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Geoscientific
Model Development
Discussions

Interactive comment on “A 1-Dimensional Ice-Pelagic-Benthic transport model (IPBM) v0.1: Coupled simulation of ice, water column, and sediment biogeochemistry” *by* Shamil Yakubov et al.

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General comments:

1. "The ms by Yakubov et al. presents a new transport model for coupled numerical simulations of sympagic, pelagic and benthic biogeochemistry. The model development itself is innovative and relevant to the scientific community. However, I have several concerns regarding the very limited description provided for the models that were used, the very little results presented, the total absence of discussion and the poor

conclusions. Although GMD journal focuses on novel model developments, I believe that the material provided by the authors so far is more suitable for a report than for a publication in GMD. However, I am sure the handling editor is the one that best can evaluate this. I have suggested several corrections already but, generally, I believe the manuscript would benefit from being reviewed by an English native speaker or being grammar checked."

- All the biogeochemical models used are quite complicated tools and have their own comprehensive description papers (with references/links provided); in the text, we provided only short descriptions of the main parts used in the demonstration runs. We have tried to concentrate on the transport model description itself, but now we have added more results, expanded the discussion and reworked the conclusions to clarify the benefits of using our model. To our knowledge, our model is the first offline biogeochemical transport model to allow integrated simulation of ice, water, and sediment biogeochemistry. It is, therefore, a novel modelling tool that, in our view, merits publication in GMD. The revised manuscript has been grammar-checked and reviewed by a native English speaker (PW).

2. "Please use standard international units as much as possible throughout the ms.When referring to parameters/forcing shown in Tables, please refer to them throughout the ms. E.g. on page 8, Line 1, for kf Line 7-8, for kscatter, Aice, Asnow, and ksnow etc."

- As far as we know we used standard international units in the all possible cases in our manuscript. On page 8 we provide a general description of the transport model, while the Tables provide specific parameter values used in the test runs. We therefore only refer to the Tables when presenting results tied to a specific set of parameter values."

3. "In the Introduction, I would suggest you have a look at Vancoppenolle and Tedesco, Numerical Models of Sea Ice Biogeochemistry in Sea Ice 3rd Edition edited by D.K. Thomas, 2017, and refer to it as needed since it is a comprehensive work on the most

novel part of your work, i.e., the inclusion of a sea ice biogeochemical module."

- Thank you for the reference; we have reviewed it and cited it in the revised introduction: “There are 3 main possibilities to implement ice algae behaviour according to the place where algae live in the ice column (Tedesco and Vichi, 2014; Vancoppenolle and Tedesco, 2017): at the bottom layer of the ice column with fixed thickness, at the bottom layer of the ice column with variable thickness, at any layer of the ice column”.

4. "In Section 3 there is a very brief description of the models (i.e., less than 20 lines), and it is overall not sufficient to make it clear to the reader what the chosen modules are about. In fact, I found Sect. 3 very confusing. Any info on growth limiting factors is for example missing. There is no description of physiological/ecological differences between the communities in different habitats. On top of the additional text, some scheme might also be good to provide. Also, there is no info on the initial/boundary conditions used, i.e. the reader has no idea where Fig. 3 comes from."

- Comprehensive descriptions of the used biogeochemistry models are provided in the corresponding articles that are cited in the text. In our revised text we have provided a short, general overview in section 3 (Test Runs):

“The first model is the European Regional Seas Ecosystem Model, ERSEM (Butenschön et al., 2016). Originally a coastal ecosystem model for the North Sea, ERSEM has evolved into a generic tool for ecosystem simulations from shelf seas to the global ocean. Model dynamics within each functional group describe processes occurring inside a ‘standard organism’ (Baretta et al., 1995; Vichi et al., 2007). ERSEM accounts for flexible elemental stoichiometry in planktonic processes by allowing decoupled fluxes of carbon, nitrogen, phosphorus, silicate, and chlorophyll a. This requires multiple state variables to describe each functional group biomass (e.g. diatom carbon, diatom nitrogen, etc.) and results in a relatively complex model.

