

Overview

In this paper, the authors use complex network theory with outputs from a model simulation of the North-West European Shelf (NWES) to identify 1) spatial correlation length scales of biogeochemical variables, 2) geographical regions with strong spatial correlation within them and weak correlation between them and 3) correlations between biogeochemical variables. Point 1) is achieved by computing the Spearman's correlation coefficient between the time series of the different grid points. For point 2), for each variable, they build a spatial network with the previous coefficient, apply spectral graph clustering to gather grid-points and identify the boundaries of these clusters. Then, they define the regions based on the fraction of variables that have a boundary in each grid point. For point 3), they compute the Spearman's correlation coefficient between the spatial distributions of each variable, build a spatial network with that and use the spectral graph clustering to cluster biogeochemical variables. A first result of this work is to show that complex network theory can be used to identify biogeochemical regions based on spatial correlation or to identify correlation between biogeochemical variables. This is of interest for reducing the complexity of biogeochemical dynamics and for helping the analysis of simulations. The correlation length scales are of interest for data assimilation as they quantify the range of the influence between grid points.

I very much appreciated to read the paper. It is clear and well written. The results are of interest and worth to be published. It presents an interesting way to analyse biogeochemical model outputs. The definition of biogeochemical provinces is particularly interesting as it can help the analysis of models. The methods are clearly explained. I do not have major comments on the paper, but rather a list of minor or specific comments that I think could further improve the paper. The comments that are more important are highlighted in red.

As a summary of my comments, here are my answers to the review criteria at Biogeosciences. I just selected the relevant questions:

1. Do the authors give proper credit to related work and clearly indicate their own new/original contribution? *Yes. Maybe a bit of comparison with the literature on correlation length scales could benefit the paper.*
2. Does the abstract provide a concise and complete summary? *Mostly. It could be improved by more clearly stating the results*

Minor and specific comments

Abstract

I think the results should be more clearly/precisely stated in the abstract. It seemed a bit too vague to me. For example:

- I. 4: « to identify the functional types », which one are they exactly?
- I. 6: « identifying the (geographically varying) connectivity lengthscales and the clusters of spatial locations that are connected. » What are the main findings concerning the length scales? What are the different clusters? For the length scales, results that seem particularly interesting is that spatial variability is quite similar between variables, requiring only to scale it using the mean length.
- I. 9: « The results of this study help to understand how natural, or anthropogenic, perturbations propagate through the shelf-sea ecosystem », it is difficult to agree with that last sentence since the results were not clearly stated before. After finishing reading paper, I also do not think the results help to understand how perturbations propagate in the ecosystem. The results rather offer an analysis framework to do that.
- I. 9: « anthropogenic » -> anthropogenic

Introduction

I. 35: « an abstraction that will allow for smarter decision-making when considering data sampling and feature selection for ML. » Not that clear to me how and why abstraction can allow smarter decision-making.

I. 37-50: Very nice paragraph clearly stating the objective of the work.

Model and Data

Sec. 2.1: I think it will be nice to have a bit more details about the configuration. Things like: numerical schemes, diffusion, viscosity, equation of state, what forcings (wind, temperature?). How the simulations are run (spin-up procedure, initialisation...). The reference to the papers should be for further details. The reader should not need to read these papers to get a basic understanding of the configuration.

Methodology

Sec. 3.1: maybe a figure showing the raw and filtered time series in the supplementaries could be useful to illustrate what are the timescale filtered? Or maybe some periodogram? It should probably be stated before (introduction? Or somewhere in the methods?) what are the timescales of interest? And why? Out of curiosity have you tried your analysis with the seasonal signal?

I. 154: « to a 21 km spatial resolution » make me wonder if the results are sensitive to the resolution of the model? Longer length scale because of eddy mixing? Or shorter one because of dynamical barrier created by filaments or eddies? This somehow questions also the isotropy assumption.

