and a detrital fraction that is exported. The chosen value therefore represents the overall within-column regeneration efficiency rather than a depth-specific dissolution rate, and it was set so that the deep silicate inventory remains stable over multi-year integrations. This introduces within-column Si recycling, reduces artificial silicate depletion, and better maintains the silicate inventory available for subsequent diatom growth.

2.2.4 Sinking and basal accumulation of ice diatoms

In the original SPBM, P1_i migrate toward the ice base at 3 cm d⁻¹ within the ice domain and, in the water column, undergo nutrient-limitation-induced sinking at a maximum rate of 5 m d⁻¹ (parameter resm) with no prescribed background sinking velocity. These values were inherited from the standard ERSEM diatom configuration and had not been adapted to the strongly bottom-enriched biomass distributions observed in the Antarctic sea ice, where the great majority of ice-algal chlorophyll is concentrated in the lowest few to ~20 cm of the ice column (Arrigo, 2017; Arrigo et al., 2003).

In SPBM v2.0 we revise the two components independently. Within the ice column, the downward migration speed of P1_i is increased from 3 to 30 cm d⁻¹ (ice_algae_velocity in spbm.yaml), implemented in the SPBM transport layer as a downward flux applied exclusively to P1_i in ice layers whose brine-volume fraction exceeds a permeability threshold of 0.05, corresponding to the percolation transition of sea ice — the brine volume fraction of about 5 % below which the ice becomes impermeable and vertical fluid transport ceases (Golden et al., 1998). This value is not a directly measured migration rate but is chosen to promote the strong basal enrichment of ice-algal biomass observed in Antarctic sea ice; in reality this basal enrichment reflects a combination of active downward repositioning along opposing light and nutrient gradients, on scales of centimetres per day (Aumack et al., 2014), and gravitational settling, which in cultured ice diatoms is accelerated under silicon limitation (Aumack and Juhl, 2015).

In the water column, the maximum nutrient-limitation-induced sinking velocity of P1_i is increased from 5 to 10 m d⁻¹ (resm), twice the value retained for pelagic diatoms. Sinking is activated only when nutrient limitation exceeds the prescribed threshold and is calculated as $SD = resm \times \max(0, esni - iNI) + rm$, where iNI is the nutrient-limitation index, esni = 0.7, and the background sinking velocity rm is zero for P1_i. Thus, P1_i cells experience no prescribed background settling in nutrient-replete water, whereas progressively stronger nutrient limitation can increase their sinking velocity up to the configured



maximum. This formulation allows enhanced settling of nutrient-stressed ice diatoms without imposing continuous sinking after their release from the ice. Pelagic diatoms (P1) retain the original $\text{resm} = 5 \text{ m d}^{-1}$.

195 **2.3 Water-only zooplankton and continuous overwintering**

2.3.1 Water-only species category

The original SPBM configuration includes mesozooplankton, microzooplankton, and heterotrophic nanoflagellates, but no representation of Antarctic krill — a keystone grazer of the Southern Ocean and a major consumer of both ice-associated and pelagic production. SPBM v2.0 therefore introduces an additional mesozooplankton group representing Antarctic krill
200 (*Euphausia superba*, Z3), which is not present in the original ERSEM configuration. Because copepods generally constitute the dominant component of Southern Ocean mesozooplankton (Atkinson et al., 2012), the existing ERSEM Z4 mesozooplankton group is interpreted here as a copepod-dominated functional group and is referred to as “copepods” for brevity. Krill (Z3) and copepods (Z4) are the two large grazers to which the developments described below — the water-only constraint, the continuous overwintering scheme (Sect. 2.3.2), and the two-species seasonal vertical migration (Sect. 2.4) —
205 are applied.

Z3 is not a duplicate of the copepod group but is parameterised to reflect the feeding ecology of Antarctic krill, an omnivorous, swarm-forming grazer that readily supplements phytoplankton with animal prey such as copepods (Price et al., 1988), and that feeds across the water column, the sea ice and the benthos, including on ice algae and detrital material (Schmidt and Atkinson, 2016). Relative to Z4, Z3 is therefore given a stronger preference for ice algae and for detrital particulate matter and a weaker
210 preference for microzooplankton, together with a lower maximum specific ingestion rate (Table 2). The two groups also differ in their overwintering physiology (Sect. 2.3.2, Table 1).

In the original SPBM, all biological tracers, including zooplankton, could diffuse passively into the sea-ice layers. This is ecologically unrealistic for the large pelagic grazers represented here: the sea-ice interior is inhabited by small sympagic meiofauna (typically 20–500 μm , such as harpacticoid copepods, turbellarians and foraminifers), whereas the brine-channel
215 network — generally narrower than 1 mm — largely excludes larger-bodied animals such as krill and large pelagic copepods, which instead occupy the water column and the ice–water interface (Bluhm et al., 2017; Krembs et al., 2000). SPBM v2.0 therefore introduces a water-only species category: for zooplankton flagged as water-only (Z3 and Z4), any biomass diffusing into the ice or sediment layers is reset to zero at every timestep. This enforces the physical constraint that these organisms remain confined to the liquid water column throughout the annual cycle, regardless of numerical diffusion across the ice–ocean
220 interface.

Table 2. Feeding and physiological parameters that distinguish Z3 from Z4 in SPBM v2.0. Overwintering parameters are listed separately in Table 1.

Parameter	Z3 (krill)	Z4 (copepods)	Rationale
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Preference for P1_i	0.25	0.20	Krill graze ice-associated diatoms efficiently
Preference for Z5 (microzooplankton)	0.10	0.20	Krill rely less on microzooplankton prey
Preference for detrital POM	0.20	0.10	Krill ingest aggregated/detrital material
Maximum specific ingestion rate (d ⁻¹)	0.55	1.2	Lower maximum specific ingestion assigned to the larger-bodied krill functional group

225 2.3.2 Continuous overwintering scheme

The original ERSEM mesozooplankton module uses a binary threshold: when total prey carbon falls below a minimum food concentration (Minprey), animals switch instantaneously to a dormant overwintering state with reduced metabolic rates. This binary switching produces discontinuous seasonal transitions that are physiologically unrealistic and numerically problematic near the threshold. SPBM v2.0 replaces it with a continuous food-availability index:

$$f_{\text{active}} = \frac{C_{\text{prey}}^k}{C_{\text{prey}}^k + K_{\text{min}}} \quad (2)$$

230 where C_{prey}^k is the total prey carbon available to the species in layer k (mg C m⁻³), computed as the preference-weighted sum over all its prey (Table 2), and K_{min} is a half-saturation constant set to 15 mg C m⁻³ for both species. The active state — full respiration, active feeding and the standard background mortality (sd) — is weighted by f_{active} and the overwintering state (reduced dormant respiration repw and dormant mortality mort) by $(1 - f_{\text{active}})$, so that all metabolic fluxes vary continuously with food availability and produce smooth autumn–winter transitions into dormancy and back.

235 The continuous formulation is also a prerequisite for coupling dormancy to vertical migration. The index is evaluated on the local rather than the column-integrated prey field, so that an animal at its overwintering depth responds to the food actually available there; with a column-integrated index, a surface bloom would keep the deep population in the active state and the deep overwintering state could not be represented appropriately. Under the binary switch, an animal that descends below the productive layer crosses the prey threshold within a single timestep and switches instantaneously to full dormancy, which
 240 neither reflects the gradual physiological transition observed in overwintering krill and copepods nor allows the population to sustain itself through the descent. The smooth index makes the metabolic state a continuous function of the food field the animals actually encounter as they migrate.

This continuous scheme is applied to both large grazers —Z3 and Z4 — but with species-specific overwintering physiology (Table 1) that reflects their contrasting winter strategies. Large Southern Ocean calanoid copepods can undergo pronounced
 245 seasonal overwintering at depth, supported by lipid reserves and strongly reduced metabolism (Schnack-Schiel et al., 1991; Bathmann et al., 1993). Z4 is therefore parameterised as a diapause-like copepod group: its dormant respiration is roughly twenty times lower than that of krill and its dormant mortality is set to zero, consistent with the very high overwinter survival



of these copepods. Antarctic krill, by contrast, do not undergo true diapause; adults depress metabolism and feeding activity but can continue low-rate opportunistic feeding through winter (Schmidt and Atkinson, 2016; Schmidt et al., 2014; Meyer, 2011). Z3 therefore retains both a higher dormant respiration and a small background mortality during overwintering.

2.4 Two-species seasonal vertical migration

2.4.1 Conceptual framework

Seasonal vertical migration (SVM) — a seasonal shift in mean residence depth, deeper in winter and shallower in summer — is a widespread trait of polar zooplankton (Bandara et al., 2021). SPBM v2.0 introduces a target-depth relaxation scheme for two large grazers, krill (Z3) and copepods (Z4), each independently parameterised, with species-specific overwintering depths, relaxation timescales and food-retention thresholds. Antarctic krill tend to occupy the surface layer in summer and shift to greater depth in winter, but this behaviour is highly plastic and varies within seasons even at small spatial scales (Bahlburg et al., 2023); where food, including ice algae, remains available beneath winter sea ice, part of the population stays near the surface (Flores et al., 2012). Large Southern Ocean calanoids such as *Calanoides acutus* can overwinter at several hundred metres in a lipid-based resting state (Schnack-Schiel et al., 1991; Bathmann et al., 1993), deeper than the winter depths typically reported for krill, and Z3 and Z4 are parameterised accordingly. The scheme operates at seasonal rather than diel timescales, a consequence of the light forcing used to trigger it (Sect. 2.7.7); the implications are discussed in Sect. 4.5.