The second model is the Bottom RedOx Model biogeochemistry module (Yakushev et al., 2017). This model represents key biogeochemical processes in the water and

upper sediments, with a focus on oxygen dynamics and redox biogeochemistry. Compared to ERSEM, it simulates the coupled cycles of more elements (N, P, Si, C, O, S, Mn, and Fe), resolves more structure in the bacterial community (4 functional groups), and calculates carbonate chemistry in more detail; however it assumes fixed stoichiometry for all forms of organic matter (nitrogen currency), resolves only one functional group each for phytoplankton and zooplankton, and does not resolve dissolved organic matter into different lability classes.”

We are reluctant to give a more detailed description than this because: (1) such detailed descriptions are provided in existing cited literature, and (2) the new model (SPBM) is not specifically tied to either ERSEM or BROM, but rather can use any model that is included in the rapidly-expanding FABM library. Growth-limiting factors and the physiological/ecological differences between the ERSEM communities in different habitats are discussed partly in the new section 3.1 (Test Case 1), but more discussion is available in the cited literature. A scheme of the FABM model coupling was and is provided in Figure 2. Information about the specific initial/boundary conditions used in the test cases is now provided in section 3 (Test Runs) (links to tables in an appendix).

5. Section 4 presents and describes way too little model results in my opinion and no sensitivity to any of the many choices that for sure the authors had to make. I don’t think this model is anyhow validated at this point and/or ready to be used for ice/water/sediment studies. If the authors are confident it is, then much more supporting results should be presented and discussed. There is currently no discussion at all in this work.

- We have added a discussion section to clarify the range of applicability of SPBM, and we now provide more model output (two test cases) with different parameterizations as examples. The first test case simulates 5 different phytoplankton functional types in the ice and water column, the second shows different redox transformations in all three domains. Also, we have compared the model output ranges to observed ranges for the Arctic taken from the literature (new section 3.1). To be clear: SPBM is an offline transport model that allows integrated simulation of biogeochemical transformations and transports within and between ice, water, and sediment domains ("offline" meaning that the physics of sea ice and water hydrodynamics is provided as input forcing and is not computed by SPBM). To our knowledge, there exists no other tool for such integrated offline simulation. The transport formulations and numerical solution techniques within SPBM are quite standard within each domain; the main novelty is in their integration, and in the FABM interface that allows biogeochemical models to be constructed using modules from a range of existing models within the FABM library (Bruggeman and Bolding, 2014). SPBM is a flexible, computationally-efficient, offline biogeochemical solver that accounts for the strong interactions between ice, water, and sediment biogeochemistry that often characterize Arctic marine ecosystems. As such it should facilitate the development of well-parameterized biogeochemical models for such systems. The test cases are only intended to demonstrate the kind of output that can be generated by SPBM with relevant configurations of physical inputs and FABM biogeochemical modules. Of course, it is desirable that the test cases show realistic behaviour (this is to some extent supported by the range comparisons) but they are not intended as validations of any particular physical or biogeochemical model formulation or parameter set. This has been clarified in the new manuscript.

Specific comments:

1. Title. To be consistent with the rest of the title, you should replace "Ice-Pelagic-Benthic" with "Sympagic-Pelagic-Benthic", and thus "IPBM" with "SPBM"

- We have changed ice to sympagic, thank you for the correction.

2. "Simulation" or "simulations"?

- It is not a specific simulation or simulations, just general simulation.

3. "I don't really have a preference for version numbering systems, but I'd rather name

this first version as "1.0" than "0.1". Just a suggestion, up to the authors."

- There are a lot of ways to version software. We would try to use https://semver.org/.

Abstract

4. Line 1. "Aquatic" or "Marine"? I suppose it is "Marine" what you want to refer to.

- Thank you, you are right. We corrected it to "Marine".

