



Metabarcoding of marine zooplankton communities in the North Sea using nanopore sequencing

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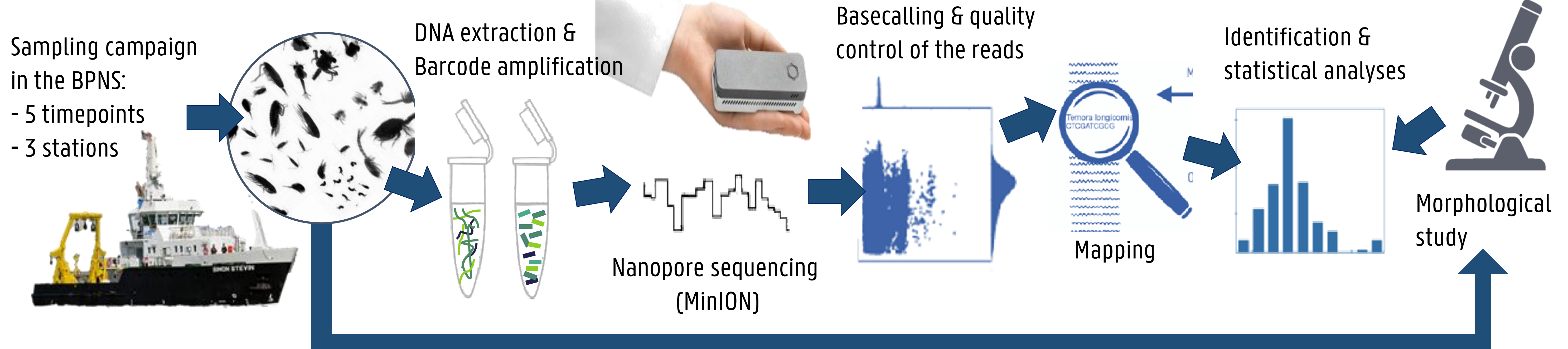
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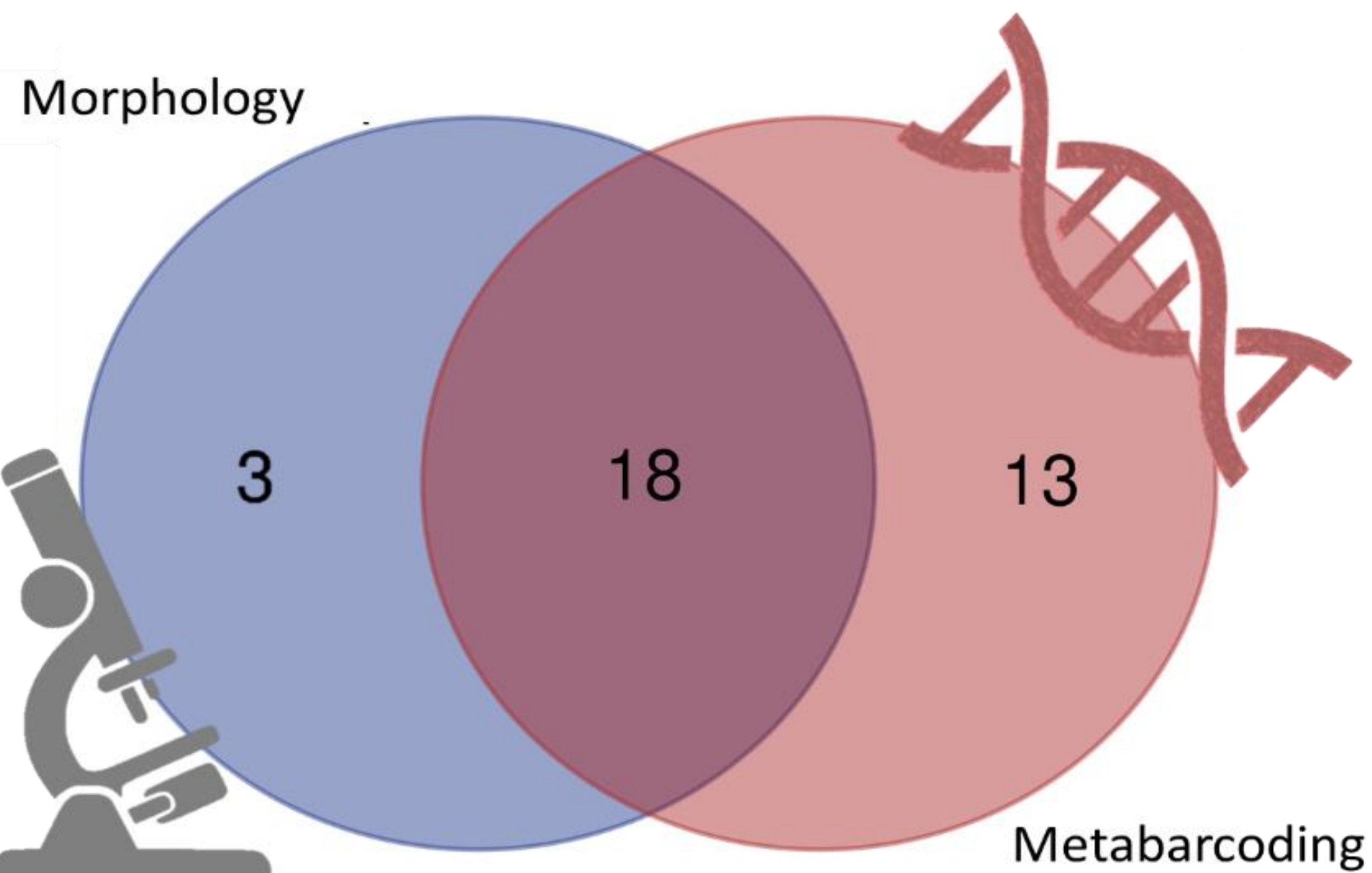
Introduction