2.4.2 Target depth and migration velocity

For each species, a smooth light-dependent target depth is defined as:

$$z_{\text{target}}(t) = z_{\text{deep}} + f_{\text{light}} \times (z_{\text{shallow}} - z_{\text{deep}}) \quad (3)$$

where z_{shallow} is the shallow (high-light season) target depth, z_{deep} is the deep (low-light, overwintering) target depth, and f_{light} is a logistic function of surface irradiance:

$$f_{\text{light}} = 0.5 \times [1 + \tanh(\frac{(\text{PAR} - \text{PAR}_{50})}{\text{PAR}_w})] \quad (4)$$

with $\text{PAR}_{50} = 10 \text{ W m}^{-2}$ (light-level midpoint) and $\text{PAR}_w = 5 \text{ W m}^{-2}$ (transition width). f_{light} approaches 1 (target $\rightarrow z_{\text{shallow}}$) in summer and 0 (target $\rightarrow z_{\text{deep}}$) during polar night. The migration velocity for layer k is:

$$w_k = \left(\frac{z_{\text{target}} - z_k}{\tau} \right), \quad |w_k| \leq v_{r,\text{max}} \quad (5)$$

where τ is a relaxation timescale (d) and $v_{r,\text{max}}$ is a maximum migration speed (m d^{-1}). For layers far from the target depth the relaxation term exceeds $v_{r,\text{max}}$, so that migration proceeds at the maximum speed and τ acts to decelerate the approach as the target is neared; the cap therefore sets the migration rate over most of the descent or ascent. Mass is redistributed between adjacent layers using an explicit, CFL-stable scheme (maximum fractional transfer of 0.5 per timestep per layer) that conserves total biomass (Sect. 2.8).



2.4.3 Food-dependent behavioural suppression

275 Migration velocity is modulated by local prey concentration, representing the tendency of actively feeding animals to remain at profitable food patches rather than migrate toward their depth target:

$$w_k \leftarrow w_k \times \left(1 - a_{\text{food}} \times \frac{C_{\text{prey},k}}{(C_{\text{prey},k} + K_{\text{food}})}\right) \quad (6)$$

where a_{food} is the food-retention weight (0 = no suppression, 1 = complete suppression), K_{food} is the half-saturation prey concentration (mg C m^{-3}), and $C_{\text{prey},k}$ is the local phytoplankton carbon in layer k (mg C m^{-3}). This term allows animals to remain near a productive layer even under high surface light, consistent with the ability of euphausiids to detect and remain within algal patches (Price, 1989) and with observations of krill remaining near the surface under food-rich winter sea ice (Flores et al., 2012). The retention threshold is lower for krill than for copepods ($K_{\text{food}} = 20$ versus 50 mg C m^{-3}), so that krill are held at food patches at correspondingly lower prey concentrations, consistent with these observations. Parameter values for both species are listed in Table 3.

285 **Table 3.** Two-species SVM parameters (identical across all three sites).

Parameter	Z3	Z4	Description
Z_{shallow} (m)	15	15	Shallow (high-light season) target depth
Z_{deep} (m)	100	300	Deep (low-light, overwintering) target depth
τ (d)	0.5	1.0	Relaxation timescale
$v_{r,\text{max}}$ (m d^{-1})	50	50	Maximum migration speed
PAR_{50} (W m^{-2})	10	10	Light-fraction midpoint
PAR_W (W m^{-2})	5	5	Light-fraction transition width
α_{food}	0.9	0.9	Food-retention strength
K_{food} (mg C m^{-3})	20	50	Prey half-saturation for retention

2.5 Corrections to the ERSEM iron cycle

Extended spin-up experiments revealed three pathways through which dissolved iron (dFe) is permanently removed from the model domain in the standard ERSEM formulation, so that the iron field declines steadily and never reaches equilibrium. Such losses have limited practical consequences in configurations in which iron biogeochemistry is inactive or iron is non-limiting. In the Southern Ocean applications considered here, however, iron exerts a first-order control on production, and a closed iron budget is a precondition for any meaningful application of the model; each pathway was therefore identified and corrected before the simulations reported here were performed.

Remineralisation of particulate iron in the water column. In the standard formulation the carbon, nitrogen and phosphorus constituents of the sinking detrital pools are subject to water-column remineralisation, but their iron constituent has no equivalent dissolution pathway, so that all particulate iron reaches the sediment, where the limited benthic–pelagic exchange



represented in the model prevents its return to the euphotic zone. We added a switchable first-order dissolution term to the pelagic base module, in which particulate iron is transferred directly to the ambient dissolved pool:

$$\frac{\partial[R_f]}{\partial t} = -k_{1,f}[R_f] \quad (7)$$

where $[R_f]$ is the iron content of the particle class and $k_{1,f}$ is a rate constant prescribed independently for each class (Table 1).

300 The term is activated per pool through a switch in the configuration file and is applied to R4 and R6; R8 carries no iron constituent and is therefore unaffected. Combined with the sinking velocity of each class, these rates dissolve a substantial part of the particulate iron before it reaches the sea floor, returning it to the dissolved pool within the water column.

Scavenging without return. ERSEM parameterises abiotic iron scavenging following Aumont et al. (2003), removing dFe in excess of a threshold concentration (0.6 nM) at a prescribed rate. In the standard implementation the scavenged iron is
 305 subtracted from the dissolved pool without a corresponding source term anywhere else, and is therefore lost from the system. We added an optional coupling (fe_scav_sink) that directs scavenged iron to the detrital pool R6_f, from which it is recycled to the dissolved pool through the dissolution term described above, so that scavenging redistributes iron within the column rather than removing it.

Grazing-mediated iron loss. The largest of the three pathways arises in the zooplankton grazing routine, which reduces all
 310 prey state variables — including their iron constituent — in proportion to the ingestion rate. The ingested iron is intended to be egested to a particulate pool through the target variable prey Nf_sink, but this variable is registered as an optional dependency and no coupling is provided in the standard configuration. Because the dependency is optional, FABM silently ignores the unresolved flux and the iron removed from prey is lost. This affects every predator–prey interaction in which the prey carries an iron state variable. We resolved it by adding explicit couplings from all iron-bearing prey types to the detrital
 315 iron pool R6_f, across the mesozooplankton, microzooplankton and heterotrophic nanoflagellate functional groups.

With the three corrections applied, iron is retained within the coupled model domain and recycled through resolved pools rather than being irreversibly lost through unresolved fluxes; the domain-integrated iron inventory is conserved over the spin-up. These corrections concern the ERSEM iron cycle itself rather than any feature specific to SPBM, and are therefore relevant to any ERSEM configuration in which iron biogeochemistry is dynamically active.

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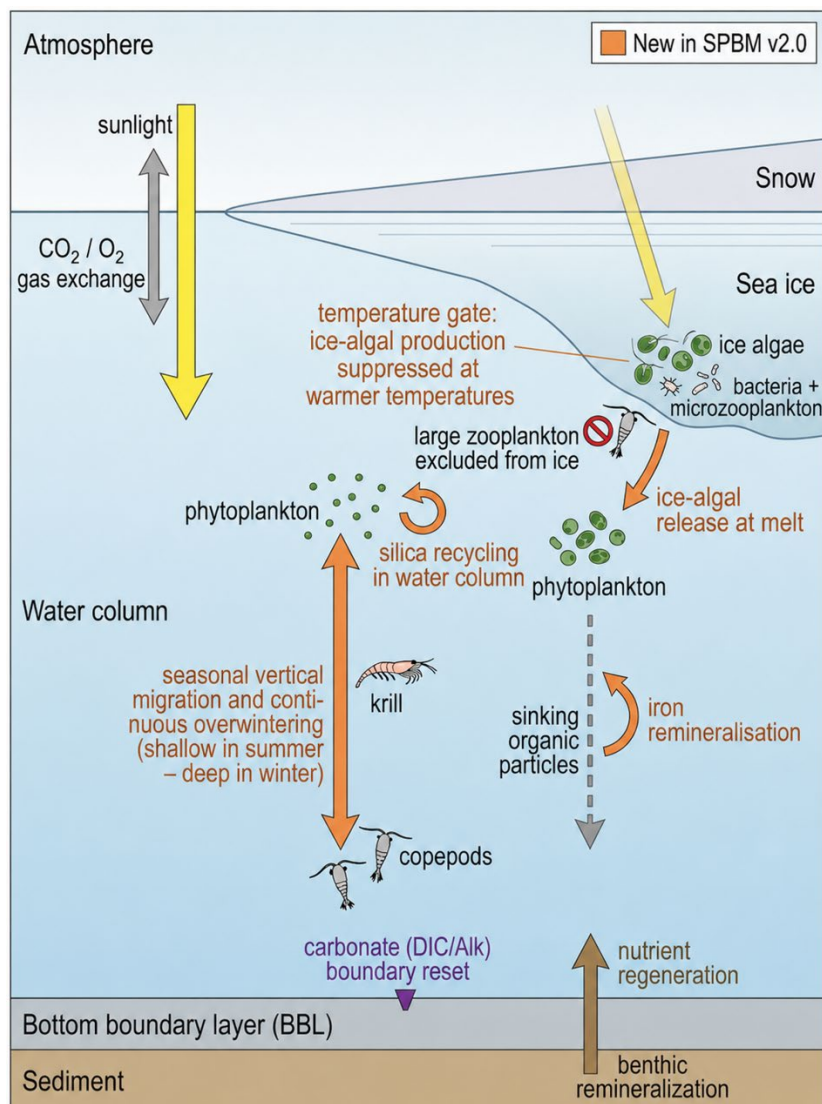


Fig. 1. Schematic of the coupled sea-ice–pelagic–benthic system represented by SPBM v2.0. The tapering ice illustrates the seasonal transition between ice-covered and open-water conditions within a single column. Processes newly introduced or revised in v2.0 are shown in orange.

325

2.6 Technical corrections

Two technical issues affecting the simulations were identified and corrected. First, the day-of-year variable used by ERSEM for zenith-angle and photoperiod computations was evaluated incorrectly. The NetCDF time coordinate (in seconds since a reference date) was converted to days but was not offset by the starting day-of-year parsed from the time-units string, so that a run beginning on 1 June was treated as beginning on 1 January. The solar forcing was thereby displaced by roughly five

330



months, inverting its seasonal phase. In SPBM v2.0 the day-of-year is computed as the elapsed days plus the starting day-of-year (152 for the 1 June forcing start common to all three sites). The error surfaced during development of the SVM scheme, where it produced an inverted seasonal phasing of the migration signal, and it underscores the importance of independently verifying calendar logic in long coupled simulations. Second, a density-handling error was identified during preparation of the physical forcing, in which 1000 kg m^{-3} could be added to a field that already represented absolute in-situ seawater density. The forcing-preparation procedure was corrected so that the archived input files contain full in-situ seawater density, which SPBM passes unchanged to ERSEM. Because ERSEM uses density to convert carbon and alkalinity concentrations to mass-specific units (mol kg^{-1}) for its carbonate-chemistry calculations, this error would otherwise distort the modelled carbonate system.

