FACULTY OF BIOSCIENCE ENGINEERING

Scaling Up Biomonitoring: Metabarcoding-driven Assessment of Eukaryotic Biodiversity and Community Shifts Under Local Emission Pressures

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Current limitations in environmental monitoring

Water Framework Directive

- Requires the monitoring of biodiversity or ecosystem structure to assess ecological status.

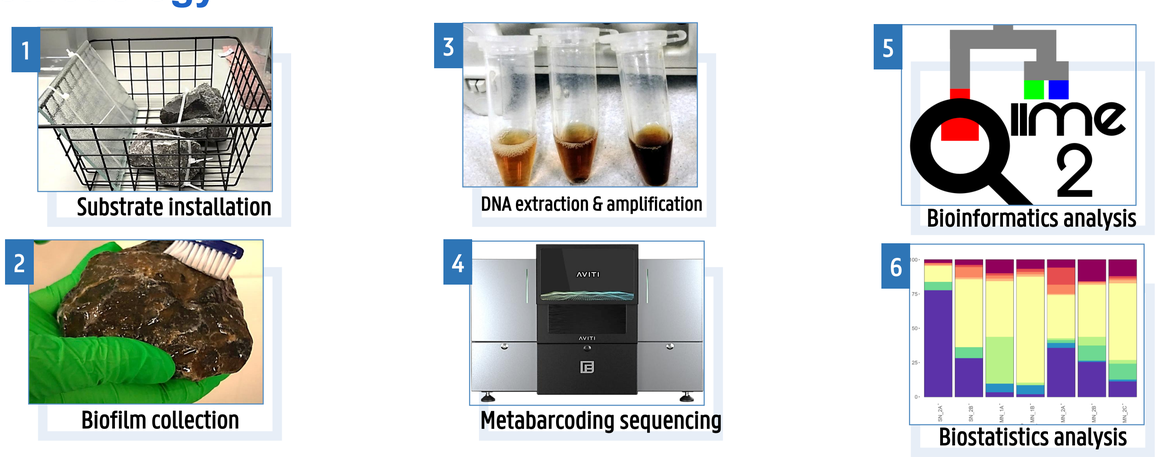
Conventional environmental biodiversity monitoring

- Apply a few indicator groups of organisms with a proven history of sensitivity to contamination (e.g., diatoms).
- Targeted species provide an incomplete picture of the community's full taxonomical range and its diverse contaminant response profile.
- Biodiversity indices condense complex community structure into simple values, masking important ecological features such as taxonomic turnover, functional replacement, and stressor-driven shifts, all essential to understand the effects of contaminants.

