Geoscientific
Model Development
Discussions

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.

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The authors present the development of a new evolutionary model of phytoplankton (SPEAD) that represents for the first time the mutation of two distinctive traits (half-saturation constant and optimal temperature) in a continuous trait space. The primary question is to see if we can develop a computationally faster model of plankton diversity that accounts for trait evolution using a Trait Diffusion term (aggregate models). The authors couple their model to a 1D vertical water column to compare their results with seasonal observations at the station BATS. They also compare the new model

with a "discrete" version. This already tested modelling approach represents diversity with hundreds of different phytoplankton types (sampling the trait space available in the evolutionary model). Once the new model is validated, the authors explore the role of mutation rate on the diversity dynamics as this is a critical term that is poorly constrained. The primary outcomes are: (1) Despite its strong assumption that traits are normally distributed, SPEAD is shown to agree precisely with the observations and a discrete model explicitly representing all phenotypes, with only minor deviations at depth in Summer, where the optimal temperature is underestimated, and in early Winter, where trait variances decrease too fast; (2) The trait dynamics depends strongly on the imposed trait diffusivity parameters; (3) SPEAD has a computational cost two orders of magnitudes lower than a discrete model, making aggregate models promising tools to explore high-dimensional trait spaces of the ecology and evolution of microbial ecotypes. The model's code is also available online on two open sources with instructions on getting the model running.

I think this is a critical work for evolutionary marine biology and ecosystem modelling. It is a step forward testing for the first time the simultaneous mutation of more than one trait, which requires the inclusion of the covariance between traits. The authors carefully explain, validate and test their new approach. Besides, this work provides a detailed overview of the history of modelling diversity and evolution, some in-depth discussion on the meaning of their method, its strengths and weaknesses, and some ideas of what could be done differently to improve their work (a multiple Gaussian approach). I strongly favour the publication of this work in GMD. It provides the necessary step toward computationally fast evolutionary modelling with an in-depth analysis of their new modelling approach's implications and unknowns.

Main comments:

Overall, the manuscript lacks a brief discussion (ideally in the introduction and discussion) on what evolutionary models bring over the traditional diversity functional types models (like Darwin). What are the processes missing in the PFT models that evolu-

tionary models get and in which environments are these processes essential? Including such a discussion will help make the paper less niche by bringing the non-evolution community up-to-speed with your approach.

The introduction provides a really detailed and useful review of the development of evolution modelling for phytoplankton. Can I suggest that you make a diagram showing the different approaches with their assumptions, cost and benefits? This would help to see how your work fits in with previous model developments.

P23, line 7: You need to justify why the ratio of mutation rates are assumed to be the same and discuss the implication on your model results. It seems that might significantly affect your results - see p26, line 7 and line 23.

Specific comments:

Abstract (p1, l2-3): Here, you highlight the main challenge of modelling evolution, I don't think that is the only one. Can you amend your sentence to reflect this?

In general, the abstract lacks a definition of your primary question that the work tackles, which you do very well in the manuscript. Can you include it in the abstract?

Introduction P2, 1st line: Some phytoplankton can be multicellular. Please amend here.

P2, line 10: The production of DMS by marine plankton is now highly debated. Can you reflect this here?

P3, lines 14-16: Can you define clearly and quite early on in the introduction the term "aggregate model"? You refer to it in line 8 (continuously distributed traits) but do not link the two. This is confusing and key for the paper.

The Methods section needs some clarifications:

P9, lines 33-35: Here you assume that $f_{pu\infty p}$ is independent of x, with x the half-saturation constant but below you define $K_n = u_{\infty p}/f_p$. Can you clarify this point? It seems that x depends on $f_{pu\infty p}$ because $K_n = x = 1/(f_p)2\, f_{pu\infty p}$.

C3

Equation 15 does not seem consistent as it assumes that $K_n(x) = e(x)$. Is that correct?

Equation 16: why did you define the maximum nutrient limitation with a squared root?

P11, line 7: Here you define, in my mind, a critical assumption that probably has a significant impact on your result: $f_{pu\infty p}$ is a constant. Can you add more discussion on this assumption (where it comes from and its limitation and influence on your results)?

P14, lines 11-14: The definition for "a" is too vague. Can you provide an equation of "a" with its correction terms and describe the meaning behind them?

P14, lines 16-17: Is that based on the theory, on what your equations predict or on your model's results? Please amend.

P19, line 22: should be observed (rather than "observated").

Section 3.1 could be more concise if the model's values and observations were presented in a table.

Figure 6: please zoom in for the x and y axis as currently too small.

P34, lines 8-9: Not a question. Please rephrase.

P35, lines 1-2: This is an essential point but not the most straightforward sentence (it is too long). Can you amend to make this information more readable?

P37, line 5: replace "an aggregate model" with "a new aggregate model".

P37, line 23: Modify to include "intermediate values of mutation rates (or diffusivity).