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Comment on gmd-2021-366

Anonymous Referee #2

Referee comment on "Water Ecosystems Tool (WET) 1.0 – a new generation of flexible aquatic ecosystem model" by Nicolas Azaña Schnedler-Meyer et al., Geosci. Model Dev. Discuss., https://doi.org/10.5194/gmd-2021-366-RC2, 2022

Review report for Manuscript ID gmd-2021-366 by Schnedler-Meyer et al. entitled:

Water Ecosystems Tool (WET) 0.1.0 - a new generation of flexible aquatic ecosystem model

General comment:

The present study elaborated to introduce a new aquatic ecosystem model - WET, based on the previous model FABM-PCLake. A number of major new features are added to the model such as the flexible food web configuration, vertical migration of organisms, and N fixation, which all make the new model more powerful in addressing key ecosystem principles in lakes. I find this working quite interesting and believe it will become a major step forward of the WET model family, and serve as a milestone for the field of aquatic ecosystem modeling. Nevertheless, I do have several major concerns as I have explained below in detail, and based on these concerns, I suggest that the manuscript need a major revision before acceptance by the journal of GMD.

- My major concern is a lack of sufficient validation for the new functions to the model in the current manuscript. Clearly these new features, such as vertical migration and N fixation of cyanobacteria, are crucial for modeling the food web interaction and ecosystem dynamics, which jointly improve the applicability of the WET model. However, the test case of Lake Bryrup and the available dataset are insufficient to explicitly test the adequacy of the new functions. The lake is also a bit too shallow to reflect the features of the deep lakes with pronounced vertical migration of organisms. More importantly, the main advance of the ‘flexible food web’ is also not addressed in the test case. Nevertheless, I can understand that field data to validate these new features are rare, particularly the spatial distributions of the organism along the vertical dimension. Therefore, I recommend to use the case of Lake Bryrup, but rather than validating the model, the main focus here should be on providing a more detailed evaluation of the new features. In additional to the existing analyses, the authors may consider the following (but not limited to): 1) compare the modeled cyanobacteria with and without N fixing function (ideally with two types of cyanobacteria), and illustrate how the N limitation regulates the growth of the cyanobacteria and potentially other algae groups; 2) design a gradient of the vertical migration parameters for zooplankton, as shown currently in Fig. 5 as an nice example (but now only with one parameter set). Such additional evaluations will help readers to better understand the importance of the new features for modeling and unravel the sensitivity of the key parameters, thereby opening up the opportunities to test the new model in other lake cases with more comprehensive datasets in the future.

- I found that some details of the new features are not clearly described. This could be fine for current users but may puzzle the new users in the future, thus obscure the application and further development of the model. The authors may consider using more Tables to list the new features of some modules with the explanation of the related parameters and meaning of the values in the configuration files. Below I list some specific points in the minor comments, but overall I would appreciate taking advantages of Tables in such model description papers as the key document.
- It remains unclear how to practically change the structure of the model by adding or deleting organism components. Likely it will be done in the configuration file, but it is not described (if I did not miss anything). Tutorial cases and/or a detailed manual for such configuration procedure should be provided because such flexible feature is one of the major advantages of the new WET over the previous version and also many other aquatic ecosystem models. Besides, I recommend to briefly discuss the possibility to implement the flexible food web in a more user-friendly way (such as the GUI of ECOPATH or AQUATOX), if such function would be envisioned for further model development.
- It is uncommon to number the first version of the WET by '0.1.0'. The first release of software or model is usually numbered as '1.0' or '1.00' etc. Current version of '0.1.0' gives the impression that the model is still at the very beginning stage and far from completed for first release. Please consider changing the version numbering, if appropriate.

Below please find additional minor points for the author to consider:

- Line 57: -coding -> recoding
- Line 66-67, this is a duplication of the information in line 59-61. Recommend removing one of them.
- Line 84: I am not sure if all the biogeochemical processes equation are 'unchanged' in WET compared to PCLake. If so, it is contradictory to the previous statement that processes such as resuspension are changed compared to previous model. Better add 'mostly unchanged', if proper.
- Figure 2: suggest to change the subtitle in vertical 'FOOD WEB MODULES' to 'FLEXIBLE FOOD WEB MODULES' to highlight the features of the model.
- Line 105, this paragraph lacks the description whether new phytoplankton groups can be added to the community, and whether they can be at least pre-parameterized with readily available parameter values (like a database). In addition, the new algal properties, e.g. Si dependency, N fixation, are better to list in the Table with details of how they can be switched on/off in the configuration file. This would be highly useful for the users.

- Line 110, the same issues here: rather than the descriptive text, a Table summarizing the new features and method to implementation in the configuration file would be helpful.
- Equation 1: reverse the super- and subscript of the ∑ (i.e. i=1 and nPISC), and delete the first product sign (×) in the inner equation, both in the numerator and denominator.
- Line 138: need to clarify how to calculate the terms such as aFunVegAss and uFunTmFish, or at least refer to related references.
- Line 142: population structure, or age structure? Please clarify this statement.
- One comment about the N fixation modeling in section 2.2: removing the 'aNLim' term in the growth modeling of algae with N fixing may be not fully realistic. Recent field observations imply that N fixation cannot compensate for the N depletion in lakes with reduced external N laoding over a long-term scale, and phytoplankton still exhibits N limitation in summer (see Shatwell et al. 2019 L&O for the long-term study in Mueggelsee, Germany). No need to change anything here, but maybe keeping this in mind and slightly discuss in the end of the manuscript.
- Line 185-195, This paragraph fits better to the introduction rather than the model description section here.
- Line 213 and 217, better describe each qTrans option in one individual paragraph. It is confusing to read such as (qTrans = 2 or 4) or (qTrans = 3 or 4) at the first glance. The same applies to the zooplankton and fish migration section below.
- Section 4.2, I feel that the results demonstration in this section can be improved by (1) adding the location of the thermocline during summer and (2) making parallel panels showing the model results of original FABM-PCLake without the newly added features such as the vertical migrations. This can be used as part of the additional evaluation of the model, as I mentioned in the major comments above.