- Although easily collected in large numbers, the subsequent processing and identification of zooplankton samples has usually been a barrier to large-scale biodiversity assessments.
- Our objective was to establish an efficient method for capturing the biodiversity of the zooplankton community across space and time in the Belgian Part of the North Sea (BPNS) using nanopore sequencing.

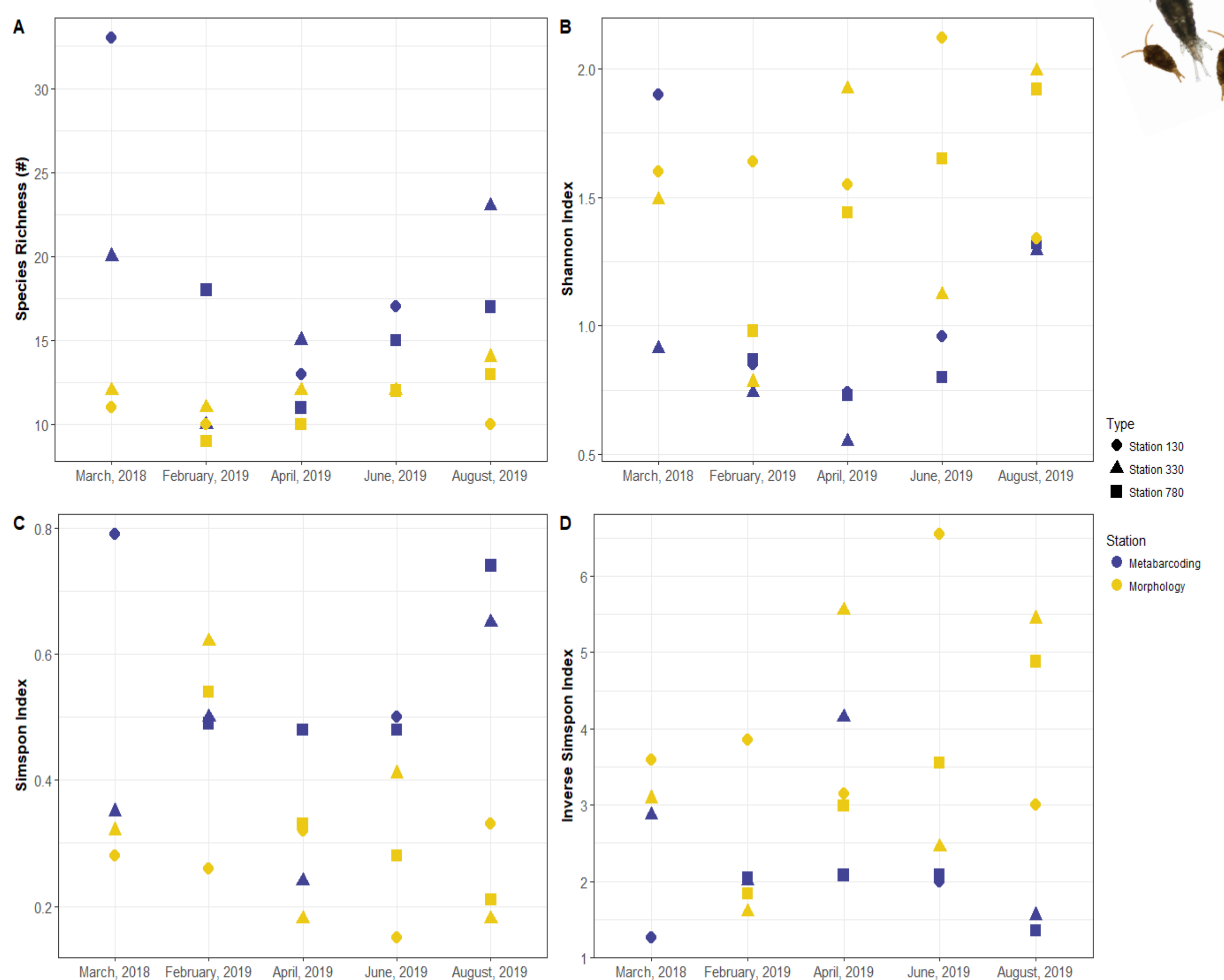
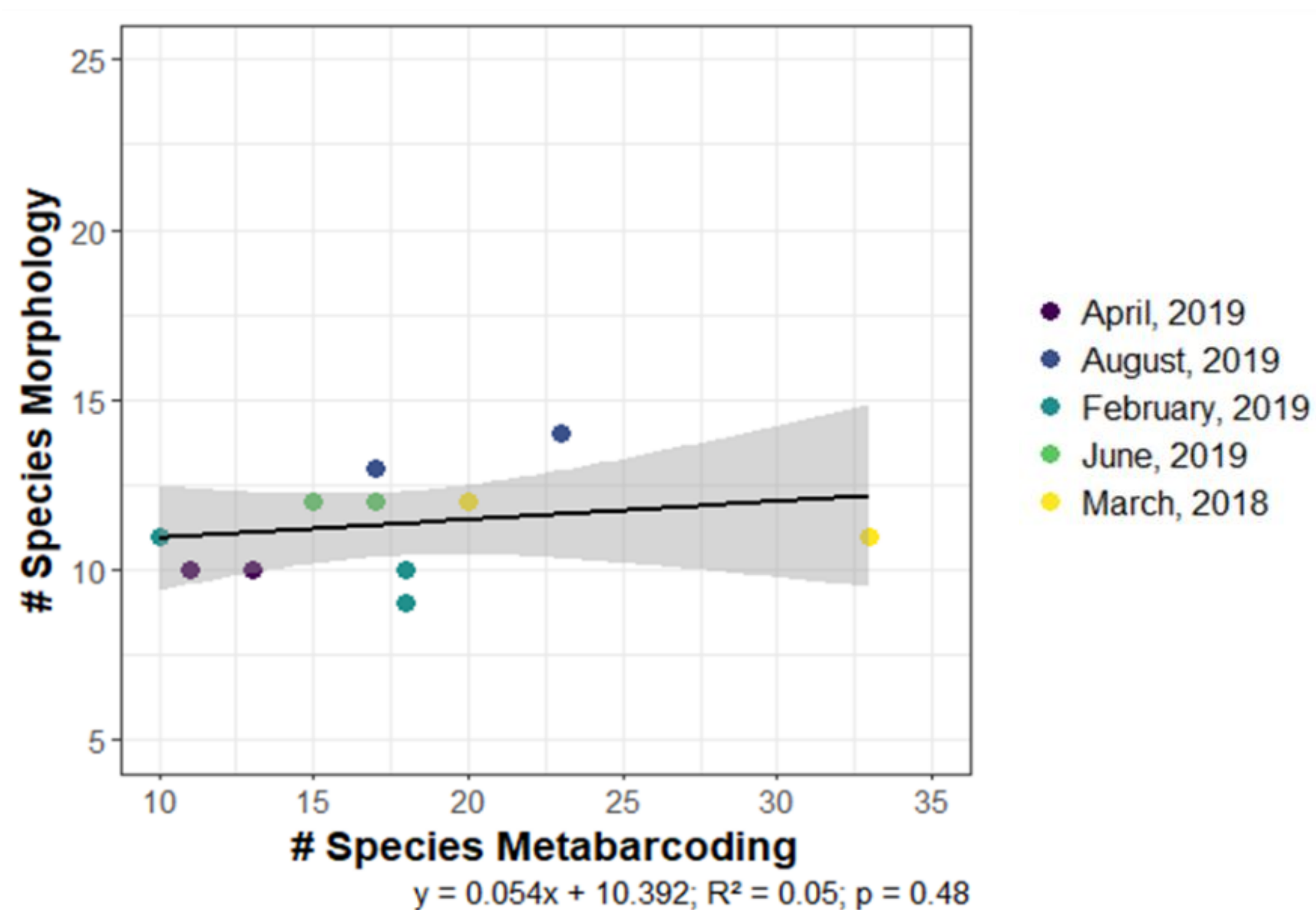
Material & Methods



Results & Discussion



Venn diagram of number of taxa detected by each method. The numbers are based on lowest morphological annotation level



Above: Comparison of a diversity measures for both the metabarcoding and the morphological approach. A) Species Richness. B) Shannon Index. C-D) (Inverse) Simpson Index.

Left: Comparison of species number in water samples for both the metabarcoding and the morphology approach.

Conclusions

We have demonstrated the feasibility of detecting taxa with a higher resolution using nanopore seq. Metabarcoding allowed for comparisons of diversity and community composition, but not all groups were detected.

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