

Benthic eDNA metabarcoding provides accurate assessments of impact from oil extraction, and ecological insights

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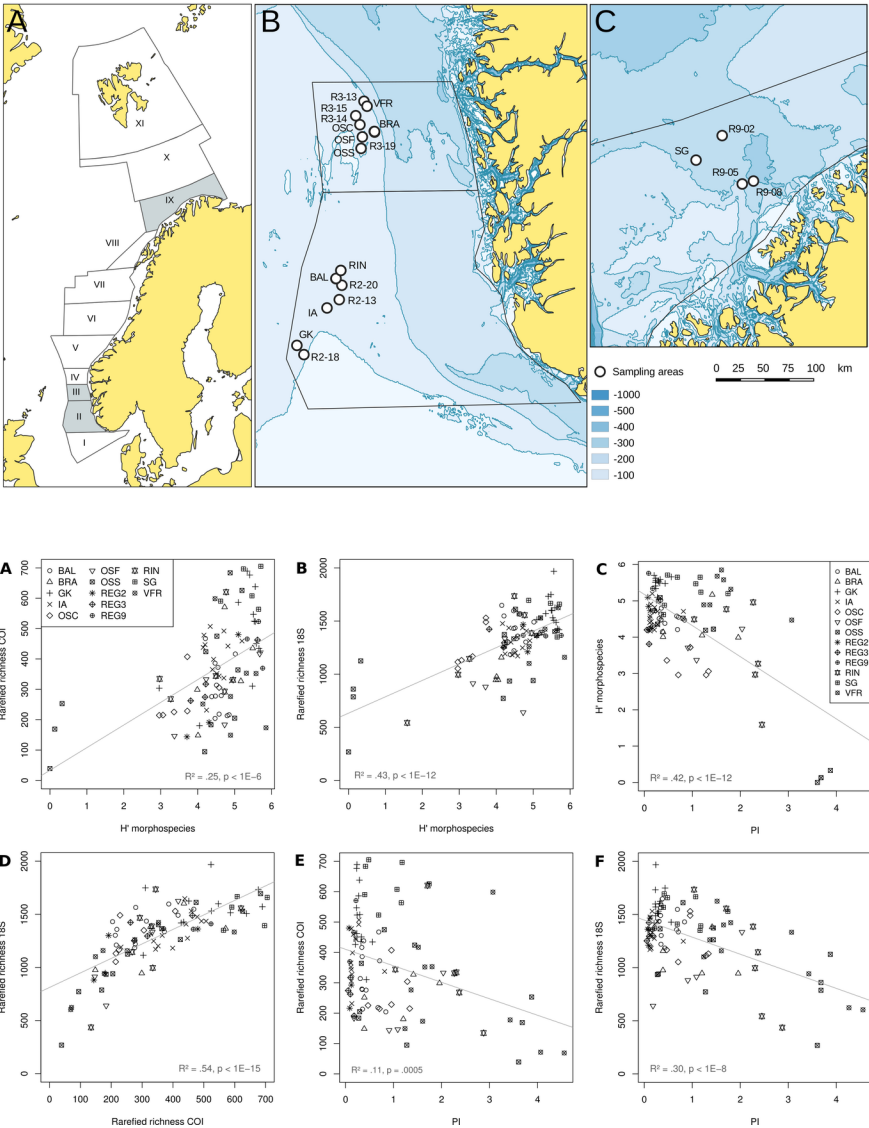
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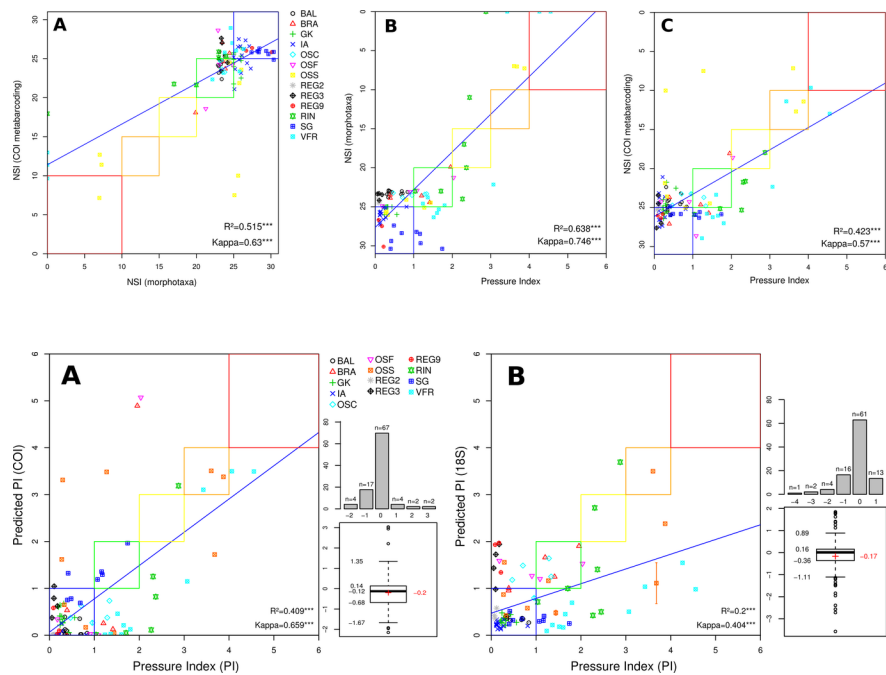
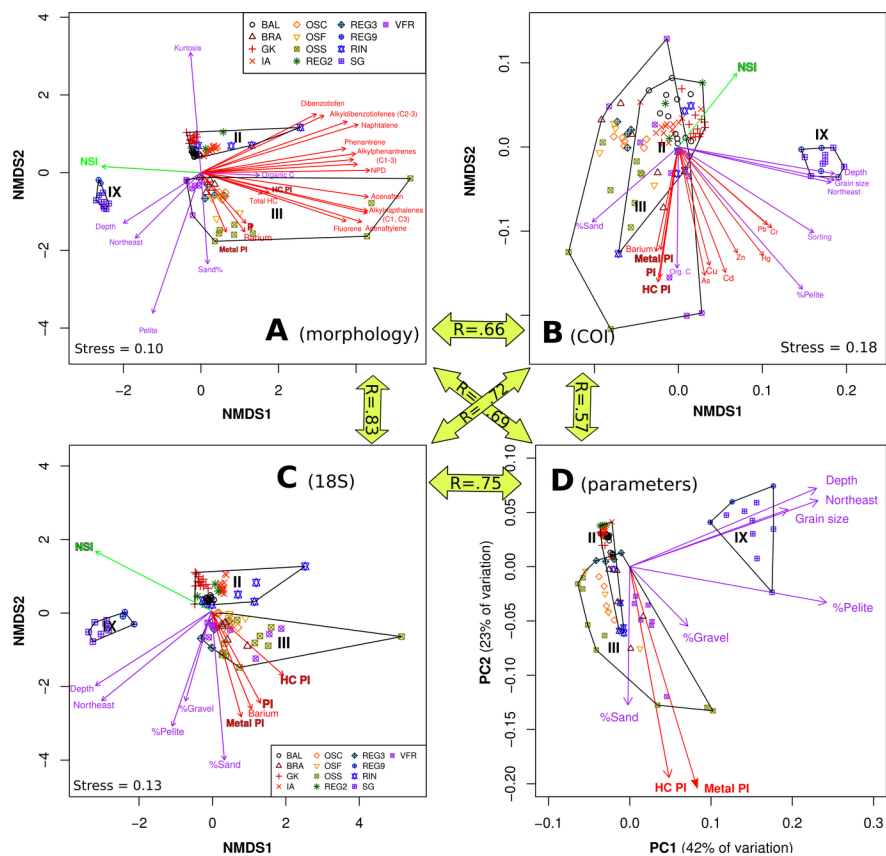
Abstract

