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Where meiofauna?
An assessment of interstitial fauna at a Belgian beach

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Introduction

Although meiofauna have an important role in global ecosystems, they are often neglected in biodiversity assessments. Their high species richness and rapid response to environmental change make them promising targets for ecological and biomonitoring studies. Meiofaunal organisms measure roughly between 0.045 and 1 mm in size, but no fixed size definition exists. Meiofauna are exceptionally diverse and encompass representatives from all major phyla. The organisms typically reside in the space between sediment grains.

Meiofauna are often overlooked because of their small size. Furthermore, expertise in meiofauna taxonomy is limited by several factors, including the large number of unknown species (Linnean shortfall) and the lack of researchers in the field, combined with the lack of studies on individual meiofaunal taxa (Prestonian shortfall). This study marks a new effort to characterize meiofaunal communities along the Belgian coast, an area largely unexplored in this respect. The intertidal zone of the Small Beach in Ostend serves as a first case study for this purpose.

Primary goal

Document and report on the diversity of meiofaunal communities present and identify any emerging seasonal patterns.
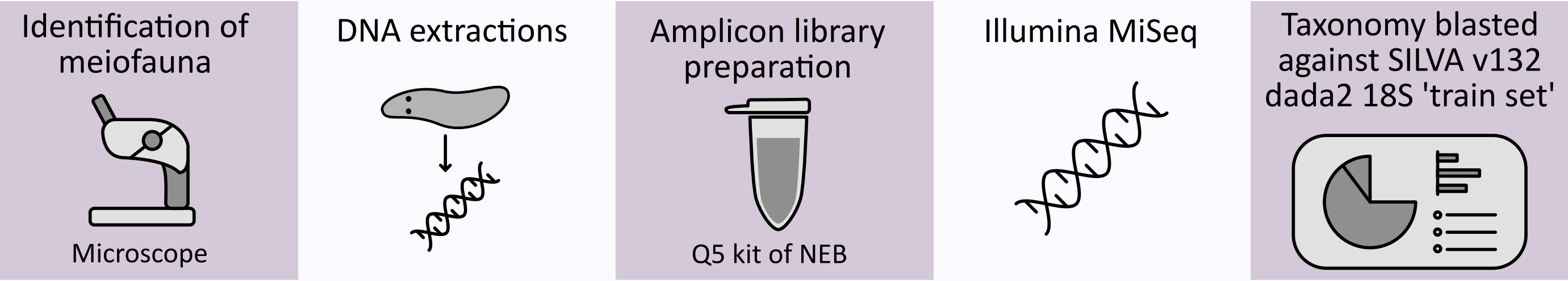
Materials and Methods

Five sampling campaigns were conducted: a pilot sampling in July (12/07/2022), followed by official samplings in August (30/08/2022), September (30/09/2022), November (12/11/2022), and December (10/12/2022).
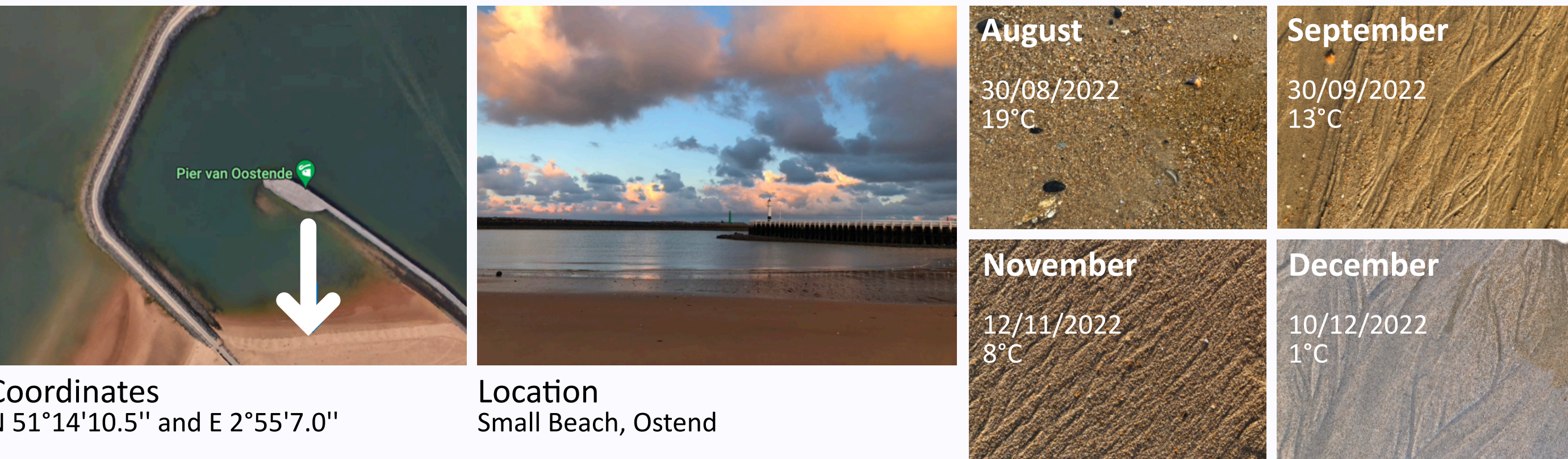
Meiofauna were extracted using the MgCl₂-method.

