Review 1 of Elsworth et al. (2022) "Anthropogenic climate change drives non-stationary phytoplankton variance", submitted to Biogeosciences.

This is a very interesting study on the impacts of climate change on the internal variability of phytoplankton, based on an Earth System Model ensemble. While I believe this study is quite important and of interest in terms of results (the main result being a reduction in phytoplankton internal variability under anthropogenic driven climate change) as in terms of implications(especially the link with fisheries stock assessment, whose uncertainty could be reduced as a consequence of this reduced phytoplankton internal variability), I have major concerns about the MLR method used to estimate the physical and biogeochemical drivers of trends in phytoplankton internal variability. I elaborate on these and other issues below.

MAJOR COMMENTS:

My first concern is the choice of explanatory variables for the MLR:

MLR is a great tool for exploring relationships between variables, but as you have indicated in the text, it is unable to distinguish between bottom-up and top-down relationships that link two variables. For these reasons, in order to be able to interpret the results with causality relationship, you should :

- 1. 1) Use only variables for which the causal relationship with phytoplankton biomass is known (or for which the first order of this relationship is known), e.g., SST (the first order is a bottom-up relationship: warming drives phytoplankton biomass by increasing metabolic rates, a positive effect, and by increasing nutrient stratification, a negative effect. At second order, one could have a top- down feedback of phytoplankton biomass change modifying carbon cycling and indirectly temperature, but one would neglect this effect). For this reason, I think that including zooplankton/zooplankton grazing in such an analysis is not appropriate because you are not able to separate top-down and bottom-up effects on phytoplankton biomass.
- 2. 2) Use only variables for which the causal relationship with the target variable is the same. In your case, use the variables for which phytoplankton biomass is a consequence, not a cause. Again, while I believe that zooplankton do exert top-down control over phytoplankton (so that phytoplankton biomass would be a consequence), PFT models with small numbers of zooplankton are likely to be dominated by bottom-up control (so that zooplankton would be the consequence and phytoplankton the cause). To support this claim, trophic amplification under climate change in these models has been described as a good indicator of bottom-up control of zooplankton by phytoplankton (Chust et al., 2014, Kwiatkowski et al., 2019), a pattern that is altered when higher trophic levels are considered (Dupont et al., 2022).
- 3. 3) MLR analysis assumes independence of explanatory variables, which is clearly not the case (e.g., MLD and Nutrient are highly correlated). I agree that this is a classic problem in multivariate analysis on climate variables, but this point should be discussed further, by providing at least one correlation matrix between all explanatory variables.

Nevertheless, your signal on zooplankton is clearly related to the strong relationship between zooplankton and phytoplankton, which is expected but clearly interesting. I think you should analyze (with simple linear regression) the relationship between phytoplankton and zooplankton separately from the other variables, which would clearly fit the main message of your paper: showing that the effect of climate change on the internal variability of phytoplankton is transferred to the internal variability of zooplankton would demonstrate a transfer of the trend in internal variability to the higher trophic levels (in this case, zooplankton), which you could then extrapolate in the discussion to even higher trophic levels (e.g. fish). It would also be interesting to compare trends in phytoplankton and zooplankton internal variability. Is it higher? Lower? Why? You could also do the same MLR analysis with trends in total plankton with the bottom-up effect.

We thank the reviewer for their constructive comments and appreciate their careful reading of the manuscript. We agree that the manuscript would benefit from extending our analysis to include these methods. To more quantitatively assess the relationship between phytoplankton and zooplankton, we will revise the manuscript to include this analytical approach. We thank the reviewer for this correction and will adapt our results section accordingly.

My second concern is about the MLR method itself, which I think is wrong in its current form:

First of all, I am missing some details to understand what exactly you did with the MLR. You would need to make it clear which variables are used for each step of the method. In particular, it is not clear which variable depends on i) time, ii) space, and iii) the member of the model set. For the rest of my argument, *t* will refer to

time, x to the grid cell (spatial position) and i to the model set member. Y will refer to the phytoplankton biomass and X to any explanatory variable.

A) So, for what I understand, your first step was to prepare linearly detrended annual anomalies. So, for a variable *X*, with a trend *a*, the considered variable in the MLR is

 $X^{d}(t,x,i) = (X(t,x,i)-X(0,x,i))-a(x)*t$, a field with 3 dimensions : space, time and model ensemble member. The same calculation gives you $Y^{d}(t,x,i)$.