2.7 Model configuration and experimental setup

2.7.1 Site configuration and parameterisation

The extended model is applied to three contrasting Antarctic sites: Terra Nova Bay (TNB) in the western Ross Sea, the West Antarctic Peninsula (WAP), and the Amundsen Sea Polynya (ASP). The three sites share a common ERSEM biogeochemical parameter set, whose changes from the baseline configuration are summarised in Table 1, and common SVM parameters (Table 3), including identical water-only species designations, overwintering physiology, ice-algal ecophysiology settings; the feeding parameters distinguishing krill from copepods are given in Table 2. The sites differ in geographic position, water-column configuration, physical forcing and initial dissolved-iron concentration (Table 4), while the biological parameterisation is held fixed. This design allows inter-site ecosystem differences to be interpreted without site-specific biological parameter tuning.

Table 4. Site configuration and physical setting.

Property	TNB (Ross Sea)	WAP	ASP (Amundsen Sea)
Longitude	165° E	68.5° W	115° W
Latitude	75° S	68.5° S	72.5° S
Water depth (m)	900	540	540
Water-column layers	100 (9.0 m)	100 (5.4 m)	100 (5.4 m)
Initial dissolved Fe (nM)	2.0	0.8	2.0
Simulation period	1 Jun 2023 – 18 Dec 2025	1 Jun 2023 – 18 Dec 2025	1 Jun 2023 – 18 Dec 2025
Maximum ice thickness (m)	1.17	0.88	1.48
Ice-covered fraction of days	89.8 %	87.2 %	94.4 %

2.7.2 Physical forcing and input data

Physical forcing for each site was generated by running the General Ocean Turbulence Model (GOTM; Burchard et al. (2006)) in an offline, one-dimensional configuration to produce an internally consistent set of vertically resolved hydrodynamic fields.



Temperature and salinity were relaxed toward the monthly EN4 quality-controlled subsurface ocean analyses (Good et al., 2013) on a one-month timescale, and the atmospheric boundary was forced by hourly ERA5 reanalysis fields (Hersbach et al., 2023), comprising 10 m winds, air temperature, humidity, sea-level pressure, and downwelling shortwave radiation. The GOTM run produced daily-mean vertical profiles of temperature, practical salinity, in-situ density, and scalar eddy diffusivity at each layer interface, together with the daily-mean downwelling shortwave radiation at the sea surface. Sea-ice thickness, snow thickness, and ice-surface temperature were taken from the GLORYS12v1 global ocean reanalysis (Jean-Michel et al., 2021) and supplied as daily time series. The temperature of the interior ice layers is interpolated linearly between the ice-surface temperature and the freezing point of the underlying seawater across the evolving ice thickness. Snow thickness is used to attenuate the light transmitted into the ice, following the original SPBM formulation (Yakubov et al., 2019). The model does not include a thermodynamic sea-ice component; ice thickness is prescribed from GLORYS12v1 rather than computed internally.

All physical fields were compiled into a single NetCDF forcing file per site and supplied to SPBM as offline forcing. The forcing fields are updated once per model day, while the biogeochemical and transport equations are integrated on an internal timestep of 300 s; the model is not iteratively coupled to a hydrodynamic model. Vertical mixing is prescribed directly from the offline GOTM eddy diffusivity and is not recomputed within SPBM. The simulations use SPBM v2.0 coupled through FABM (Bruggeman and Bolding, 2014; branch spbm_v0.2.2, commit 1944b09) to the study-modified ERSEM source and to BROM (Yakushev et al., 2017; based on branch spbm_v0.2.2, commit 1542fd6, with study-specific modifications). The modified ERSEM and BROM source snapshots and patches used in this study are archived together with SPBM v2.0 (see Code and data availability). The hydrodynamic forcing was generated offline with GOTM (Burchard et al., 2006). The exact source snapshots and study-specific modifications used for the simulations are archived with SPBM v2.0 (Kwon and Rhee, 2026).

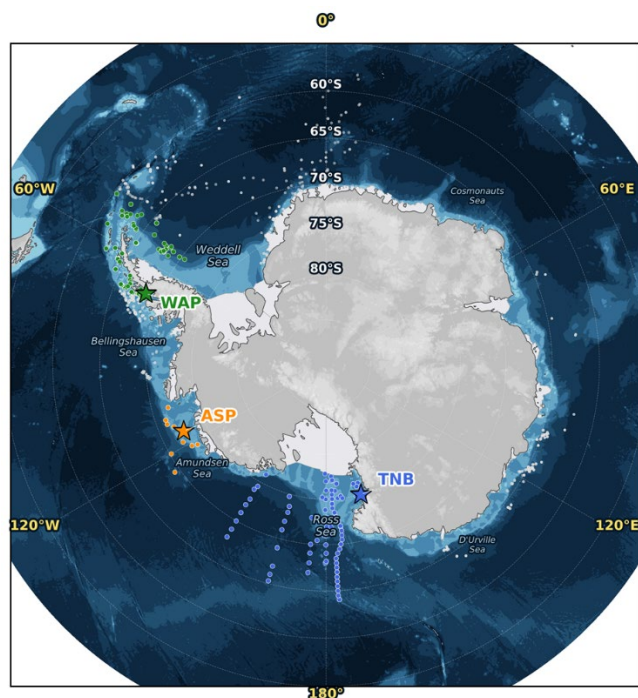


Fig. 2. Map of the study region showing the three model sites (stars): Terra Nova Bay (TNB, blue), the western Antarctic Peninsula (WAP, green) and the Amundsen Sea polynya (ASP, yellow). Coloured dots mark the ASPECT ice cores used to evaluate each site, in the same color as the corresponding star; light grey dots show the remaining cores of the ASPECT database, which were not used here.

2.7.3 Vertical grid and domain

The water column is resolved on a uniform grid of 100 layers extending from the surface to 900 m at TNB (9.0 m layers) and to 540 m at WAP and ASP (5.4 m layers). Beneath the water column, a bottom boundary layer (BBL) of 0.5 m is resolved with five 0.1 m layers, and a 0.1 m sediment column with five 0.02 m layers. Sea-ice layers are added dynamically above the water column as ice forms, each with a fixed thickness of 0.06 m, so that the number of ice layers scales with the prescribed ice thickness; the water-column and sediment grids are fixed, and only the ice domain grows and shrinks over time. Sea ice (thickness > 0.01 m) is present for 89.8 % of the simulated days at TNB, 87.2 % at WAP, and 94.4 % at ASP (Table 4). When new ice layers form during freezing, each layer inherits the tracer concentrations of the underlying surface-water layer, scaled by the ice-to-water layer-thickness ratio so that mass is conserved. The water-only zooplankton groups (Z3 and Z4) are instead set to zero in newly formed ice, reflecting their exclusion from the ice matrix (Sect. 2.3.1). During melting, ice-layer tracers are released into the uppermost water layer weighted by the same thickness ratio.



2.7.4 Biogeochemical boundary and initial conditions

395 Carbonate-system boundary conditions are imposed on dissolved inorganic carbon (DIC) and total alkalinity (Alk) at the bottom of the water column only, where they are reset each day to prescribed target values (2280 mmol C m⁻³ for DIC and 2350 μmol kg⁻¹ for Alk). The surface carbonate system is left free to evolve under biological cycling and gas exchange. The deep target constrains the carbonate system against long-term drift, which a one-dimensional column cannot otherwise avoid in the absence of lateral exchange. By contrast, no boundary relaxation is applied to the macronutrients (NO₃, PO₄, Si) or to dissolved iron (Fe); these are deliberately left unconstrained and evolve freely under biogeochemical cycling and vertical mixing, so that their seasonal cycling and long-term inventory emerge from the simulated ecosystem rather than being imposed. Gas exchange is computed prognostically by the corresponding ERSEM modules.

All biogeochemical state variables are initialised with vertically uniform profiles. Initial conditions are identical among the three sites except for dissolved iron: dFe is initialised at 2.0 nM at TNB and ASP and at 0.8 nM at WAP. The lower WAP value was chosen to represent the relatively Fe-poor upper-ocean conditions reported for parts of the WAP shelf (Annett et al., 2015; Sherrell et al., 2018). These concentrations prescribe contrasting site-specific initial Fe inventories within the horizontally closed one-dimensional columns, rather than climatological vertical profiles or site-specific biological tuning. Because no lateral Fe exchange or Fe restoring is imposed, the prescribed initial Fe inventory can exert a persistent influence on the simulated iron regime. The remaining initial concentrations are NO₃ = 31.0 mmol N m⁻³, PO₄ = 2.5 mmol P m⁻³, Si = 80 mmol Si m⁻³, O₂ = 250 mmol m⁻³, DIC = 2200 mmol C m⁻³ and Alk = 2300 μmol kg⁻¹. Living biomass pools are initialised with small non-zero seed concentrations, also identical at the three sites, so that populations can develop from the first spin-up cycle. The complete set of initial conditions, including the elemental and chlorophyll components of each functional group, is given in the archived configuration files (see Code and data availability). All biological state variables are initialised identically across the three sites, and all biological parameters are held fixed across sites.

