Tracing Sarno river freshwater run-off into coastal areas using eDNA microbial indicators

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River runoff strongly impacts coastal ecosystems by discharging freshwater, nutrients, sediments, pollutants and organisms. Some freshwater microorganisms can tolerate salinity gradients and persist in mixed or purely marine environments, making them promising biomarkers of riverine input.

In this study, environmental DNA (eDNA) datasets originally collected through multiple independent monitoring activities and research campaigns were merged to identify microbial tracers of riverine input across land-to-sea gradients. Samples spanned the English Channel, Bay of Biscay, and Mediterranean Sea, covering river-influenced (mixed) to fully marine conditions. Microbial communities were analysed through V4 16S rDNA amplicon sequencing. To identify indicator taxa, a multifaceted data analysis approach was applied, combining methods to detect taxa significantly associated with freshwater influence, responsive to salinity and rainfall values. Across the European regions, Comamonadaceae and Flavobacterium consistently showed strong associations with freshwater influence, regardless of local variability and geographic differences, highlighting their tolerance to salinity gradients and their potential as robust tracers of riverine input. To further validate this framework, a targeted case study was conducted in the Sarno River system (Italy), including estuarine and adjacent coastal samples collected after rainfall events. The Sarno dataset was screened for the 14 previously identified freshwater bioindicator taxa, of which six were detected, confirming their applicability across independent systems. Overall, this study demonstrates that eDNA-based microbial indicators can reliably trace freshwater inputs into coastal environments, offering a scalable tool to monitor land–sea connectivity and assess ecological impacts.