Title:
A 15 year long depth-resolved time series of metagenomic data from Lake Zurich

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Abstract (300 words maximum): :
Microorganisms in freshwater lakes regulate biogeochemical cycles and thus affect water quality. Owing to the limitations of widely used cultivation-dependent techniques and single-gene metabarcoding, we still lack comprehensive information about the physiology and ecology of environmentally abundant bacterial lineages. Over the last decade, metagenomics has become one of the most used approaches in environmental microbiology, aimed at overcoming these limitations to create a complete picture of microbial community functioning. It allows for the exploration of microbial diversity and evolutionary dynamics, as well as helping to establish the phylogenetic and functional relationships between microbes and their environments.

We present a context-rich database of microbial metagenomes with unmatched depth and resolution. LTS-LZ (Long Term Series – Lake Zurich) is based on a collection of depth-resolved bi-weekly samples of microbial communities from Lake Zurich, gathered over 15 years (2009–2024), along with corresponding climatic and physicochemical data from the entire lake depth profile. Physicochemical profiles, including oxygen and phosphate concentrations, water temperature, and conductivity, were interpolated at 1-meter depth intervals from the surface (0 m) to 120 m. Metagenome sequencing was performed on samples from the epilimnion (5 m depth), metalimnion (20 m depth), and hypolimnion (80 m depth).

Time series of physicochemical parameters alone have already demonstrated their usefulness to detect shifts in ecosystem functioning—such as alterations in water turnover (mixis) resulting from climate change. We aim to go beyond such knowledge by elucidating the effects of climate-induced changes in lake stratification on bacterial diversity and evolution. We also seek to apply this new insight to improve cultivation efficiency, using enrichment cultures of the Nomurabacteria lineage (a CPR/Patescibacteria representative) derived from Lake Zurich, which are currently considered non-culturable bacteria.