If it is based on globally averaged values, I would recommend to keep the space dimension. B) With the MLR, you fitted the following relationship and thus estimated the coefficients dYd/dXd:

 $Y^{d}(t,x,i) = sum \left((dY^{d}/dX^{d}) * X^{d}(t,x,i) \right)$

An approximation of the first order taylor development which would give

 $Y^{d}(t,x,i) = sum ((dY^{d}/dX^{d})(t,x,i) * X^{d}(t,x,i))$ C) Then, by linearity, you compute (*t* being a 10-year average)

 $Sigma_i(Y^d(t,x,i)) = sum (dY^d/dX^d sigma_(X^d(t,x,i)))$

BUT : Variance isn't linear (neither is the standard deviation). Even if two variables are independent (which is definitely not the case), $VAR(aX+bY) = a^2 Var(X) + b^2 Var(Y)$.

In your case, if you wanted to reconstruct your variance, you would use the following formula (*ai* being your MLR coefficient dY^d/dX^d and Cov being the covariance and not the coefficient of variance here):

You can calculate this value perfectly well, but I'm not sure that's what you want to do.

Indeed, I'm not sure what kind of information you expect from the relationships between linearly detrended variables and linearly detrended phytoplankton carbon biomass: do you want to explain the internal phytoplankton variability by the internal variability of others variables or do you want to explain it by the trends of other variables ? I think the second option, or both, would be more appropriate (e.g., is the increase in temperature related to the reduction in internal variability of phytoplankton biomass?)

While I think your current method is wrong, I keep in mind that too few details have been provided to be certain, and perhaps I will be convinced of your method when more details are included. Nevertheless, I suggest another approach:

You have introduced CoV (Coefficient of Variance), and I think this variable is indeed more appropriate than standard deviation because it removes the effect of reduced mean state values on the change in internal variability (i.e., a lower mean state will lead to lower internal variability in absolute magnitude, but not necessarily to a reduced coefficient of variance).

$$egin{aligned} \operatorname{Var}\!\left(\sum_{i=1}^N a_i X_i
ight) &= \sum_{i,j=1}^N a_i a_j \operatorname{Cov}(X_i,X_j) \ &= \sum_{i=1}^N a_i^2 \operatorname{Var}(X_i) + \sum_{i
eq j} a_i a_j \operatorname{Cov}(X_i,X_j) \ &= \sum_{i=1}^N a_i^2 \operatorname{Var}(X_i) + 2 \sum_{1 \leq i < j \leq N} a_i a_j \operatorname{Cov}(X_i,X_j). \end{aligned}$$

You could perform the MLR on CoV directly (which would mean using the mean anomalies of the entire model ensemble), i.e., estimate a linear relationship between $CoV_phyto(t,x)$ and other variables:

$$CoV_phyto(t,x) = CoV_phyto(0,x) + a * anomaly_var1(t,x) + b * anomaly_var2(t,x)...$$

Or if you want-to keep detrended variables:

 $CoV_phyto(t,x) = CoV_phyto(0,x) + a CoV_var1(t,x) + b CoV_var2(t,x)...$

We thank the reviewer for this helpful insight. To address this suggestion, we are revising our MLR analysis to use CoV rather than standard deviation to identify drivers of phytoplankton variance. We will revise the figures associated with the MLR analysis as well as the associated text to reflect this new analytical framework.

MINOR COMMENTS :

Discussion : The discussion is quite short, I would like to see a discussion of the mechanisms that might lead to this reduction in internal phytoplankton variance. In addition, the discussion focuses on the top-down control of zooplankton on phytoplankton. Although the authors no longer assert in the current version that zooplankton are a driver of trends in internal phytoplankton variability, they continue to discuss it, which is not necessarily relevant. Given my main comment on how to study the relationship between phytoplankton and zooplankton variability, I would focus on the bottom-up effect of phytoplankton on zooplankton to support the impact of changes in phytoplankton variability on higher trophic levels, and then discuss top-down effects as a limitation to the interpretation of your results.

Wording : Consider using "internal variability" instead of "variance" throughout the text, starting with the title. While variance can refer to many temporal scales (seasonal, interannual,...), I think internal variability is much more accurate (e.g., L7, "internal variability" instead of "internal variance")

We agree with the reviewer and will revise the manuscript text to reflect this clarification.

