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Interactive comment on "Vertical distribution of chlorophyll a concentration and phytoplankton community composition from in situ fluorescence profiles: a first database for the global ocean" *by* R. Sauzède et al.

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Answers to Referee #2:

We are grateful to the reviewer for his constructive suggestions to clarify our manuscript. We have modified it accordingly and think that the new version is now improved. Our responses as well as the description of actions taken in regards to the comments are detailed below. We hope that we have sufficiently addressed the issues that were raised by the reviewer.

General comments from Referee:

The authors need however to provide more information on the method limits that are not listed clearly. In my opinion, the reading of Sauzede et al. 2015a was required and then several questions appeared after that. An efficient synthesis of the main limitations of the methodology without going back to the previous article is thus required. For example (like all methodologies using a training set), the authors indicate some limitations for applying it on profiles prior 1991. It was assumed that the relationship between the phytoplankton biomass and the community composition with the fluorescence profile is similar to that one after 1991. In a context of global scale, climate change and validation of long simulations, I'm thus wondering how some modifications of the phytoplankton composition over time would be detected from the algorithm?

The authors indicate also that the method "is robust with slightly less accurate results for the Arctic basin and the Indian Ocean which are two areas known for data scarcity". I think the authors should provide a specific quality index for this data base for helping to weight correctly their estimates for some comparison with model outputs. Are the authors able to produce some potential errors or a quality index in the classification according to the number of HPLC samples available for one period and one area? This step is very relevant because, at least in [TChl], this data base could be reuse by a large community of modelers by providing a higher resolution that WOA13.

Author's response:

We agree that FLAVOR method described in Sauzède et al. (JGR, 2015) is at the heart of this study and was likely not enough detailed in this paper. This was our initial deliberate choice as the main focus of paper was to present the "calibrated data base". However given this issue is raised by both reviewers, we have subsequently tried to explain the algorithm more thoroughly in the Section 2.3 "Conversion of chlorophyll fluorescence into chlorophyll a concentration and phytoplankton community composition". Additionally a new paragraph also explain the limitations of the method in this

Section.

To assess the spatial quality index for the database, the user has just to refer to the statistics given in the paper of Sauzède et al. (2015). We have subsequently added a sentence to guide the user for easily finding the information if needed.

Author's changes in manuscript:

The main modifications to the manuscript made were:

1- Page 374 line 1, we added details about FLAVOR algorithm:

"FLAVOR is composed of two different neural networks: the first one was trained to retrieve the vertical distribution of [TChl] and the second one to retrieve simultaneously the vertical distributions of [microChl], [nanoChl] and [picoChl]. Both neural networks were trained and validated using a large database including 896 concomitant in situ vertical profiles of HPLC pigments and chlorophyll fluorescence. These profiles were collected as part of 22 oceanographic cruises representative of the global ocean in terms of trophic and oceanographic conditions, making the method applicable to most oceanic waters. The diagnostic pigment-based approach of (Uitz et al., 2006), based on (Claustre, 1994) and (Vidussi et al., 2001) was utilized to estimate the biomass associated with the three pigment-derived size classes for each profile. Finally, the dataset of concurrent fluorescence profiles and HPLC-determined [TChl], [microChl], [nanoChl] and [picoChl] at discrete depths was used to establish the neural network-based relationships between the fluorescence profile shape and the vertical distributions of [TChl] and phytoplankton community. The schematic overview of the FLAVOR method is shown on Figure 4 in Sauzède et al. (2015a). The global absolute errors of FLAVOR retrievals are 40%, 46%, 35% and 40% for the [TChl], [microChl], [nanoChl] and [picoChl] respectively (Sauzède et al., 2015a). The global absolute errors of FLAVOR retrievals are 40%, 46%, 35% and 40% for the [TChl], [microChl], [nanoChl] and [picoChl] respectively (Sauzède et al., 2015a)."

2- Page 374 line 3, we have added a specific paragraph that reports the potential limitations of our method:

"Admittedly, the FLAVOR method has some limitations. The dependence of chlorophyll fluorescence on light environment is probably intrinsically accounted for in the algorithm thanks to the geolocation and date of acquisition used as inputs for the training. However, one of the potential concern with FLAVOR is that the impact of the daytime Non-Photochemical Quenching (NPQ; see, e.g., Cullen and Lewis, 1995), responsible for a decrease in chlorophyll fluorescence values at high irradiance, is not accounted for by the method. The NPQ uncorrected fluorescence profile shape is indeed used to retrieve the vertical distribution of phytoplankton biomass (see details in Sauzède et al., 2015a). Note that, if density profiles are available together with fluorescence profiles, NPQ can be corrected using the method of Xing et al. (2012). This method involves substituting the fluorescence values acquired within the mixed layer by the maximum value within this layer.

