Biogeosciences Discuss.,
https://doi.org/10.5194/bg-2019-289-RC3, 2019

Biogeosciences Discussions

Interactive comment on "On modeling the Southern Ocean Phytoplankton Functional Types" *by* Svetlana N. Losa et al.

Anonymous Referee #3

Received and published: 6 September 2019

General comments:

The paper by Losa et al. (2019) describes marine ecosystem model development in order to better represent the marine phytoplankton community in the Southern Ocean. This is a worthwhile endeavour, and, if done correctly, could lead to major improvements in our understanding of marine ecosystems, and global biogeochemical cycling in the high latitudes. However, unfortunately, the current manuscript has multiple severe shortcomings, that - in my view - preclude a publication in Biogeosciences in its current form. In essence, I have strong reservations about (1) the lack of a scientific purpose of the paper presented, (2) the modelling work itself, which is not following standard protocols in the field with regard to model set-up, testing and quantitative validation, and (3) the interpretation of the results as a result of point (2). Since reviewers

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1 and 2 have done an excellent job in pointing out specific shortcomings of the current work already, I would like to highlight my concerns with regard to these three general issues.

1. No scientific hypothesis pursued

As becomes clear from the abstract, and later throughout the entire manuscript, no concrete scientific question is pursued by the paper. Hence, this paper is not suitable for publication in Biogeosciences in its current state. Rather, the current development work should be published in journals such as “Geoscientific Model Development,” or “Ecological Modelling” instead. For a successful submission to any of these journals, however, a proper documentation of the model, a documentation of its sensitivity to parameters chosen and assumptions made, and thorough model evaluation and validation would be required.

2. Model set-up characterised by substantial flaws that preclude a conclusive assessment of the main model dynamics and conclusions of this paper

[redacted] This becomes evident from an under-referenced introduction section, which is limited in scope and does not point out current gaps in marine ecosystem development, a poor, incomplete and flawed methods section that reveals major critical issues with the model set-up, spin-up, the initialisation and documentation of the runs conducted, and major critical issues with model stability and tuning. The paper is further characterised by a complete lack of a suitable model evaluation that would show that the model decisions taken (e.g. two diatoms, Phaeocystis parameterisation, etc.) are sound and robust (how do your nutrient patterns look like compared to observations, what is your NPP and export, what are your zonal and vertical standing stocks of carbon and chlorophyll-a for each of the biological tracers, what is the zonal and vertical biomass of your zooplankton functional types, how sensitive is your model to each of the parameters of your new tracers, are these values and dynamics realistic?), a profoundly disorganised documentation of model equations and parameters (no units in tables, wrongly declared equations, random selection of topics presented), followed by an erratic presentation of random model results, and finally, as a consequence of the above, a questionable interpretation of the model results that documents a severe lack of understanding of the model behaviour. [redacted]

An example that will illustrate why I have strong doubts about the methodology used is found in the description of the model set-up described in the Methods section. Here, the authors mention, that

- they use a spin-up period of 6 years for the physical model, which is far too short to equilibrate even the surface layer of the Southern Ocean,

- then initialise biomasses and nutrient fields with results from a model coupled to another, completely different biogeochemical model (Recom-MITgcm) without carefully validating these fields,

- and finally run the coupled model for 13 years only, without spinning up the biogeochemical module first (the authors point out that coccolithophores die out by the end of the simulation, which shows that the model isn't in a stable equilibrium yet for that target region),

- and present results from random months within the first and last few years of the simulation (across all figures we see patterns from: January, June, July, August, December 2003 and January, February, March 2004, February 2008, March 2012), where the biogeochemical model is not even remotely in equilibrium.

Needless to say that common practice in the field is to carefully spin up the physics for multiple decades, then couple to the biogeochemical model, initialise that model

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from observations (available as gridded and extrapolated products in standard netcdf format, so no excuses here), spin-up the coupled model for another ten years or so until the biogeochemistry does not drift anymore, and then run the model with varying forcing and finally quantitatively (!!! -> Taylor diagrams, other model evaluation metrics, observational constraints, etc.) analyse the 5- or 10-year averages (or whatever is appropriate to filter out inter-annual and multi-decadal variability in the target region) of the last few decade of the simulation, provided that the point of the study is to present average biogeographic patterns (well, if that was the point of the study, other approaches may hold for other scientific questions). And needless to point out that many of the required observations for the model are actually carefully processed by and available within the team of senior co-authors. [redacted]

Since the modifications of the biological module are documented even more poorly, there is no quantitative model evaluation, and neither is there a comprehensive documentation of carefully designed sensitivity tests that would allow us to understand the model sensitivity to the new parameterisation, it is impossible to critically evaluate the biological results of this work. Furthermore, the reported model instability with a high sensitivity of model results to parameter choice, as well as the disappearance of major functional groups (coccolithophores) throughout the simulation shows that this model configuration has major stability issues and a huge drift in the biological compartments with likely substantial consequences for productivity, nutrient distribution and biogeochemical cycling in this basin, and is thus unsuitable for publication at this point in time, as it clearly needs to be further tested.