Other comments :

L1: Bopp et al., 2001, 2013; Laufkötter et al., 2015; Kwiatkowski et al., 2020 are model studies. If you want to keep past tense, please add data-based reference. Or use another tense.

Thank you for this suggestion. We will revise the tense in which we refer to modelling studies to reflect this comment.

L4: I would mention the impact of phytoplankton on the carbon cycle. Also in the discussion.

We agree that the manuscript would benefit from elaborating on the role of phytoplankton in the carbon cycle. We will add text to the abstract and introduction to reflect this important role.

L45-46: As formulated, the results of the Resplandy's study are not clear.

Thank you for this clarification. We will revise the text to more accurately convey the results of the Resplandy study.

L54: The last sentence of the paragraph does not flow well with the rest.

Fig 1 and L160: "by ensemble member 1 of the CESM1-LE": why not using the average of the model ensemble members ?

Thank you for bringing this point to our attention. We have refined our analytical method to use the average of the model ensemble members. We will modify both the text and the equation to reflect this change.

Eq. 1: use a separate symbol for internal variability (you have twice sigma) Eq. 2: Specify on which variable your mean LE is computed (time, space and model ensemble members)

This is an excellent suggestion. We will revise the equation to reflect the precise variables for which the mean LE is computed. We will modify the equation to reflect time, space, and model ensemble variables.

L132: unclear, why not using the same term as above, i.e., "ensemble mean", i guess that LE(x,y,t) is the same as LE but this needs to be specified.

Thank you for this clarification. We will revise the text to reflect this clarification.

L134: Please avoid using variance if you refer to internal variability. L164: use interannual instead of temporal which is no precise

We agree with the reviewer and will revise the manuscript text to reflect this clarification.

L179 (and L290): I disagree with this statement: the comparison between the observed variance and the modeled variance does not give any information about the trends in the variance.

Thank you for clarifying. We will revise the text to reflect this comment.

Fig 3. Specify the variables on which you have applied a t-test, at least as supplementary material. The reader should be able to assess the validity of your test (sample size, normality assumption, etc.).

We agree that the manuscript would benefit from elaborating the precise variables on which we have applied a t-test. We will revise the supplementary material to provide more information.

L239: Why not use the total biomass of phytoplankton everywhere?

Fig 4: Please add the regions to the map (at least ASP, SAP, SOC, and EQP), and consider showing diatom biomass over small phytoplankton biomass ratio, as diazotrophs are not dominant anywhere and to be more quantitative.

We thank the reviewer for this helpful insight. We will add a revised figure which includes the overlayed regions to the manuscript. This will allow better visualization of the precise locations of the regional analyses.

L260: The wording of the sentence suggests that zooplankton exert top-down control over phytoplankton, which is uncertain or even false.

Thank you for this clarification. We will revise the text to resolve this issue.

L275-279: I think this result (with an appropriate MLR method) is very interesting in explaining what is driving the zooplankton variability (see main comment) and should be interpreted from a zooplankton perspective.

Absolutely. We agree that the manuscript will benefit from applying a more statistically robust MLR analysis. We will modify the results and the accompanying figures to reflect this revision.

L287: I do not believe that either of these references is relevant to this statement.

Thank you for this comment. We will revise our selection of references to better reflect the statement.

Review 2 of Elsworth et al. (2022) "Anthropogenic climate change drives non-stationary phytoplankton variance", submitted to Biogeosciences.

My only remaining recommendation is to remove Diazotrophs from the color bar for Figure 4. If Diazotrophs to not dominate in any region (as specified in the authors' responses to the initial review), it seems unnecessary to include them in the figure. If the authors have some other reason for including Diazotrophs, it should at least be specified in the caption that Diazotrophs are not actually visible in the figure.

Thank you for this suggestion. We have removed diazotrophs from the color bar in Figure 4 and have revised the figure caption.



"Figure 4: Distribution of the dominant phytoplankton functional type in biomass carbon averaged across the RCP8.5 forcing scenario (2006 to 2100). The CESM1-LE simulates three phytoplankton functional types: diatoms, diazotrophs, and small phytoplankton. Regions where diatoms dominate are shown in yellow and regions where small phytoplankton dominate are shown in purple. Diazotrophs do not dominate in any region of the global ocean."

Review 3 of Elsworth et al. (2022) "Anthropogenic climate change drives non-stationary phytoplankton variance", submitted to Biogeosciences.