It has been previously mentioned that FLAVOR is not adapted for the retrieval of chlorophyll a concentration on a fluorescence profile-by-profile basis (Sauzède et al., 2015a). Rather, FLAVOR and, hence, the resulting database are relevant for large scale investigations, e.g. development of climatologies of the vertical distribution of chlorophyll a from which regional anomalies or temporal trends might be evidenced. In fact, the method was validated using a global database and it is not excluded that the retrievals from FLAVOR might be regionally biased. For instance, Sauzède et al. (2015a) have shown that FLAVOR retrievals for the Southern, Arctic and Indian Ocean are slightly less accurate than for the other basins. This is likely because the method is not enough constrained in these specific areas, which are known for data scarcity. Additional details about the performance of the method for various oceanic basins are given in Sauzède et al. (2015a), in Figures S3, S5-S7. Finally, it is worth recalling here that the relationships between the phytoplankton biomass or community composition profiles and the fluorescence profiles is assumed to be identical for profiles acquired

before 1991 (not involved in the training data set because of lack of HPLC data) and after 1991 (only used for the training process). In the context of possible use of this database for supporting analysis looking for trends or shift in chlorophyll a time series, this assumption will have to be taken into consideration."

General comments from Referee:

I'm also wondering if the authors could provide some recommendations on the sampling protocols to improve FLAVOR results (exp: not sampling at fixed depth but according to the shape of the profile) and to be consistent over time for the next decade (could you recommend some HPLC measurements with a minimal frequency for one area?). This one could be tested by under sampling (spatially and temporally) different size of training sets, to evaluate the impact on the estimates quality.

Author's response:

Although this comment is totally right, it is relevant to the performance of the FLAVOR method and not to the production of the dataset presented here. We therefore believe this comment is beyond the scope of this paper that only deals with the application of the method. Additionally before such types of recommendations become really useful, which means accepted and used by the community, it deserves first discussed within the community before becoming a kind of HPLC sampling core protocol.

Specific comments from Referee:

P8: How did you manage temporal trends due to fouling for autonomous in-situ Chl sensors? Did you use some quality indices associated with these platforms?

Author's response:

As part of the Bio-Argo program, some procedures are being developed to deliver quality-controlled data, in real-time as well as in delayed-mode. Our lab is deeply engaged in developing these procedures, in particular with monitoring of quality indices (i.e. monitoring of deep (1000m) fluorescence, comparison with remote sensing esti-

mate of Chla). Some documentation, discussed as part of the Argo Data Management Team are being produced. The analysis of the float data that we have conduct to date does not reveal any biofouling effect on the Chla fluorometer. One of the reasons is that floats spend most of their time (90%) at 1000m, i.e. in the dark, at low temperature and high pressure, maybe one of the most efficient way to prevent fouling.

Specific comments from Referee:

P8, lines 22-23: How can you have less than five values per profile with at least ten values per profile??? If condition-4 was satisfied, the condition-5 should be fine? Not clear

Author's response:

The condition is "a minimum of five different values per profile is required (i.e. condition on the sensor resolution)." (p. 372 line 23) because there are some cases where there are more than ten points per profile and less than five different values (not equal). This is the case when the sensor resolution is not good.

Author's changes in manuscript:

We have replaced different by "not equal" to be more specific. (p.372 line 23)

Specific comments from Referee:

P9, line 6: Have you really checked 48 600 profiles visually??

Author's response:

Yes, it was a very long and tedious work. Obviously, like every visual verification, we are not safe from having forgotten some "bad" profiles.

Specific comments from Referee:

P11: First sentence of section 3.1 is a repetition of the previous section and can be removed. P11, line7: Is the "FLAVOR use" a real calibration process? Probably not, in

spite of the good quality of the algorithm.

Author's response and changes in the manuscript:

Thank you for the referee for these comments. The first sentence of Sect. 3.1. was removed and we have replaced "calibrated" (p. 375 line 7) by "transformed".

Interactive comment on Earth Syst. Sci. Data Discuss., 8, 365, 2015.