Response to Reviewer #2

We thank the reviewer for their review and suggestions. Below, the original comments of the reviewer are quoted verbatim, and our responses are provided right after each comment.

"General comments
The article presents the first spatially-resolved implementation of an "Instant Acclimation" approach to modelling plankton ecosystem. The authors found that the Instant Acclimation model performance was very close to that of a more computationally expensive Dynamic Acclimation version. Both of these models where markedly different from a physiologically less realistic Fixed Stoichiometry model. This is an important contribution that will allow biogeochemically and ecologically important stoichiometric variation to be efficiently included in computationally expensive global ecosystem and biogeochemistry models.
The objectives of the article where clearly communicated, and the approach accurately described. From my perspective the main weakness of the article was the 'Model Description' section, which I felt could be made a lot more coherent. As it stands, the article attempts to describe three versions of the general model in parallel. As the model contains a number of subsections, each subsection needs to be described in multiple different ways before we can move on to the next subcomponent. I found that this made it hard to understand how each version of the model works as an integrated whole. My recommendation would therefore be to first describe the Dynamic Acclimation model in full, before going on to describe how the Instant Acclimation and Fixed Stoichiometry models deviate from this. This makes more sense to me, as both of the latter models are effectively simplified versions of the former."
Response: we can understand the concern of the reviewer. In fact, in the first draft of the manuscript, the model description was structured exactly as suggested by the reviewer: first an uninterrupted description of the IA model, then an explanation of the differences in the FS and DA variants. The main problem with that approach was that the physical gap (in the order of 2-3 pages) between the formulations and logic made it difficult to see and understand the difference between the variants, as we had realized based on a friendly review. Moreover, the presented description follows the model code more naturally, noting that we do not have 3 different modules, but a single one where the individual process descriptions are chosen based on the specified variant. We would also like to point out that a full description of the DA model can be found in Pahlow et al. (2013) and the IA model can be found in Smith et al., (2016) with minor differences (as explained in Appendix A2). For these reasons, we would prefer to keep the structure of the model description in its current form, but indicate more clearly that the full description of the DA and IA variant can be found in the aforementioned publications.

"My other main comment is that I did not see the benefit of varying the way photoacclimation is handled in the three models. This mechanism is included in many 'fixed stoichiometry' models, so it is not a unique benefit of the two more sophisticated approaches. Given the not insubstantial level of complexity in the rest of this article, I wondered if it might not make more sense to fix this part of the model across the three cases, and focus on the more novel developments in the C:N ratios."

Response: we again understand the concern of the reviewer, and agree that photoacclimative response adds an additional layer of complexity. Nevertheless, in this study we would like to provide an analysis of the presented IA model together with its photoacclimative response in its entirety, as it was used in another study (Anugerahanti et al., 2021, which was earlier cited as 'in prep.') and was planned to be extended further in follow-up studies (e.g., Anugerahanti et al., in prep.). It should be noted that the behavior of the instantaneous photoacclimation model that we used here had not been analyzed in a vertically resolved setup until our study, therefore we consider the results presented to be useful in this regard as well. For these reasons we would like to keep the photoacclimative response in the model. Despite the additional complexities imposed by the photoacclimative response, we believe that our analysis is fairly complete, but we are fully open to any suggestions that may help improve our analysis and cover/point to any potentially open issues.

"Specific comments
Line 34: 'Models that account for variations in cellular composition are indeed more likely to provide more realistic estimates' - Suggest 'Models that account for variations in cellular composition are in principal more likely to provide more realistic estimates'"
Response: we agree that the suggested reformulation is more accurate, since no examples are cited to support the statement until that point. We changed the statement as suggested.

"Line 68: 'The key assumption is that growth and nutrient uptake are at all times strictly balanced [w.r.t. the internal C:N stoichiometry of the cell]'"
Response: thank you, we will add the statement in brackets to be more specific.

"Line 76: 'the inclusion of transport terms may lead to additional complications'. Please could you explain how/why this leads to extra complications?"
Response: We will include the following explanation: In a spatially structured environment, transport of cells with a certain internal state to a zone where the typical (average) cell composition is different, can create a \`resource storage' effect (e.g., Grover, 2009; Kerimoglu et al., 2012). A typical example of this is nutrient-replete cells (as represented by high N:C) at the deeper layers diffusing towards the surface layers across the thermocline where the cells are typically nutrient starved. In principal, this effect can be resolved only by explicitly tracing the constituents of the cell dynamically.

