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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.

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This study attempts to address issues inherent to the spatial and temporal variability of phytoplankton community structures in marine ecosystems. The authors present an interesting novel method to help improve estimates of phytoplankton community structure derived from satellite imagery using calibration from high-resolution flow cytometry data. The authors conducted a 4 days-survey of the phytoplankton communities in the North Sea using a scanning flow cytometer and compared their results with estimates derived from PHYSAT algorithm, a model that estimates the dominant phytoplankton

groups based on anomalies in satellite-based ocean color. While the authors used a interesting method a significant and collected a significant amount of data, I think the authors failed to present and discuss their results in a meaningful way. The authors did not address a specific question with that method and no substantial conclusion was reached. In my opinion, the manuscript is lengthy, there are too many figures (5-8 can be supplemental), and the discussion section does not discuss the findings in a broader context. The manuscript focuses too much on the scanning flow cytometer and not enough on the coupling between flow cytometry data and PHYSAT model output. The author's conclusions are 1) Abundances of phytoplankton vary along the transect (line 14-15), 2) the sum of the red fluorescence of each individual phytoplankton cells correlated with bulk chlorophyll estimates (line 15-18), 3) the high-frequency Cytobuoy enable 2-3 more matchups with satellite data than traditional, low-frequency water sampling. As is, these three main results feel short of my expectations considering the amount of data collected in this study. I was disappointed after reading the manuscript due to the high expectations built in the title, which are not met by the current version of the manuscript. I recommend the authors to rewrite the discussion and resubmit a more concise version of the manuscript.

Reply: We thank the reviewer for his interest in the PHYSAT method andhis expectation of a more detailed description of the importance in getting synoptical basin scale phytoplankton community distribution. However, our main aim is not to furnish a new PHYSAT method with an improve and exhaustive labeling adapted to the North Sea in this paper. We only want to show that cytometry observations can potentially be used in association with remote sensing data. It's the first time that specific composition (not only dominance based on pigments analysis) can be associated with specific anomalies. We don't have the objective to give a new PHYSAT method or a regional PHYSAT observation at this stage. To clarify this, the title was modified in order to decrease the level of expectation although the importance of getting high resolution phytoplankton community structure at the basin scale either for ecological or biogeochemical purposes is clearly mentioned in the discussion.

The suggested title is: "High resolution analysis of a North Sea phytoplankton community structure based on in situ flow cytometry observations and potential implication for remote sensing."

The paper describes the distribution of phytoplankton community structure, size and contribution to chlorophyll from high frequency in situ analysis, and then the data set enables a first attempt to label two different types (not all of them...) of PHYSAT anomalies with in situ automated flow cytometry. We think that presenting the in situ phytoplankton datasets (distribution, size and contribution to fluorescence) is still an important descriptive part useful for any ecological survey in the area or comparison with other datasets. Furthermore, at this stage of research and with such little sampling days, the use of the data set is not representative enough for any broad conclusion on phytoplankton distribution in the North sea. It is not possible with this little level of time/seasonal resolution to get substantial and mean full conclusion. It would overtake the capacity afforded by the present dataset. However, we really think that our work is interesting enough by showing, for the first time, that two sampling days of cytometry can furnish matchups for a first remote sensed anomalies labeling, with a description of the phytoplankton community instead of the phytoplankton dominant group only as previously described.

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