I. 162: I do not understand why the authors say : « As opposed to the biogeochemical lengthscales computed in Sect. 3.2.1 [...] here we manipulate the spatial networks to look at the spatial dependency of this length scale. » In section 3.2.1 you also have a map of the length scales that give you the spatial information (Fig. 2). I do not get the interest of these two definitions. Note that this also bring a bit of confusion about which are the length scales used for the different plots. For example in Fig. 4 which one is it? And for Fig. 5? I kind of got that Fig. 4 is the length scale define in sec. 3.2.1 and Fig. 5 the one in sec. 3.2.3 but it is not so clear.

I. 167: « black » rather than « red »?

Sec. 3.3: This part is not easy to follow. Maybe a short description of the objective at the beginning could help the reader. What are the objects to be clustered, following which criteria? If I understood well, the goal is to clusters grid-points depending on their temporal correlation between each other for each variables so that grid-points with strong correlation are group together.

Results and Discussion

Sec. 4.1: As mentioned before, mentioning which length scale (the one from sec. 3.2.1 or sec. 3.2.3) the authors refer to would help the reader. Since two definition of length scale seems to be used, it feels natural to wonder how they compare?

I. 275-278: I think I got the general idea here: the spatial distribution of the length scale of a specific variable is the product between Fig. 5a and Fig. 4. However, as it seems that it is not the same definition of the length scale between Fig. 4 and Fig. 5a it is a bit confusing.

Sec. 4.1: I am not familiar with length scale, but it seems that there is some literature on length scales (just saying that based on a quick search on google scholar). Some comparison of the results and the methods with the literature is missing there. Are there other definition of length scale? How does the method used in this paper compare with other? Are the length scales similar to former estimations?

Fig. 7: How is it done? I guess it is some kind of generalisation of Fig. 6 but it would be good to know more than « We used those robust boundaries to identify 13 regions representing areas of NWES connectivity. Results of this regionalisation are represented in Fig. 7. » (line 315)

I. 350: « or build simpler models than ERSEM » I think this need to be say a bit differently. Complexity of models tends to increase to better (or hoping to better) represent the real world. NPZD models already exist with just one phytoplankton, one zooplankton... Here the issue is to simplify ERSEM while keeping an accurate representation. Maybe something like line 51 « simplified (yet realistic with respect to the objectives) ».

I. 363-366: I do not see that in Fig. 8. The mean correlation between POM (yellow) and the Higher Trophic Levels + DOM (pink) is rather low. The authors should clarify.

Conclusions

I. 410-426: You are here a bit more specific about the results and this could be used for the abstract. E.g. « we can conclude that the biogeochemical lengthscales vary significantly between variables and are not directly transferable. » or « we have provided an approximation for the lengthscale of each variable, and each spatial location, that is informed by the high correlation in the spatial variability between lengthscales of each variable »...

I. 421-424: « Our analysis demonstrated that the chemical components (e.g., nitrogen, carbon, silicon. . . etc) of each pelagic variable (e.g., diatoms, nanophytoplankton, microzooplankton) are closely linked and a simpler version of the model can be built, by reducing these variables through parametrization. » I do not know ERSEM but I assume that as many models it started from a simple version and the complexity has been increased (e.g. addition of more phytoplankton types). I am wondering how the grouping compare with a former simpler version of ERSEM? I suppose it should be relatively similar (e.g. all types of phytoplankton in gather in only one) however it will be quite interesting if some grouping where different.

Extra comments

« lengthscales »: After a quick search on google scholar, it seems that it is rather written « length scales » or « length-scales ».

The regions define in Fig. 7 could be used for sampling the domain to analyse the inter-variable interaction network. Maybe selecting grid points only within one region and to compare with the same done with another region. Are the interaction between variables different between two regions? Or sampling evenly between the regions to have a fair general representation? This point is mostly for curiosity as it seems natural to try to use these regions.

I. 367: Butenschon et al. (2015) and Butenschon et al. (2016) are similar paper (2015 is the discussion version of 2016). Better to keep only 2016.