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Interactive comment on "Phytoplankton community structure in the North Sea: coupling between remote sensing and automated in situ analysis at the single cell level" *by* M. Thyssen et al.

M. Thyssen et al.

melilotus.thyssen@mio.osupytheas.fr

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The aim of this paper is to develop specific approaches to characterize the phytoplankton community structure and its high frequency variation in time and space. For this purpose, the authors combine plankton community structure using automated flow cytometry and remote sensing algorithm such as PHYSAT. The manuscript is well written and the topic is very interesting and relevant for environmental and ocean colour researches. I do recommend it for publication, however the authors should improve the paper (see comments above).

General comments: The authors are interested in a regional area of the North Sea. They have used ocean colour data within 4 km of spatial resolution. Maybe, the study could improve using satellite images with 1.1 km of spatial resolution.

Reply: At the time the matchups were selected, the remote sensing dataset available for PHYSAT was the 4km resolution. We would like to insist on the fact that the aim of the paper was not to improve PHYSAT. PHYSAT maps are just shown as a potential application so that the question of resolution seems not essential at this stage. However, we agree with the reviewer, future application and PHYSAT development will need the best resolution.

Once PHYSAT has been applied, the frequency of occurrence of the two distinct anomalies (N1 and N2) were very low. Can you explain why these percentages are very low? Could authors explain the phytoplankton community that include N1 and N2?

Reply: Again, PHYSAT maps are shown as a potential application. The two anomalies found during the 5 days cruise can't be representative of all the variability over the area. A lot of other kind of anomalies exist (in different areas and seasons) and will potentially be identified using cytometry in the future. This explains why the frequencies of the two anomalies found in this first test are not high everywhere. Our aim is to show that it's possible to find different anomalies with different composition based on cytometry. This shows for the first time that PHYSAT is not limited to dominant cases as it was before with HPLC (pigments) data. Areas where the frequencies of the two anomalies are low correspond to other sets of anomalies not found within our 2 days matchups between the in situ measurements and the satellite pixels. At this scale of anomalies selection, the variability is high and this variability is used in the paper of BenMustapha et al., 2014. Text has been added to better explain that our aim is not to improve PHYSAT and to furnish a new method adapted to the area. We only want to show (for the first time) that cytometry analysis at high frequency can be potentially used to label PHYSAT anomalies in the future as two distinct types of anomalies have

BGD
11, C9210–C9214, 2015

been associated to two different in situ compositions. This work encourages people to develop in situ cytometry measurement and coupling with remote sensed data.

"This paper shows for the first time that SFC datasets can be used for labeling PHYSAT anomalies at the daily scale. The SCF is a powerful automated system aimed to be implemented in several vessels of opportunity and monitoring programs for future PHYSAT anomalies identification at the daily scale and at the community structure level."

Minor comments: Page 15625, Lines 14-15. You can include more studies perform with PHYSAT in regional scales such as Mediterranean Sea.

Reply: Thank you for this reminding, we have added the Navarro et al. 2014 reference in the list.

Page 15630, Lines 25. Please, give more information about the turbid mask using in this study.

Reply: The turbid mask used in this paper is the one described in the paper of Vantrepotte. As our paper is not focused on the improvement of PHYSAT, we decided not to explain again this method here. We would like to invite the reviewer to read the Vantrepotte et al. paper for more information as we have apply the method without any changes.

Page 15631, Line 5. Although PHYSAT is a well know method established in the scientific literature, I think that the authors should give more information about PHYSAT method using in this study.

Reply: We thank the reviewer for its interest in PHYSAT. However, as our paper is not focused on the development of a new regional exhaustive, we decided not to explain in detail this method here. Papers referenced in the manuscript about PHYSAT methodology are easily accessible on the internet for more detail.

Page 15635, Line 11. Which LUT has been used to calculate Ra?

BGD

11, C9210–C9214, 2015

Reply: Once again PHYSAT is not the main aim of our paper. However the LUT is based on the relationship used in Alvain et al. 2005 and 2008. This relationship has been applied to regional dataset used in this study. A sentence about that has been added in the text: "PHYSAT radiance anomalies (Ra) were calculated based on the 2005 method (Alvain et al., 2005) and the average signal was recalculated to fit the sampling area."

Page 15635 , Line 15. Explain why authors did not use the Ra 555 nm.

Reply: This wavelength was not implemented in the PHYSAT calculation for MODIS at the time it was processed for the paper. We think it's not crucial as we only want to show that the two specific phytoplankton compositions detected by cytometry can be associated with two specific anomalies at different wavelengths.

Figure 9. Please, include in fig 9c and 9d the threshold from Table 3 to compare with the individuals spectra.

Reply: The thresholds were highlighted on the figure 9. Legend was updated according to.

Interactive comment on Biogeosciences Discuss., 11, 15621, 2014.

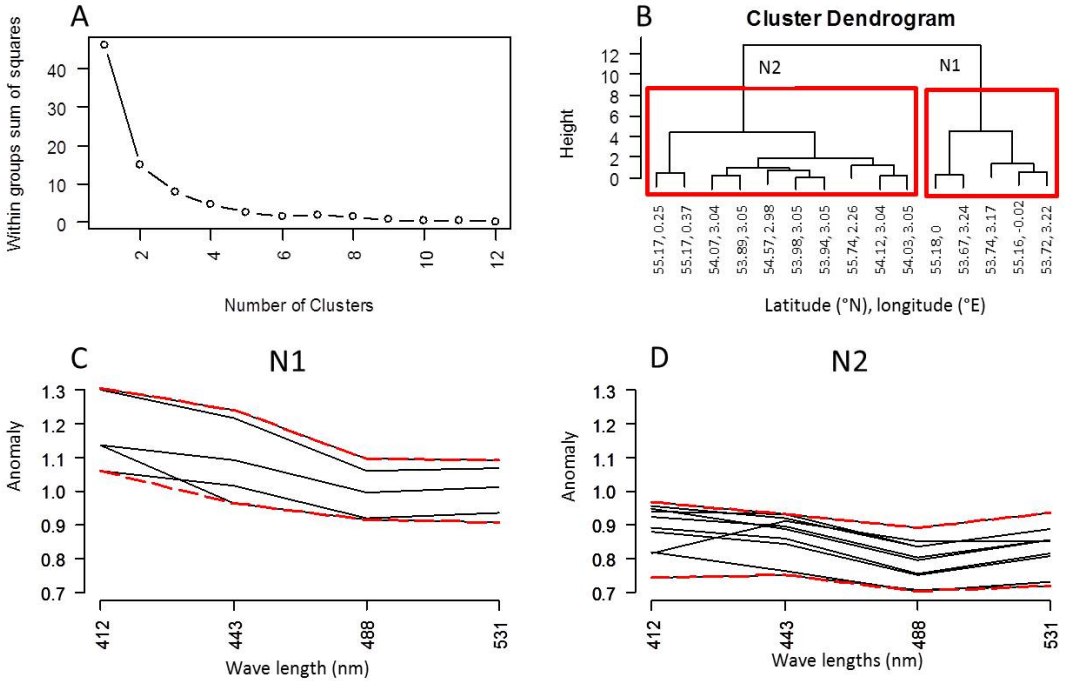

Fig. 1. Figure 9

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