Geosci. Model Dev. Discuss., https://doi.org/10.5194/gmd-2020-302-RC2, 2021 © Author(s) 2021. This work is distributed under the Creative Commons Attribution 4.0 License.



## Interactive comment on "SPEAD 1.0 – A model for Simulating Plankton Evolution with Adaptive Dynamics in a two-trait continuous fitness landscape applied to the Sargasso Sea" by Guillaume Le Gland et al.

## **Anonymous Referee #2**

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Review to "SPEAD 1.0 – A model for Simulating Plankton Evolution with Adaptive Dynamics in a two-trait continuous fitness landscape applied to the Sargasso Sea"

This study nicely demonstrates that an aggregate model may capture the key properties of functional diversity within phytoplankton communities, i.e. the means, the variances and the covariance of two physiologically important traits, over the course of a year very well, while being at the same time superior with respect to the computational efficiency when compared to a corresponding discrete multispecies model. This implies that aggregate models might be a suitable tool to study the impact of functional

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diversity on the population and community dynamics of natural plankton communities, in particular when facing a multidimensional trait space.

Despite my overall positive impression of the present study, I have the feeling that the study would benefit from more clarity in the method section where the model is initially described. Furthermore, I am not entirely convinced at this point to what extent the addition of functional diversity to the model may improve the match between the modeled and observed phytoplankton densities and nutrient concentrations over a spatial gradient and over the course of a year. For details, please see below.

## Major

- 1) The model validation is done based on e.g. the observed primary production and chlorophyll concentration of the phytoplankton in the Sargasso Sea. Overall, the model predictions match the observations quite well. However, I was wondering whether a corresponding model that only uses a mean field approach and thus neglects trait diversity and trait diffusion entirely, performs really worse when compared to the performances of the aggregate and discrete-diversity models. I mean, the sensitivity analysis performed with respect to the comparison of the 2D and two different 1D models shows that the predicted temporal development of the phytoplankton density is guite similar throughout most times of the year. Based on this, I was wondering how these models differ from a model that does not account for trait diversity at all, and thus a 0D model with respect to the functional diversity. This additional model simulation may help to answer the question whether a model that accounts for trait diversity matches the observation better than a model which does not. Furthermore, this consideration may also help to support the claim that additional measurements of functional diversity of natural communities in respect to relevant traits are needed to actually validate aggregate models, which account for trait diversity.
- 2) The uptake function up is introduced twice, i.e. with equation (11) and equation (12). The authors used equation (12) to consider two different limiting cases of the spe-

cific nitrogen uptake rate up, i.e. equations (13) and (14). Based on this, the authors motivated their choices of how the half saturation constant and maximum uptake rate should depend on the trait x given the constraint, that the species' abilities to take up nitrogen at low and high concentrations should follow a gleaner-opportunist trade-off. However, after having defined the uptake function up with equation (11), I would have found it more intuitive to proceed with the definition of the nutrient limiting factor  $\ddot{l}$ S, which is simply assumed to follow Michalis Menten kinetics with a corresponding half saturation constant and maximum uptake rate. Afterwards, with or without a limit consideration, the gleaner-opportunist trade-off could have been motivated by stating that the maximum uptake rate to the power of 2 multiplied by the half saturation constant is assumed to remain constant. Please consider a potential revision of this section!

- 3) The sign structure of the migration or diffusion terms in equation (20) seems to be mixed up. I mean, the outflow of density from the focal population should be associated with a minus sign whereas the inflow of density towards the focal population should correspond to positive signs.
- 4) In section 2.3 Physical setting, the authors describe that vertical mixing is included via vertical (physical) diffusion. However, I could not really understand how the addition of vertical diffusion have modified the equations (30) to (35) that are governing the biomass and trait dynamics of the phytoplankton community. So, please explain in a little bit more detail how this implicit scheme, which is mentioned on page 15, lines 15-18 actually works and how the corresponding terms or equations are looking like. Accordingly, please also add the terms that are reflecting sinking.

## Minor

Page 4, Lines 14/15: This statement about a future perspective seems somewhat misplaced in the introduction.

Page 5, equation (1): Is the uptake function Up that uses a capital letter U the same as the uptake function up that uses a small letter u and which is introduced later on in the

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text (e.g. equation (10))? While Up seems to depend on P, up does not depend on it. Please clarify?

Page 21, Line 2: Please add a "by" between "are caused" and "the aggregate model's assumption".

Page 24, Line 16: Please replace "is" by "are", i.e. "the standard deviations ... are significantly smaller".

Page 24, Line 20: Here, it says that Table 3 also assesses whether bimodality occurs at some moment in time. However, I was wondering how exactly this was done by the authors. I could not find any explanation. Please clarify!

Page 34, Line 9: Please substitute the "?" by a ".".

Page 34, Line 12: Spelling error: "interpretation" not "interpretation".

Page 35, Line 21: Please substitute "or" by "of".

Page 39, Line 1: Why do you mention here that cell size is independent of time? Cell size is not a trait, that you have explicitly incorporated into your model. Please clarify.

Page 39, Line 4: Please substitute the minus sign '-' by a plus sign '+' in the term  $x-\delta x$ .

Page 39, Line 5: The probability ax should be a ratio instead of a product and thus read ax=  $vx/(\delta x^2)$  instead of  $vx\hat{A}\mathring{u}(\delta x^2)$ . Otherwise the term  $(\delta x^2)$  would not cancel out in the equation that is displayed in line 29 of page 40. See also line 28 of page 40 where ax and ay are displayed correctly.

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