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Metagenome-guided machine learning unravels dynamic interactions of sulfate-reducing microbiomes with operational parameters in a full-scale wastewater treatment plant

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Sulfate-reducing bacteria (SRB) in wastewater treatment plants (WWTPs) play a pivotal role in converting sulfate ions into hydrogen sulfide as a metabolic byproduct. The release of hydrogen sulfide gives rise to significant challenges, encompassing noxious odors that adversely affect the working conditions of operators and the overall quality of daily life in residential communities neighboring WWTPs. This study has established a machine learning (ML) modeling framework employing microbiome data, with the primary objective of unraveling the intricate interactions of SRB with operational parameters within a full-scale WWTP. The research has successfully identified key SRB populations that dominate over an extended monitoring period, and the ML framework has demonstrated its capacity to forecast their spatiotemporal assembly, dynamically responding to both environmental and operational variables. The ML-based insights have been validated through the analysis of multi-omics data, which corroborate the presence of genes and transcripts associated with sulfate reduction within the WWTP. Consequently, the findings derived from this study offer a diagnostic comprehension of the SRB populations within WWTPs, holding great promise for facilitating predictive control strategies aimed at mitigating sulfur-related contaminants and odor-related issues.

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