5. Line 1. Why "especially in polar regions"? I would rephrase as: "interact in shallow areas of the polar regions with", or something like that. Line 2. I'd suggest removing "layers".

- Thank you, we changed a sentence to "Marine biogeochemical processes can strongly interact in shallow areas of the polar regions with processes occurring in adjacent ice and sediments."

6. Line 3 and further. Same comment as in the title about replacing "Ice" with "Sympagic" for consistency, and thus the acronym "IPBM" with "SPBM".

- We renamed IPBM to SPBM.

7. Line 5. I'd suggest removing "(reaction terms)".

- It was removed.

8. Line 6. "partly coupled" in which way? Do you mean "coupled to both"?

- It meant that IPBM (currently SPBM) used some parts of both models, yes, it was coupled to both. The sentence was removed.

9. Line 9. What "main variables"? Which model are you referring to? Please, specify.

- The sentence was removed, as well as results section was extended (and renamed to the test run section) and all state variables have their descriptions there. So we have rewritten the abstract according to the new test run section.

10. Line 9-11. Since the model setup explicitly stresses a benthic component, the reader is perhaps expecting a comment also on that in this sentence (on top of the others for sympagic and pelagic dynamics).

- The sentence was removed. We have rewritten the abstract to account for the new test run section: “Marine biogeochemical processes can strongly interact with processes occurring in adjacent ice and sediments. This is especially likely in areas with shallow water and frequent ice cover, both of which are common in the Arctic. Modelling tools are therefore required to simulate coupled biogeochemical systems in ice, water, and sediment domains. We developed a 1D Sympagic-Pelagic-Benthic transport model (SPBM) which uses input from physical model simulations to describe hydrodynamics and ice growth and modules from the Framework for Aquatic Biogeochemical Models (FABM) to construct a user-defined biogeochemical model. SPBM uses the physical model input and FABM modules to simulate vertical diffusion, sinking/burial, and biogeochemical transformations within and between the three domains. The potential utility of SPBM is demonstrated herein with two test runs using modules from the European Regional Seas Ecosystem Model (ERSEM) and the Bottom-RedOx Model biogeochemistry module (BROM-biogeochemistry). The first test run simulates multiple phytoplankton functional groups inhabiting the ice and water domains, while the second simulates detailed redox biogeochemistry in the ice, water, and sediments. SPBM is a flexible and computationally-efficient tool for integrated simulation of ice, water, and sediment biogeochemistry, and as such may help in producing well-parameterized biogeochemical models for regions with strong sympagic-pelagic-benthic interactions.”

Introduction

Page 1

11. Line 13. Is there a need of “marine” between “Arctic” and “ecosystem”?

- Thank you, “marine” was added.

12. Line 13. Please, consider replacing “induced” with “driven”.

- Thank you, it was corrected.

13. Line 14. Do you refer here only to CCSM? Or more generally to ESM? Please, correct in case. Line 15. Please, change “global mean” with “mean global”. Line 15. This reference might be updated. Line 17. Please, place a reference at the end of the sentence.

- Thank you, it was corrected to “The Coupled Model Intercomparison Project and the Community Climate System Model studies have projected atmospheric warming in the Arctic of 1.5 - 4.5 times the mean global warming, and the Arctic marine environment is expected to be strongly impacted by loss of ice cover, increased light exposure, ocean warming, freshening, acidification, and deoxygenation (Holland 2003)”.

14. Line 17-18. This sentence could be much better rephrased to emphasize the role that numerical models may play in the understanding of future changes of the Arctic Ocean Ecosystems.

- It was corrected to “Model simulations are needed for the analysis of present conditions and the projection of long-term impacts on Arctic marine biogeochemistry”.

15. Line 19. This sentence applies to all model developments. I’d suggest modifying as “of this region, such as the seasonal to permanent ice cover and the presence of shelf areas. Thus, the model should preferably combine: : :”, or something similar.