415 2.7.5 Spin-up procedure

The biogeochemical state is spun up by cycling the first year of physical forcing (1 June to 31 May) ten times before the main simulation. The internal timestep is 300 s (288 steps per day), while the physical forcing is updated daily. During spin-up the SVM scheme is disabled (maximum migration speed set to zero for both species). This is necessary because deep-water oxygen has no restoring or lateral-supply boundary condition, with no boundary relaxation or nudging to buffer it: in a one-dimensional column the net downward transport of organic matter by migrating zooplankton, in the absence of any lateral or vertical oxygen resupply, would otherwise drive the deep water toward anoxia before the ecosystem reaches equilibrium. Disabling migration during spin-up allows a stable, oxygenated state to establish first; the migration speed is then restored to its configured value for the main simulation. This subsurface oxygen-depletion tendency is consistent with that reported for earlier SPBM configurations (Yakubov et al., 2019) and is examined further in Sect. 4.6.



425 2.7.6 Simulation periods and analysis

All three simulations span approximately 2.6 years, from 1 June 2023 to 18 December 2025, covering three calendar years (2023–2025). The common start date is set by the availability of the GLORYS12v1 sea-ice forcing. Each run is preceded by a spin-up in which the first year of forcing (1 June–31 May) is cycled ten times (Sect. 2.7.5). Daily-mean output is written for the water column, sea ice and sediment, and the analyses presented here use the full main-simulation period unless otherwise stated. For the maximum total in-ice phytoplankton concentrations reported in Sect. 3.3, the analysis was restricted to output from 1 January 2024 onward and used thickness-weighted means across active ice layers, requiring at least three active ice layers.

2.7.7 Light forcing and the seasonal vertical migration trigger

Two distinct light quantities are used. The shortwave radiation entering the ice and water columns is taken from the ERA5-derived GOTM output and drives all photosynthesis through the ERSEM light module. The SVM scheme, by contrast, is triggered by a separate astronomical light signal: the theoretical 24-hour-mean surface irradiance, approximated from latitude and day-of-year using the simplified solar-declination formulation adopted in the OXYDEP model (Yakushev and Sørensen, 2013), with a fixed clear-sky maximum scaled by the photosynthetically active fraction. This daily-mean irradiance defines the light fraction (f_{light}) through a logistic function (midpoint $\text{PAR}_{50} = 10 \text{ W m}^{-2}$, width 5 W m^{-2}) that sets the target depth between the shallow and deep end-members (Table 3). Because the trigger integrates over 24 hours and varies only seasonally, the resulting migration is seasonal rather than diel — consistent with the overwintering behaviour represented for Z4 — and using an astronomical rather than the ERA5-based irradiance ensures that day-to-day cloud variability does not generate spurious high-frequency migration.

445 2.8 Model verification

Before evaluating the model against observations (Sect. 3), we verify that the numerical implementation solves the intended equations correctly and conserves the relevant quantities.

Mass conservation. The seasonal vertical migration scheme redistributes biomass conservatively between adjacent layers using an explicit flux-based formulation. Biomass lost from one layer is added to the adjacent layer within the same timestep, while fluxes are suppressed at the domain boundaries. Direct numerical tests confirm conservation to machine precision, with relative changes in water-column-integrated biomass of order 10^{-16} over a redistribution step. The dynamic formation and melting of sea-ice layers is likewise conservative: newly formed ice layers inherit the underlying surface-water concentration scaled by the ice-to-water layer-thickness ratio, with the corresponding mass removed from the water column. Because the water-column-only zooplankton (Z3 and Z4) are excluded from newly formed ice, no biomass is transferred to the ice domain at formation and none is discarded on melt. The water-only constraint (Sect. 2.3.1) additionally resets to zero any Z3 or Z4



biomass that reaches the ice or sediment layers by numerical diffusion, the only remaining pathway into those domains; this is a deliberate removal rather than a conservative transfer.

Positivity and numerical stability. Across all three multi-year simulations, no state variable develops numerically undefined values (e.g., NaN), and all biological and nutrient concentrations remain non-negative throughout. Negative values occur only in diagnostic quantities that are physically signed, such as net production or apparent oxygen utilisation. The migration scheme remains numerically stable under the configured timestep and migration velocities. The fractional biomass transfer across a layer interface in a single timestep is capped at 0.5. At the prescribed maximum migration speed of 50 m d⁻¹ and a timestep of 300 s, the corresponding transfer fraction is only 0.019 at TNB and 0.032 at WAP and ASP, well below the imposed cap. The configured timestep therefore introduces no numerical instability in the transport scheme.

Dissolved oxygen. Because deep-water oxygen has no restoring or lateral-supply boundary condition, with no boundary relaxation (Sect. 2.7.4), the oxygen field provides a stringent check on the spin-up protocol. The main water column remains well oxygenated at all three sites, with minima of 204 mmol m⁻³ at TNB, 171 mmol m⁻³ at WAP and 190 mmol m⁻³ at ASP, the lowest values occurring in the deepest layer of each column. This confirms that disabling migration during spin-up (Sect. 2.7.5) successfully prevents the anoxic collapse that downward organic-matter transport would otherwise trigger. Below the water column, oxygen in the bottom boundary layer and sediment becomes negative at all three sites; in ERSEM negative oxygen is the model's representation of an oxygen debt, expressing the equivalent of reduced species produced by anaerobic respiration rather than a physically negative concentration. This is not a transport instability but a structural consequence of the one-dimensional framework: sediment and BBL respiration consume oxygen that cannot be replenished by lateral advection in a single column, an effect already noted for earlier SPBM configurations (Yakubov et al., 2019). Its implications are discussed in Sect. 4.6.

2.9 Observational data for model evaluation

The simulated sea-ice biogeochemistry is evaluated against the ASPeCT circumpolar ice-core database (Meiners et al., 2012), which compiles depth-resolved measurements of chlorophyll *a*, particulate organic matter, dissolved nutrients and salinity from Antarctic sea-ice cores. Observations were grouped by sector (Fig. 2) and aggregated into four austral seasons (spring, September–November; summer, December–February; autumn, March–May; winter, June–August). Cores with a total ice thickness below 0.2 m were excluded, and any season–variable combination represented by fewer than five cores is reported but not used in the comparison. Model output was aggregated over the same seasonal windows. For the seasonal depth-averaged comparison in Table 5, model concentrations were taken directly from the archived ice output without additional porosity scaling and were thickness-weighted over the active ice column before seasonal aggregation. Seasonal medians and interquartile ranges were calculated from the resulting daily depth-averaged values. For the profile comparison, every observational core and every daily model profile was normalised by its own column maximum and averaged within five equal bins of normalised depth (0 = ice–atmosphere interface, 1 = ice–ocean interface), so that the shape of the profile is assessed independently of its magnitude.



3 Results

3.1 Physical settings

The three sites differ considerably in their physical setting, while sharing the same biogeochemical parameterisation (Sect. 2.7.1); the resulting contrasts provide the physical context for the ecosystem differences described below. The seasonal evolution of the ice and upper water column at each site is shown in Figs. S1–S3.

Maximum winter ice thickness reaches 1.48 m at ASP and 1.17 m at TNB but only 0.88 m at WAP, and the timing of the open-water season differs markedly among the sites. At TNB the ice opens completely in late January to early February and begins to re-form before early March. At ASP there is no ice-free period in 2023–2024, while in the following year the ice opens in early February and likewise re-forms in early March. WAP contrasts with both: the ice does not disappear entirely until mid-March and begins to re-form only in early May, so that the open-water season starts considerably later than at the other two sites. Snow cover, by contrast, is deepest at ASP and WAP (seasonal means of 13.5 and 8.8 cm, with maxima of 37.6 and 27.7 cm) and thin at TNB (3.5 cm, maximum 11.8 cm). Relative to the ice beneath it, however, the snow layer is thickest at WAP: the mean snow-to-ice thickness ratio is 0.34 at WAP, against 0.27 at ASP and 0.05 at TNB — a configuration that reduces the light reaching the ice and the water beneath it (Sect. 2.7.2).

These differences in the melt season and in snow thickness are the primary cause of the contrasting irradiance reaching the ice interior and the water column at the three sites. At TNB, where the ice opens relatively early and the snow is thinnest, the light penetrating the ice interior is the highest from spring onward, as is the light entering the water column. At ASP, once the year without an ice-free period is set aside, the irradiance reaching the water column in the remaining years is comparable to that at TNB. At WAP, by contrast, where the snow is thick and the ice opens late, both the irradiance within the ice and the light entering the water column are the lowest of the three sites. These differences in available light play a decisive role in the contrasting primary production discussed below.

These differences propagate into the temperature of the ice interior: the thick TNB ice develops a cold interior, reaching -28.5°C and remaining below -2.5°C for 87.5 % of the time that ice is present, and ASP is similar (73.4 %). The thin WAP ice, by contrast, stays closer to the freezing point of seawater and falls below that threshold only 52.0 % of the time. The contrast is sharper in the basal ice, where the ice-algal community is concentrated: there the ice is below -2.5°C for 82.0 % of the time at TNB, 58.6 % at ASP and 38.3 % at WAP. This contrast is central to the results that follow, because the ice-algal temperature gate operates at -2.5°C (Sect. 2.2.1). The upper water column shows a related but not identical contrast: WAP is again the warmest site (summer mean of $+0.41^{\circ}\text{C}$ over 0–30 m), but ASP is now the coldest (-1.36°C), below TNB (-0.70°C).