"Line 96: 'the trivial flux terms'. I do not see how these terms are trivial?"
Response: here, we are referring to the flux terms listed in Table 1 that are trivial (i.e., all except $F_{DIN-PhyN}$ and $F_{DIC-PhyC}$, which are indeed non-trivial). We will revise the sentence to clarify this point.

"Eqns: 1-3. I found this notation a bit confusing. I wonder if simple word equations might be the most straightforward here? (e.g. dPhyN/dt = phytoplankton uptake - linear mortality). Failing that, I think substituting in the terms from Table 1 would be a lot clearer."

Response: The flux terms make the source and target pools immediately clear, therefore we find them to be useful. However, we understand that for those who are not used to this notation, these can be difficult to read, therefore will add 1-word descriptions of the terms in underbraces.

"Line 153: "(equivalently, relative size of the chloroplast, following Pahlow and Oschlies (2013)), fC:". I found this hard to understand. Have we switched to an entirely new idea here (fV to fC)? If so wouldn't it be better to separate out, instead of adding it on parenthetically?"
Response: This is not a new idea, however we realize that our statement in parentheses might be misleading, therefore we will reformulate this in a separate sentence.

"Equation 30: Which state variables are actually transported? Presumably not C for the IA or FS models. It is noted in the Discussion that C biomass is not conserved - I expect due to issues with advecting C in IA model. This should perhaps be discussed in a bit more detail."
Response: all state variables are transported. For the IA and FS variants, Phy_C is not a state variable, but a diagnostic variable calculated based on Phy_N and Q (Fig.1), therefore it is indeed not transported. We will stress that the Phy_C is a state variable for the DA variant. We would like to clarify also that the presented N-based version of the model is fully closed, i.e., mass conserving with regard to N. Only if we had resolved a second nutrient, e.g., C, additional nutrient flux terms would have been required to satisfy the conservation of this second element. This issue has been explained previously by Smith et al. (2016). We had tried explaining this in L455-460 in the discussion, but we understand that this explanation was not clear enough, therefore we will revise the paragraph.

"Figure 4: The third row of panels (g-i) are cited out of order in the legend, which is slightly confusing."
Response: in fact, there is no inconsistency here: first the concentrations (Phytoplankton N, C and Chl) are introduced, then the ratios (N:C, Chl:C) are introduced in the figure. Referring to the variables in displayed order would lead to repetitions.

"Results section: I think it would be worth noting any differences in system level functional parameters such as overall primary production and C export."
Response: thank you for this suggestion, we very much like this idea. The water-column integrated net primary production rate and C export rate as estimated by the model variants are shown in Fig. R2.1 below. We will include this figure in the revised manuscript.

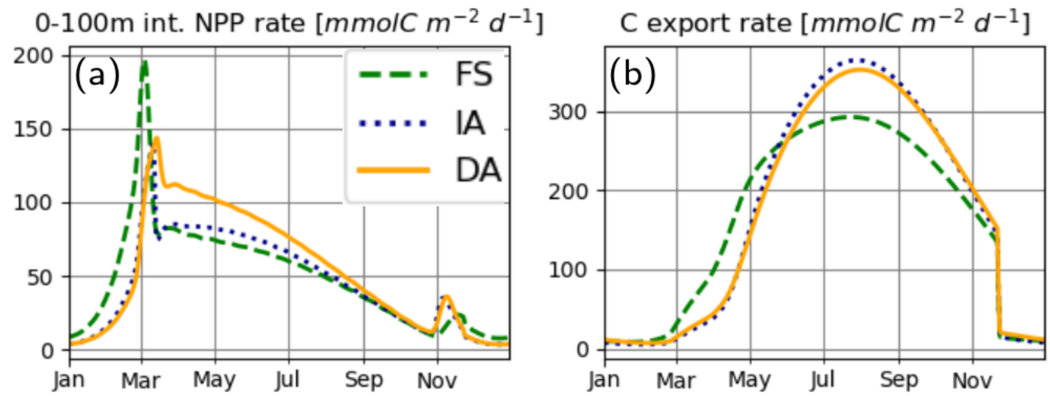

Figure R2.1 (a) Integrated Net Primary Production (NPP) Rate [mmolC m^{-2} d^{-1}] and (b) Carbon export rate [mmolC m^{-2} d^{-1}] as simulated by the IA (fine-dashed dark blue line), DA (continuous orange line) and the FS (dashed green line) variants.

References:

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Kerimoglu, O., Straile, D., & Peeters, F. (2012). Role of phytoplankton cell size on the competition for nutrients and light in incompletely mixed systems. *Journal of Theoretical Biology*, *300*, 330–343. https://doi.org/10.1016/j.jtbi.2012.01.044

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