- Thank you for the suggestion, it was corrected to “A biogeochemical model suitable for the Arctic should take into account the specific conditions of this region, such as the seasonal to permanent ice cover and the presence of shelf areas. Thus, the model should preferably combine processes occurring in 3 domains: ice, water column, and sediments.”

Page 2

16. Line 1. Please, place a reference at the end of the sentence.

- A link to "Arrigo, K. R., Mock, T., and Lizotte, M. P.: Sea ice, vol. 2, chap. Primary Producers and Sea Ice, pp. 283–325, Oxford: Wiley-Blackwell, 2010." was inserted.

17. Line 3. "2012", recent? Please, also consider overall estimates of sea ice algal production and related parameters that can be found in Arrigo, K., Sea ice as a habitat for primary producers, in Sea Ice 3rd edition, edited by D.K. Thomas, 2017 (see e.g. Tables 14.1,14.3,14.5 and 14.7). Line 4-5. Again, I suggest having a look also at other references in the same chapter just mentioned in my previous comment. Line 5. Correct reference style and update reference to 2017.

- "Recent" was deleted. Thank you for the link provided, but since we used the Sea Ice 2nd edition we provided a link to the reference we used.

18. Line 5. Please, place "algal "between "sea ice" and "production", and please, replace "from" with something like "accounting for".

- We inserted algal between "sea ice" and "production" and changed "from" to "accounting for".

19. Line 5-6. Please, also here add e.g. "primary" before "productivity".

- It was added.

20. Line 6. Please, specify "in a study area of Greenland" after "community".

- Thank you, it was specified.

21. Line 11. "Pervasive"?

- "Pervasive" was deleted.

22. Line 11. "localized"? or "local"?

- The sentence was corrected to "In the Arctic, global change is causing seawater acidification, accompanied by local changes in productivity and oxygen depletion (Bopp

et al., 2013; Henson et al., 2017)".

23. Line 11. Please, replace "the most" with "an".

- It was replaced.

24. Line 20. Please, place a comma after "Also".

- A comma was added.

25. Line 21. Please, remove the comma after "pelagic".

- It was removed.

26. Line 21-22. Repetition of "correct". Please, rephrase.

- 'correct' was replaced with 'adequate'.

27. Line 22-23. Please, change "structured in the vertical" with e.g. "vertically structured".

- It was corrected.

28. Line 28-30. Please remove parenthesis before "such" and at the end of the sentence for better readability.

- It was corrected.

29. Line 31. Please, place a comma before and after "i.e.".

- It was corrected.

30. Line 33. Missing reference after "MOM".

- We have added a link to "A TECHNICAL GUIDE TO MOM4 GFDL OCEAN GROUP TECHNICAL REPORT NO. 5" S.M. Griffies, M.J. Harrison, R.C. Pacanowski, and A. Rosati, NOAA/Geophysical Fluid Dynamics Laboratory Version prepared on February 4, 2008 Available online at www.gfdl.noaa.gov

Page 3

31. Line 16. Something wrong with line editing.

- Yes, something wrong with a “\unit” LaTeX command provided by GMD.

32. Line 16-20. It is a good practice to specify variables’ names in order of appearance. Please, correct accordingly.

- Thank you, it was corrected.

33. Line 22. Please, replace “between in” with e.g. “within”.

- It was corrected.

Page 4

34. Eq. 4. Please, consider replacing “IceGrowth” with e.g. dzs/dt. Also, if this is in cm s-1, I see a problem with units since zs is in m.

- There is no need to use Leibniz’s notation, we prefer to keep IceGrowth. We checked the units: they are ok because the coefficients in the numerator convert to cm s-1, while the denominator converts to m s-1.

35. Line 8. Where does “72” come from? Does it need a reference? Or is a tuned parameter? Please, specify.

- We have changed it to be a tunable parameter φ_min

36. Line 14. Where does “3” come from? Does it need a reference? Or is a tuned parameter? Please, specify. I don’t think sea-ice diatoms have to have a sedimentation rate. They are able to move and stick within sea ice and this has been proven now for a long time (see references e.g. in Arrigo et al, 2017, reference above)

- Thank you, the sentence was corrected to “To represent the ability of sea ice diatoms to maintain their vertical position relative to the skeletal layer (Arrigo et al., 1993) their vertical velocity is set to a constant but possibly layer-dependent value within the ice

column, and zero on the interface between ice and water domains”

Page 5

37. Line 1. Please, correct reference style.

- It was corrected.

