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THE FUTURE OF STREAM MONITORING: DNA METABAR-CODING!

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ABSTRACT

Macrozoobenthos is an essential part of stream ecosystems, and macrozoobenthic indicator taxa are widely used for monitoring and assessment of stream ecosystem health. Unfortunately, morphology-based identification of invertebrate larvae is often only possible to a crude taxonomic level, time-consuming, difficult and the result highly depends on the experience of the analyst. This can lead to inaccurate ecosystem assessment and thus inefficient stream management.

An alternative method, which allows reliable species level identification, is DNA-based. Individual specimens can be identified by sequencing a short standardized DNA fragment (Cytochrome oxidase I) and comparing it to a reference database. DNA Metabarcoding relies on the same principle, but can identify thousands of specimens of a single sample using recent advances in sequencing technology.

We present our cutting edge metabarcoding protocol for monitoring to stream ecosystems. Our first experiments show that DNA metabarcoding is best suited for generating presence / absence data and biomass estimation will be difficult with DNA based methods. However, we were already able to reliably detect and identify 83% of taxa present in artificially constructed bulk benthos sample. Detection rates will be further optimized using novel bioinformatic tools like PrimerMiner. In a next step, complete benthos samples from various streams from Finland and central Germany will be tested and the first results presented. Finally, a road map to DNA based monitoring will be presented, summarizing past and future challenges.