3. Flawed analysis and interpretation of model results

Due to the above issues, any interpretation of the findings in this paper will obviously suffer from major uncertainties due to a lack of conclusive sensitivity tests and a thorough validation of the approach, and thus must remain entirely speculative. In its current form, it is impossible to say whether (1) the implementation of two diatoms is meaningful and leads to a gain in model performance (most models suffer from an over-estimation of diatom biomass in this ocean basin), (2) the Phaeocystis module is correctly implemented, (3) the modifications of coccolithophore physiology are justified (since the author claims that they die out anyway), and (4) if, in fact, the model produces reasonable biogeography, primary production, depth patterns of biomass, and carbon standing stocks in this basin that would point at an actually improvement of the model compared to previous versions.

As an example for a section that make me doubt the validity of the entire analysis, I would like to point out the following point:

In figure 2, model results are presented for the month of July, i.e. austral winter, where biomass in this basin is clearly very low, as it is dark. Yet, much ado is made about "dominance patterns" of specific PFTs during that time. However, the quantification of dominance on very low background biomass values is meaningless, as we're looking at percentages of zeros, essentially. Furthermore, plankton biogeography in winter is very likely strongly linked to sea ice dynamics and factors not represented in current (global) models (resting spores, etc.) – whereas the authors even discuss spurious dominance patterns for areas clearly covered by ice, e.g. in the Dutkiewicz et al. (2015) set-up (which, apparently, isn't coupled to an ice model in its original configuration). In addition, dominance patterns are compared for a random year of the simulation (2003 and 2004), where biogeography is still reported to contain major drifts (as coccolithophores are reported to die out). This makes the claimed "improvement" of the model quality in terms of phytoplankton biogeography highly questionable. Furthermore, since the MITgcm set-up is likely global in scale (we do not know, as this is not described), and since the Dutkiewicz et al. (2015) set-up was likely tuned at the global scale, a comparison with a regionally tuned model is just simply unfitting – a global model will never do as well as a model tuned for a specific region, and it doesn't have to. We do not know, how the current set-up was tuned (I assume the MITgcm is still run in its global set-up, and the rest of the ocean is just not shown on the maps), and how it performs for the rest of the ocean.

As a marine ecosystem modeller, I am all in favour of seeing further modelling work published that would illuminate the drivers of phytoplankton biogeography, and the respective role of competition, predation and environmental niche dynamics in shaping phytoplankton communities and associated ecosystem services. However, unfortunately, due to the poor quality of the submitted manuscript, my recommendation for this manuscript is forced to be: reject, revise and re-submit.

Note to the author: The posted videos are in no way helpful for a quantitative (!) evaluation of the paper.

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Specific comments:

Abstract:

Lines 8-14: Revise. Vague and unsubstantiated claims. Be quantitative. Give numbers. What scientific questions would you like to address with your model?

Intro:

General: Does not identify major challenges in the field addressed by this work. Does not introduce Southern Ocean community structure and function. Poorly referenced. Lack of original references. Fairly irrelevant discussion of the multiple meanings of PFT, and the criteria in Le Quéré et al. (2005).

Lines 16-23: Poorly referenced. Give evidence for each of your claims.

Line 28-30: I disagree. Not the main planktonic calcifiers, if we trust modern estimates. The main PHYTOplanktonic calcifiers. See Buitenhuis et al. (2013) and Buitenhuis et al. (2019).

Line 32: References for Phaeocystis contribution to biogeochemical cycles missing.

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Lines 32-36: Same thing. Original references for the importance of named groups missing.

Lines 49-50: "..different algorithms. . . use various approaches. . ." Be precise. What is relevant in this context. Focus on the issue with carbon to chlorophyll conversions. Your model calculates biomass in carbon units and derived chlorophyll-a biomass. You validate against chlorophyll-based algorithms (e.g. PHYSAT). What are the challenges? How can DARWIN help?

Line 54-55: Do not use multiple names for the same thing. One term – one meaning.

Line 56: No. Le Quéré and Follows were not the only researchers to initiate efforts in PFT modelling. They, as many others, contributed important material and thoughts to an ongoing discussion and effort. Have you read Hood et al. (2006)? Anderson et al. (2005)?

Line 61: NOBM is not the only model with 4 PFTs. In fact many others do. BFM, GFDL, BEC (see e.g. Krumhardt et al. (2019)), etc.

Line 63: No. DARWIN in its 2007 configuration does not contain all PFTs proposed by Le Quéré et al. (2005).

Line 75 ff: What is the point of your paper? You state no scientific purpose. Model development should be published elsewhere.