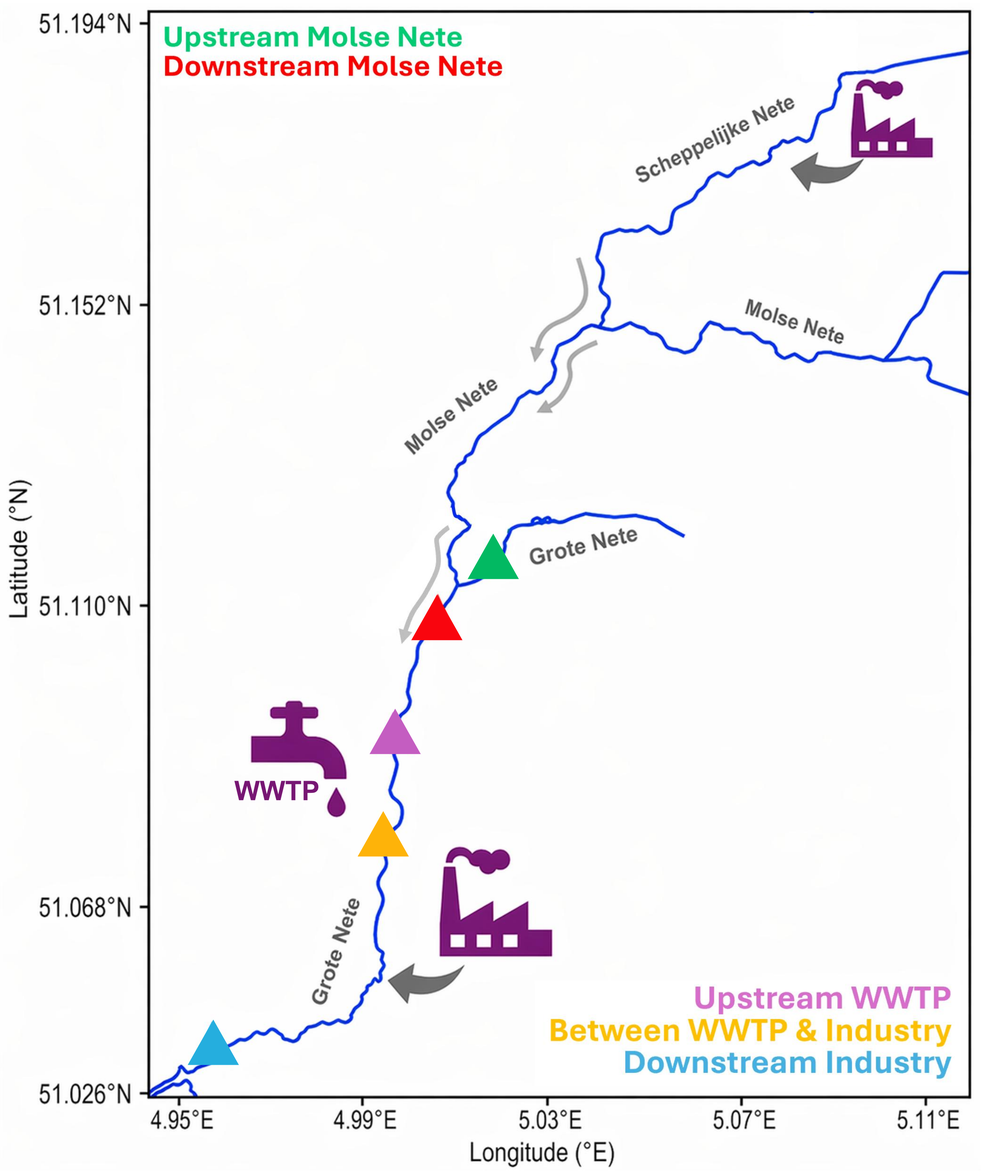
Filling the gap: AQUADIVERS project

- Apply **eukaryotic 18S rRNA metabarcoding** as a **holistic screening tool** to capture **multi-phyla responses** to local pollution, by **combining overall and phylum-level diversity.** As the number of sequences often reflect biomass and functional dominance, this approach improves comparability across sites, while **shifts in relative abundance** reveal **ecologically meaningful community changes**.

Methodology



Study Area: Grote Nete (Flanders, Belgium)

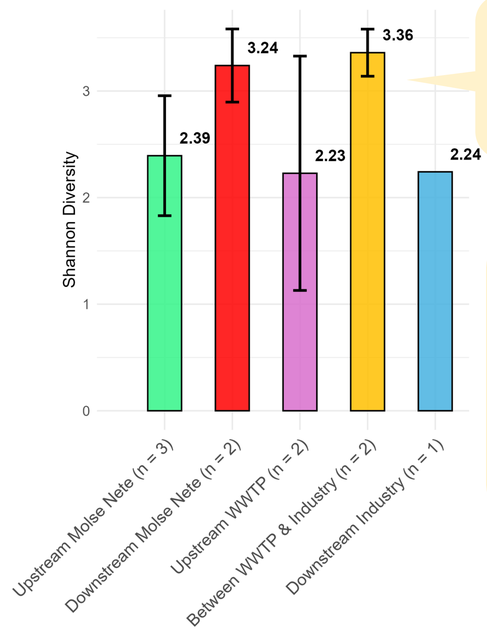


Preliminary results

Overall Eukaryotic Shannon Diversity

Shannon diversity was computed considering all species detected at each site.

(Whiskers represent the standard error - SE).



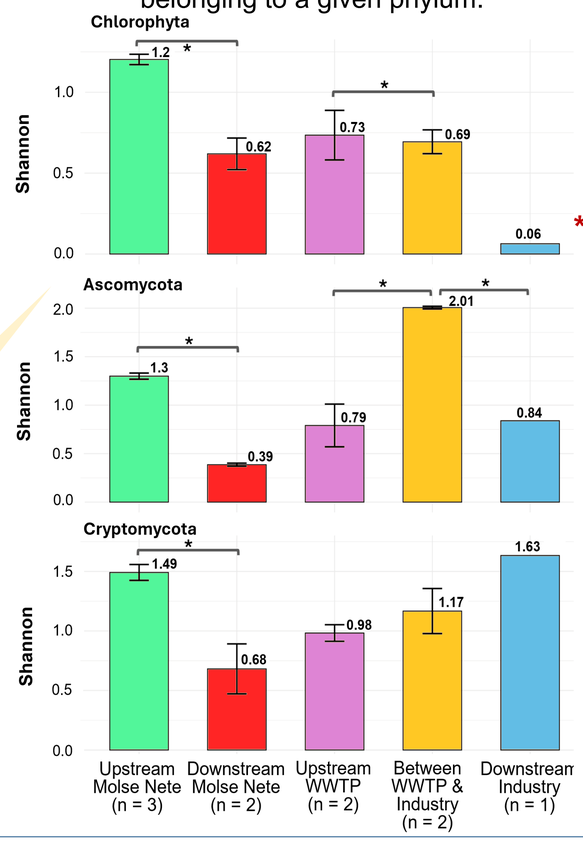
There were **no significant changes** in the **Shannon diversity** between upstream and downstream sites (ANOVA, $p > 0.05$).