38. Line 20. Should "width" be replaced with "thickness"?

- It was corrected.

Page 6

39. Line 1. Please, correct reference style. Also, why do solutes have a sinking velocity?

- The reference was corrected. We changed “sinking velocity” to “sinking/burial velocity”. Solutes are buried. All velocities are in the reference frame of the SWI. In this frame, the settling of sediment gives the bottom water velocity a very small component downward through the SWI (since it is porous, see Boudreau 1997, p34: “The burial component of porewater advection results from the sediment-water interface moving away from porewater as sediment accumulates”). To be strictly consistent, the solute burial velocity could be extended through the water column as an advection velocity, but the contribution of this to transport in the water column is safely negligible since the deep burial velocity is of order 10ˆ-10 m s-1 (Table C3).

40. Alg.1 Is this the same "IceGrowth" as earlier in the ms? To me, it looks like something different.

- It was renamed.

Page 7

41. Line 13. Something wrong with line editing.

- Thank you, it is again some problems with the \unit LaTeX command provided by

GMD. Hope the new version of their package will solve the problem.

42. Line 15. Please replace “depths” with “depth z in the water column, which” and specify according to which scheme (with reference, possibly). Also, consider replacing “propagate” with e.g. “compute”.

- We do not describe FABM family biogeochemical model routines in this paper; the reader can consult the published literature on the relevant FABM family models. We rephrased the introductory part of the irradiance formulation section as follows: “FABM biogeochemical models generally need to know the photosynthetically active radiation (PAR) in each layer of the model grid. Some FABM models compute water column PAR given only surface PAR, but they do not assume the existence of the ice column and consider all grid points to be located within the water column. SPBM, therefore, provides the following simple approach to calculate PAR in both ice and water column domains.”

43. Line 17. Please, remove one “is”. - It was corrected.

Page 8

44. Alg. 2 If this refers to melting, I suppose that the sign for "IceGrowth" should be rather negative than positive, right?

- The parameter IceGrowth (currently renamed) can be positive, negative, or null. A value of |IceGrowth| in Alg.2 should be positive according to the modulus definition.

45. Line 1-12. Please refer to related Tables for parameters such as kf, kscatter, etc.

- The Tables report the specific values used in the test runs; they do not give a general description of parameters within formulations used by SPBM, rather we do this in the main text.

Page 9

46. Line 1. Same comment as above.

- There are no related Tables, all tables refer to the test runs in the results section. Here we are giving a general description of the model routines.

47. Line 4-5. Please, explain this further.

- We mention here that SPBM uses FABM to initialize variables, which in turn uses YAML files for configuration. The further explanation of both is not a purpose of this manuscript, but a citation is provided (Bruggeman and Bolding 2014) if one wants to know more about FABM routines, also it is widely known standard (https://en.wikipedia.org/wiki/YAML).

48. Line 6-8. So, which option was used here? If both according to ice presence, then please, rephrase to make it more clear.

- In the 2nd section “SPBM: A 1D transport model” we provide only a general description of the routines used. Options and specific parameter values used in the test runs are reported in the 3rd section “Test Runs”. We added more information about the work structure in the introduction part.

49. Line 10-11. Not clear the sentence in brackets. Should the comma before salinity be replaced by an “and”?

- We rephrased it to “... (turbulent diffusivity [m2 s-1] on layer interfaces; temperature [°C] and salinity [psu] on layer centres) . . .”

50. Line 13-15. Bad wording, please, rephrase with e.g. “More accurate estimates of downwelling shortwave radiation and PAR can also be read from..”

