Dear Eva Álvarez et al.,

We received one review on your revised manuscript. The other reviewer was not available, but I think you have addressed most of his/her previous comments and therefore I decide to proceed with the current evaluation from reviewer #2. Reviewer #2 thinks that the revised manuscript has addressed their comments and is much easier to follow. There are a few additional comments and suggestions, but it should be easy to address. I consider this a Minor revision.

Reviewer comments are appended below for your reference.

Looking forward to seeing your revisions.

Best sincerely, Yuan Shen Associate Editor

Dear Editor,

Thanks a lot for handling the review of our manuscript. We have revised the manuscript according to the Reviewer #2's comments. Find below our point-by-point response to the comments that includes a list of all changes made in the manuscript.

We would like to sincerely thank our two reviewers for taking the time and effort necessary to review the manuscript, and providing feedback in such a constructive and useful way. We have updated the Acknowledgements section to recognize their support.

Best regards,

On behalf of all the authors, Eva Álvarez

Review #2:

The authors have addressed my comments and the updated manuscript is much easier to follow. It is good to see that the parameter estimates converge to similar values in replicate experiments. The figures are useful (they look great, too) and the results are convincing. At this stage, I have only a few specific comments, and two remarks about the updated naming which reflect my personal preferences and which the authors may choose to ignore.

We thank the reviewer for revising so carefully our work and for the really useful comments. We have revised the manuscript to improve readability following the specific comments of the reviewer, change the name of the two EXP-Biology simulations and update the y-axis label to "depth (m)" in some figures. Following each reviewer's comment, we detail the changes we have made to the manuscript which are marked in green font in the revised version of the manuscript. The line numbers indicated in our responses refer to the revised version of the manuscript.

The new variable names are much more intuitive, and a new reader is no longer in constant need to look up the meaning of the previously numbered variables. I am not certain why the naming was not extended to the DOM and CDOM variables ($X^{(labile)}$) or $X^{(l)}$) is more intuitive to me than $X^{(1)}$) but with a total of 6 numbered variables left ($X^{(1)}$), $X^{(2)}$, $X^{(3)}$, $R^{(1)}$, $R^{(2)}$, and $R^{(3)}$) it is not a big issue.

The names of R and X were not updated in order to keep short names, especially for the parameters associated to the dynamics of each state variable (e.g. f^maxX2[P(i)], b[X(3)], f^X1[Z] ...). We have clarified earlier the correspondence (labile, semi-labile, semi-refractory) with (1,2,3) as follows:

L 171 "three pools of dissolved organic matter differentiated by reactivity into labile ($R^{(1)}$), semi-labile ($R^{(2)}$) and semi-refractory ($R^{(3)}$), and CDOM differentiated by the same reactivities ($X^{(1)}$, $X^{(2)}$ and $X^{(3)}$)."

I welcome the new names for the experiments, EXP-Biology and EXP-Physics, which are more intuitive as well. The names of the simulations have also improved. A minor issue is that "Constant leakage" and "Constant dpp" experiments do not use a constant value for leakage or dpp, but a constant (CDOM/DOM) ratio in leakage or dpp. I would prefer "Constant leakage ratio" and "Constant dpp ratio" but these names are longer, and I leave it to the authors to decide.

Thanks for the suggestion, we have taken it and changed the name of the simulations from "Constant leakage" to "Constant leakage ratio" and from "Constant dpp" to "Constant dpp ratio" (L497, Table 2, L708 and Figure 12).

specific comments (line numbers are based on the "tracked changes" version of the manuscript)

I 40: "plays" → "DOM plays". Changed, thanks.

I 56: "The latter" is more difficult to interpret now that the previous sentence has changed, I suggest changing it to "Remote-sensing platforms". Modified as suggested.

I 86: "dynamics at the surface is" → "dynamics at the surface are". Corrected, thanks.

I 125: A different study testing and comparing different genetic algorithms, including DE, in the context of BGC models is: Mattern and Edwards (2017): Simple parameter estimation for complex models — Testing evolutionary techniques on 3-dimensional biogeochemical ocean models.

https://doi.org/10.1016/j.jmarsys.2016.10.012

Thanks for the suggestion, we included the reference in L127.

I 172: "The subscript appended to each living and non-living component indicates ..." No subscripts have been shown yet, I would suggest either giving an example or slightly rephrasing it to: "In the following, subscripts are appended to the symbols for the constituents, indicating..."

We have rephrased to: "In the following, subscripts are appended to the symbols for the components to indicate the elemental constituent for which the state variable stands, including carbon (C), nitrogen (N), phosphorus (P), Chl-a (only in phytoplankton) and silica (Si, only in P^(DIATOM))."

I 188: "is indicated before the vertical bar" → "appears in front of a vertical bar". Changed.

