One fish calender in a metabarcoding era – lessons from a temperate bayment

(Reliability of the quantitative information of metabarcoding fish diversity)

DNA metabarcoding is an efficient method for measuring biodiversity, but the process of initiating long-term DNA-based monitoring programmes, or integrating with conventional programs, is only starting.

Sequence numbers are impacted by the widely varying sizes of organisms, variation in PCR amplification efficiency or primer bias, and differences in copy number of the target rRNA genes, among others. Acknowledging this,

One major concern for both science and management communities is … Statistical comparison of temporal and spatial patterns of variation based on molecular metabarcoding and morphological taxonomic analysis is an important step toward integration and application of metabarcoding results for ocean ecosystem assessment and management.

The challenge of quantification of taxa (either abundance or biomass) based on metabarcoding is of central importance for applications for ocean monitoring and assessment

1. Provide an eDNA fish calendar to fill in knowledge gaps regarding finfish community composition when traditional sampling is not available in cold seasons. Provide suggestions on best practices for effective environmental DNA sampling especially when biomass is low, for which knowledge is still lacking.
2. Temporal variability in a relatively open coastal estuarine (including diversity indices?) Time-series studies is essential in understanding spatiotemporal patterns of microbial communities and the environmental factors shaping these patterns (Duan et al 2018). Macroorganisms such as finfish, more mobile and with many underlining factors contributing to their distribution, can be expected to demonstrate higher variability in temporally. Interpreting data from restricted bodies of water systems such as ponds and lakes is subjected to potentially less uncertainties as opposed to open systems in coastal and oceanic environments.
3. Spatial variation of finfish at three habitats representing different oyster farming techniques.
4. Demonstrate the potential effects of sampling periods on spatiotemporal implications by subsampling the dataset.
5. Evaluate the potential effects of a changing climate through finfish eDNA distribution in the context of a coastal embayment.

Part of the reason why monitoring benthic communities is done sparsely is because traditional methods are often time and effort-consuming, ignore rare and cryptic species, and often require SCUBA or trawling/netting gear (Deiner et al. 2017). It also requires taxonomic expertise for accurate species identification (Dickens et al. 2011). These difficulties prevent the collection of continuous, quantitative, comprehensive, and long-term data of biodiversity. The ever-decreasing price of second-generation DNA sequencing provides alternatives to monitor biodiversity. Environmental DNA (*e*DNA) is one of these alternatives to infer species richness (Taberlet et al. 2012b, Creer et al. 2016).