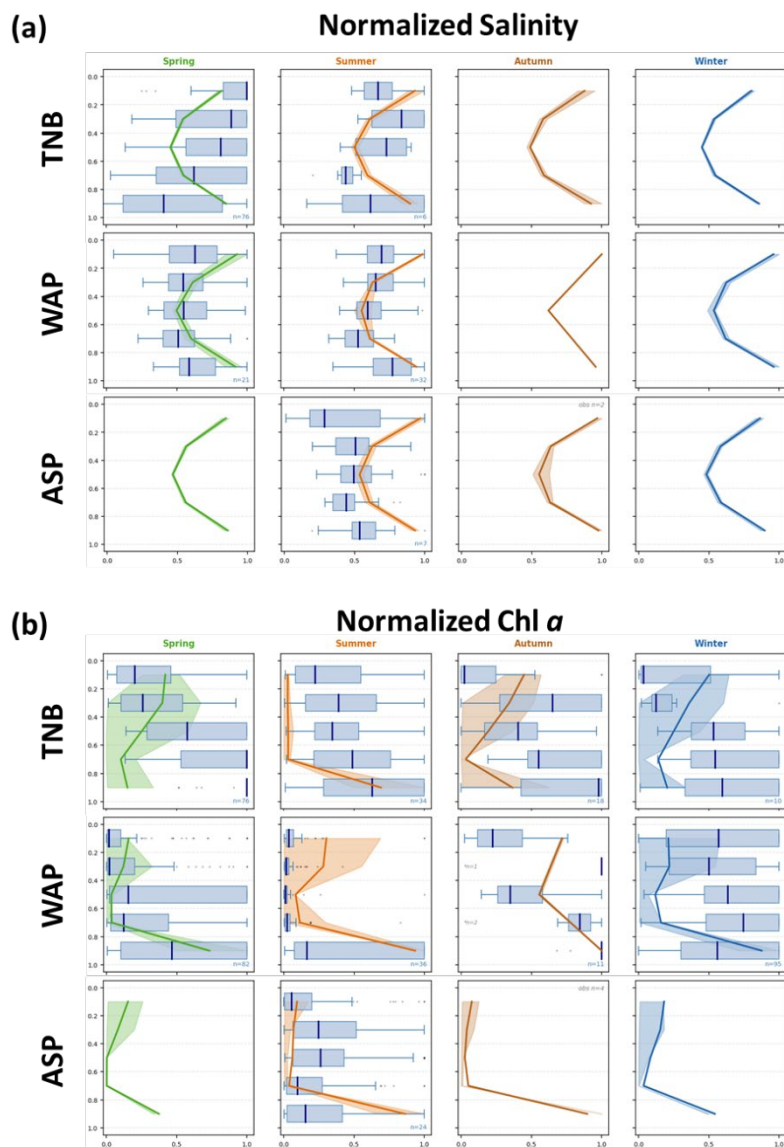


Fig. 3. Seasonal vertical profiles of (a) normalised bulk ice salinity and (b) normalised chlorophyll a within the sea ice, comparing SPBM simulations (coloured lines, with shading showing the interquartile range across daily model output) with ASPeCT ice-core observations (boxplots; box = interquartile range, line = median, whiskers = $1.5 \times \text{IQR}$, dots = values beyond). Rows are the three sites and columns the four austral seasons, with colours denoting season. Depth is normalised within the ice column (0 = ice–atmosphere interface, 1 = ice–ocean interface), and each observational core and each daily model profile is scaled by its own column maximum, so that the shape of the profile is compared independently of its magnitude (Sect. 2.9). The number of observational cores is given in each panel; panels showing a model line without boxplots are seasons for which no core data are available. Profiles of particulate organic matter and dissolved nutrients are given in Figs. S4–S6.



3.2 Sea-ice biogeochemistry: evaluation against ASPeCT observations

The simulated sea-ice biogeochemistry is compared with the ASPeCT ice-core observations in two complementary ways (Sect. 2.9): as seasonal depth-averaged concentrations, given in Table 5 as medians with interquartile ranges, and as normalised vertical profiles, shown in Fig. 3.

Chlorophyll a. The agreement in absolute sea-ice chlorophyll varies strongly among sites and seasons (Table 5). At TNB, the simulated spring median (3.01 mg m^{-3}) is close to the observed median (3.83 mg m^{-3}), and the autumn value is likewise similar (0.56 versus 0.61 mg m^{-3}). By contrast, the model substantially underestimates chlorophyll in summer (0.25 versus 6.84 mg m^{-3}) and winter (0.23 versus 3.18 mg m^{-3}). At WAP, chlorophyll is underestimated in all four seasons, with the largest discrepancy in spring (0.04 versus 7.38 mg m^{-3}). At ASP, the simulated summer median of 6.14 mg m^{-3} lies within the observed interquartile range of $4.17\text{--}13.4 \text{ mg m}^{-3}$ and is close to the observed median of 7.31 mg m^{-3} . Thus, the model reproduces the observed chlorophyll magnitude in some site–season combinations, particularly ASP summer and TNB spring and autumn, but underestimates absolute ice biomass in others.

Vertical structure of chlorophyll. The normalised profiles (Fig. 3) show that the model reproduces some aspects of the vertically structured chlorophyll distribution observed in Antarctic sea ice, including basal enhancement in several site–season combinations, but substantial seasonal biases remain. The simulated profiles are generally more strongly structured than the observations, indicating that the current representation of transport through the ice matrix does not reproduce the observed vertical distribution uniformly across sites and seasons. The physical origin of these biases, including the role of temperature-dependent porosity and permeability, is discussed in Sect. 4.2.

Bulk ice salinity reproduces the broadly C-shaped vertical structure characteristic of sea ice at all three sites, with enhanced values near the ice–atmosphere and ice–ocean interfaces and lower values in the interior (Fig. 3). The observed profiles are generally flatter and more variable, indicating that the prescribed physical structure represents a more idealised ice column than the heterogeneous conditions sampled by the ice cores.

Particulate organic matter. POC and PON are substantially underestimated wherever observations are available (Table 5). At TNB in spring, simulated POC is 48.9 mg C m^{-3} compared with 490 mg C m^{-3} observed, while simulated PON is 10.2 mg N m^{-3} compared with 64 mg N m^{-3} observed. The discrepancy is also large at WAP, particularly in spring, where simulated POC and PON are 1.10 and 0.22 mg m^{-3} , compared with observed values of 54 and 9 mg m^{-3} , respectively. The summer discrepancy at WAP is smaller but remains substantial (9.43 versus 45 mg C m^{-3} for POC and 1.80 versus 6 mg N m^{-3} for PON). These biases are consistent with the generally low simulated particulate organic matter concentrations.

Dissolved nutrients. At WAP, simulated NO_3 exceeds the observations in both spring (3.48 versus $2.03 \text{ }\mu\text{M}$) and summer (3.89 versus $1.00 \text{ }\mu\text{M}$), while Si is likewise overestimated (9.32 versus $7.13 \text{ }\mu\text{M}$ in spring and 10.38 versus $2.90 \text{ }\mu\text{M}$ in summer). PO_4 is reproduced more closely in summer (0.33 versus $0.31 \text{ }\mu\text{M}$). At ASP, summer NO_3 and Si are also overestimated (3.18 versus $1.62 \text{ }\mu\text{M}$ and 10.67 versus $4.80 \text{ }\mu\text{M}$, respectively), whereas PO_4 is underestimated (0.23 versus $0.57 \text{ }\mu\text{M}$). At WAP, the coexistence of low simulated particulate organic matter with relatively high residual NO_3 and Si is consistent with weak



560 biological utilisation of the available nutrients. The elevated residual NO_3 and Si at ASP likewise indicate incomplete nutrient
 drawdown, although particulate organic matter observations are unavailable there.

Overall, the evaluation indicates that SPBM v2.0 reproduces selected aspects of the observed seasonal magnitude and vertical
 organisation of Antarctic sea-ice biogeochemistry but retains substantial site- and season-dependent biases in absolute biomass
 and nutrient utilisation.

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Table 5. Seasonal comparison of depth-averaged sea-ice biogeochemical properties between the SPBM simulations and
 ASPeCT ice-core observations at the three sites. Only season-variable combinations for which observations are available are
 listed. Values are medians with the interquartile range in parentheses. Model concentrations are taken from the ice output
 without additional porosity scaling and are depth-weighted over the active ice column as $\Sigma(C_i \Delta z_i) / \Sigma(\Delta z_i)$, and are computed
 570 from daily output over the full simulation period (2023-2025). Observations are per-core depth-weighted averages from the
 ASPeCT merged database, filtered by sector. n is the number of observational cores. No in-ice nutrient observations are
 available at TNB, and no particulate organic matter observations at ASP.

Variable	Unit	Season	Model, median (IQR)	Observed, median (IQR)	n
TNB					
Chl <i>a</i>	mg m ⁻³	Spring	3.01 (0.21–9.34)	3.83 (2.96–6.08)	66
		Summer	0.25 (0.08–2.06)	6.84 (4.44–12.0)	34
		Autumn	0.56 (0.45–1.64)	0.61 (0.32–3.96)	18
		Winter	0.23 (0.08–1.35)	3.18 (0.21–10.2)	10
POC	mg C m ⁻³	Spring	48.86 (23.17–103.10)	490(304-751)	62
PON	mg N m ⁻³	Spring	10.21 (5.35–20.84)	64 (45–102)	62
WAP					
Chl <i>a</i>	mg m ⁻³	Spring	0.04 (0.02–0.17)	7.38 (4.62-10.91)	82
		Summer	0.35 (0.11–0.85)	3.71 (3.02–5.14)	36
		Autumn	0.67 (0.51–1.28)	4.06 (2.74-6.16)	11
		Winter	0.17 (0.07–0.34)	0.56 (0.12-1.55)	90
POC	mg C m ⁻³	Spring	1.10 (0.88–3.75)	54(42-63)	9
		Summer	9.43 (2.87–23.52)	45(30-67)	14
PON	mg N m ⁻³	Spring	0.22 (0.18–0.73)	9(6-10)	8
		Summer	1.80 (0.55–4.47)	6(2-10)	8
NO ₃	μM	Spring	3.48 (3.26–3.81)	2.03 (1.64–2.65)	9
		Summer	3.89 (3.58–4.05)	1.00 (0.52–2.23)	15
PO ₄	μM	Summer	0.33 (0.30–0.34)	0.31 (0.12–0.44)	15
Si	μM	Spring	9.32 (8.86–10.16)	7.13 (5.90–7.96)	9
		Summer	10.38 (9.55–10.79)	2.90 (2.69–3.57)	15
ASP					
Chl <i>a</i>	mg m ⁻³	Summer	6.14 (3.06–8.54)	7.31 (4.17–13.4)	24
NO ₃	μM	Summer	3.18 (2.29–4.15)	1.62 (1.60–1.93)	7
PO ₄	μM	Summer	0.23 (0.20–0.39)	0.57 (0.46–0.61)	7
Si	μM	Summer	10.67 (9.05–16.88)	4.80 (3.06–6.23)	7



3.3 Simulated ecosystem dynamics in the water column

575 Having evaluated the ice component against observations, we now describe the simulated dynamics of the water column and of the migrating zooplankton, which follow from the site-specific environmental conditions without further constraint by data.