Eq 4: I don't want to be too pedantic here, but it looks like G_P and $G_P'\{balance\}$ are dependent on i (plankton-specific). I would suggest adding "(i)" to the subscript, like for the symbol $f_p'\{X2\}$ in Eq (5).

Thanks for pointing this out. We refer now to G[P] and G[P]-balance of each phytoplankton type as G[P(i)] and G[P(i)]-balance, both in the text (L220) and in Eq. 4.

Fig 1 caption: "only for" \rightarrow "only used for". Changed.

I 432: This decision is up to the authors, but I would prefer having the table with the optimized parameters in the main text, and the table with the remaining parameters in the appendix.

We have decided to keep the order of the parameter tables as they were in the previous version. Although the alternative order could also be informative, we have chosen to combine all the results related to the optimization experiments in a single Appendix.

I 447: "We kept constant a and optimized \phi because these parameters are not well documented in literature...": This sentence still does not make it clear why a lack of documentation motivates the optimization of a parameter. Maybe add some more information, such as: "We kept constant a and optimized \phi, opting to optimize only one of these two interdependent parameters because they are not well documented in literature..."

We realize now that the original sentence suggested that both parameters (aPS and phi) were not well documented. We reformulated this part to clarify that the lack of documentation motivates the choice to optimize one parameter (phi, which is not very well documented) and not the other (aPS, which is much easily derived from observed aPH spectra).

I 457: I would suggest changing the introductory sentence to DE so that it says that the parameters represent individuals and not model simulations.

We removed: "(i.e., one model simulation)"

I 462: I like the updated text, but adding a bit more information removes ambiguity: "from a total of $M" \rightarrow "from a$ total number of M observed variables". Changed.

I 463: This N should be an N m, or more description is needed.

Yes, thank you, we changed it.

I 463: Again, a small suggested change to improve readability: "consisting of the simulation P_n and the corresponding observation O_n " \rightarrow "consisting of observation O_n and corresponding simulation-based estimates P_n (model results at the temporal and spatial observation locations)"

Thanks for the suggestion. We have reformulated following the reviewer's proposal.

I 468: In the description of the DE algorithm, make sure to point out that this represents one possible implementation. For example, the mutation scheme described here is one of many. I am not suggesting to name them all, but to keep the phrasing a bit more general, e.g.: "Each mutant vector is created selecting" → "In this implementation, each mutant vector is created selecting".

Thanks for pointing this out. We have accepted this suggestion of the reviewer (L474 & 477). The reference suggested above (Mattern & Edwards, 2017) was also very useful to read several possible ways the new samples are generated from an existing population.

I 473: "Crossover is performed between each target vector and its corresponding mutant vector, retaining the target vector in the population with a probability of 0.9, ..." In a typical implementation, this procedure is applied to each element (parameter) of the vectors, sometimes mutating one element for certain. In other words, would it be correct to say "Crossover is performed between each target vector and its corresponding mutant vector, retaining each element of the target vector in the population with a probability of 0.9, otherwise introducing the corresponding element from the mutant vector."?

Thanks for the suggestion. We took it and now the sentence reads: "Here, crossover is performed between each target vector and its corresponding mutant vector, retaining each element of the target vector in the population with a probability of 0.9, otherwise introducing the corresponding element from the mutant vector."

I 494: Again, I do not want to be pedantic but 4 of the 5 following sentences start with "In EXP-Biology", "In Constant leakage", "In Constant dpp", and "In EXP-Physics" and the sentences do not make it clear that the two hypothesis-testing experiments are "EXP-Biology" and "EXP-Physics", and that "Constant leakage" and "Constant dpp" are simulations/sub-experiments of "EXP-Biology". I would suggest modifying the text to add more information: "In the first experiment EXP-Biology, we investigated [...] This experiment consisted of comparing the results of Optimized with two additional simulations. These additional simulations are: (1) Constant leakage, in which we [...] (2) Constant dpp, in which we [...] In the second experiment, EXP-Physics, ..."

Thanks for the suggestions, we do agree the structure of the sentences was a bit redundant in the previous version. We took the reviewer's alternative and reformulated slightly the paragraph L493-512.

Fig. 3 - 6: I like the figures and the changes made to them, my only suggestion is to change the y-label from "m" to "depth (m)".

All y-axis in figures that show vertical profiles now display "depth (m)" (Fig. 3, 4, 5, 6, 8 and 13).

I 701: A reference to Eq (5) may be useful in this paragraph.

The first sentence introducing the results of EXP-Biology has been modified to: "EXP-Biology focuses on the physiological processes affecting CDOM production by phytoplankton examining which is the coloured fraction of the total DOC of phytoplankton origin (Eq. 5)."