This work investigates the internal variability of phytoplankton biomass in an Earth System Model large ensemble (CESM1-LE). The results show a decrease in internal variability under RCP8.5.

The manuscript is well written and well laid out and the results are novel and important. I have only some minor suggestions.

We thank the reviewer for their constructive comments and appreciate their careful reading of the manuscript.

Comments

Line 128: The coefficient of variance seems to be much more commonly referred to as the coefficient of variation. Is there any reason why you use the term "coefficient of variance"?

We thank the reviewer for this clarification. We will revise the text to reflect this point.

Line 130: Should the nominator in this equation read LE(x,y,t) (with a line above) as it is defined on line 132? In that case I would rephrase the sentence on line 131 to say something like: where LE(x,y,t), the forced response of the large ensemble, is calculated as the mean of ensemble members at a given location and time.

We appreciate this suggestion. We will revise both the equation and the accompanying text to clarify this point.

Line 140: Should be biomass standard deviation instead of variance? Also on line 145. Also check other places throughout the manuscript like on lines 225-229.

Thank you for noting this discrepancy. We will revise the manuscript to make sure we are using the correct terminology at each point in the text.

Line 169 - 175: It is not specified in the text that it is surface chlorophyll that you are using. Also, could you please clarify why you used surface chlorophyll for the validation of internal variability instead of biomass as in the rest of the analysis?

Thank you for this clarification. We use surface chlorophyll for the validation of internal variability, because we are building on previous work in which we created a synthetic ensemble of observed surface chlorophyll to emulate observed variability. We will revise the text and the associated figure captions to clarify the motivation for this decision.

212: Specify that it is surface chlorophyll.

We will specify that we are referring to surface chlorophyll.

Review 4 of Elsworth et al. (2022) "Anthropogenic climate change drives non-stationary phytoplankton variance", submitted to Biogeosciences.

The authors are to be commended for taking on an interesting and important scientific challenge. However I do have a primary concern with the analytical framework applied using an MLR approach to evaluate the drivers of future changes in biomass variance. I believe that the methodology applied is sufficiently problematic that the primary result (grazing) is not convincing.

A biomass framework has been developed and applied for looking at marine ecosystems, namely that of Behrenfeld and Boss (2014; Annual Reviews), or more concisely the Behrenfeld framework. This method provides a quantitative and mechanistically-based means to connect biomass fluctuations with the underlying drivers at the timescales resolved by the model output (presumably monthly here). Within the Behrenfeld framework, decomposition into the underlying drivers is based on mass conservation using fields that should be saved for the model. For the case of the case of entrainment as it impacts biomass (a viable mechanism) there is not a convincing case that this will be properly represented by the fluctuations in annual mean MLD. This may be the case, but it is important for the authors to demonstrate this rather than simply assume it to be the case. Likewise temperature and nutrient dependencies in the model work into growth rates for phytoplankton, and the representation in the MLR approach is not convincing or state-of-the-art. The burden is really on the authors to justify their decision to use an MLR approach, rather than the mechanistically-based biomass framework of Behrenfeld.

I would urge the authors to apply the biomass framework of Behrenfeld to identify properly the relative roles of light, nutrient, and temperature drivers, with the analysis performed at the (monthly?) timescales resolved in the model output. Otherwise in my view the main ideas emphasized in the interpretation of the results are somewhat unsubstantiated.

We thank the reviewer for their constructive comments and appreciate their careful reading of the manuscript. The reviewer makes a general comment to revise our MLR analysis to make it more statistically robust. This also reflects the comments of Reviewer 1. We will address this by revising our MLR analysis to use CoV rather than standard deviation and will extend the discussion section of the manuscript to reflect his revised analysis.

While the Behrenfeld and Boss, 2014 analytical framework is applicable to the study of bloom dynamics on the scale of days to months, our analysis relates to drivers of phytoplankton variance on the scale of centuries. The difference in relevant timescales between the studies result in different analytical approaches. This study does not attempt to address drivers of bloom dynamics, but rather drivers of phytoplankton variance.

The CESM1-LE does not provide output for phytoplankton growth rate. Without information about phytoplankton growth rate, we cannot reconstruct the change in phytoplankton or the change in phytoplankton variance over time using the analytical approach suggested from Behrenfeld and Boss, 2014. However, we have explored a more statistically robust approach to reconstruct drivers of phytoplankton coefficient of variance in response to Reviewer 1's comment.