- It was corrected to: “Downwelling shortwave radiation and PAR can be read from an input file instead of using the formulae provided in Subsect. 2.4”

51. Line 16-20. Not clear, please rephrase and correct writing style. - We rephrased to “Other optional input forcings include: brine volumes and diffusion coefficients in the ice, input fluxes at the water surface, and horizontal mixing fluxes at any depth.

Page 10 From page 10: - To fix a lot of misunderstandings we have restructured the text, moved explanation of biogeochemical models to the "Test Runs" Section and provided more output and more test cases in order to better demonstrate the model capabilities.

52. Line 2. Please, remove double brackets.

- It was corrected.

53. Line 4. I wonder why "non-bacterial" since ERSEM does have a bacterial component. Also considering that you did consider bacteria in the sea ice. How do bacteria end up in the ice if they are not in seawater? And please notice that strictly speaking, plankton definition does include bacteria (i.e., bacterioplankton).

- On Line 9 you can see that the bacteria part was taken from another model. On Line 4 "ERSEM modules are used to model the non-bacterial lower trophic levels (plankton)." - meant only that we did not simulate it with ERSEM, not that we neglected bacteria in seawater. Thank you for the remark, the word "plankton" was erased.

54. Line 4-5. Please, replace "conception of the functional groups" with "concept of functional group (..), which". And please, reformulate better the rest of the sentence to make it clear what a functional group describes.

- With hindsight, this concept is not very specific to ERSEM and does not need to be explained in our text. The paragraph has been revised to: "The first model is the European Regional Seas Ecosystem Model, ERSEM (Butenschön et al., 2016). Originally a coastal ecosystem model for the North Sea, ERSEM has evolved into a generic tool for ecosystem simulations from shelf seas to the global ocean. Model dynamics within each functional group describe processes occurring inside a 'standard organism' (Baretta et al., 1995; Vichi et al., 2007). ERSEM accounts for flexible elemental stoichiometry in planktonic processes by allowing decoupled fluxes of carbon, nitrogen, phosphorus, silicate, and chlorophyll a. This requires multiple state variables to de-

scribe each functional group biomass (e.g. diatom carbon, diatom nitrogen, etc.) and results in a relatively complex model."

55. Line 6-8. Why was this choice made? For technical reasons? For lack of observations? Or? Please, explain also the consequences/limitations due to this choice either here or later in the ms.

- In the revised test case we take the standard ERSEM groups (4 phytoplankton, 3 zooplankton) and add an additional group "ice diatoms" based on modifying the ERSEM parameterization for diatoms. As we explain in the revised text, such a model extension is very easy to perform within SPBM because of its use of the FABM, which requires only a few extra lines in the fabm.yaml model specification file (mostly duplicating lines for the diatom specification). The issue of reasons for simplification therefore no longer arises.

56. Line 16. I would call it "site" rather than "point". What is also the ROMS grid point? Is it one of ROMS test case study? If so, please, rephrase. Also, a location map of the site with also bathymetry would be a nice addition.

- We have significantly modified the test cases and extended the results section. We only meant that the forcing required for the model were taken from the ROMS test case study in the mentioned position. We have removed reference to a grid point in the revised text.

57. Line 17. 1984 is a curious number, any explanation for this choice?

- Originally this year was chosen after repeating the first day of 1 january 1980 100 times, then the first year 10 times, then skipping the first 4 years to ensure full spinup. Our new choices are fully explained in the new text.

58. Line 20-21. I don't think this is the way that the problem should be faced. What was too high? The snow depth provided by the physical model? How high? Did you compare with observations? Sea ice is rarely snow-free and ice algae can cer-

tainly grow under thin snow. If the model was not able to produce any growth, then perhaps you should review algal growth parameterizations rather than removing snow from the model, which has e.g. the effect to anticipate unrealistically the bloom timing and even causing photoinhibition, as shown by both field experiments (e.g. Campbell et al., 2014) and modelling work (e.g. Tedesco and Vichi, 2014). Campbell, K., Mundy, C.J., Barber, D., Gosselin, M., Characterizing the sea ice algae chlorophyll a-snow depth relationship over Arctic spring melt using transmitted irradiance, Journal of Marine Systems (2014), doi: 10.1016/j.jmarsys.2014.01.008 Tedesco, L., Vichi, M., Sea ice biogeochemistry: a guide for modellers. PLOS ONE, (2014), doi: 10.1371/journal.pone.0089217.