Phytoplankton dynamics and ice-to-water coupling. Phytoplankton dynamics differ markedly among the three sites in their partitioning between ice and water, in the timing of the blooms, and in the contribution of ice-derived phytoplankton to the water column (Figs. 4–6). Total in-ice phytoplankton carbon reaches its highest value at ASP (up to 540 mg C m^{-3}), followed
 580 by TNB (280 mg C m^{-3}), and remains much lower at WAP (16 mg C m^{-3}). At TNB and ASP, biomass accumulates within the ice before the seasonal melt, whereas accumulation remains weak at WAP, where the ice is thinner, warmer, and more heavily snow-covered.

The timing and strength of the water-column bloom also vary by site. At WAP, a distinct bloom recurs after ice melt, reaching 136 mg C m^{-3} . At TNB, a summer-to-early-autumn bloom reaches 97 mg C m^{-3} , whereas ASP develops the strongest water-
 585 column bloom, reaching 327 mg C m^{-3} during summer. The resulting water-column phytoplankton maximum therefore follows the order $\text{ASP} > \text{WAP} > \text{TNB}$.

Water-column chlorophyll shows the same site ordering but differs in relative magnitude. The 0–50 m mean chlorophyll reaches its highest maximum at ASP (5.27 mg m^{-3}), followed by WAP (2.64 mg m^{-3}) and TNB (1.50 mg m^{-3}). The corresponding bloom-period Chl:C ratio is lowest at TNB (0.016), higher at ASP (0.021), and highest at WAP (0.024),
 590 reflecting site-to-site differences in photoacclimation.

The contribution of P1_i to the water-column community differs particularly strongly among the sites. At ASP, P1_i accounts for about 51 % of water-column phytoplankton biomass and contributes about 26 % at TNB. At WAP, by contrast, its contribution is negligible ($\sim 0.1\%$), and the water-column community is dominated almost entirely by pelagic phytoplankton. The simulations therefore span a pronounced gradient in direct ice-to-water phytoplankton coupling, from strong at ASP
 595 through intermediate at TNB to very weak at WAP.

Heterotrophic community: zooplankton and bacteria. The two large grazers develop contrasting community structures among the three sites. At TNB, the column-integrated Z3:Z4 biomass ratio ranges from 1.85 to 10.0, indicating persistent krill dominance. At WAP the ordering is reversed, with a Z3:Z4 ratio of 0.06–0.38 and copepods consistently dominant. At ASP the ratio spans 0.29–9.21, but its median value of 1.61 indicates krill dominance overall despite substantial seasonal variation.
 600 These contrasts emerge under the common biological parameterisation but differing environmental and food-web conditions at the three sites.

The two groups also differ in their vertical distribution. During the non-bloom period (May–September), Z4 concentrates near 300 m and Z3 near 100 m, close to their prescribed overwintering depths (Table 3), so that Z3 responds more quickly to the developing surface bloom. Z4 rises toward the upper water column as the productive season develops, producing a later
 605 response than Z3.

The spatial and temporal variability of bacteria follows the supply of organic matter. Surface B1 reaches its highest biomass at ASP (277 mg C m^{-3}), followed by TNB (105 mg C m^{-3}) and WAP (46 mg C m^{-3}). Bacterial biomass increases rapidly following the phytoplankton bloom as phytoplankton mortality and zooplankton feeding supply dissolved and particulate organic matter, with the largest response occurring at the two sites with the stronger overall seasonal production.

610

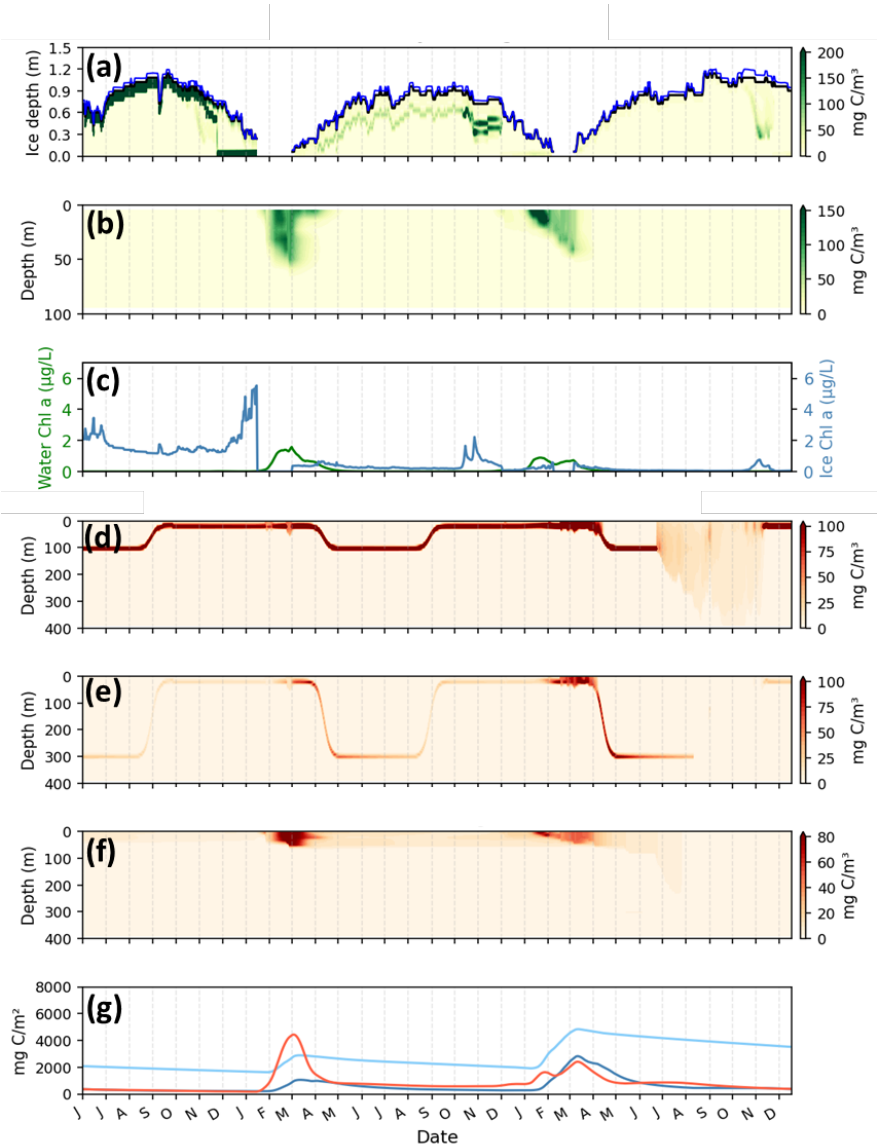


Fig. 4. Simulated phytoplankton and zooplankton dynamics at TNB over the simulation period. (a) Total phytoplankton carbon within the sea ice, with the black line marking the ice surface and the blue line the snow surface; ice depth is measured downward from the ice surface. (b) Total phytoplankton carbon in the upper 100 m of the water column. (c) Depth-averaged chlorophyll a in the water column (0–50 m; green, left axis) and in the sea ice (blue, right axis). (d) Krill (Z3), (e) copepods

615



(Z4) and (f) bacteria (B1) in the water column. (g) Column-integrated biomass over the full depth of krill (light blue), copepods (dark blue) and bacteria (orange). Note the differing depth ranges between panels (b) and (d)–(f).

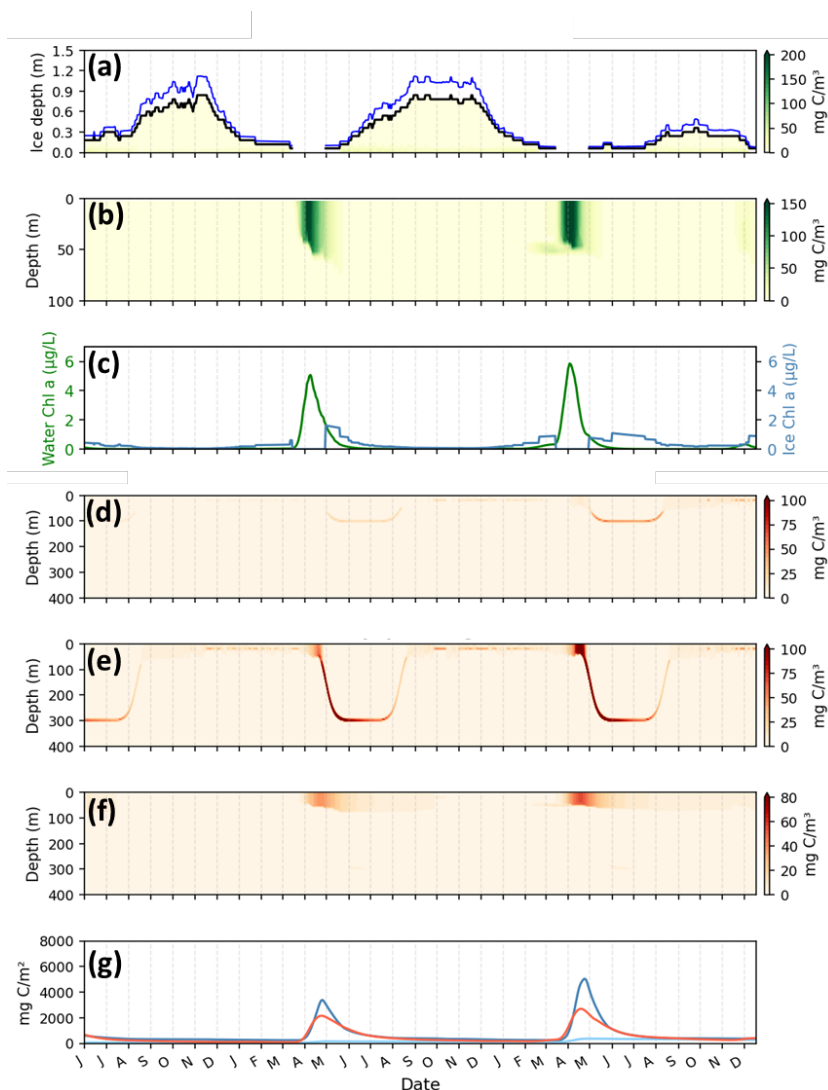


Fig. 5. As Fig. 4, but for WAP.