Among the 48 Phyla detected in Grote Nete, there were **significant changes** in the **Intra-phylum Shannon diversity** across upstream vs. downstream sites comparison **for only 3 phyla** (post hoc Tukey, $p < 0.05$).

This suggests **changes in the internal structure of these phyla**.

Intra-phylum Shannon Diversity

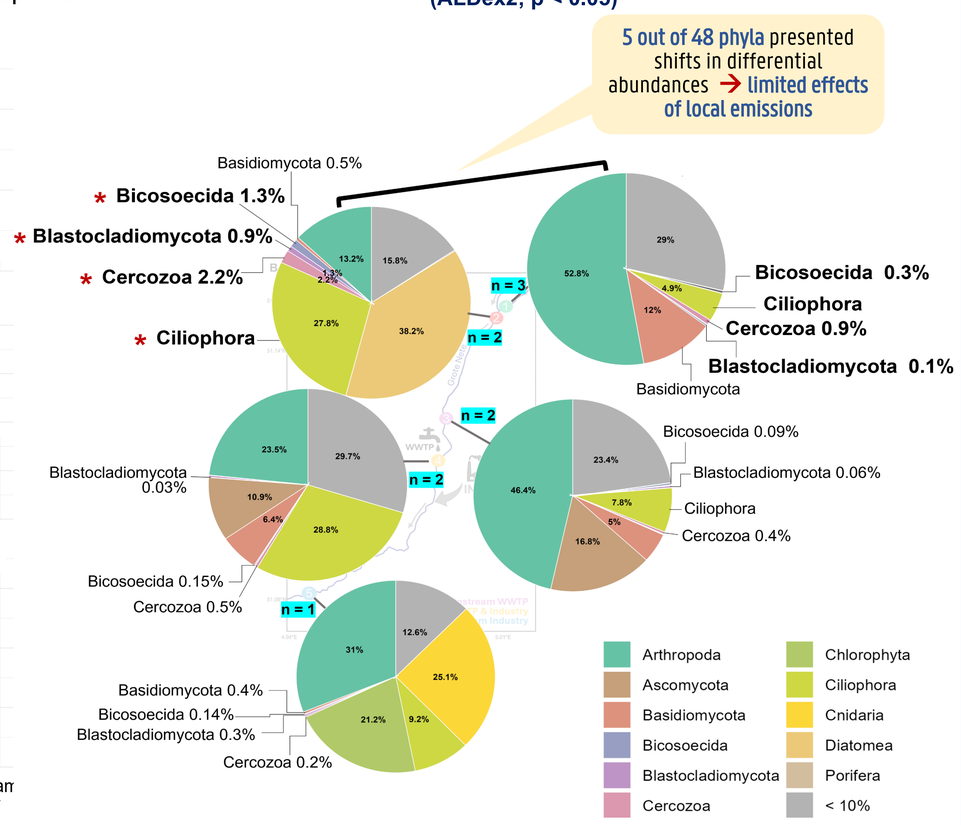
Shannon diversity was computed considering all species belonging to a given phylum.



Differentially Abundant Phyla

(ALDex2; $p < 0.05$)

5 out of 48 phyla presented shifts in differential abundances → limited effects of local emissions



Preliminary conclusions

- Using all species, **site-level Shannon diversity did not differ across the Grote Nete** (~~ANOVA; $p > 0.05$~~), suggesting **limited or no impact of emissions on eukaryotic diversity**.
- **Intra-phylum diversity** (i.e., restricting analyses within each phylum) tends to minimize cross-phyla biases in biomass, body size, and life-history traits. Given that metabarcoding reads often reflect biomass and functional dominance (Mass Ratio Hypothesis), **this approach improves comparability of phylum-specific distribution patterns across sites**.
- Under this framework, **Shannon diversity differed significantly between upstream and downstream only for 3 out of 48 phyla**, indicating **shifts in richness and/or evenness within specific phyla that likely reflect** (i) **responses to local pollutant inputs** and (ii) **associated changes in ecological interactions driven by environmental filtering**.
- **Shifts in relative abundances between upstream and downstream sites** for **5 out of 48 phyla** (representing a small fraction of the community), suggest **compositional restructuring not captured by overall diversity metrics**; however, low replication (1–3 samples/site) limits statistical power, supporting the need for increased replication.

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