Comment on egusphere-2022-493

Anonymous Referee #2

Referee comment on "FABM-NflexPD 2.0: testing an instantaneous acclimation approach for modeling the implications of phytoplankton eco-physiology for the carbon and nutrient cycles" by Onur Kerimoglu et al., EGUsphere, https://doi.org/10.5194/egusphere-2022-493-RC2, 2022

Kerimoglu and colleagues developed an updated version of their previously published plankton model FABM-NflexPD. In this version, they track both N and C biomass of phytoplankton assuming instantaneous acclimation (IA version of the model). In comparison to its previous version, this new version conserves both carbon and nitrogen in the system. Mass balance is ensured by analytically computing the temporal change in cellular N quota. In 0-D and pseudo 0-D setups, mass conservation is excellent and the model performs very well compared to a fully explicit treatment of the N quota (DA version of the model). However, the IA setup is not cheaper in terms of computing cost.

The paper is very well written, very clear and complete. I don't have any major issues on what is presented in the study. However, I should admit that I have trouble finding this paper interesting and useful. The main objective of this study, as stated by the authors, is to develop a model that mimics the behavior of a full quota model but that is cheaper so that it can be embedded in a global biogeochemical model. As a global biogeochemical modeller, I agree that it is a crucial point. And having less tracers in a global 3-D model is generally a good strategy to reduce the computing cost as transport of a tracer is very expensive. In the case of this study, I think that this main objective is not reached. First, the study is restricted to a pseudo 0-D (closed and opened) framework where transport with neighboring cells is not relevant and computing not an issue. Second, they claim that transposing this framework to a 1-D setup failed because mass is no more conserved. Obviously, spatial transport of a variable quota leads to the same problem as temporal evolution of this quota. As said in the manuscript, conserving mass in a 1-D or 3-D configuration would require to track the evolution of the quota due to transport to compute the additional fluxes of nutrients. To me, this is equivalent to explicitly transport the quota. Furthermore, it would require additional fluxes of nutrient that could possibly, especially when transport and spatial gradients are strong, significantly alter the model behavior. In other words, the computing cost would be identical for a result that may differ from the fully explicit model.

I have additional small questions. In T1, mass is not fully conserved in both model

versions. Could the authors be more specific on why this is the case? In DA, is it simply truncation errors in single precision? In T2, differences in total N seem to be 0? Obviously, this is not exactly 0 because it is not the case in T1. Is the difference larger than in T1? In other words, I suggest to change the y-axis in a way similar to what is done in T1. Finally, in T3, the authors only show two figures. From these figures, it is difficult to see if the temporal evolution of the total phytoplankton biomass is changed and by how much.

To conclude, I find that the authors did not make the demonstration that the framework they developed in the study provides an interesting, cheaper alternative to model flexible nutrient quota in spatially explicit biogeochemical models. To be convinced, I think that including a 1-D experiment is necessary. This would also present how additional fluxes due to transport can be represented and if that framework is really cheaper than a full model. Without such an experiment, I think that this manuscript should be rejected.