1. Sandy   2. Anesthetized   3. Rinsed   4. Awake
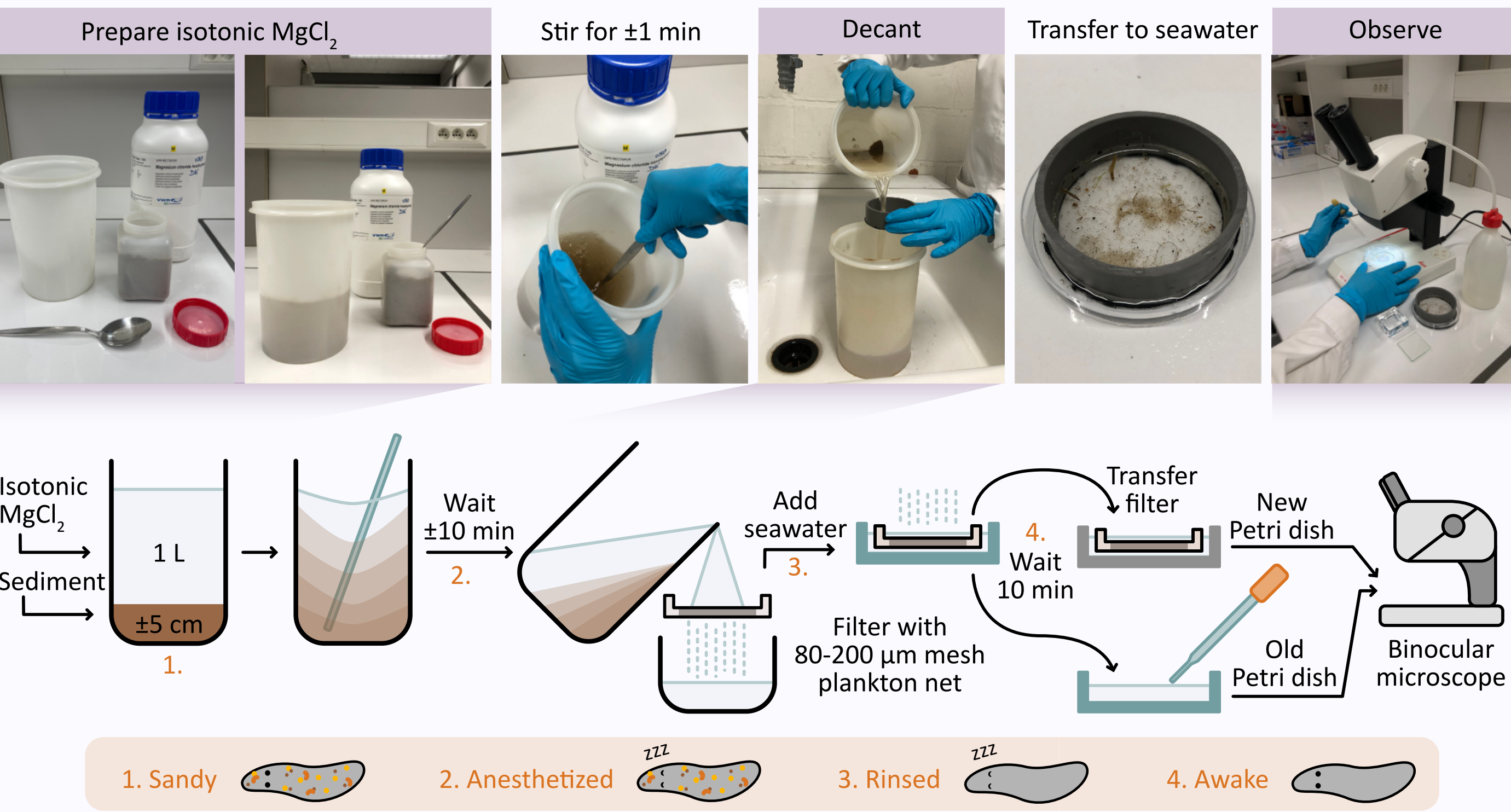
Samples were fixated in liquid nitrogen and stored in the -80°C freezer for metabarcoding. DNA extractions were performed following a salting-out protocol. Amplicon libraries for Illumina MiSeq Sequencing were prepared. Two primer pairs were selected for metabarcoding, targeting 18S (SSU-F04; (SSU)R22mod) and COI (mICOIintF; LoboR1) regions. As the COI primers did not yield sufficient results for any of the collected samples, downstream sequencing was performed only for ribosomal regions. After index PCR, all samples were pooled. Sequencing was carried out on an in-house MiSeq machine, following manufacturer's instructions. After sequencing, the guidelines of DADA2 for big data were followed. Taxonomy was blasted against the SILVA v132 dada2 formatted 18S 'train set'.

