

## Deterministic community re-assembly shapes bacterioplankton diversity across a freshwater plume

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Marine bacterioplankton communities vary across seascape. While DNA-metabarcoding studies greatly facilitated our access to bacterioplankton community data, the underlying causes of seascape community variation remain poorly understood. In this study, we used a metacommunity framework and phylogenetic and network analyses to unravel causes of seascape level variation in bacterioplankton communities across the Rhine-Meuse-Scheldt freshwater plume off the coast of Belgium in the southern part of the North Sea. We observed three nested communities across the freshwater plume, with the most offshore community having the lowest alpha diversity. Phylogenetic clustering (as opposed to overdispersion) of communities indicate habitat filtering as an important force driving the community assembly. However, we also observed a mismatch between community differentiation and variation of the physicochemical seascape, indicating that other mechanisms (biotic interactions?) may play an equally important role in structuring bacterioplankton communities across a freshwater plume.

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