

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.

Anonymous Referee #2

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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 an

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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.

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