

Test-casing the integration of plankton imaging and genomics data for biodiversity indicator assessments in the Southern North Sea

Authors

Christina Pavloudi¹, Willem Boone², Luz Amadei Martínez², Cymon J Cox³, Hanneloor Heynderickx², Jonas Mortelmans², Carlota Muñiz², Stelios Ninidakis⁴, Ioulia Santi¹ and Klaas Deneudt²

¹ European Marine Biological Resource Centre (EMBRC-ERIC), Paris · ² Flanders Marine Institute [Vlaams Instituut voor de Zee (VLIZ)] · ³ Centro de Ciências do Mar, Universidade do Algarve, Faro · ⁴ Institute of Marine Biology, Biotechnology and Aquaculture (IMBBC), Hellenic Centre for Marine Research (HCMR), Heraklion

Presenting author

Christina Pavloudi

Keywords

eDNA, EOVs, MSFD, plankton indicators

Abstract

Planktonic organisms are the most abundant organisms in the oceans and are considered to be excellent indicators for environmental changes; they are the basis of the food web and, thus, ecosystem functioning. Changes in plankton diversity have been used extensively as an indicator of ecosystem health. Two of the Essential Ocean Variables (EOVs) (i.e., “Phytoplankton biomass and diversity” and “Zooplankton biomass and diversity”), as well as one Essential Climate Variable (ECV) (i.e., “Biological/Ecosystems: plankton”), are focusing on plankton. In addition, plankton is incorporated in the assessment of Marine Strategy Framework Directive (MSFD) Good Environmental Status (GES) (e.g. Descriptors 1, 2 and 5). Further, assessments of planktonic groups that perform similar functional roles, called “lifeforms”, are also used to evaluate GES under the Convention for the Protection of the Marine Environment of the North-East Atlantic (OSPAR). eDNA-based biodiversity observations are now being employed on a large scale, within coordinated networks at European level such as the European Marine Omics Biodiversity Observation Network (EMO BON). Despite eDNA-based observations currently not being used as data source for MSFD assessments, the coordinated nature of EMO BON offers great potential for their use for large-scale assessments. The aim of this study is to test-case EMO BON eDNA data against image-based observations to identify the similarities between the two methodological approaches and the potential for eDNA to serve as an input source for EOV assessments or MSFD indicators’ calculation. We used phyto- and zooplankton imaging data collected within

the scope of the VLIZ biodiversity observatory, which are already being used for MSFD reporting at national level. The considered time series consists of biodiversity data from seventeen stations which are monitored in the Belgian part of the North Sea (BPNS) on a monthly or seasonal basis (zooplankton: since 2014; phytoplankton: since 2017). Phytoplankton (55-300 μm) was analysed with a FlowCAM, and zooplankton ($>200 \mu\text{m}$) with a ZooScan. The identification of these images (zooplankton: order level; phytoplankton: genus level) was done using automatic image-recognition analysis, followed by manual validation. eDNA data was obtained from one EMO BON observatory in the BPNS where water samples are collected bi-monthly since 2021, filtered sequentially (0.2-3 μm and 3-200 μm) and sequenced using shotgun metagenomics. Part of the study's computational analyses will be conducted on the European Digital Twin Ocean (EDITO), and make use of tools (developed for the Demonstrator Use Cases of DTO-BioFlow project) facilitating the calculation of pelagic habitat indicators. This (proof of concept) study is a practical assessment of the suitability and validity of eDNA data for calculation of plankton based indicators and EOVs. It will provide insights on functional diversity in the Southern North Sea and showcase the potential of this approach to be replicated in other areas at European level, capitalising on the EMO BON network. The validity of the information deriving from both the eDNA and the imaging approaches will allow a better and holistic understanding of coastal biodiversity and its status.