Apart from its contribution to climate change, offshore oil and gas extraction is also a potential threat to the diversity and function of marine ecosystems. Routine monitoring of the environmental status of affected areas is therefore critical for proper management. While current morphology-based monitoring is relatively time-consuming, costly and prone to identification bias, environmental DNA metabarcoding offers an attractive alternative, including for impacts of oil drilling, extraction or spills. However, to be ready for routine monitoring, its performance needs to be demonstrated, through agreement with assessments based on physicochemical measurements and current bioindicators. To this end, we applied metabarcoding to sequence the metazoan and total eukaryotic benthic components. We targeted an range of sites, from high to low impacts, located near active production platforms and reference sites, in the North and Barents Seas. Alpha diversity and community structure of both datasets correlated strongly with a physicochemical pressure index (PI), based on total hydrocarbons, PAH16, Ba and Cu. The macroinvertebrate-based Norwegian Sensitivity Index (NSI) based on the COI metabarcoding data also agreed well with morpho-taxonomy based values, and with PI. Further, we identified a set of bioindicator taxa from both metabarcoding datasets, to develop novel biotic indices and demonstrate their predictive performance using cross-validation. Finally, we compared co-occurrence networks from impacted v less disturbed sites, to improve the understanding of the ecological consequences of impacts. Our study demonstrates that metabarcoding is comparable to the morpho-taxonomic approach in terms of accuracy, and could eventually be used to replace it, given further efforts.

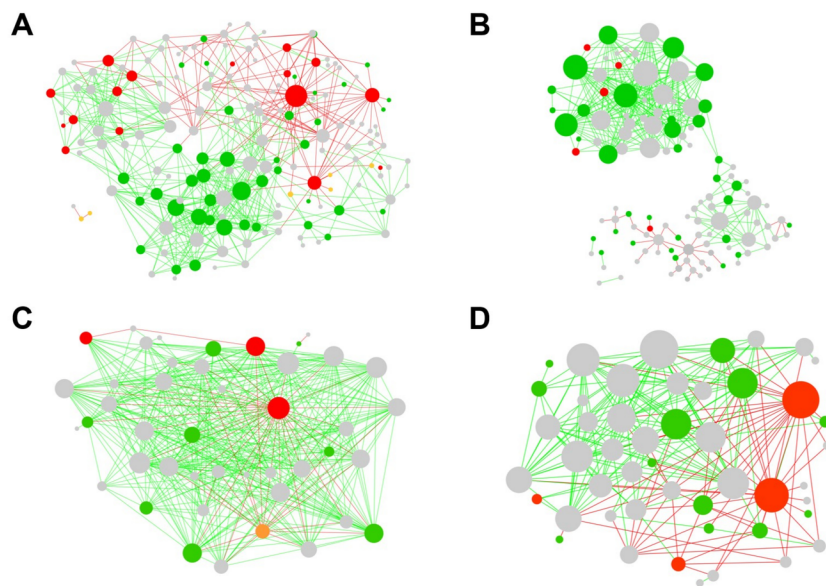
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