



Benthic monitoring of salmon farms in Norway using environmental DNA metabarcoding

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Environmental DNA metabarcoding allows characterizing benthic communities using DNA isolated from the sediments. Here, we apply eDNA approach to assess the environmental impact of salmon farming on benthic communities. Traditionally, benthic monitoring is based on the diversity of macro-invertebrates that are sorted, morphologically identified and counted. This traditional approach is time-consuming, expensive and requires a taxonomic expertise, which is rare. To overcome these issues, we develop rapid and highly sensitive genetic tests that allow measuring the benthic diversity based on eDNA analysis.



Target species

Two major groups of benthic meiofauna have been examined:



Foraminifera

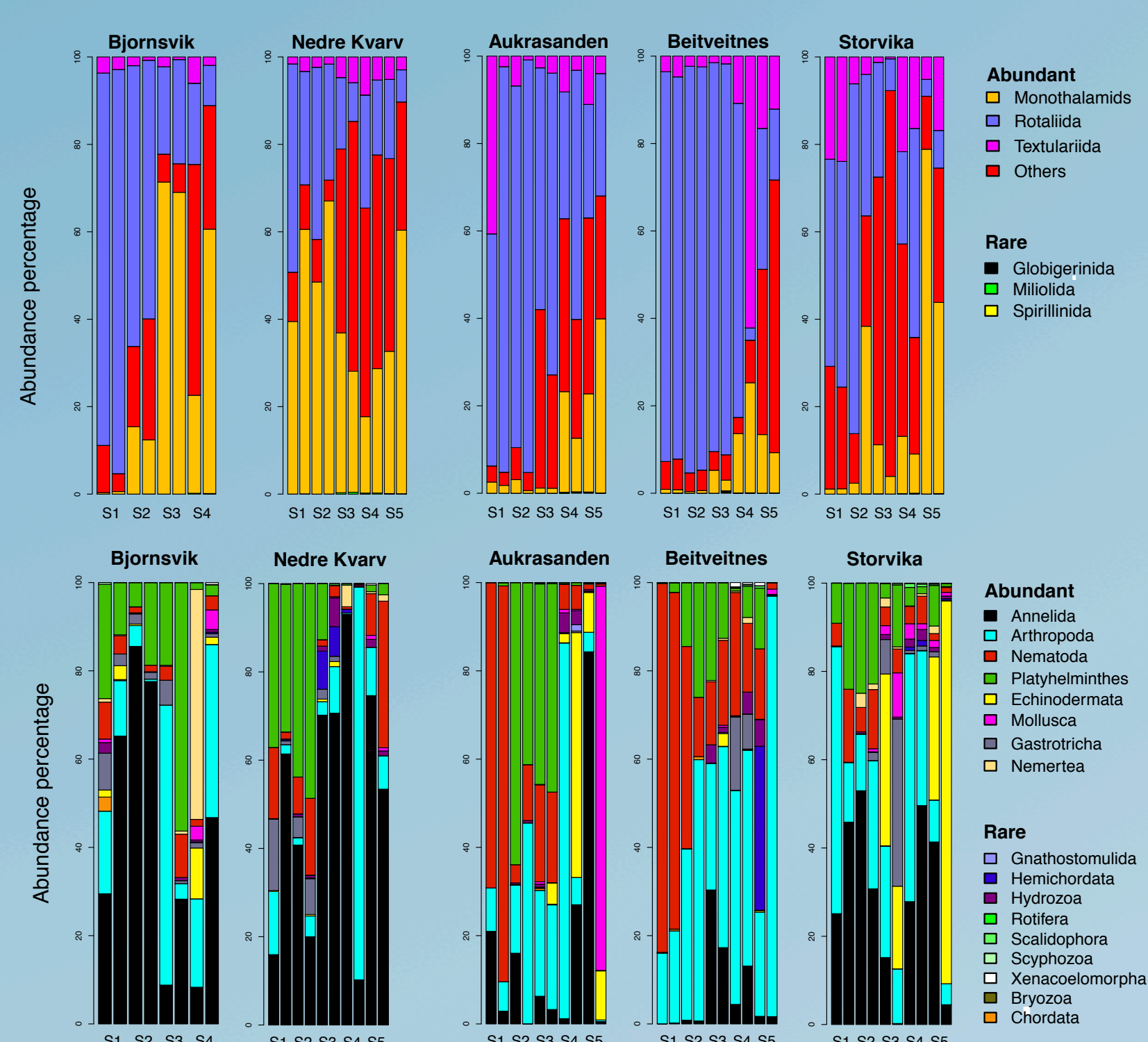


Metazoans

Why meiofauna? Because meiofauna species are:

- abundant,
- highly diverse,
- and sensitive.

