

14. Januar 2026, 16 ct - 18 Uhr
Hörsaal Fahrenbergplatz, Friedrichstr. 39

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(Meta)genomic comparisons to predict prokaryotes integral for building soil organic carbon

Billions of years of evolution have shaped prokaryotes to be the primary drivers of biogeochemical cycling, providing them with the most varied genetic reservoir for carrying out these functions. The physiology needed to perform these functions are encoded as genes within their genomes, which can vary greatly between species.

This Kolloquium presentation will begin by considering the phylogenetic diversity of extant prokaryotes that live in temperate terrestrial environments, including land use factors that determine “who lives where”. This holds particular significance for soil organic carbon turnover, as the genomes of these different species encode for distinct repertoires of anabolic and catabolic processes. A role for Machine Learning in predicting rates of enzyme function, growth and cellular carbon use efficiency from metagenomic sequencing data will be discussed.

The identification of specific species, or functional genes, linked to building soil organic carbon could lead toward biologically-sound land use management or bioremediation strategies to improve this important resource.