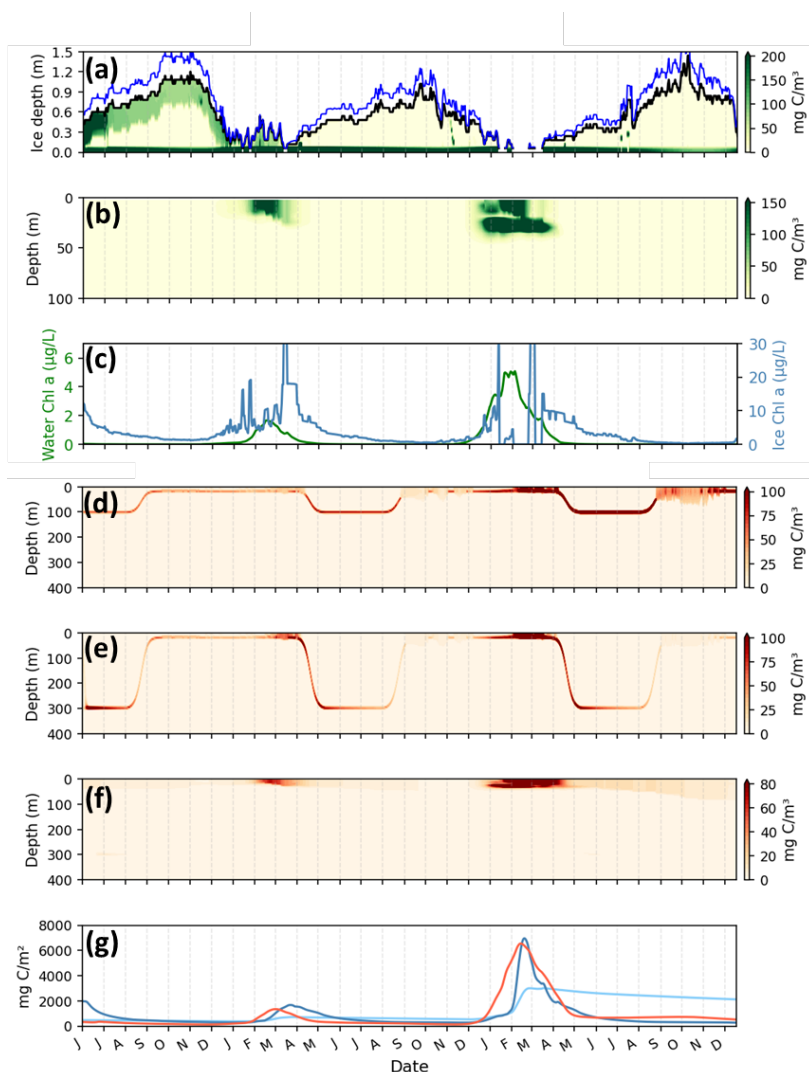


Fig. 6. As Fig. 4, but for ASP.

4 Discussion

4.1 Ice–pelagic coupling as an emergent, site-dependent property

625 The central result of the multi-site simulations is that the strength of sea-ice–pelagic coupling emerges under contrasting local environmental conditions rather than through site-specific biological parameterisation. Because the three sites share a single biogeochemical parameter set (Sect. 2.7.1), the pronounced differences in ice–pelagic coupling among the sites arise under a common biogeochemical parameter set and reflect their contrasting physical forcing and prescribed initial Fe inventories. This



provides a stringent test of the ice–pelagic coupling that is the primary target of SPBM v2.0, and one that a single-site application cannot offer.

The coupling is clearest at the two ice-rich sites. At TNB the thick, cold ice sustains the coldest basal ice of the three sites (below -2.5°C for 82 % of the time ice is present; Sect. 3.1) and a high total in-ice phytoplankton biomass (up to 280 mg C m^{-3}), while ASP reaches higher values still (540 mg C m^{-3} ; Sect. 3.3). At ice melt, ice-associated biomass is released to the surface layer, including P1_i cells that can contribute directly to the pelagic phytoplankton pool. The contribution of P1_i to the pelagic phytoplankton differs sharply among sites, accounting for about 51 % of water-column phytoplankton biomass at ASP, about 26 % at TNB, and only ~ 0.1 % at WAP (Sect. 3.3).

That a common biological parameterisation produces this gradient — from substantial ice-derived contributions at ASP and TNB to negligible direct P1_i contribution at WAP — demonstrates the strong site dependence of ice–pelagic coupling under contrasting physical and iron regimes. The simulated TNB regime, with its strong ice-algal bloom contributing biomass to the summer pelagic community, is consistent with the established view of the Ross Sea as a system in which sea-ice algae make a large seasonal contribution to shelf production (Arrigo et al., 2003; Peloquin and Smith Jr, 2007). The weakness of the coupling at WAP, however, is not a statement about the real West Antarctic Peninsula, where sea-ice conditions can be thicker and more persistent than represented by the forcing used here; it reflects the simulated local environmental conditions, including the weak ice-associated production and more iron-limited regime, as examined in Sect. 4.3.

4.2 Temperature-controlled ice-algal habitat and its consequences

The thermal state of the sea ice influences the simulated P1_i community through two distinct pathways. First, the logistic temperature gate (Sect. 2.2.1) directly regulates P1_i gross production, strongly suppressing new production under comparatively warm conditions. Second, ice temperature controls brine-volume fraction and therefore the permeability of the ice matrix, which determines whether P1_i can be transported downward within the ice (Sect. 2.2.4). These two mechanisms act independently but both respond to the local thermal state of the ice and together contribute to the site-to-site differences in the simulated ice-algal community.

The production gate produces a strong contrast among the three sites. At the cold TNB and ASP sites, where the basal ice lies below -2.5°C for 82 % and 59 % of the time, respectively, the ice-diatom group P1_i forms a substantial component of the simulated ice-algal community. In the thinner and warmer WAP ice, which remains below the threshold only 38 % of the time, P1_i is strongly suppressed. P1_i is most abundant in the TNB ice, remains substantially lower at ASP, and is nearly absent at WAP. This ordering follows the thermal state of the basal ice rather than the total in-ice phytoplankton biomass, which is highest at ASP (Sect. 3.3). The resulting contrast is qualitatively consistent with observations that Antarctic sea-ice algal community composition varies with the thermal and structural regime of the ice (Arrigo, 2014). The temperature gate should nevertheless be interpreted as a pragmatic constraint on P1_i production under comparatively warm conditions rather than as an explicit representation of physiological cold adaptation.



Ice temperature affects the vertical distribution of $P1_i$ through a separate mechanism. Because ice porosity in SPBM is determined by the interior temperature, sufficiently cold ice can fall below the permeability threshold of 0.05, restricting the prescribed downward transport of $P1_i$ even when production is permitted by the temperature gate. As the ice grows from its base, algae established earlier can therefore be displaced upward without being efficiently redistributed downward through the low-porosity interior. This mechanism provides a plausible explanation for the seasonal biases in the simulated chlorophyll profiles at TNB (Sect. 3.2). The structural bias therefore reflects the porosity-controlled transport formulation rather than the production gate alone. Representing the basal skeletal layer, where much of the bottom-ice algal biomass is concentrated, would require a finer treatment of the ice–ocean interface and transport through the ice matrix.

A related simplification concerns the thermal role of snow. In the current formulation, ice-interior temperature is interpolated linearly between the ice-surface temperature and the freezing point of the underlying seawater and therefore does not explicitly account for the insulating effect of snow. Because snow is thickest at WAP and ASP (Sect. 3.1), its omission may bias the simulated thermal structure of the ice, particularly at WAP. Incorporating snow insulation into the ice-temperature calculation, rather than using snow only for light attenuation as at present, is therefore a natural direction for future development.

4.3 Underestimation of the water-column bloom at WAP

The simulated water-column bloom at WAP is weak relative to what is known of the real shelf, and its origin is not a single limiting factor but a combination of the structural, forcing and parameter limitations discussed below.

A major limitation is the one-dimensional structure itself. A single column cannot supply the lateral fluxes that sustain shelf production in this region: neither the episodic intrusions of warm, nutrient-rich Circumpolar Deep Water that periodically ventilate the WAP shelf (Martinson et al., 2008), nor the sedimentary, glacial and iceberg sources that dominate the coastal iron budget (Annett et al., 2015; Sherrell et al., 2018; Dinniman et al., 2020). On the real WAP inner shelf, dissolved Fe is supplied primarily by shallow sediment-derived inputs transported laterally from the surrounding coastline rather than by upwelling of deep water (Sherrell et al., 2018), with glacial meltwater acting as an additional source in some coastal embayments (Annett et al., 2015); nearshore surface concentrations near Palmer Station average about 1 nmol kg^{-1} through January (Sherrell et al., 2018). WAP is also initialised with a lower dissolved-iron concentration (0.8 nM ; Table 4) than TNB and ASP (2.0 nM). This lower initial inventory is consistent with the sub-nanomolar upper-ocean dissolved-Fe conditions reported for parts of the WAP shelf (Sect. 2.7.4). Because no iron restoring is applied, this lower initial inventory contributes to a more iron-limited simulated regime. Together with the absence of lateral iron replenishment, this helps explain the weak WAP bloom in the model. The weak simulated WAP bloom should therefore be interpreted within this iron-limited, horizontally closed model setting rather than as a property of the real West Antarctic Peninsula, which supports some of the most productive waters of the Southern Ocean (Ducklow et al., 2013).