- Thank you for the links provided. We have significantly modified the test cases to exclude such issues. In fact we now modify the algal growth parameterization (for “ice diatoms”) instead of modifying the input snow depth.

Page 11

59. Fig. 3,4,5. Please, invert the scale of the y-axes, i.e. sea ice thickness should be represented in the y-axes, as normally done for sea-ice plotting.

- When considering the 3 domains together this representation can be better since the most important areas are the boundaries and it can be more convenient to represent them as straight lines. We added more figures in the test run section to show it.

60. Fig. 3. Labels of Chl-a concentrations should be changed for better readability in the upper two panels, i.e. 0.8 rather than 8.00 x 10-1, etc. What is the yellow band at the end of February in panel c)? What is the sense of presenting Chl-a in the deep if there seem to be only a “spike” in the data?

- We have redone the figures to make them more representative and to include more results and test cases. The new figures have more readable colorbar tick labels as advised. The idea was to show that we can use one model for all domains and there is

no need to rewrite and reimplement models for different media.

61. Line 1. How do you define it as a “bloom”? Also considering the very little number, I’d rather call it a “small growth”.

- Thank you, we have deleted this sentence.

62. Line 2-4. I don’t agree. Sea ice algal Chl-a can have a tremendous spatial and temporal variability (see e.g. the very many Chl-a values reported in Table 14.1 of Arrigo et al, 2017 (reference above)). One cannot compare model results just like this; especially for a 1D model development when the reader does expect that the site has been chosen also for the availability of observations/measurements to compare the model with. Also, 0.8 mg Chl m-3 is certainly among the lowest concentrations ever seen, not very typical.

- The referee is right that we should avoid this sort of casual “validation” against model output, and we have avoided it in the revised manuscript. SPBM is intended to facilitate the rigorous calibration and validation of biogeochemical models for strongly coupled sympagic-pelagic-benthic systems, but this remains no small task and this model description paper is not aiming to present a rigorous validation for any particular site. The test runs are merely intended to demonstrate the kinds of output that SPBM can produce and its relevance for modelling coupled ice-water-sediment systems. That said, it is, of course, desirable that the demonstration runs produce output that is broadly realistic. To that end, we have added a table that compares model output ranges with observational ranges from Vancopenolle et al., (2013, Figure 3, p 210). But we stress in the new text that this is not a rigorous validation for any particular site (rather, such validation is a goal for future work).

63. Line 4. Could this be just “export” rather than “deep Chl-a maximum”? And what about the non-diatom Chl-a?

- We have completely reworked the results section and this figure and text were removed. Actually, the deeper Chl-a maximum was connected with the primary productivity maximum (that is a diagnostic variable in ERSEM), that along with non-diatom Chl a was not shown. Now we have added more variables in the supplementary materials.

64. Line 7. As far as I know values in Fig. 4a are way too low. Do you have any reference to provide here? Any measurement?

- The illustrated values of 20-70 μM for springtime dissolved oxygen in sea ice are perhaps somewhat low compared to the observational range of (Vancopenolle et al., 2013, Figure 3, p 210 suggests 50-250 μM for bulk concentrations, whereas our bulk concentrations may be 30-60 μM). In the revised test case the bulk concentrations show somewhat better agreement (50-80 μM vs. 50-250 μM in the new Table 2).

65. Line 11. Is really "oxygen transported down"? Please, rephrase.

- This phrase has been deleted in the new text.

66. Line 12. This is not correct. Not all brine channels have very high salinity. Their values vary both vertically and seasonally. Please, rephrase.