Methods:

General: Poor and disorganised. Documents strong lack of understanding of model structure and functioning.

Lines 85-876: Use consistent nomenclature to designate the PFTs included in the model. Your statement here lists other groups than those, e.g. represented in Figure 2.

Lines 90-100: You must show all parameters and all equations for novel tracers. Need to document how diatoms differ, justify coccolithophore modifications, give equations for full Phaeocystis module. Justify each and every parameter, back up with literature values. You also need to show the results of your sensitivity analysis. Any deviation from the conventional PFT equation structure, i.e. the inclusion of life stages needs to be carefully motivated and evaluated. Get Phaeocystis data for the Southern Ocean. Evaluate fraction of biomass in colonial versus single-cell stage. Yes, there is data.

Line 100: Why did you choose to replace other large phytoplankton with Phaeocystis, and not nitrogen fixers? Nitrogen fixers have been shown to only play a very minor role in the Southern Ocean due to their temperature limitation. On the contrary, other large phytoplankton species, such as dinoflagellates, are regularly observed in this ocean basin. This decision seems questionable.

Line 105ff: The light module is completely irrelevant in this context. Move to appendix, or omit.

Line 109; Same holds for kCDOM. You don't ever discuss this. Omit.

Table 1: No units given. No references included. What is mfunc? It does not appear in equations (3) – (6). Use consistent abbreviations and names for all PFTs throughout entire paper.

Line 118: I am 100% positive it was not Geider et al. (1998) who invented the growth functions. This parameterisation is quite similar to what Riley developed in 1946 (!). Please check your referencing.

Lines 119 – 123: Not all parameters defined, all functions named must be given as equations. Incomplete set of equations. For example, what is f(k_sat)? Formulation for Phaeocystis is clearly not as given in (3) – (6).

Line: 130: This is not a Holling II function. Also, you state that DARWIN has two zooplankton types on line 84. Where are the zooplankton traits? Need to report. In general, the role of zooplankton grazing pressure on plankton biogeography is not discussed in this manuscript. Since zooplankton usually play a vital role in determining the relative biomass fractions and dominance patterns in these models, the role of top-down control must be addressed else in the manuscript.

Line 140ffff: Where does this parameterisation come from. Why did you not choose to follow e.g. Schoemann et al. (2005), the most comprehensive review on Phaeocystis dynamics. What temperature function did you choose, and why? Do you use one or two tracers for Phaeocystis (Phaeo versus Phaeo_cell)? Are there two combined? Do you get realistic fractions of biomass in colonial stage?

Line 144-145: Rewrite. Utterly unclear.

2.1.2. Physics:

6 years is not a spin-up. What are you spinning up? What is the temporal resolution of your simulation? Are you using a global model? Documentation of model set-up is insufficient – do not just say it was "similar" to something else. And, by the way, it was not similar to the model used in Taylor et al. (2013), since these authors used a completely different coupled GCM-biogeochemical model. Why do I care about light penetration, when you haven't even described the ice module? Which ice-model do you use? Is it dynamic?

2.1.3 Biogeochemical tracer initialisation

[redacted] Initialise from observations, not from unvalidated model runs conducted with a completely different model. These observations are generated in your group. Spin up the biogeochemistry. Evaluate (quantitatively) your NPP, export, nutrient fields, total chlorophyll-a before you even start thinking about a reference run. Spin up your biogeochemistry module. Initialisation of biomasses from Recom is absolute nonsense. Below you describe your satellite validation data. Use that as an initialisation. Do not point to Taylor et al. (2013), as this leads me to Losch et al. (2010), and they use a different model. Use new World Ocean Atlas nutrients, for instance. Equilibrate your model. If major Southern Ocean players show a strong drift in their biomass (e.g. your coccolithophores die out, as you write), then there is a major problem in your model.

2.2.1 In situ observation

Cryptic and poorly written. List all data sets used. Which units does the data have, which spatio-temporal resolution, are these surface data, or are they depth-resolved. Pointing at another study is insufficient. How do you treat, bin, grid, quality control this data to be useful for model validation? Do you convert any of this to biomass, in order to evaluate biomasses? What about the vertical pattern? What about the comprehensiveness of this data – how many months, years, seasons, latitude bands, depth levels does your data cover (all this needs to be described in the main text). What do the "measurements" by Smith et al. 2017 comprise.

Line 173: Table 2, in fact, does not contain any useful information.

Figure 1: What kind of observations do you show? Cite the appropriate reference. Why do you show the Longhurst provinces? These are of no relevance in the rest of the paper. They only confuse the reader. Else aggregate and evaluate your model based on these provinces throughout the entire manuscript.

2.2.2 Remote sensing

Why would you use the old 2008 PHYSAT product? There is an updated algorithm using a neural network approach. This should be far better than this outdated version. What type of "abundance" are you referring to, and how can this be compared to the model output? You mention this data is high resolution – did you regrid the data to fit the model grid?

