

Interactive comment on “Calibration of a simple and a complex model of global marine biogeochemistry” by Iris Kriest

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I thank referee 4 for his/her critical yet helpful comments. Below is my reply, indicated by "IK"

"My overall feeling is that the paper is badly lacking in focus. Reading through I was always struggling to understand what major point the author was hoping to make. Is it that the simple model is nearly as good as the complex model, or is it that different parts of the model are better constrained by different kinds of observations? At the moment the article reads as if two separate (and somewhat poorly developed) stories have been combined into one, with very little thought as to what connects them. I think that the author either needs to pick one theme, and develop it better, or needs to do a much better job of finding a narrative thread linking the two themes together. It is up to

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the author to identify how that might be achieved."

IK: I am sorry that the paper appears to be so unfocused, and will try to explain my reasoning better here, and in a revised version of the paper. In short, given the sometimes high structural complexity of global biogeochemical models there are only sparse observations to constrain them, the two main findings of the paper:

- complex, biological dynamics are not well constrained by a rather biogeochemical misfit to nutrients and oxygen
- the simple model performs almost as good as the more complex one, with respect to the given misfit function

are somehow connected. Calibrating a complex model would possibly require either a much more complex misfit function (with respect to observations; e.g. using Chl a, observations of zooplankton abundance, and DOP). Given that

- models of higher complexity, such as MOPS, are usually applied to research questions that relate to more biogeochemical issues (such as ocean carbon inventory, or deoxygenation)
- these models are expensive in terms of computing time, thereby hampering exploitation of model (parameter) sensitivity and skill in spun up state, and
- more "sophisticated" data sets are sparse, and many of the observations may contain a high uncertainty, or noise

I find it important to raise some awareness about the necessary level of model complexity, and the uncertainty associated with model structure and parameters. In some cases it may be more appropriate to spend more time on carefully exploiting the parameter space instead of adding more complexity. Of course, this tightly relates to the research question addressed with the model. I will do my best to render the paper more focused and clear in a revised version.

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Specific comments

Abstract

"Line 7: "a complex seven-component model (MOPS), and a very simple two- component model (RetroMOPS)" and "The simple model, which contains only nutrients and dissolved organic phosphorus (DOP)". RetroMOPS clearly has four components: PO₄, NO₃, O₂ and POM."

IK: Yes, thank you. This will be corrected.

"Line 13: Please do a better job of explaining what is "the global bias"."

IK: I will add "(global inventory of oxygen and fixed nitrogen)"

1 Introduction

"Line 29: "[Kriest et al. (2017)] showed that annual mean tracer concentrations do not provide much information on parameters related to the dynamic biological processes taking place in the euphotic zone". Should be "annual mean tracer concentrations did not provide much information", as I am not convinced this is a general result for all models."

IK: It would be interesting to see other models when facing optimisation against the same misfit (volume weighted RMSE of annual mean nutrients and oxygen); Until then, I agree, it should be "did".

2.2.1 Primary production

"Equation 1: Why use the mean phytoplankton concentration at all? It would be more consistent with the rest of the model (i.e. Equation 5) to convolve the specific growth rate and the phytoplankton concentration into a single growth rate of the phytoplankton population (mmol P m⁻³ d⁻¹)."

IK: I used this particular decomposition to clearly illustrate the specific assumptions

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that may be inherent in simple models such as RetroMOPS (similar to Kriest et al., 2010). In addition, deriving the specific growth rate from MOPS, and transferring this to RetroMOPS, would involve accounting for nutrient concentration and limitation - which in turn depend on the remineralisation rate and sinking speed. I therefore chose this way of aligning both models, and would prefer to keep it that way. Note that the resulting specific growth rates (including limitation by nutrients, temperature and light) between both models are not too different: 0.1021 d⁻¹ (RetroMOPS) and 0.1267 d⁻¹ (MOPS). I will add a sentence on this in the revision.

2.2.2 The fate of primary production: Export, DOP production and remineralisation

"Line 19: "DOP then decays to phosphate and nitrate". To me it would make sense to call it POM."

IK: POM would be something that sinks, which clearly distinguishes it from DOM.

"Line 19: "To allow for a potential, fast recycling loop at the surface, RetroMOPS parameterises an additional decay rate". Presumably this is inspired by (Oschlies 2001), but why would this be necessary in the absence of assimilated primary production observations?"

IK: There are three reasons why I have embedded this fast recycling loop: first, DOP production and decay in RetroMOPS has to mimick all dynamic surface processes of MOPS, so I initially expected it to require a specific degradation rate constant for the surface. As it turned out, this is not necessary (this parameter during optimisation was reduced to nearly zero). Second, at a later stage it might indeed be interesting (and helpful) to include primary production into the misfit function, with possibly different resulting best parameters surface DOP decay. Finally, data by Hopkinson et al (2002) indicate that DOP recycling rates may be much higher than commonly applied in global models. I will add some discussion on this in a revised version of the paper.

"Equation 4: I think a bit more could be said about the interdependence of sO₂(j)

and $sDIN(j)$. For example, their sum forms a coefficient for remineralisation, so it is important to note that their sum is constrained between 0 and 1."

IK: I will comment more on this function in a revised version of the paper.

2.5 Misfit function

"Equation 11: I am a bit confused by how the misfit function and its components are defined. In particular, I cannot see how \bar{o} (the global average observed concentration of the respective tracer) is included in the RHS. "

IK: This was a mistake by me; The RHS was missing $1/\bar{o}_j$ after the first sum, but it should have been after $J(j)$. Thank you for drawing my attention to this.

"Also, it seems that the model is being compared to gridded observations, instead of observational equivalents being extracted at the spatiotemporal locations of the observations. As the gridding process will introduce its own set of errors, this choice needs some justification."

IK: Although regridding the observations onto the coarser model grid removes much of the variability in the observations, this procedure is much more efficient (in terms of computing time) during the optimisation process. Further, by following this approach the model is not penalised for its apparent lack of resolution. It could be worthwhile adding the variance, that arises from the regridding process, and the variance in the data themselves, as weight to the misfit function. However, in an earlier study (Kriest et al., 2010) we could not find any large effects of this on model assessment. Testing different misfit function with respect to observational data sets, weighting schemes, etc., will be subject of follow-up work, but possibly exceed the scope of this paper.

2.6 Optimisation of MOPS

"Line 15: I don't think including results from the hand-tuned model brings anything of value to the paper."

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