- Thank you, this sentence was misleading. This association has been avoided in the revised text.

67. Line 13. What is the carbonate system constant?

- It should have read “carbonate system equilibrium constants”. The phrase is not used in the revised text.

68. Line 15. You would need to place here at least a reference.

- This statement has not been included in the revised text.

69. Line 17. “habitats” would stand better than “media”. Please, consider rewording.’

- We have stuck to “media” in the revised text in the interests of generality (to avoid assuming that all three media can sustain living organisms).

Page 12

70. Fig. 4. Labels of O2 concentrations should be changed for better readability, i.e. 70.0 rather than 7.00 x101, etc.

- Corrected as advised

71. Fig. 5. Labels of pH should be changed for better readability, i.e. 11.0 rather than 1.10 x101, etc.

- Corrected as advised

Page 13

72. Line 1-3. The multilayer approach advantages’ were not discussed at all in this work. The same applies to BBL and multilayer sediments.

- We mentioned it and provided a reference in the introduction “Recent research suggests that ice-algal models should resolve vertically the ice to avoid biases that may result from either assuming that ice algae are solely at the bottom layer or that they are homogeneously distributed vertically (Duarte et al., 2015).” In the revised manuscript the advantages are discussed more fully with reference to the test run vertical variability of biogeochemical variables within sea ice and upper sediments (new Figures 4 and 5).

73. Line 4. Please, remove “of”.

- It was corrected.

74. Line 5-6. I am not sure this is a scientifically sound approach. E.g., not every model might fit any habitat. And this could be the case for sea ice algae that did not grow under snow. In general, the approach the authors chose has not been discussed properly in my opinion. If the authors are confident this is a scientifically sound approach, they should add a discussion about it.

- We do not claim that every model might fit any habitat, but the user can and should take advantage of existing model parameterizations to accelerate the development of new parameterizations for new habitats. Approaches for biogeochemical models construction are often quite similar in different habitats. In particular, approaches for modelling primary producers in ice are often adapted from models used for the water column. We added a new test case with all the standard pelagic primary producer functional types from ERSEM plus one more functional type to simulate ice algae. The current modular ERSEM code and the FABM interface allow users to easily generate any number of primary producer or other functional groups, which can be useful for model development. Also, there are other ecological models available that can be suitable to simulate ice algae e.g. Wirtz KW and Kerimoglu O (2016) Autotrophic Stoichiometry Emerging from Optimality and Variable Co-limitation. Front. Ecol. Evol. 4:131. doi: 10.3389/fevo.2016.00131. Of course, our approach does not require only using modules that currently exist within the FABM: new modules can and will be developed and these will be accessible to SPBM as long as they are coded to be compatible with the FABM. We have included some discussion of these matters in the new manuscript.

75. Line 7-8. What the authors suggest for further work, i.e., a "validation to a particular a case", I believe it is something missing from their own work in here.

- We aimed to provide an efficient computational tool for flexible, offline simulations of coupled biogeochemistry in ice, water, and sediment domains. It is not our aim in this work to parameterize or validate a particular physical or biogeochemical model (new or old) for a particular site. This has been clarified in the revised text.

76. Appendix A. Why the author choose such a simple sea-ice model? A discussion on this choice should be added.

- There is no sea-ice model per se, only empirical relationships used to calculate the volume of brine channels and diffusion coefficients in ice. To enhance this part the user can take these parameters from a thermodynamic sea-ice model and use it as

forcing. We chose this as a useful default because the calculation of all together is time-consuming and adding an online sea-ice model can slow down the process. We have added a remark about this in the revised discussion section.

77. Line 23. Duarte et al., 2015 is a wrong reference here.

- Thank you, it was corrected.

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78. Line 1. Duarte et al., 2015 is a wrong reference here.

- Thank you, it was corrected.

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79. Table C5. Where do those values come from?

- It was roughly mean parameters for the Kara sea area. We have included citations in the revised tables.

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