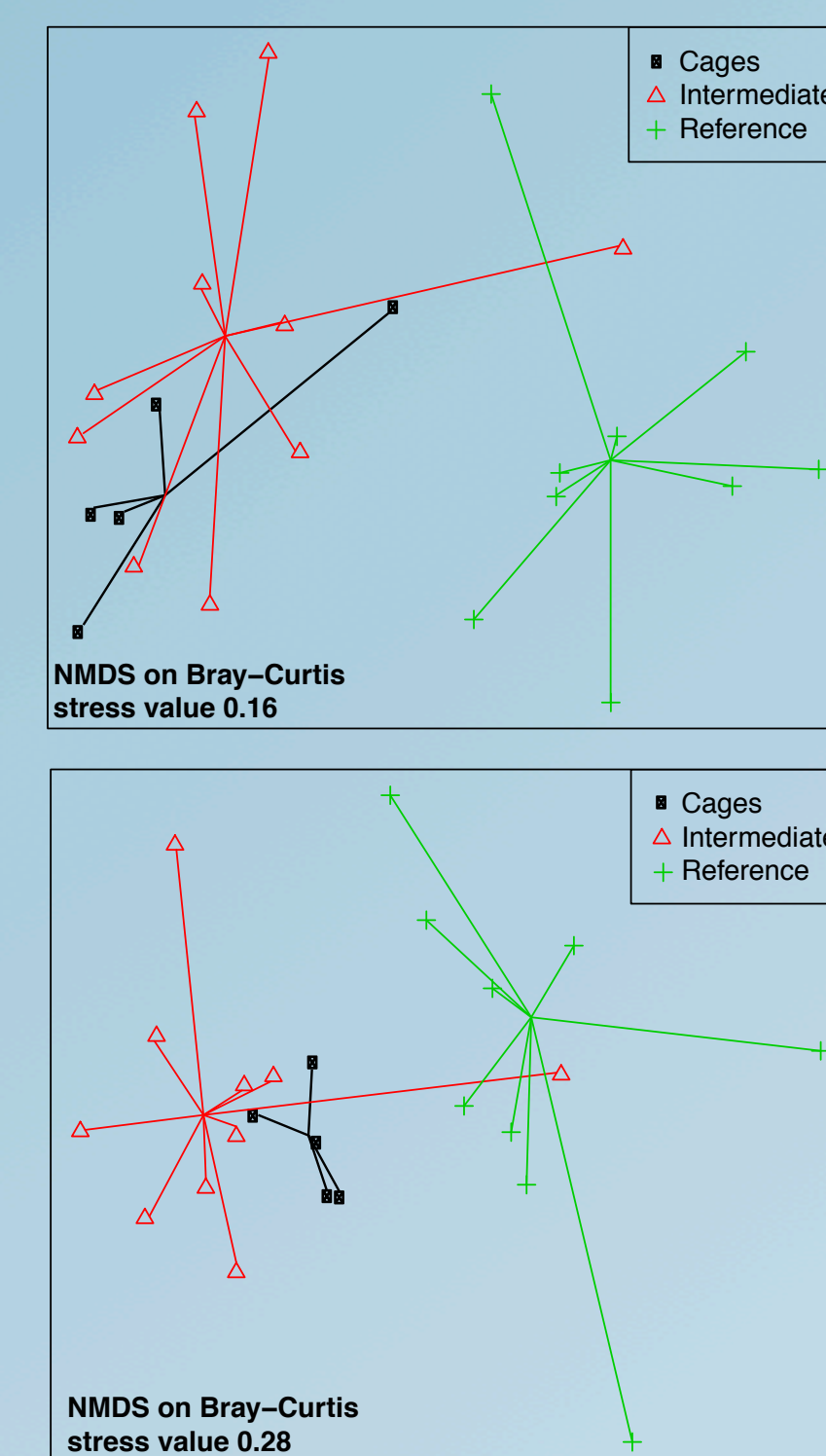
Taxonomic composition



Variable regions of 18S rRNA gene were used (V1/V2 for metazoa and helix 37F for foraminifera).