Identification of meiofauna — Microscope
DNA extractions
Amplicon library preparation — Q5 kit of NEB
Illumina MiSeq
Taxonomy blasted against SILVA v132 dada2 18S 'train set'

Morphological results

Meiofaunal samples were collected once a month. All samples were collected during low tide at the same locality. Sampling date and time were selected to maintain a maximum water-level difference of 0.15 meters. Location coordinates, time, weather conditions (wind and temperature), water level, and an estimate of the total number of algae present on the beach were recorded for each sampling. A total of 1,742 organisms were retrieved. The peak number of organisms was observed in August, whereas the lowest count was recorded in December. In August, Acoela and Nematoda displayed the highest abundance, while Polychaeta was the dominant group in November. Copepods reached a peak abundance in December, whereas the isopods exhibited their highest count in September and November. Among all the organisms encountered during the samplings, Platyhelminthes was the most frequently observed taxon. Isopods were the least commonly found organisms throughout the sampling period.
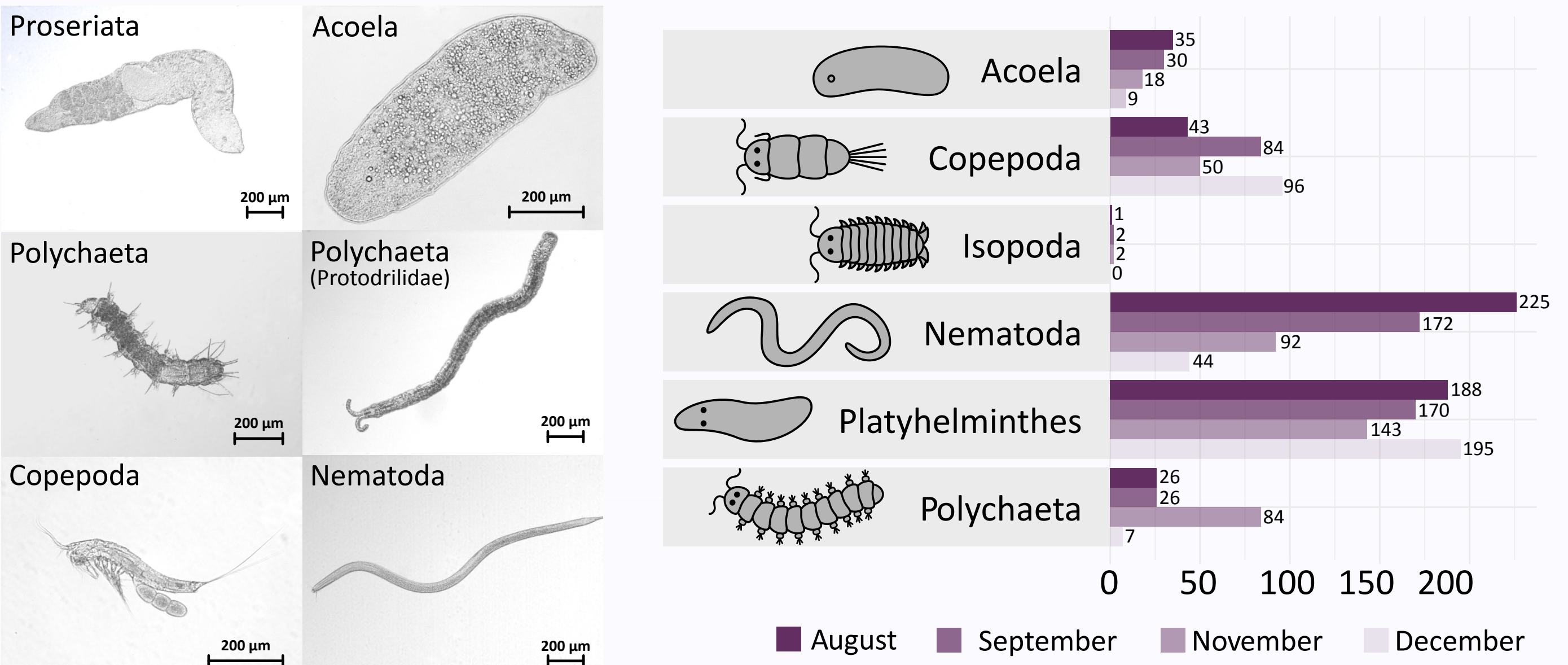
Molecular results