Results & Discussion

General: This section is characterised by a complete chaos in terms of information presented, spatio-temporal scales shown. None of the figures are in any way useful to evaluate the quality of the model development you presented in your methods section. All you show is colourful surface ocean maps, and most of these maps are useless. Redo entire section from scratch. Does not contain any discussion, as there is no quantitative evaluation and interpretation of the work.

Line 205: You do not discuss phenology in this section.

Lines 207: The satellite estimate you are comparing your results against is not “the truth”, merely another algorithm. Be sure to correct. Why, on Earth, would you compare winter values for the Southern Ocean? It’s dark in winter, and background biomass is likely very challenging to model, as it will depend on features not included in the current generation of ecosystem models, such as resting spores, overwintering strategies, ice associations, etc. Hence, your entire dominance analysis is severely flawed, see detailed comment above. Why don’t you evaluate e.g. a 5-year seasonal average over December – February period (most commonly used)?

Lines 219: This comparison appears flawed. As far as I know, Dutkiewicz et al. (2015) was tuned for a global fit.

Figure 2: Names in legend do not match those given for your PFTs elsewhere in the manuscript. Do not show results for random months and years.

Lines 213-2014: This must be included in the main text, not the supplementary. Along with a thorough discussion of the parameter choices in the methods section.

Lines 220 – 223: This, if true, would deserve a paper on its own. Unfortunately, you do neither quantify nor show phonological patterns. All we see in figure 2 is dominance plots for two selected months in random years.

Line 225: Claimed “augmentation” hasn’t been shown. What is augmented? NPP? Export? Nutrient fields? Silicification and calcification rates? Opal export? Relative biomass fractions? None of this has been shown so far.

Line 228: “in agreement with” How is anything shown so far in agreement with anything.

No quantitative evaluation has been provided.

Line 230: "..results are supported.." How, and in which way? Quantitative comparison with data is missing (model evaluation).

Line 233-236: "However, ..." This shows that your model is not stable, not in any kind of sensible equilibrium, with likely large consequences for all tracers associated with global biogeochemical cycles, and thus not publishable yet. Absolute game stopper. And by the way, in fig 8 you show us coccolithophore biomass for March 2012, which is "towards the end of your simulation", and thus it looks like coccolithophores are abundantly populating the low latitude Southern Ocean, with a substantially overestimated chlorophyll-a biomass relative to the SynSenPFT estimate.

3.3.

"To cope with the aforementioned chaoticity of the system. . .."

I stop my detailed review of this section here. All the remainder is speculation. If the model couldn't be tuned to reliably reproduce the biogeography of major players, then this paper shouldn't have been written, but the model should have been developed further.

Figure 3: Why do you show another month? Evaluate model results on same spatio-temporal scales throughout entire manuscript. Compare total model chlorophyll-a estimate to total satellite chlorophyll-a. Compare group-specific chlorophyll-a to your different SynSenPFT etc. algorithms. Quantitatively.

Figure 4: Label your axes. What is the total biomass level in each of these plots? There seem to be far too many nitrogen fixers at 40South. Same for coccolithophore contribution in this area. Are you under- or overestimating total biomass here? Why have you chosen to present a zonal view of the community structure? In figure 1 you show Longhurst biomes. Can you evaluate the depth pattern? What is the link between zooplankton biomass dynamics and the relative fractional contribution of individual groups

to total biomass? Furthermore, Phaeocystis is not usually known to dominate biomass between 60-50S.

Figure 5: Why, again, do you show another month? Compare total chlorophyll-a to observations. Compare the groups to observational estimates from space, or in situ data. Do not just show model nutrients. Compare quantitatively with observational estimates, e.g. from World Ocean Atlas.

Figure 6: Why would you only show modeled PIC? Compare to observational PIC from space. Where is the "Great Calcite Belt"? Do you represent it well? And if your coccolithophores die out throughout your simulation, how does this affect PIC patterns? 2004 does not seem to represent a "typical" year, as there is no typical year in a model with a strong drift.

Figure 7: Same comments as Fig 2. Winter patterns unrepresentative, and very likely very tricky to model. Where is the "Great Calcite Belt"?

Fig 8: Merge with Fig. 5.

Fig. 9 - 11: These figures do not contain any quantitative information. Omit.

4 Concluding remarks and outlook

Same as above. It is impossible for me to evaluate this section. Since the modelling work does not seem to be up to the standard in the field, the model evaluation is missing and the analysis of the results is severely flawed, it is impossible for me to judge the scientific interpretation of the findings. Any conclusions based on this work must remain mere speculations at this point in time.

Note from Copernicus Publications: Some parts of this comment have been redacted on 28 April 2020 on request by the BG Executive Editors.

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