A second factor specific to the light environment is the snow forcing. Unlike the thermal role of snow, which the model does not represent (Sect. 4.2), its optical effect is resolved, although the imposed snow depth may be overestimated. The GLORYS reanalysis used here places thick snow on the WAP ice (seasonal mean of 8.8 cm , with the highest snow-to-ice thickness ratio



of the three sites; Sect. 3.1), and because snow attenuates light far more strongly than ice, an overestimate of snow depth directly suppresses both ice-algal and under-ice water-column production. Snow thickness is among the least constrained fields in sea-ice reanalyses, and a possible overestimate of snow depth at WAP could therefore provide an additional explanation for the weak simulated bloom. Finally, most of the physiological parameters in the standard ERSEM configuration were not optimised for Antarctic conditions and may not be appropriate for a Southern Ocean setting such as WAP — a limitation that applies equally to the other two sites. Disentangling this parameter effect from the structural and forcing limitations above would require targeted sensitivity experiments, which we leave to future work; representation of lateral nutrient and iron exchange and a polar recalibration of phytoplankton parameters are corresponding priorities for model development.

4.4 The chlorophyll-to-carbon ratio

One aspect of how the model represents phytoplankton, as distinct from the amount of phytoplankton biomass it simulates, bears directly on the evaluation. At TNB the simulated water-column phytoplankton biomass remains of the same order as at WAP, yet the maximum 0–50 m mean chlorophyll is lower (1.50 versus 2.64 $\mu\text{g L}^{-1}$). The ERSEM photoacclimation module likewise produces a lower bloom-period Chl:C ratio at TNB than at WAP (0.016 versus 0.024), with ASP intermediate (0.021; Sect. 3.3). Within the ice, simulated spring chlorophyll at TNB is of the observed order of magnitude, whereas bulk POC and PON remain substantially underestimated (Sect. 3.2). Because the observed POC and PON include non-phytoplankton particulate material, this mismatch cannot be interpreted directly as evidence of a bias in phytoplankton Chl:C. It nevertheless highlights uncertainty in relating simulated chlorophyll to bulk particulate carbon and nitrogen. Photoacclimation of this kind is a well-established property of polar algae (Cota and Sullivan, 1990), and its representation is appropriate in principle; the concern is quantitative. Because chlorophyll is widely measured in ice cores and field programmes and is also commonly used in remote-sensing assessments, a Chl:C ratio that is biased under the polar light regime could misrepresent the chlorophyll field independently of biases in simulated carbon biomass. Further evaluation and, if necessary, recalibration of the Chl:C parameterisation under Antarctic light conditions would therefore be a useful model refinement.

4.5 Zooplankton behaviour and community structure

The two-species migration scheme produces distinct seasonal depth distributions for the two large grazers. During the non-bloom period, copepods concentrate near 300 m and krill near 100 m, close to their prescribed overwintering depths, whereas both groups move toward the upper water column during the productive season (Sect. 3.3). The seasonal displacement is similar among the three sites — approximately 60 m for krill and 200 m for copepods — because the target depths are prescribed identically. What differs among the sites is primarily the relative dominance of the two groups and their timing of response to the surface bloom.

Community structure varies with the contrasting environmental and food-web regimes simulated at the three sites. TNB remains persistently krill-dominated, whereas WAP is copepod-dominated in association with its weak direct $P1_i$ contribution and more iron-limited pelagic regime. ASP spans both grazer states seasonally but remains krill-dominated overall. These



contrasts are qualitatively consistent with the strong association of Antarctic krill with sea-ice habitats (Schmidt and Atkinson, 2016; Flores et al., 2012) and with the more omnivorous, water-column feeding of dominant Southern Ocean copepods (Bathmann et al., 1993; Schnack-Schiel et al., 1991).

730 The scheme resolves seasonal, rather than diel, vertical migration. It operates on daily-mean irradiance and therefore does not represent the dawn–dusk vertical movements that occur at sub-daily timescales. Resolving diel migration would require sub-daily light forcing and finer near-surface temporal and vertical resolution. The present formulation is instead intended to represent the large seasonal redistribution associated with overwintering and the return to the productive upper water column.

4.6 Structural limitations of the 1D framework

735 Several of the biases discussed above share a single origin in the one-dimensional design, and it is useful to consider them together as the price of the column approach rather than as independent shortcomings. In the Antarctic coastal setting, three consequences follow.

The first is the absence of lateral nutrient and iron exchange, discussed for the bloom at WAP in Sect. 4.3. On the real shelves, winter macronutrient inventories are replenished by intrusions of Circumpolar Deep Water (Martinson et al., 2008), whereas 740 the growth-season iron supply is dominated by sedimentary and glacial sources, whose relative importance differs between shelves, with deep-water upwelling contributing comparatively little directly (Gerringa et al., 2012; Sherrell et al., 2018; Dinniman et al., 2020); a column that evolves its dissolved pools without boundary relaxation cannot replenish them, so that both the weak bloom at WAP and any slow drift of the deep nutrient reservoir over the multi-year integration are expected features of the framework rather than model errors to be tuned away.

745 The second appears at depth, where dissolved oxygen in the bottom boundary layer and sediment becomes depleted at all three sites and remains so throughout the simulation. This is not a numerical artefact but a direct consequence of the column geometry: organic matter settling to the sea floor is respired in the boundary layer and sediment, consuming oxygen that a single column cannot replenish through the lateral advection and deep-water renewal that ventilate the real Antarctic shelves. Oxygen depletion of this kind was likewise reported for the original SPBM, where a prolonged ice-melt season produced 750 strong stratification that inhibited downward oxygen supply, while organic matter produced during the phytoplankton bloom drove oxygen consumption in the subsurface layers (Yakubov et al., 2019); more generally, such oxygen depletion can arise in horizontally closed 1-D biogeochemical columns that resolve benthic respiration without a lateral oxygen supply. The effect is confined to the bottom boundary layer and sediment; the overlying water column remains well oxygenated at all three sites, with minima of 171–204 mmol m⁻³ in the deepest layer (Sect. 2.8). We therefore treat the bottom boundary layer as a sink 755 boundary rather than a quantitative representation of near-bottom oxygen, and exclude it from the interpretation of water-column biogeochemistry.

The third is the absence of horizontal ecological connectivity: in reality krill and copepods advect between regions and the ice-derived material disperses laterally, whereas here the column is treated as horizontally closed. These limitations are common



to horizontally closed single-column biogeochemical models and are the counterpart of the framework's principal strength. By holding the biological parameters fixed, SPBM v2.0 provides a controlled comparison of ecosystem responses to contrasting local physical forcing and prescribed initial Fe inventories. The site-to-site contrasts identified here should therefore be interpreted as responses of biologically identically parameterised columns to different local environmental conditions, rather than as fully realistic regional budgets. Capturing the lateral fluxes on which the real Antarctic shelves depend would require coupling the column to a regional circulation model, which remains a central direction for future development.

5 Conclusions

SPBM v2.0 extends the original one-dimensional sea-ice biogeochemical model into a tool for studying coupling between the sympagic and pelagic subsystems of Antarctic coastal ecosystems. The extension combines a temperature-gated, bottom-accumulating ice-algal ecophysiology; a water-only zooplankton formulation with continuous overwintering; and a two-species seasonal vertical migration scheme, together with corrections to the solar forcing and ERSEM iron cycle required for iron-sensitive Southern Ocean applications.

Applied with a common biological parameterisation to Terra Nova Bay, the western Antarctic Peninsula and the Amundsen Sea polynya, SPBM v2.0 reproduces several observed features of Antarctic sea-ice biogeochemistry. The model captures the observed spring and autumn sea-ice chlorophyll magnitude at TNB and the summer magnitude at ASP, reproduces the broadly C-shaped vertical salinity structure, and represents basal chlorophyll enhancement in several site–season combinations. At the same time, substantial biases remain, including underestimated chlorophyll during summer and winter at TNB and across seasons at WAP, as well as underestimated particulate organic matter and imperfect vertical chlorophyll structure.

The simulations also produce strong site dependence in ice–pelagic coupling without site-specific biological parameter tuning. $P1_i$ contributes about 51 % of water-column phytoplankton biomass at ASP and about 26 % at TNB, whereas its direct contribution is negligible at WAP. The contrasting physical forcing and prescribed initial iron inventories are accompanied by different pelagic food-web structures, with krill dominance at TNB and ASP and copepod dominance at WAP. The new zooplankton formulation also produces distinct seasonal depth distributions, with krill occupying shallower overwintering depths than copepods and both groups returning toward the upper water column during the productive season.

The model's principal limitations are traceable to identifiable structural and forcing constraints. The one-dimensional framework excludes lateral nutrient and iron exchange, the representation of transport within the ice does not reproduce the observed vertical chlorophyll structure uniformly, and several standard ERSEM physiological parameters remain uncalibrated for Antarctic conditions. These limitations define concrete directions for future development, foremost coupling SPBM to a regional circulation framework. Within those constraints, SPBM v2.0 provides a FABM-compatible process model for investigating how contrasting Antarctic coastal environments influence coupled ice–pelagic biogeochemistry and lower-trophic ecosystem structure.



790 **Code and data availability**

The exact version of SPBM v2.0 used in this study is archived on Zenodo at <https://doi.org/10.5281/zenodo.22668073> (Kwon and Rhee, 2026). The archive includes the SPBM source code, study-specific modifications to ERSEM and BROM, final configuration files for TNB, WAP and ASP, the physical forcing files used in the simulations, the derived ASPeCt-Bio observational dataset used for model evaluation, and scripts for building and running the model and reproducing the main manuscript Figs. 2–6. FABM is used as an external dependency at commit 1944b09237e093c06d9adb0bd06de59c2d3d894e, with build instructions provided in the archive. The GEBCO bathymetry required only for reproducing Fig. 2 is not included and can be obtained separately from GEBCO.

Author contributions

YSK developed the model code, performed the simulations, analysed the model results, and prepared the manuscript. TSR contributed to the analysis of observational data and manuscript editing. Both authors contributed to the interpretation of the results and revision of the manuscript.

Competing interests

The authors declare that they have no conflict of interest.

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