Through metabarcoding of the 18S ribosomal region, a preliminary biodiversity assessment was conducted, yielding a total of 106 Amplicon Sequence Variants (ASVs). After filtering out rare reads, 65 metazoan ASVs were retained: 12 representing Polychaeta, 17 Proseriata (Platyhelminthes), 15 Copepoda, 4 Acoela, 16 Nematoda and 1 representing Rhabdocoela (Platyhelminthes). Identification of the ASVs through blasting, generated a rather low species richness. The highest species richness was observed among Proseriata and Nematoda, each comprising six different species. Additionally, four different species of Polychaeta and Copepoda, two species of Acoela, and one species of Rhabdocoela were identified.
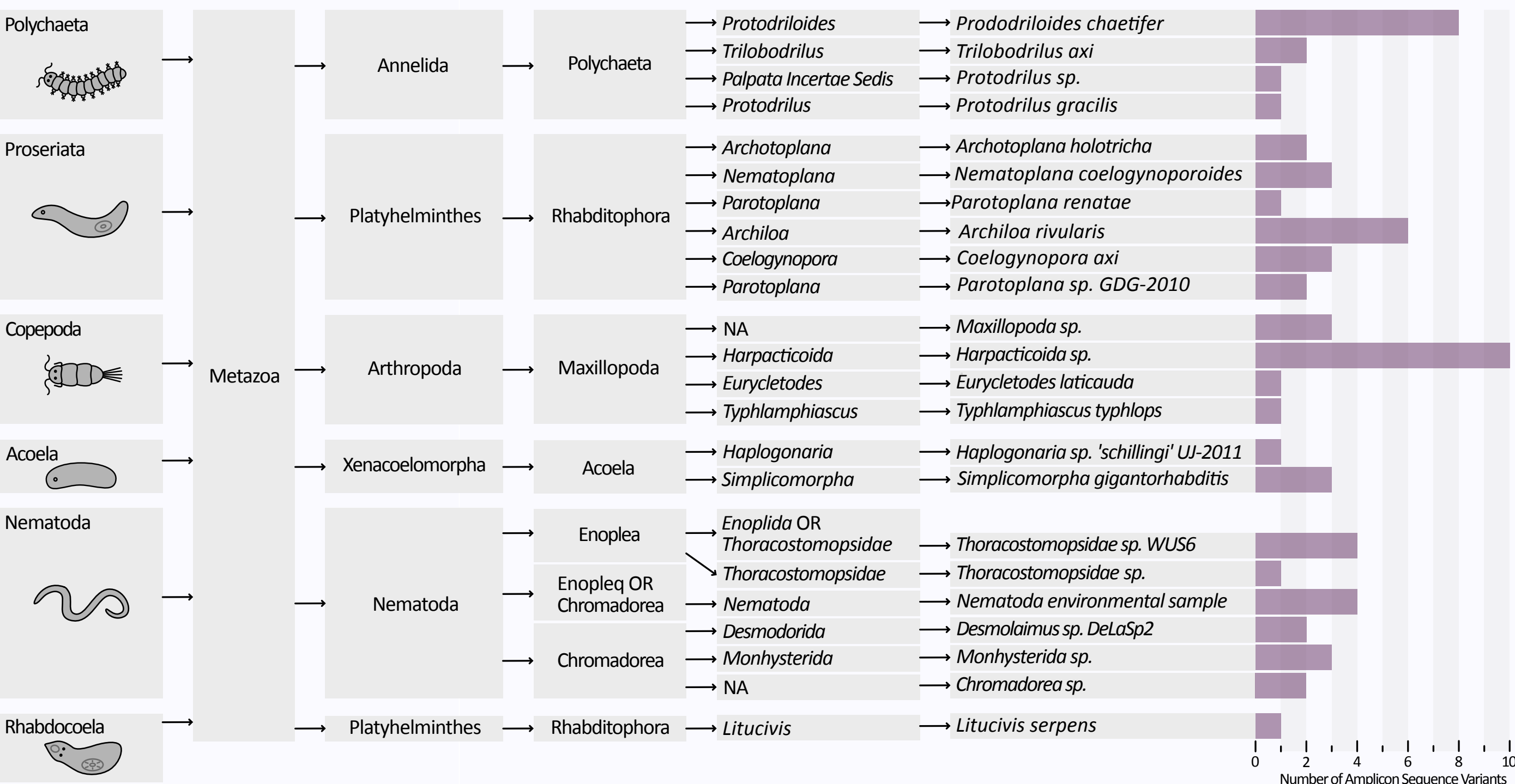
Conclusion

This study marks the first assessment of meiofaunal communities at the secluded 'Small Beach' in Ostend. Abundance patterns were evaluated morphologically, highlighting Proseriata, Polychaeta, Nematoda, Copepoda, and Acoela as the dominant taxa. While a potential seasonal trend was perceptible, quantifying it statistically awaits future investigations with a more extensive, time-sensitive dataset. The interrelationship between diversity, abundance patterns, and the observed abiotic factors remains uncertain, and should be assessed in future repeated studies. Ribosomal (SSU) metabarcoding provided a finer taxonomical resolution of the meiofaunal diversity at the beach, revealing a relatively modest species richness in the investigated area. Proseriata and Nematoda exhibited the highest diversity, each comprising six distinct species. However, limitations in species-level assessment persist due to the overall limited availability of reference data for meiofauna. Hence, we argue that the combination of morphological and molecular methodologies is paramount to yield a robust estimation of the fauna present.

Acknowledgements