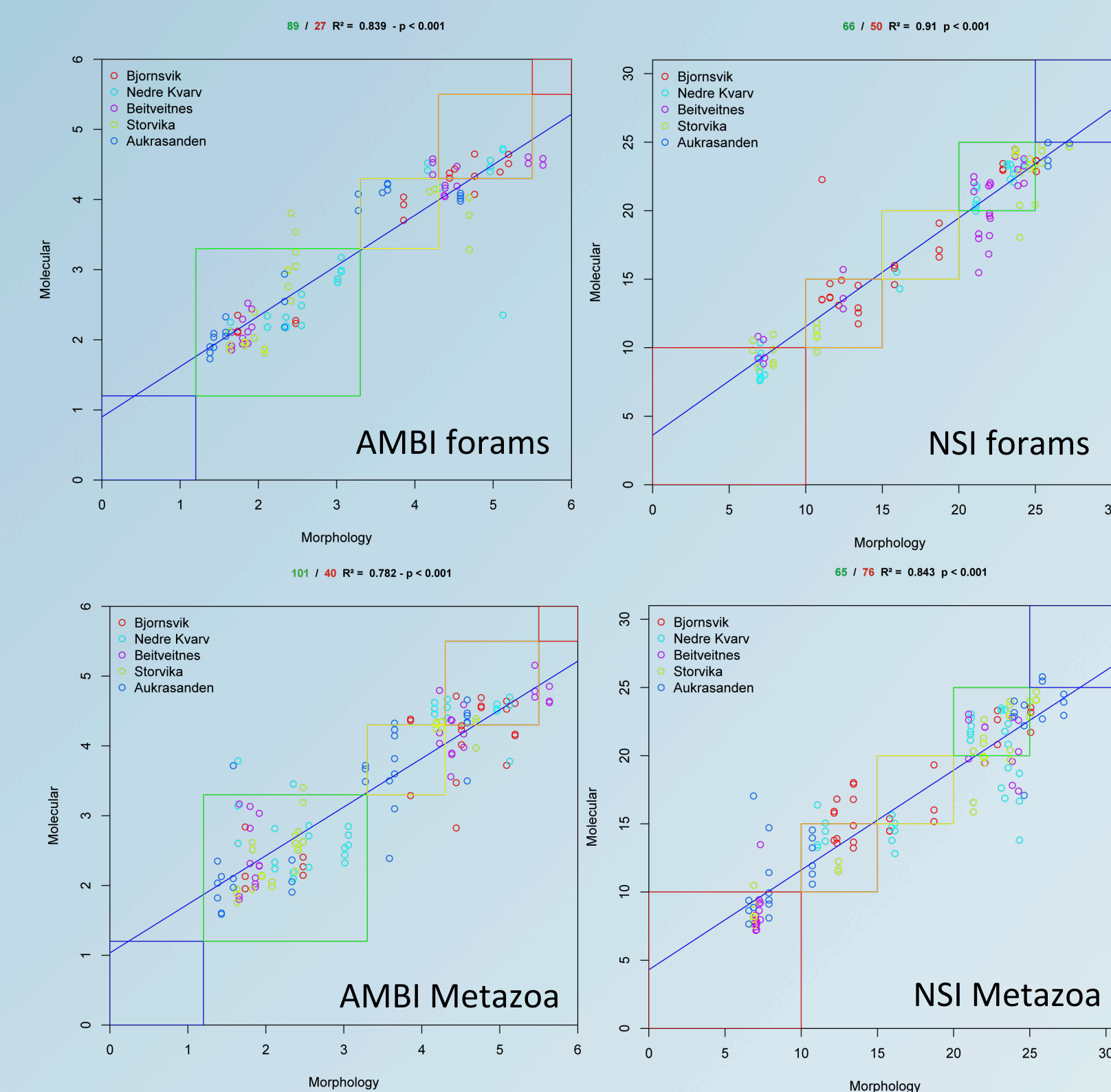
The proportion of major groups changes between sites and between stations. Annelids, copepods, and nematodes, and dominate the metazoan assemblage.

Testing the response to organic enrichment



Foraminiferal and metazoan assemblages are different in stations close to the cages (black) and in reference stations (green).

Predicting molecular indices



The values of molecular indices (AMBI, NSI) predicted by machine learning from foraminiferan and metazoan DNA sequences provide very similar assessment to indices based on macrofauna morphological studies.

Advantages of eDNA benthic monitoring

- time saving** - allowing faster assessment of benthic biodiversity and more rapid certification
- cost-effective** - allowing economy for salmon producers and consulting agencies
- sensitivity** – allowing better risk assessment and evaluation of ecosystem based on cumulative evidence
- automatization** - allowing more reliable standardized processes and results
- accuracy** – using comprehensive global database instead of personal expertise

Further readings:

Pawlowski J, Esling P, Lejzerowicz F, Cordier T, Visco JA, Martins CIM, Kvalvik A, Staven K, Cedhagen T (2016) Benthic monitoring of salmon farms in Norway using foraminiferal metabarcoding. *Aquacult Environ Interact*.

Lejzerowicz F, Esling P, Pillet L, Wilding TA, Black KD, Pawlowski J. (2015) High-throughput sequencing and morphology perform equally well for benthic monitoring of marine ecosystems. *Sci Rep*. 2015 5:13932.

Pochon X, Wood SA, Keeley NB, Lejzerowicz F, Esling P, Drew J, Pawlowski J. (2015) Accurate assessment of the impact of salmon farming on benthic sediment enrichment using foraminiferal metabarcoding. *Mar Pollut Bull*. 100(1):370-82.

Pawlowski J, Esling P, Lejzerowicz F, Cedhagen T, Wilding TA. (2014) Environmental monitoring through protist NGS metabarcoding: assessing the impact of fish farming on benthic foraminifera communities. *Molecular Ecology Resources* 14(6):1129-1140.